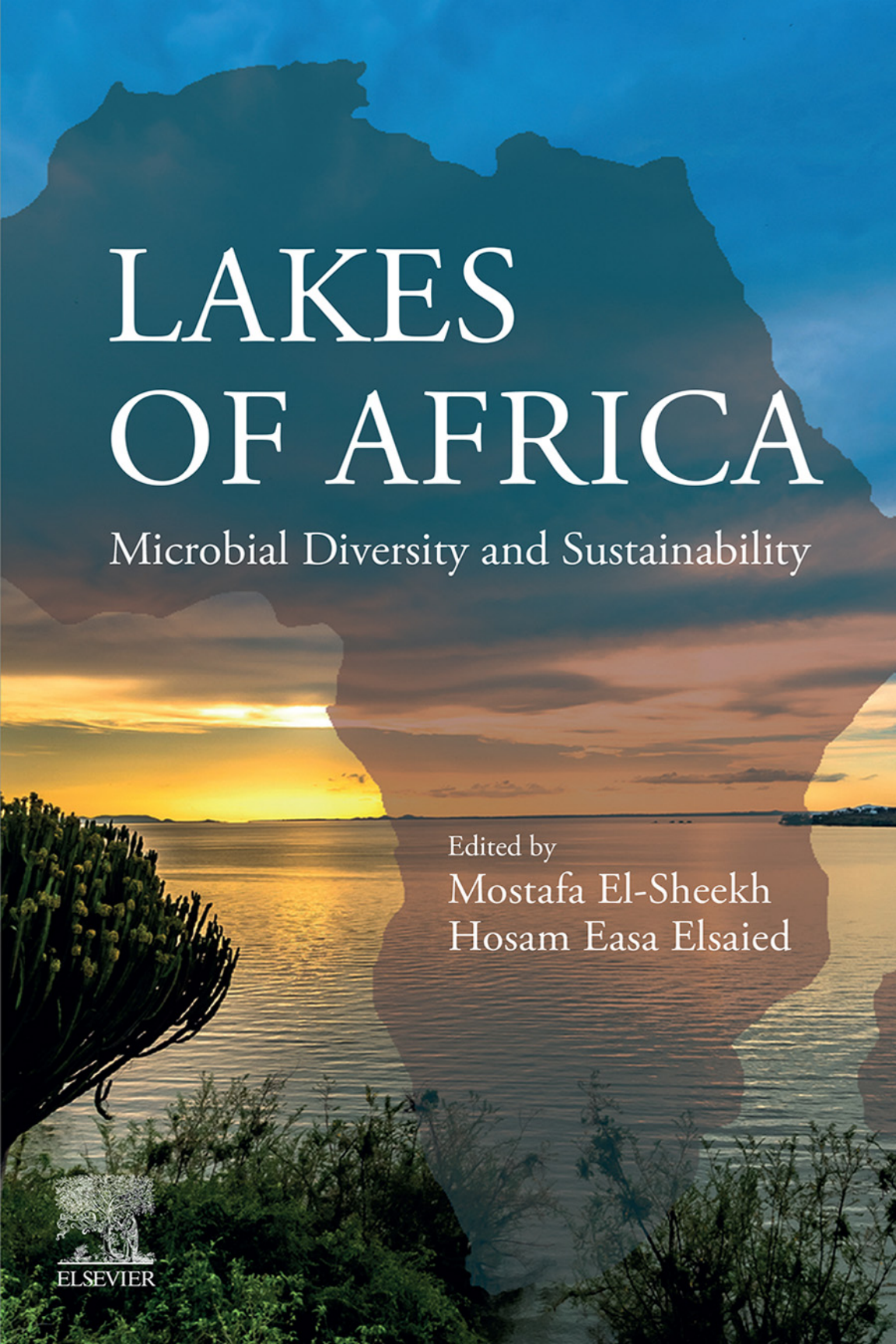
LAKES
OF AFRICA
Microbial Diversity and Sustainability
Edited by
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Lakes of Africa

Microbial Diversity and Sustainability

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Preface

This book contains the perspectives of researchers and academics with extensive scientific understanding and practical expertise. We are confident that the book will improve the foresight of present and future researchers working on African lakes as a source of sustainable useful microbial bioprocesses. This book offers an all-in-one resource for researchers, graduate students, and professionals working in the areas of microbiology, climate change, and blue biotechnology. Furthermore, this book includes structured foundational content on microorganisms and their contribution to sustaining African lake habitats for both undergraduate and postgraduate students working in the field of hydrobiology of African lakes. The editors are thankful for the help provided by Tanta University, the National Institute of Oceanography and Fisheries, NIOF, Egypt, and the *Egyptian Journal of Aquatic Research*. Writing a book is harder than we thought and more rewarding than we could ever have imagined. None of this would have been possible without the continuous support and encouragement of the staff members of the home universities and research institutes. Lastly, a warm thanks to the families and friends who stood with us at all times of struggle and consolidated us to move on.

Mostafa El-Sheekh
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CHAPTER 1

History and formation of African Lakes

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Africa is the oldest inhabited continent on Earth and the second largest continent of the world, which is why it is sometimes called "Mother Continent." The continent is made up of eight primary physical regions: the Sahara, the Sahel, the Ethiopian Highlands, the savanna, the Swahili Coast, the rain forest, and the African Great Lakes. The Saharan and Sahelian regions cover large swathes of the continent, while the Ethiopian Highlands and the Great Lakes are isolated areas.

The terrain of Africa is varied, comprising low-lying coastal areas, mountains, and valleys that affect catchment areas and, in accordance, embrace water to form lakes. Therefore, the lakes in Africa are confined to certain regions where water, either fresh or marine, is available. In addition to the natural lakes of Africa, humans have created a number of artificial lakes either on rivers by building dams to retain water to meet their needs for fresh water and hydroelectric power or by opening an inlet near the coasts to trap marine water for obtaining food from different marine species.

According to the WORLDLAKE database [1], Africa has the largest number of lakes in the world (677 lakes), of which 88 are recognized as principal lakes. The African lakes hold significant aquatic biodiversity by providing critical habitat for an amazing range of plants and animals, including bacteria, fungi, algae, plankton, mussels, snails, crustaceans, insects, fish, amphibians, reptiles, birds, and mammals. They are the centers of tourist activities and support very important fisheries. Most African societies rely on lakes for life and livelihood, but they are also the main cause of natural catastrophes, tropical diseases, and pandemics. Several human activities and climate change are significantly affecting Africa's lakes, with potentially severe impacts on people's livelihoods and aquatic biodiversity [1].

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In this chapter, we will discuss the history and formation of lakes in the continent of Africa and describe their origin, trophic status, productivity, and biodiversity. Also, morphometric and ecological characteristics of the African lakes have been addressed.

1.1 The Sahara region

The Sahara region is the world's largest hot desert [1,2], covering 8.5 million km^2 and making up 25% of the continent. Oases are water centers in the desert, typically in the form of springs, wells, or irrigation systems, which make up only 2071 km^2 of the desert's vast area. North Africa is one of the subregions in Africa, which sits squarely on the Sahara Desert. The region is made of seven countries: Egypt, Sudan, Libya, Tunisia, Algeria, Morocco, and Western Sahara.

Morocco has the highest number of lakes—26 lakes in North Africa—representing 3.8% of all the lakes in the continent, followed by Egypt with 16 lakes, representing 2.4% of all lakes, and Tunisia with only 16 lakes, representing 2.2% of all the lakes in Africa. Thus, North Africa contains less than 10% of the total number of lakes in Africa.

The water bodies in North Africa can be divided into two major groups: natural lakes and human-made lakes. Natural lakes can further be divided into lagoons along the Mediterranean Sea and closed or endorheic lakes. Most natural lakes are not large and some are seasonal lakes.

1.1.1 Natural lakes

1.1.1.1 Lagoons along the Mediterranean Sea

Coastal lagoons play a crucial role in preserving biodiversity and the ecological integrity of coastal systems [3]. As a result of massive nitrogen and phosphorous discharges from domestic and industrial wastewater, as well as urban drainage, the quality of water of coastal lagoons has deteriorated in many regions of the world in recent years [4,5]. Recent decades have seen the preservation of biodiversity and natural processes in coastal lagoons challenged by human pressures such as fishing, tourism, population growth, and global climate change [6].

The Egyptian Mediterranean coast exhibits five lagoons (Fig. 1.1). Four of them are the Nile Delta lakes, namely Mariut, Edku, Burullus, and Manzalah. These lakes are the final basins of the Nile water before it drifts into the Mediterranean. These lakes take the main bulk of the drainage water from the Nile Delta land and occupy an area of about 1100 km^2.

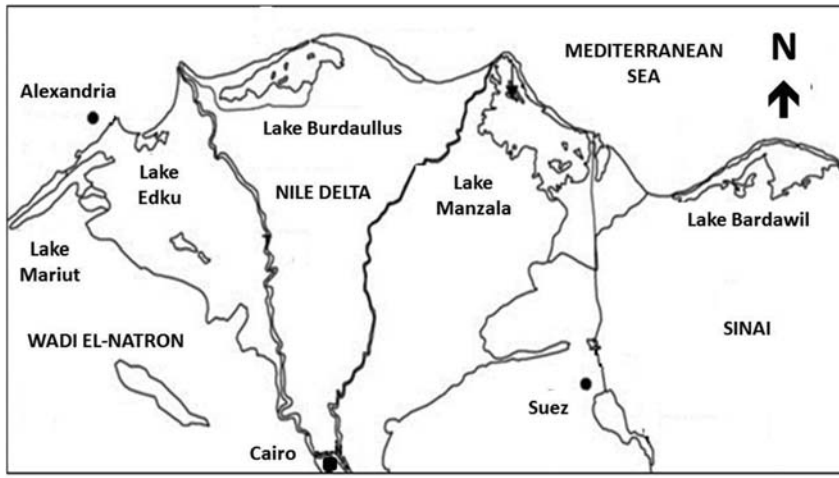

Figure 1.1 Egyptian coastal lakes: Bardawil, Manzala, Burullus, Idku, and Mariut.

They are shallow (average 1.10 m depth) and their salinity changes from fresh to brackish in the seaward direction [7]. All of them, except Lake Mariut, are directly connected to the sea. The fifth lagoon, Lake Bardawil, is located to the east of the Suez Canal. The northern lake fisheries play an important role in the Egyptian economy, where they provide a rich and vital habitat for estuarine and marine fish and their regeneration, and more than 75% of Egyptian lakes' production is harvested from them [8,9]. Also, they are internationally important sites for wintering water birds providing valuable habitat for several hundred thousand birds [10].

Lake Tunis is a lagoon off the Mediterranean Sea located near the capital, between Tunis and the Gulf of Tunis. It is a small shallow lake. After the restoration program, the lagoon appears as an eclipse stretching about 10 km long and 3.5 km wide (Fig. 1.2). It extends for 7.2 km^2 with a regular depth of about 2.1 m, except on the east side, where it reaches a maximum depth of 5 m. Its shores are rectilinear and protected by large rockery stones [11].

Bizerte Lagoon, the second largest lagoon in Tunisia, is located in an economically important area in Northern Tunisia. It extends for over 150 km^2 (the maximum width is 11 km and the maximum length is 13 km) and has an average depth of 7 m. It connects with the Mediterranean Sea through a straight channel that is about 6 km long, 300 m wide, and 12 m deep (Fig. 1.3) [13]. The Bizerte lagoon is populated by typical marine species [12]. In the south, it is connected by the Tinja stream along 5 km to the Ichkeul Lake.

Figure 1.2 Lake Tunis.

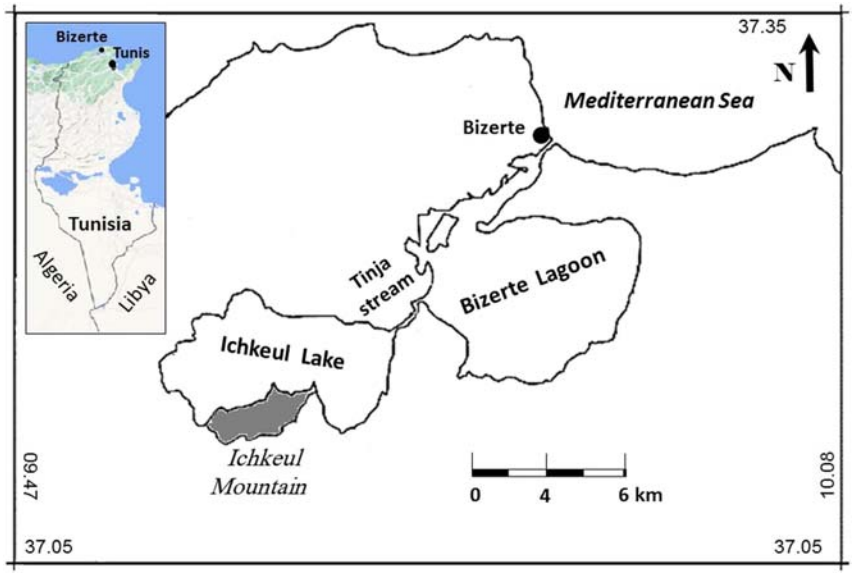

Figure 1.3 Location map of the Bizerta lagoon in connection with the Ichkeul Lake [12].

Lake Ichkeul is located in northern Tunisia, 20 km to Bizerte, the northernmost city in Africa on the Mediterranean Sea (Fig. 1.3). The lake is 90 km^2 in area and is 1.5 m deep in summer but rises to 2.5 m during winters [14]. The Lake is a Ramsar site, a MAB Biosphere Reserve and a UNESCO World Heritage Site since 1980 for its biodiversity. Its National Nature Park was one of the top overwintering Africa's stopover points for large waterfowl populations (180,000–230,000 birds) [15]. However, the construction of three dams in the Ichkeul catchment between 1983 and 1994 has produced major changes to hydrological and physicochemical variables [15]. These impoundments reduced river inflows into the lake, which replaced the freshwater plants with salt-loving ones [16], as well as another biota, such as invertebrates and fish. Due to these changes, the migratory bird population has sharply declined as it once relied on a unique plant mix.

1.1.1.2 Closed or endorheic lakes

In northeastern Libya (Sirte Basin), the Sahara is green, contained forests, grasslands, and permanent rivers and lakes in wet periods [17], for example, Bi'r al Kharijah, Màţan al Jafr, and Marada are desert oases that form seasonal lakes in the Al Wahat District of the Cyrenaica region.

Chott El Djerid is the largest saline depression, located in the southwest of Tunisia (Fig. 1.4), forming a large endorheic ephemeral salt lake [18]. It represents a characteristic wetland of northern Sahara. The site also hosts an important steppe fauna and flora and supports between 3000 and 15,000 Mediterranean flamingos (*Phoenicopterus ruber*), or 3.5% of the individuals for this species in this biogeographical region. Chott El Jerid exhibits an extremely halophilic ecosystem with remarkable microbial diversity [18]. Climate change and overgrazing on the borders of the chott risk provoke a loss of vegetation cover and erosion.

Lake Tonga, together with *Lake Oubeira* (Fig. 1.5), which is situated east of the El-Kala town in the most northeastern part of Algeria, is part of the El-Kala National Park, Biosphere Reserve, and Ramsar site. It is a mosaic of wetlands ecosystems including sea inlets, lakes, rivers, wet forests, marshes, sand dunes, and alder thickets. The El-Kala complex is generally recognized as one of the four major wetland complexes in the Western Mediterranean. This seasonal freshwater lake is linked to the Mediterranean Sea. Lake Tonga is about 27 km^2 with an average depth of 1.2 m [19]. *Lake Oubeira* is a naturally occurring, permanent freshwater body with an area of 22.57 km^2 and a depth of 4 m, with no flow toward the sea [20].

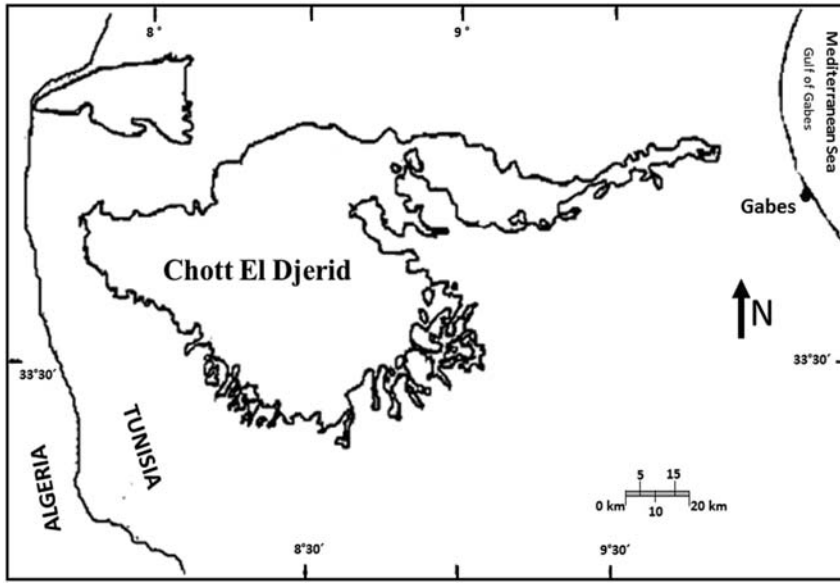

Figure 1.4 Location map of Chott El Djerid.

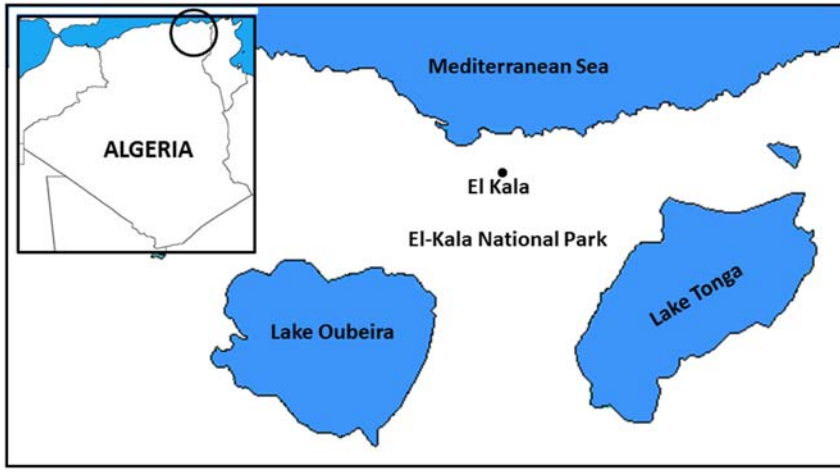

Figure 1.5 Location map of Lake Tonga and Lake Oubeira.

These lakes play an essential role in maintaining high biodiversity; however, water withdrawals for irrigation and a significant reduction in water supply are the main threats, which alter its ecological nature [21,22].

Most of Algeria's lakes are seasonal, that is, they are filled during the rainy season and dry up when the rainy season ends, morphing into salt flats with a crust of up to 60 cm thick. Lake **Chott Melghir** in Algeria is the largest lake [23], flowing straight from the mountains of Ores during winter. In the summer, this pond usually dries out and becomes a salt marsh. It is a closed lake situated in the west at 26 m below sea level, with an area of 6700 km^2 and a width of 131 km. **Chott Melghir** is protected by the Ramsar Convention [24].

The Ink Lake is located near the town of Sidi Bel Abbes. It is a truly mysterious natural phenomenon. Its water is toxic to organisms and neither fish nor plants live there. People, therefore, called it the Ink Lake, Devil's Eye, or Black Lake. Two rivers join in the Ink Lake; one contains dissolved iron salts, while the other contains organic compounds. Upon entering both rivers, the water undergoes complex chemical reactions which result in ink.

1.1.2 Human-made lakes

1.1.2.1 Lake Qarun and Wadi El-Rayan Lakes

The El-Fayium Depression, 100 km southwest of Cairo, is a natural depression below sea level, formed by wind erosion ca 1.8 million years ago, covering 12,000 km^2 [25]. It consists of two lacustrine complexes, Lake Qarun (or Birket Qarun) and two artificial Wadi El-Rayan lakes.

The lowest part of the depression is occupied by the Qarun Lake (Fig. 1.6), which is about 45 m below sea level and about 200 km^2 in area [25]. Lake Qarun is a saline remnant of the historical freshwater Lake Moeris, which became the center of a prosperous agriculture area in the days of Pharaoh Menes. It is connected to the Nile by a canal called Bahr Yussof, dug in 2000 BCE and carried abundant water into the lake making the first human-made flood regulator (the canal is still in use at present). The Pharaohs of the 12th dynasty are known to have used the lake as a regulator of the Nile flow, useful to store water [26]. The lake is no longer connected to the Nile and collects agricultural drainage water through two drains. Consequently, the salinity of the lake has increased. Since 1973, about 30% of the agriculture drainage water has been diverted to a second depression, Wadi El-Rayan [26]. The artificial Wadi El-Rayan Lakes are situated southwest of the El-Fayum Depression (Fig. 1.6).

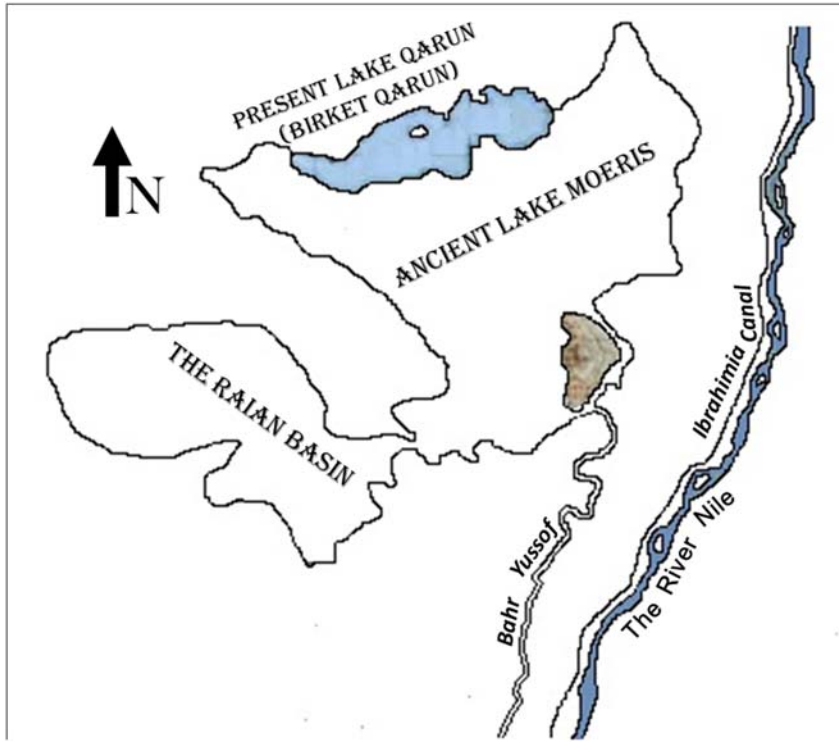

Figure 1.6 El-Fayium Depression, Qarun Lake (also known as Birket Qarun), and the Wadi El-Rayan Lakes.

1.1.2.2 Aswan reservoir

The Aswan reservoir is the lake formed after the construction of the "Aswan Dam" on the River Nile at the Aswan Cataract (2 km width) in 1902 (Fig. 1.7). Before the construction of the Aswan High Dam, some 7 km upstream of the old dam, the reservoir contained 5300 million m^3 of water and extended as far back as the Second Cataract [27]. The reservoir bottom is granite with silt deposits. The dam was subsequently heightened twice, the first in 1912 and the second between 1929 and 1933; it now stands at 40 m high. The outflow is used to generate hydroelectric power [28].

1.1.2.3 The High Dam Lake

The High Dam Lake was created as a result of the construction of the Aswan High Dam in the 1960s. It aimed to increase economic production

Figure 1.7 Aswan Reservoir between the Aswan Dam and the High Dam.

by further regulating the annual river flooding and providing storage of water for agriculture, and later, to generate hydroelectricity. Egypt's economy and culture have been significantly affected by the dam [28]. It is a transboundary lake that extends 480 km from the High Dam at Aswan in Egypt to the Dal Cataract in Sudan (Fig. 1.8), 300 km within the Egyptian borders (as Lake Nasser), and 180 km within the Sudanese borders (as Lake Nubia) (Table 1.1). Lake Nasser is the world's second largest human-made lake after the Bratsk Dam Lake in Russia [28]. Lake Nasser has long, narrow arms, which are called "Khors" (Fig. 1.8). There are 100 major khors, 58 on

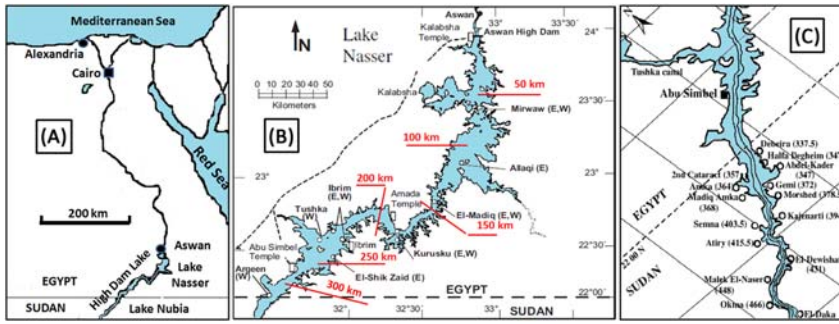

Figure 1.8 High Dam Lake: (A) the whole Lake of the High Dam across the Egyptian-Sudanese borders, (B) Lake Nasser in Egypt, and (C) Lake Nubia in Sudan.

Table 1.1 Morphometry of the High Dam Lake, Lake Nasser, and Lake Nubia.

Parameters		High Dam Lake		Lake Nasser		Lake Nubia	
		160 m	180 m	160 m	180 m	160 m	180 m
Length	(km)	420	482	292	292	128	190
Surface area	(km^2)	3057	6215	2585	5237	472	978
Volume	(km^3)	65.9	156.9	55.6	132.5	10.3	24.4
Shoreline	(km)	6027	9250	5380	7844	647	1406
Mean width	(km)	7.1	12.5	8.9	18.0	3.7	5.2
Mean depth	(m)	21.6	25.2	21.5	25.2	20	26
Maximal depth	(m)	110	130	110	130	110	130

the eastern shore and 42 on the western shore [29]. For 50 km from the dam and the last 150 km in the Sudan territory, the banks of the lake are of granite basement. Along the 300 km in between the lake cuts is the Nubian formation of sandstone. The Lake Nasser region, which was previously an undeveloped desert, is developing and has created considerable possibilities for fisheries, navigation, agriculture, and tourism, although Lake Nubia in Sudan remains largely undeveloped. Lake Nasser is a subtropical monomictic lake [30]. It is a mesotrophic lake [31].

Fish landings increased with the gradual expansion of the impounded lake. The highest production ever was 34,206 tonnes in 1981. A total of 50 fish species have been recorded in the lake. Tilapia fish (*Oreochromis niloticus* and *Sarotherodon galilaeus*), Nile perch (*Lates niloticus*), and tiger fish (*Hydrocynus forskalii*) are the essential economic fish that make up more than 95% of the fish production of the lake.

1.1.2.4 The Toshka Lakes

The Toshka Lakes are a by-product of the rising level of Lake Nasser and lie in the same general region as much of the New Valley Project. The maximum water level of Lake Nasser is 183 m above sea level. Water levels higher than 178 m are drained off into the Toshka Depression at the south end of the Eocene limestone plateau via Wadi Toshka at the west of Lake Nasser (Fig. 1.9). The 1970s and 1980s were items of mediocre to low floods, and it took well over 20 years for the reservoir to fill its capacity. As Lake Nasser became filled in the 1990s, Khor Toshka was flooded. The easternmost depression was flooded in November 1998 forming Lake 1 (Fig. 1.9A). By late 1999, three additional lakes (2, 3, and 4) had formed further westward. The westernmost one (Lake 4) started filling between September 2000 and March 2001 (Fig. 1.10). In 2002, the estimated total surface area of the Toshka Lakes was 1540 km^2, distributed over lakes 1, 2, 3, and 4 from east to west as follows: 449, 265, 20, and 807 km^2, respectively (Fig. 1.9B). However, in 2006, the lake surface area had dropped to 937 km^2. Lake 3 vanished and the surface area of lakes 1, 2, and 4 had become 286, 101, and 550 km^2. The calculated stored water volumes of lakes 1, 2, 3, and 4 for the years 6.78, 2.21, 0.044, and $16.23 \times 109\ m^3$; by the year 2006 these had declined to 3.45, 0.44, 0, and $8.78 \times 109\ m^3$ [33]. By 2015, the flooded regions of the Toshka Lakes had significantly decreased, and lakes 1 and 3 disappeared. Only lake 4 existed. In 2018, lake 4 surface area was significantly reduced, representing minimum water surface area in the Toshka Depression. In 2019, lake 1 has grown again, whereas lake 4 had considerably shrunken. The flooding of the Toshka Depression in 2020 created five wide lakes [32]. Fig. 1.10 shows the historical development of the Toshka Lakes.

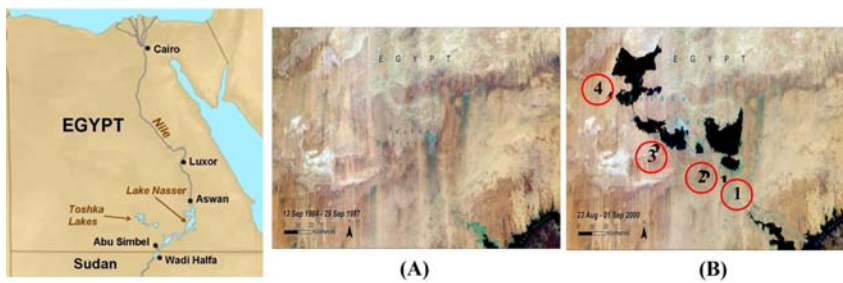

Figure 1.9 Lake Nasser and Toshka Lakes in Egypt (left) and Landsat mosaic of Toshka Lakes in 1987 (A) and 2000 (B) (right).

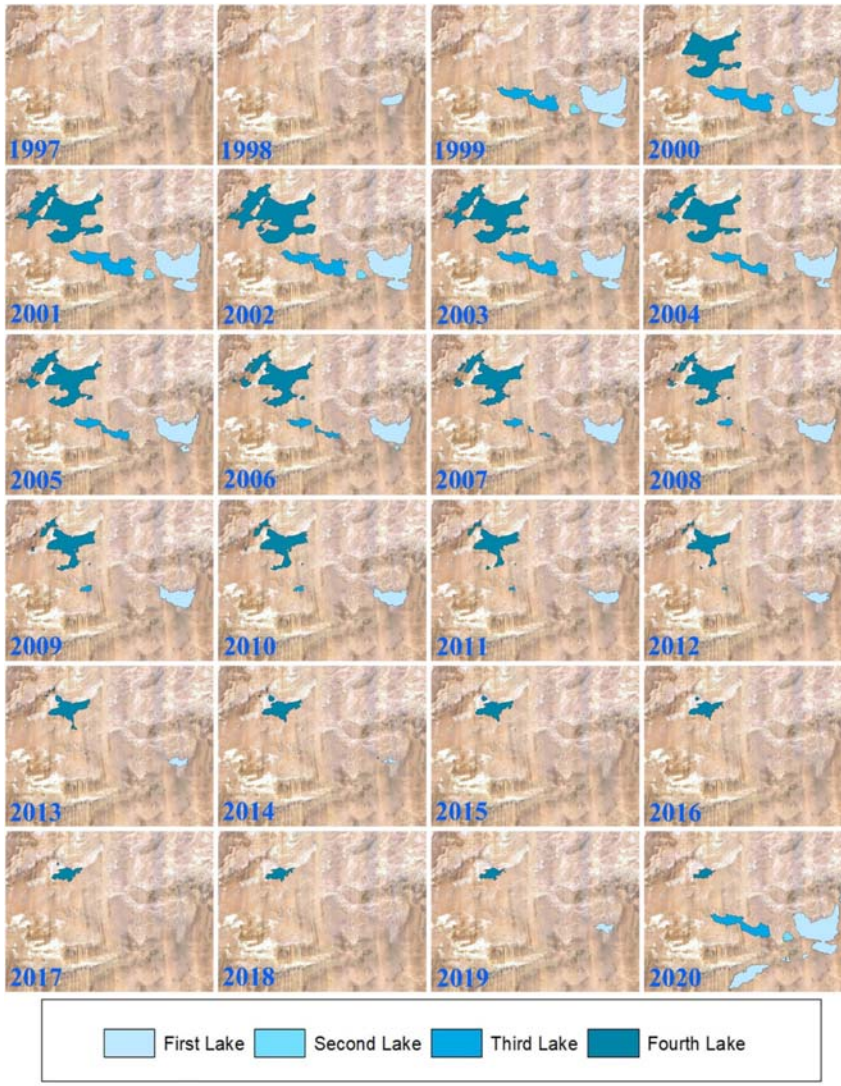

Figure 1.10 Development of Toshka Lakes from 1979 to 2020 [32].

1.1.2.5 The Al Wahda reservoir

The Al Wahda reservoir is an artificial lake with a capacity of 3800 million m^3, which resulted after the construction of the Al Wahda Dam on the Ouergha River near M JAARA in the Taounate Province in the El Obeid Basin in central Morocco. It was completed in 1996 for flood control, drinking water supply, irrigation, and hydroelectric power production. The lake

generates about a third of the electricity supply to Morocco. The dam is located 18 km from the entrance to the lake and is considered the second most important dam in Africa after the Aswan High Dam in Egypt, but the largest in Morocco [34].

In the winter-spring season from December to May, the average monthly precipitation is up to 80 mm, and the average monthly temperature is between 10°C and 17°C. The dry season lasts from June to October with average monthly precipitation not exceeding 5 mm and an average monthly temperature between 17°C and 28°C.

1.1.2.6 Bouhouda Lake

The Bouhouda Lake was formed after the construction of the Bouhouda Dam in 1999 on Wadi Sra, a tributary of Wadi Ouergha, about 18 km north of the Taounate city, Morocco. Although the region receives abundant rainfall, geological formations limit the potential for groundwater storage [35]. This compact concrete dam with a capacity of 55 million m^3 is intended for irrigation, especially during long dry periods (from May to October) and for the supply of drinking water [36,37].

1.2 The Sahel region

The Sahel region is a narrow strip of the semiarid biogeographic realm (transitional zone) that separates the Saharan desert to the north and the Sudanese Savanna to the south. The region is located in the northern part of Africa and extends from the Red Sea to the Atlantic Ocean. It consists of flat and arid plains that stretch for nearly 5900 km across Africa and cover an area of 3,053,200 km^2, from Sudan to Senegal. The Sahel portion of Africa from west to the east includes parts of northern Senegal, southern Mauritania, central Mali, northern Burkina Faso, southernmost Algeria, Niger, northernmost Nigeria, northernmost Cameroon and the Central African Republic, central Chad, central and southern Sudan, northernmost South Sudan, Eritrea, and northernmost Ethiopia. Most of the area lies between 200 and 400 m in height. Lake Chad is one of the most important lakes in the Sahel.

1.2.1 Lake Chad

Lake Chad is a shallow, endorheic lake in Central Africa, which has varied in size over the centuries. The lake stretches across the borders of Nigeria, Chad, and Cameroon. Its surface has shrunk by as much as 95% to

300 km^2 [38], which was once the second largest wetland in Africa [38–40], supporting rich biodiversity of endemic animals and plant life.

About 90% of Lake Chad's water comes from the Chari-Logone River, which enters the lake from the southeast, and its sources are in the humid highlands of the Central African Republic. The Komadougou-Yobe River, which enters the lake in the northwest, contributed about 10% of its water. In addition to being a vital source of fresh water for local communities, Lake Chad's unique mixture of terrestrial and aquatic habitats hosts globally important biodiversity, although most large mammal species have been hunted nearly to extinction. Crocodiles and hippos have been particularly important in maintaining a healthy wetland ecosystem [41]. Today, however, the replacement of these mammals by livestock has severely degraded the wetland ecosystem. The main plant communities within Lake Chad itself consist of floating "suds", permanent reed swamps, and seasonal turf swamps [42]. Grasslands predominate the flooded areas, interspersed with *Acacia* forests, with dry land forests in sandy soils far from the lake [41].

The lake's water level has changed significantly over time, leading to significant changes in its size and surface area. At low lake levels, the lake resembled a vast swamp with small northern and southern pools. With increasing rainfall, the northern and southern pools are connected. The lake has also become very shallow, but before the decline of Lake Chad in the 1970s, the maximum depth of the lake was 12 m. The bottom of the lake itself is not flat but rests on an ancient bottom of petrified sand dunes, many of which appear as islands when the lake level drops [43]. Climate and human factors often play a part in the dramatic fluctuations of Lake Chad.

As a result of climate change and resource extraction, the size of Lake Chad, once one of Africa's largest freshwater bodies, has drastically decreased. The lake is now one-twentieth of the size it was 35 years ago [44].

1.3 The Ethiopian Highlands region

The Ethiopian Highlands region is a rugged mass of mountains in Ethiopia in northeastern Africa. Much of the Ethiopian Highlands is part of a large igneous province, an area with a large accumulation of large lava rocks. The Ethiopian Highlands are the highest in Africa, comprising 80% of the highest African mountains, with peaks reaching heights of up to 4550 m (Jabal Ras Dashen). The prevailing climate in the Ethiopian Highlands is the alpine climate. The highlands are divided into

northwestern and southeastern parts by the main Ethiopian Rift, which is situated in the central part of the country.

1.3.1 Lake Tana

Lake Tana, the source of the Blue Nile, is the largest lake in Ethiopia and is located in the Amhara Region in the north-western Ethiopian Highlands, at an elevation of 1788 m. The lake was formed by volcanic activity, blocking the course of inflowing rivers in the early Pleistocene period, around 5 million years ago [45]. It is the largest lake in the Ethiopian Highlands being 84 km long, 66 km wide, and a maximum depth of 15 m [45]. The lake was originally much larger than it is today. It receives water from seven large permanent rivers and 40 small seasonal streams. Gilgel Abbay (Little Nile River), Megech, Gumara, and Rib rivers are the main tributaries of the lake [45]. Its surface area ranges from 3000 to 3500 km^2, depending on the season and rainfall. A control weir, where the lake discharges into the Blue Nile, has regulated the lake level since it was constructed. This controls the flow to the Blue Nile Falls and hydropower plant. Ethiopia is currently building the Grand Ethiopian Renaissance Dam, formerly known as the Millennium Dam, since 2011 on the Blue Nile River. It is located in the Benishangul-Gumuz Region of Ethiopia, 45 km east of the Sudanese border [46]. The primary purpose of the dam is to produce electricity to relieve Ethiopia's acute energy shortage and to export electricity to neighboring countries. By the time the dam is completed, it will be the largest hydroelectric power plant in Africa as well as the seventh largest in the world [47]. The filling of the reservoir began in July 2020. Depending on the hydrologic conditions during the filling period, it could take between 4 and 7 years to be filled with water [48]. Egypt and Sudan did not agree to the second phase of filling, so it was completed without their consent on July 19, 2021. The dam began producing power for the first time on February 20, 2022, supplying electric power to the grid at a rate of 375 MW.

In the southeastern part, the Ethiopian Rift Valley is located at the northernmost part of the East African Rift Valley. The lakes within the Ethiopian Rift Valley occupy the floor between the two parts of the Ethiopian Highlands. Most of these lakes do not have an outlet and most are alkaline. A common feature of the rift valley is small, shallow, and terminal lakes within closed drainage basins [48]. These lakes are in altitudes ranging from 1200 to 1680 m. The region supports great biodiversity and is of significant importance to the Ethiopian economy. The morphometric

measures according to Kebede et al. [49] of the major lakes of the Ethiopian Rift Valley are shown in Table 1.2 and Fig. 1.11 shows the locations of the Ethiopian Rift Valley lakes.

Lake Awasa lies south of Addis Ababa within the Main Ethiopian Rift. Lake Awasa is a freshwater lake with a subterranean outlet, although it has an endorheic basin. Lake Abijatta is an alkaline lake in the Abijatta-Shalla National Park. It is located south of Addis Ababa. Several hot springs are found in the northeastern part of Lake Abijatta that attract tourists. Reserves of soda ash are mined on the shores of the lake. Further, Lake Abijatta is an important habitat for flamingos. Lake Langano is situated 200 km south of Addis Ababa in the Oromia region. It is a freshwater lake with high mineral content giving its water a brown color. The forest surrounds the lake and has abundant wildlife and numerous resorts. Lake Shala lies in the Abijatta-Shalla National Park. It is the deepest lake in the Ethiopian Rift Valley (Table 1.2). Many hot springs surround the lake and sulfur springs emerge from its bed. The fog is observed around the lake due to steam rising from the boiling water of the hot springs. Lake Shala provides an excellent habitat for several birds particularly great white pelicans and flamingos. Lake Zway is a freshwater lake situated 160 km south of Addis Ababa. It contains many islands. One of them is Tulu Gudo, which features an ancient monastery. The lake and a large number of birds and hippopotamuses live in the surrounding area. The lake produces 2454 tons of fish annually, providing the local population with an important source of income. The Zway town lies on the western shore of the lake, and the people of the Zay tribe live on islands and shores of the lake. Lake Chamo is located in the Southern Nations, Nationalities, and Peoples' Region (SNNPR) of southern Ethiopia. The Kulfo River and

Table 1.2 Lakes of the Ethiopian Rift Valley.

Lake	Area (km^2)	Length (km)	Width (km)	Max. Depth (m)	Elevation (m)
Awasa	90	16	9	23	1680
Abijatta	176	17	15	14	1578
Langano	241	18	16	48	1582
Shala	329	28	12	266	1558
Zway	442	31	20	7	1636
Chamo	551	32	13	13	1233
Abaya	1162	60	20	13	1285

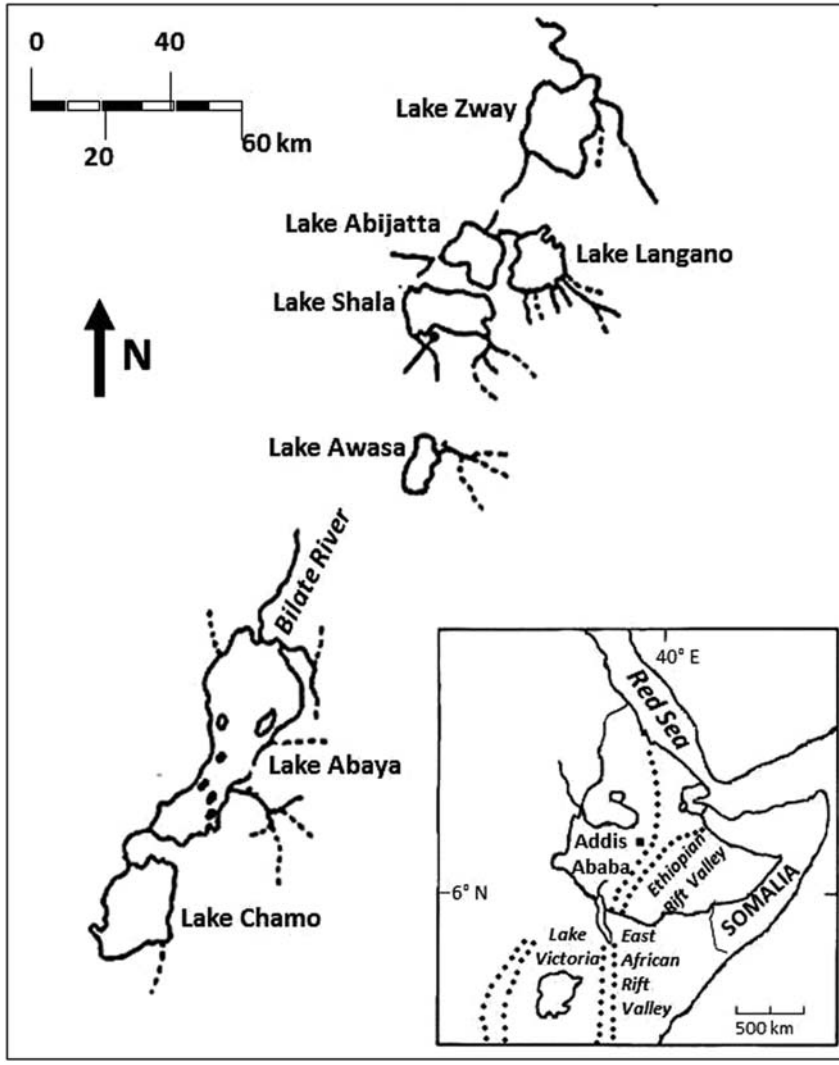

Figure 1.11 The Ethiopian Rift Valley lakes.

the overflow from Lake Abaya are the main sources of Lake Chamo's water. The lake is inhabited by the Nile crocodile, hippopotamus, Nile perch, and catfish. Lake Abaya lies east of the Guge Mountains in the Main Ethiopian Rift near Lake Chamo. Three rivers feed Lake Abaya: the Bilate River, the Gidabo River, and the Gelana River. The lake is an essential fishing area for the local people, and the adjacent savanna supports varieties of birdlife and wildlife.

1.4 The Savanna region

The Savanna area covers 13.5 million km^2, that is, nearly half of Africa [50]. A majority of Central Africa is covered by this type of grassland, which begins south of the Sahara and ends just north of the southern tip of the continent. The Serengeti River is the most famous of the wide, undulating plain that stretches for 30,000 km^2 from Kenya to Tanzania. One of the highest concentrations of large mammals on the continent can be found in the Serengeti, including lions, hyenas, elephants, giraffes, and zebras. The African Savanna ecosystem is a tropical grassland with year-round warm temperatures with the highest seasonal precipitation in summer. It contains a diverse community of organisms that interact to form a complex food web.

1.5 The Swahili Coast region

The Swahili Coast region is a narrow strip of land, running along the eastern edge of Africa from Somalia in the north to Mozambique in the south on the eastern coast of Africa at the western edge of the Indian Ocean.

1.6 The Rainforest region

The rainforest region is predominantly to the west and covers more than 3.6 million km^2 of land in West, East, and Central Africa. The Congo River basin contains 80% of the rainforests in Africa, which are confined in Central Africa. This biogeographical area is by far the most diverse. In West Africa, a chain of rainforests up to 350 km in length stretches from the eastern border of Sierra Leone to Ghana. In Ghana, the forest area is gradually dissipating near the Volta River, after a 300 km stretch of savanna gap in Dahomey. The West African rainforest continues from eastern Benin through southern Nigeria and officially ends at the Cameroon border along the Sanaga River.

1.7 The Great Lakes region

The African Great Lakes region is found in 10 countries surrounding the Great Rift Valley (Burundi, Dr Congo, Ethiopia, Kenya, Malawi, Mozambique, Rwanda, Zambia, Tanzania, and Uganda). The rift valley formed when large deep cracks formed on the earth‘s surface; it was later

filled with water. This geological formation has produced a number of the largest and deepest lakes in the world. The African Great Lakes are a chain of lakes that form the portion of the Rift Valley Lakes in and around the East African Rift. Lake Victoria, Lake Tanganyika, Lake Malawi, Lake Turkana, Lake Albert, Lake Kivu, and Lake Edward are the major seven African lakes. The major drainage basins are the Congo-Zaire which drains into the Atlantic Ocean; the Nile basin pours into the Mediterranean; and the Zambezi River basin, which empties into the Indian Ocean. Among the world's largest freshwater lakes by surface area, Lake Victoria is the second, and Lake Malawi is the eighth; and by volume and depth, Lake Tanganyika is the second. They hold a total of 31,000 km^3 of water, which is about 25% of the earth's unfrozen surface freshwater. Approximately 10% of the world's fish species live in the Africa Great Rift Lakes, which are the ancient habitat of great biodiversity. It is relatively cool in the highlands, with temperatures averaging 17°C to 19°C and heavy rainfall. The average temperatures in the lowlands are around 35°C.

A significant amount of hydrocarbons discovered in the tropical rift lakes along the Ugandan margin of Lake Albert offer a valuable opportunity for the formation of high concentrations of oil and gas. Most of the world's extant long-lived lakes are associated with continental extensional basins in which organic-rich rocks of lacustrine origin are dominant sources of hydrocarbons. High biological productivity and prolonged bottom water anoxia are two factors that contribute to the exceptional organic nature of sediments in tropical lacustrine systems [51,52]. Due to the discovery of hydrocarbons along the Uganda margin of the Lake Albert Rift, modern tropical rift lakes are important sites to study oil and gas formation and concentration. Table 1.3 summarizes the morphometric characteristics of the Great Rift Valley lakes.

1.7.1 Lake Victoria

Lake Victoria is the largest African freshwater lake and the second largest in the world by surface area. In the Nile River basin, it is situated at the uppermost reaches and is shared by three East African countries of Kenya (6%), Uganda (45%), and Tanzania (49%) [53]. The lake receives 80% of its water from rainfall, while the remaining 20% comes from the numerous rivers and small streams that flow into the lake. The Kagera River is the major river that empties into the lake.

Table 1.3 Morphometric measures of the Great Rift Valley lakes.

Lake name	Surface area (km^2)	Max. length (km)	Max. width (km)	Mean depth (m)	Max. depth (m)	Shore length (km)	Volume (km^3)	Altitude (m) a.m.s.l.
Lake Victoria	68,870	359	337	41	81	7142	2424	1135
Lake Tanganyika	32,826.6	670	72	50	1470	2126	18,900	767
Lake Malawi	28,800	580	87	290	704	1500	8400	471
Lake Turkana	7560	257	44	31	114	1025	237	365
Lake Albert	5300	160	35	25	58	781	138	615
Lake Kivu	1977	90	50	220	475	*	*	1460
Lake Rukwa	5760	180	32	3.5	15	590	20.632	801
Lake Mweru	857	131	56	7.6	27	572	38.2	921
Lake Edward	759	77	40	34.2	112	307.5	76.7	912

As a result of natural processes and inappropriate human actions, people living around the lake have been more affected by environmental change over the past two decades [54]. Only a small area of the land around the lake can be cultivated, which tends to be the most densely populated area. Some areas are prone to flooding, have low fertility and poor soil texture, and suffer from vital constraints such as the tsetse fly. Therefore, the urgent need to bring about rapid land-use change has caused fast population growth in the region, accelerating the rate of degradation of dwindling land resources around the lake and growing agricultural pollution, freshwater biodiversity loss, and overfishing [1]. Lakeshore residents depend heavily on fishing for their livelihoods.

The Lake Victoria Basin suffers from extensive water erosion. As soil erosion and other degradation forces in the basin increase, the lake will silt up, and flooding risks will increase in estuaries [55].

The eutrophication in Lake Victoria is due to land-use changes and, subsequently, agriculture and industrial effluents are released into the lake and, in addition, fast population growth around the lake [1]. This habitat was favored by the water hyacinth that invaded Lake Victoria in the 1990s. Transport and fishing were disrupted, municipal water pipes were clogged, and disease-causing insects flourished, which prompted the removal of hyacinth infestations from Uganda's severely affected bays [1].

In the last 50 years, many endemic fish species have become extinct after introducing invasive species to the lake, for example, the Nile perch and Nile tilapias. Victorian haplochromines and lake tilapias are the most dominant fish species in the lake. Cyprinids, catfish, African tetra, spiny eel, elephant fish, marbled lungfish, and climbing gourami are some of the fish found in the lake. Also, freshwater crabs, snails, and bivalves are found in the lake.

1.7.2 Lake Tanganyika

Lake Tanganyika lies within the Albertine Rift, in the western part of the East African Rift. The lake is shared by four countries: Tanzania (46%), the Democratic Republic of the Congo (40%), Burundi (7%), and Zambia (7%). Worldwide, it is the longest lake, the second largest freshwater lake by volume [56], and the second deepest lake [57]. It is Africa's second largest lake by surface area (after Lake Victoria). It accounts for about 18% of the entire world's unfrozen surface freshwater. Lake Tanganyika is one of the 20 ancient lakes on this planet, and its age is

expected to be someplace between 9 and 12 million years old [58]. Lake Tanganyika has three basins: the middle basin is a wide ridge of 700 m (deep), the Kigoma Basin is in the north (1310 m deep), and the Kepili Basin is the deepest (1470 m) [57].

The bottom of the lake comprises "fossil water" which absences oxygen because the lake is exceptionally deep and positioned in a tropical area. The lake generates 6 m waves during its ferocious storms. Despite these storms, surface and bottom waters do not mix, making the lake meromictic. The lake water temperatures are astonishingly uniform, with the lower regions slightly cooler at 3°C than the surface; however, the cause for this is indefinite [59]. Annual seasonal temperatures change at the surface layer are experienced. Transparency is on average 11 m. Solar radiation varies slightly during the year because the lake lies close to the equator. Where photosynthesis takes place in the mixed layer, nutrients provided are habitually internal to the lake itself. Atmospheric and riverine nutrient contributions are considered negligible.

Along the lake's shores, the Gombe Stream National Park and Mahale Mountains National Park in Tanzania, Rusizi Natural Reserve (also a Ramsar site) in Burundi, and Gombe Stream National Park and Nsumbu National Park in Zambia are protected areas.

1.7.3 Lake Malawi

Lake Malawi is the southernmost lake of the East African Rift. It is named "Nyasa" in Tanzania and "Lago Niassa" in Mozambique. As the African tectonic plate split into two parts, the East African Rift opened, creating the lake. The estimated age for Lake Malawi is up to 2 million years. The lake is shared by Malawi, Mozambique, and Tanzania. It is the third largest lake in Africa by surface area. The lake holds an impressive quantity of water, about 7% of the total available world surface freshwater. It is also the second deepest lake in Africa [60], after Lake Tanganyika.

The lake's main inflow is the Ruhuhu River (Malawi 43%; Mozambique 4%; Tanzania 53%). The Shire River flowing out of the lake in the southern section is its only outflow into the Zambezi River in Mozambique.

Lake Malawi is a meromictic lake, which means that its layers of water do not mix, as it is always stratified (being anoxic below 170–200 m in depth [61]), which is maintained by chemical and thermal gradients [60]. The bottom is an oxygen-poor layer [62], where very few organisms can live, for example, purple sulfur bacteria. These bacteria use sulfur

compounds produced by the decomposition of organic sediments, such as sulfides in photosynthesis [63].

An amazing number of 1000 cichlid species live in Lake Malawi, which makes it the world's richest lake in fish species. The vast majority of the cichlids in the lake are endemic. Overall, 100,000 tons of fish are harvested annually from the lake by more than 56,000 fishers. Fishing is a major economic activity around the lake. Numerous fishing villages line the lake shores, boasting rich harvests. From afar, the lanterns on the boats of fishermen on Lake Malawi resemble starry skies, hence, the name "Lake of Stars," given to the lake by David Livingstone. More than 1.6 million people depend on the fishery for their livelihoods.

Contaminated tailings from uranium mining and habitat degradation by intensive agriculture and clearing forests by fire are the most important environmental threats to Lake Malawi. Also, the pelagic waters in the region from the shore to 200 m along the lake are overfished, leading to extinctions of local species, especially the cichlid fish, which are most susceptible to overfishing.

In June 2011, the section of the lake in Mozambique was declared a reserve and its section in Malawi contains the Lake Malawi National Park on its shores. Also, Cape Maclear, south of the lake, comprises the first freshwater national park in the world, established in 1984. The park which consists of many islands and a peninsula is a UNESCO World Heritage Site.

1.7.4 Lake Turkana

Lake Turkana formerly known as Lake Rudolf, after Rudolf, Crown Prince of Austria-Hungary in 1888, or Jade Sea (due to its beautiful turquoise color, caused by algae rising on top of the lake calm water) is a vast shallow lake in the Kenyan Rift Valley, in the arid zone in the north of Kenya, which extends to Ethiopia. The lake is the largest alkaline desert lake in the world. By volume, this salt lake ranks fourth in the world [64]. Volcanic rocks surround the lake, which is located on the tectonic ground. Lake Turkana lies in the arid region with a low yearly rainfall of less than 250 mm, hot temperature, and powerful winds. Water from the lake is essential to over a million people who live in the surrounding arid regions.

The lake gets most of its water from three main rivers (Omo, Kerio, and Turkwel) with no outflow and receives a slight amount of rain and water mainly lost by evaporation. The construction of the Gilgel Gibe III Dam in Ethiopia along the Omo River alone delivers 90% of the lake

inflow, threats Lake Turkana and severely reduces the lake water level causing it to split into two smaller lakes.

The lake has abundant plankton that include microalgae and cyanobacteria. In total, 50 fish species are recorded in Lake Turkana, 12 of them are endemic, comprising cichlids, barbs, catfish, and robber tetras. Also, tilapia, Nile perch, African knifefish, and African Arowana are found. The lake has diverse aquatic animals, including hippos, crocodiles, migratory birds, and flamingos. The mammals include giraffes, zebras, rhinos, elephants, and cheetahs. In 1997, Lake Turkana National Parks, including the lake itself, was inscribed on the UNESCO World Heritage List [65].

1.7.5 Lake Albert

People called it "Mwitanzige" (locust killer) because numerous locusts died while overpassing the lake. Samuel Baker gave it a new name "Lake Albert" after Prince Albert in 1864. Lake Albert formed over 10 million years ago and is Africa's seventh largest lake. Lake Albert is shallow by comparison with most other large East African rift lakes found to the south (e.g., lakes Tanganyika and Malawi) [66]. At the northern end of the East African rift system lies Lake Albert. The lake is situated in east-central Africa on the Dr Congo-Uganda boundary and is part of the complex upper Nile system. It is shared by Dr Congo (54%) and Uganda (46%). Many other African Great Lakes border the lake, including Lake Edward (south), Lake Victoria (southeast), and Lake Kyoga (east). The Semliki River from Lake Edward and Victoria Nile from Lake Victoria are its primary sources. Fisheries and water are the main uses of the lake. Numerous animal species live in Lake Albert, among them being the Nile crocodiles, hippos, turtles, water birds, and frogs. Although it has lower fish diversity than other African Great Lakes, the lake hosts about 55 fish species.

1.7.6 Lake Kivu

Lake Kivu is one of the African Great Lakes. It lies on the border between the Democratic Republic of the Congo and Rwanda and 58% of the lake's waters lie within Dr Congo borders. Its irregular shape makes measuring its precise surface area difficult. It is Africa's eighth largest lake. The lake bed sits upon a rift valley that is slowly being pulled apart, causing volcanic activity in the area.

Lake Kivu has enormous amounts of carbon dioxide ensnared beneath its depths [67]. In geology, mazuku (Swahili for "evil wind") is referred to

as a toxic pocket of carbon dioxide-rich air. Around Lake Kivu, the term mazuku is usually used to describe areas where secretive deaths happen as a result of the free up of toxic quantities of carbon dioxide into the air. Carbon dioxide forms mazuku when accumulated in depressions close to the ground by gravity because it is heavier than air. Lakes Kivu, Nyos, and Monon have huge amounts of carbon dioxide trapped beneath the depths [65]. Regular geological actions can make the stuck carbon dioxide to lease to the surface, threatening the lives of residents.

1.7.7 Lake Rukwa

Lake Rukwa stands midway between Lakes Tanganyika and Nyasa and is of tectonic origin. It is an endorheic lake, without any outlets, in the west of the Africa Rift Valley, in the southwestern part of Tanzania, where earthquakes are quite common. In the nineteenth century, it was described as an "impossible swamp" because, sometimes, the lake partly dried up, and its shore remained wet. Its size changes according to the amount of rain. Rivers Rungwa and Momba are the main inflows from the northern and western sides, respectively. The Lupa, Chambua, and Songwe rivers are the other three large inflows feeding the lake in the south. The basin in the north is often dry, and the western part is shallow, making it a perfect habitat for crocodiles. The southern basin is deeper, where hippopotamus and otters are frequently observed, and more than 80,000 great white pelicans, which come across and breed there annually. Also, a large number of nonbreeding wetland birds frequently congregate around the lake. Almost 60 fish species live in Lake Rukwa, one-third of which are endemic. Commercial fishing is the principal source of income for the local people. Agricultural runoffs and subsequent aggravation of erosion have been increased, which could result in the disappearance of this African rift lake.

1.7.8 Lake Mweru

Lake Mweru is situated between Zambia and DR Congo. The Luapula River in the South and the Kalungwishi River in the East are the main inflows. The northern part is deeper while the southern area is shallower.

The swamps of Bangweulu surround the southeastern part of the lake. They have the Itigi-Sumbu-thicket with over 100 species of trees and bushes which no human or animal can penetrate.

The local economy relies heavily on Lake Mweru. Zambia's fishing industry (smoked, dried, and salted fish) relies heavily on it. People of this area rely on it for their food and livelihood. Among these fish, some types are the bream, catfish, tilapia, tiger fish, and elephant fish.

The Mweru Lake was the center of a transcontinental trade route for ivory, copper, and slaves among Arab and Swahili traders. The Mweru Wantipa and the Lusenga Plain National Parks are two main reserves, which once had an abundance of wildlife (buffalos, lions, and antelopes mainly), but not anymore. These large animals can be seen in big herds because of hunting and poaching, and crocodiles and elephant populations have been completely wiped out. Leopards, lions, hyenas, and buffalos are found in small numbers.

1.7.9 Lake Edward

Lake Edward is the 15th largest lake in Africa. It is situated west of the East African Rift at the Albertine Rift. It is surrounded by the high Rwenzori Mountains (5119 m at Margherita Peak) in the west, less steep lands and hills in the east, lined with savanna and swamps in the valleys of the Rwindi, Rutshuru, and Ishasha rivers in the south.

Many endemic species (e.g., the mountain gorillas) are living in the rich mountain forests of the Albertine Rift in the northwest part. Rolling hills, forests, and savanna characterizes the east zone.

The lake shores comprise two national reserves, the Queen Elizabeth National Park in Uganda and the Virunga National Park in Dr Congo. On the southeastern shores of Lake Edward, the Kigezi Game Reserve is found.

The main outflow is the Semliki River in the northwest of the DR of Congo, through which the lake is joining the River Nile. In the northeastern region, Lake George discharges its water into Lake Edward through the Kazinga Canal (32 km).

Fishing is an important activity for the locals, as the lake is inhabited by many fish. Chimpanzees, elephants, crocodiles, lions, and hippopotamuses inhabit the shoreline, along with perennial and migratory birds.

1.8 The Southern Africa region

It is the southernmost region of the African continent. The United Nations Scheme of Geographic Regions divides Southern Africa into five states: Botswana, Eswatini, Lesotho, Namibia, and South Africa. Southern

Africa has a diverse landscape that includes forests, grasslands, and deserts. The region has both low-lying coastal areas and mountains. The region has the world's largest resources of platinum and the platinum group elements, chromium, vanadium, and cobalt, as well as uranium, gold, copper, titanium, iron, manganese, silver, beryllium, and diamonds.

1.8.1 Lake St. Lucia

Lake St. Lucia is a large estuarine lake system (350 km^2) on the northeast coast of South Africa, comprising three interconnected shallow lakes (South Lake, North Lake, and False Bay) that are joined to the Indian Ocean via a 21 km channel known as the Narrows [68] (Fig. 1.12). The estuary is 60 km long, 1–20 km wide, and mean depth of 0.9 m [69]. The lake is fed by direct rainfall from five major rivers. The main water body is connected to the sea only in the south by a 22 km long channel, "The Narrows", with very limited tidal influence beyond the first 14 km from the sea [70,71]. Along the Indian Ocean coastline, the high forested coastal

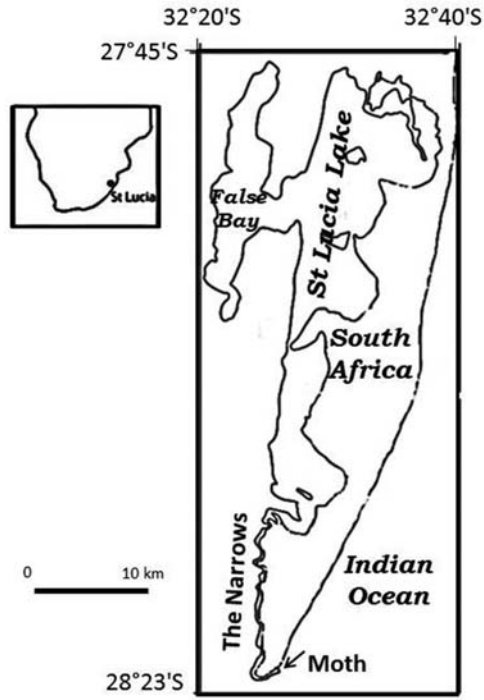

Figure 1.12 Location Map of St. Lucia Lake, South Africa.

barrier dune reaches up to 180 m asl. This prominent dune cordon forms river estuaries and creates isolated coastal lakes and lagoons with restricted marine influence along the coast [72,73]. The St Lucia Lake system is part of the iSimangaliso Wetland Park, South Africa's first UNESCO World Heritage Site, and a RAMSAR Wetland of International Importance [74]. It is also the most biodiversity-rich lake in Southern Africa [1].

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CHAPTER 2

Exploring and phylogenetic characterization of microbial communities in African lakes

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2.1 Introduction

According to the world lake database, International Lake Environment Committee Foundation, Africa has the greatest number of natural and artificial lakes. There are 677 lakes distributed among the African countries with the most in Cameroon, Kenya, and Uganda. Each country in Africa has lakes with unique features, which differ from each other in microbial content and diversity. The microbial content includes microbes comprising bacteria, viruses, archaea, and protists. Microbial growth depends on several factors such as temperature, NaCl concentration, pH, nutrients, radiation, CH_4 cycle, pressure, heavy metals, toxic components, and other environmental factors [1]. The availability of certain factors in a lake makes the environment conducive to bacterial growth and diversity [2]. Variability of the physiochemical properties in African lakes is the cause of the diversity of bacterial assemblages [3]. For example, Soda Lake is considered the best lake in Kenya for fungal diversity due to the presence of optimal growth conditions and the variation in the temperature [4]. Lakes Olden and Olbolosat exhibit the highest prokaryotic diversity among all the

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equatorial lakes due to the freshwater that floods the lakes [5]. Climate change enables new mutated microbial strains to appear and adapt to climatic modifications. The mutated microbial strains are a potential threat to human health. Mutated microbes generate new diseases, which increase incrementally with microbial growth [6,7]. Egyptian lakes, such as Lake Nasser, show changes in the microbial community because of the noticeable modification in biotic and abiotic parameters between pre and postflood periods. The analysis of the lake contents has shown that there are more cyanobacterial phytoplankton and coliforms in the preflood era, while zooplankton is more abundant in the postflood era [8].

Taxonomical studies of African lakes have revealed higher archaeal diversity, containing at least five different phyla [5,9,10]. The taxonomical classification is based on the phenotypic characteristics of cultivated strains as well as noncultivated strains [11]. It is worth noting that the phylum *Nanoarchaeota* is also found in the Soda Lake Magadi, the lake with the greatest *archaeal* diversity. Due to the vast microbial diversity in African lakes, it is important to study and understand the factors and related threats that affect the diversity. Microbial diversity is characterized by different microbes that contain more than one kind of organism, including archaea, protists, bacteria, and fungi with their varied distribution [12,13]. One threat is the planting industry, fish aquaculture, and stock-farming activity [14]. Also, agricultural and aquaculture activities that use pesticides, antibiotics, and organic matter to promote growth, change microbial diversity [14,15]. Pesticides trigger changes in microbial diversity and community structure, which disrupts ecosystem functions when microorganisms are unable to or lose microbial function when utilizing them [16]. These changes affect bacterial and archaeal communities' growth, survival, and reproduction, which subsequently change the population and communities [16]. Heavy metal contamination also changes the bacterial community structure [17]. For example, *Verrucomicrobia* and *Planctomycetes* are not found in polluted soil contaminated with uranium and chromium, but Proteobacteria are resistant to heavy metal contamination [17]. This chapter focuses on the microbial ecology of African lakes and their taxonomical classification. Furthermore, intrinsic and extrinsic factors, as well as current threats that change microbial diversity, are clarified.

2.2 Microbial ecology of African lakes

The Great African Lakes are a group of lakes in and around the East African Rift Valley. Lake Victoria is the world's third largest freshwater

lake by area, followed by Lake Tanganyika, by volume and depth, which is also the world's second-biggest freshwater lake. Lake Malawi is the world's eighth-largest freshwater lake by area [18]. The lakes contain more water than Lake Baikal or the Great Lakes of North America with a combined 31,000 km^3 (7400 cm). This accounts for almost a quarter of the planet's unfrozen surface freshwater. Africa's massive rift lakes are the ancient home of remarkable biodiversity, with 10% of the world's fish species. The most famous lakes that are characterized by biodiversity are the soda lakes [19].

Soda lakes are saline and alkaline habitats said to have existed throughout the Earth's geologic history. Many soda lakes have high amounts of heavy metals. The soda lakes are examples of terrestrial biomes and are geologically interesting areas such as the Great Rift Valley. They are found all over the globe but are especially widespread in deserts and steppes. The peculiar geochemistry encourages the development of a diverse range of microorganisms with commercial and eco-significance [20].

Soda lakes contain the main trophic groups and include haloalkaliphilic bacteria and archaea. There are numerous functional categories of bacteria in soda lakes, such as methanogens, methanotrophs, phototrophs, denitrifiers [21], syntrophs, sulfate reducers, and sulfur oxidizers, all of which suggest environments with complex microbial food webs. Soda lake microbes contain biotechnologically important microbial enzymes and biomolecules (e.g., cellulases, amylases, and tetrahydro pyrimidines), and new integrated approaches are needed to complement bioprospecting in these habitats. Importantly, some saline lake habitats must be safeguarded from environmental pressures, which could jeopardize their long-term survival.

2.2.1 Microbial ecology of African soda lakes

The soda lakes of the East African Rift Valley, as well as the Kulunda-Transbaikal steppes and those in the United States, are well-studied, with several novel autotrophic and heterotrophic microbial genera and species described [22]. Notably, the East African soda lakes have been considered to exhibit around 10^5–10^6 CFU/mL cultivable aerobic and anaerobic bacteria [23,24]. Novel alkaliphilic bacteria have been recorded in East African soda lakes [19].

Bacteria belonging to genera *Halomonas*, *Bacillus*, and *Arthrobacter*, the alkaliphilic archaea *Natronococcus* and *Natronobacterium*, and new cyanobacterial

species related to *Cyanospira*, *Synechococcus*, and *Chroococcus* have been identified regularly. According to Jones and colleagues [23], *Arthrospira sp.* is responsible for the majority of photosynthetic production in these lakes.

Ectothiorhodospira and other anoxygenic phototrophs are proposed to contribute to primary productivity in lakes [22,25]. The most frequent anaerobes discovered in the sediments of East African soda lakes are chemoorganotrophic Halanaerobiales and Clostridiaceae [23].

The presence of acetogenic bacterial species, including *Natroniella acetigena, Thermosyntropha lipolytica*, and *Tindallia magadiensis* in soda lakes sediments [21,26] indicates that acetogenins digest waste products of other anaerobic microbes [22]. Many novel 16S rRNA gene sequences associated with possibly the archaeal phylum Euryarchaeota have been recorded in alkaline saltern water adjacent to Lake Magadi, Kenya, [24]. Haloalkaliphilic archaea, belonging to genera *Natrialba, Natronomonas, Natronolimnobius*, and *Halorubrum* have been observed in Lake Magadi and Inner Mongolian soda lakes [22].

The presence of both autotrophic sulfur-oxidizing and heterotrophic sulfate-reducing microorganisms in Lake Magadi shows that they may be functionally linked via redox junctions between the C and S cycles [27]. Heterotrophic denitrifiers such as *Halomonas, Pseudomonas*, and *Paracoccus* spp. mediate the denitrification process. In the presence or absence of other sulfur autotrophs, syntrophic relationships between sulfur autotrophs related to *Thioalkalivibrio* have been observed in the Wadi Al-Natrun's hypersaline soda lakes, Egypt [28].

2.2.1.1 Microbial ecology of Kenyan soda lakes

The world's most prolific microbial systems are found in soda lakes in tropical Africa. The Kenyan Rift Valley was screened from October 1989 to September 1989 and included soda lakes Bogoria, Elementaita, Magadi, and Nakuru, all with a unique combination of microbial, geological, geographical, and climatic factors [29,30]. Lake Bogoria is an exceedingly salty and alkaline soda lake, making it unsuitable for fish. For the Endorois people, who have been the lake's caretakers for millennia, it holds significant spiritual and cultural value. However, it was not until the turn of the last century that the Endorois learned about the lake's economic value. The lake, which is known for its flamingos and fresh waterspouts, includes uncommon bacteria such as gram-negative bacteria. The high G + C gram-positive bacteria in the soda lake environment include novel *Streptomyces spp.* that grow at pH 10 and hydrolyze proteins and

carbohydrates, a novel genus *Bogoriella*, a new species of *Dietzia*, and uncharacterized relatives of *Nesterenkonia* and microorganisms that can be used to make valuable enzymes [21]. Companies in Europe and the United States harvest the microorganisms from Lake Bogoria to make medicine, detergents, and color fabrics, sharing financial gains with Kenya [31].

In less saline soda lakes, Cyanobacteria, like *Spirulina platensis*, are the primary producers, whereas, in the more salty Lake Magadi, purple sulfur bacteria, like Ectothiorhodospira, are the predominant producers [32]. Two big cyanobacterial blooms have been recorded in Lake Magadi, where the conductivity of the water influenced the algae population and species compositions [33]. At higher conductivity, Spirulina was the most prevalent cyanobacterium [34], while *Nitzschia* and *Navicula* were the most common diatoms [35]. However, the algal communities did not appear to be affected by minor alkalinity variations. The algae in Lakes Nakuru and Elementaita showed modest nitrogen limitations, but no nitrogen limitations were seen in Lake Bogoria, which had slightly higher total nitrogen levels. In the lakes of Bogoria and Elementaita, total phosphate was a limiting factor for algae. Generally, organotrophic aerobic bacteria from the studied Kenyan soda lakes were high and steady [36].

2.2.2 African Great lakes ecology and evolution

East Africa's great lakes are the world's most species-rich freshwater lakes. Much of the lakes' astonishing biological diversity evolved through evolutionary (often adaptive) radiation and explosive speciation, [37] thanks to intrinsic biological variables and extrinsic ecological chances. Ecosystem functioning and complex biotic interactions, such as coevolution, are highlighted in the review, in addition to evolutionary patterns and mechanisms that led to the biodiversity and morphological differences. Through the late Cenozoic, comparative biogeographic patterns for vertebrates and invertebrates [38], as well as patterns of diversity and disparity, are explored. The African Great Lakes are fantastic locations for integrating micro-and macroevolution because of their fossil archives. Unfortunately, these ecosystems are vulnerable to human-made stressors on global and regional scales, which have already harmed their stability and jeopardized some of the biodiversity.

2.2.2.1 Microbial ecology of Lake Kivu

Lake Kivu is one of Africa's great lakes and is located in the Albertine Rift, the western arm of the East African Rift, on the boundary between the Democratic Republic of Congo and Rwanda [39]. The Ruzizi River

empties into Lake Kivu, which empties into Lake Baikal to the south. These lakes' peculiar geochemistry encourages the growth of a diverse range of microorganisms. Lake Kivu, along with Lake Nyos and Lake Monoun in Cameroon [40], is one of the three freshwater lakes in the world known to produce limnic eruptions. Around the lake, geologists discovered evidence of massive local extinctions every thousand years, which were most likely triggered by outgassing. The cause of the Lake Kivu overturns is uncertain, however, it is thought to be volcanic activity. Each erupting lake has its chemical makeup of gaseous chemicals. As a result of the lake water interaction with volcanic hot springs, methane (CH_4) and carbon dioxide (CO_2) are produced in Lake Kivu [41].

Early microbiology studies focused on microbes involved in the CH_4 cycle, with indications of CH_4-oxidizing bacteria present and active in Lake Kivu's anoxic deep waters [42,43]. A study on the phylogenetic diversity of the microbial community involved in the CH_4 cycle in Lake Kivu was published by [44]. The authors used the functional gene sequences of particulate CH_4 monooxygenase (*pmoA*) and methyl coenzyme M reductase (*mcrA*) as molecular markers for methanotrophic aerobic bacteria and anaerobic archaea, respectively.

The steep oxycline and oligotrophic nature of the lake's mixolimnion provides an ideal environment for the formation of autotrophic nitrifying archaeal communities [45]. A considerable number of sequences belonging to the marine Crenarchaeota were attributed to a single operational taxonomic unit (OTU) associated with *Nitrosopumilus maritimus* have been recorded in Lake Kivu, confirming the presence of active archaeal nitrifiers in the water column [46]. The occurrence of archaeal ammonia monooxygenase subunit A (*amoA*) genes at depths where nitrate and nitrite maxima have been detected in two basins of the lake implicates that planktonic archaea may be involved in the oxycline nitrification processes [46].

2.2.2.2 Microeukaryotes of Lake Kivu

The diversity of microeukaryotes in Lake Kivu is unknown. Although phagotrophic protists may contribute to the food chain, little reliable data have been gathered [47]. Using 18S rRNA gene fingerprinting, a recent biodiversity study of microeukaryotes in Lake Michigan's surface waters offered data for comparison of the microeukaryote assemblage with that of Lake Tanganyika [47]. The microeukaryote assemblage in Lake Kivu included heterotrophic and photosynthetic uncultured taxonomic groups,

Stramenopiles (21.4%), Alveolata (21.4%), Cryptophyta (21.4%), Chytridiomycota (8.9%), Kinetoplastea (7.1%), and Choanoflagellida (5.4%), accounting for 78.6% of the total retrieved diversity (87.3% of the clones) [41]. No clones belonging to Chlorophyta have been recorded in the Lake Kivu clone library [40]. However, no significant difference in microeukaryote taxonomic composition between sampling times has been observed in the lake.

2.3 Patterns and processes of morphological evolution of microbial diversity

Bacteria, archaea, protozoa, fungi, and viruses all come in a variety of different shapes and there are a few theories on why these shapes evolved. Apart from the basic shapes (rod, coccus, and spiral), some bacteria are amorphous, ovoid, square, stellate, filamentous, or stalked. Bacteria can be grouped as clumps, chains, rosettes, cuboid packets, flat squares, networks, mycelia, or fruiting bodies [48].

The question to answer is whether morphology has biological relevance. Different microbial genera usually have a limited subset of morphologies, and some can change shape in response to environmental cues. This suggests that shape must have selective value if it merits regulation [49]. One evolutionary argument suggests that some shapes have an advantage in certain environments. For example, archaea have morphological forms similar to that of bacteria [30]. Both bacteria and archaea are also diverse in terms of adaptations for motility. Motility in prokaryotes is generally restricted to moving along concentration gradients toward nutrients or away from repellent chemicals [50]. Shape thus contributes to the survival value in the face of selective pressures that determine whether cells live or die, such as nutrient acquisition and predation.

2.3.1 Nutrient acquisition

It is generally accepted that prokaryotic cells are so small because they require a large surface-to-volume ratio for optimal internal biochemistry. However, it has also been suggested that the small size arises from competition for nutrients, which is won by smaller, faster-growing cells. Another explanation is that bacteria alter their morphology to increase the efficiency of their nutrient harvesting. *Caulobacter crescentus*, for example, has a stalk (prostheca) that extends from the organism and attaches the organism to a solid surface in water. The stalk length increases in

phosphate-poor conditions; this has also been observed in similar bacteria [33]. Fluctuations in water levels, during wet and dry seasons, change the nutrient composition of the lakes, and as a result, microbial communities adapt for nutrient uptake. The structure of these communities also changes due to a shift in nutrient availability [51].

2.3.2 Predation

Predation is one of the most pronounced evolutionarily selective forces affecting larger organisms. However, research on predation in microbes has only recently gained traction. Bacteria have diverse ways in which they adapt to escape protistan grazing. Protists can only ingest bacteria that are of the right shape and size [52]. Some bacteria adapt morphologically and in other ways becoming so-called "grazing-resistant bacteria." Bacteria can change their size (i.e., become too small, too large, or elongated) [53–55], by filamenting [55,56], producing prosthecae [57], and grow as microcolonies or biofilms [58,59]. The food web of Lake Kivu in Rwanda has undergone substantial changes since the introduction of the zooplanktivorous Tanganyika sardine in the 1950s. It caused the disappearance of the most efficient grazing zooplankton [60] and lowered grazing pressure, resulting in higher biomass of phytoplankton. Diatoms are currently the most abundant phytoplankton in Lake Kivu. With the abundant diatoms being large, slow-growing, inedible diatoms such as *Fragilaria danica* and *Nitzschia bacata* [61].

2.3.3 Intrinsic and extrinsic factors affecting microbial diversity

Microbes including bacteria, archaea, some unicellular eukaryotic organisms, protozoa, fungi, and viruses are present in lake water. Many factors influence the composition of these microbial communities. The intrinsic factors that affect the diversity of microbial life in lakes include biotic interactions (predation, parasitism, competition, and symbiosis), the salinity, pH, nutrient availability, and barriers caused by lake stratification. The extrinsic factors include land-use change, water pollution due to anthropogenic activity, and global warming. Of the intrinsic factors, salinity seems to be the principal determining factor of microorganism diversity. In the case of external factors, global warming has a large effect on most other factors and parameters (both intrinsic and extrinsic).

2.3.3.1 Intrinsic factors

2.3.3.1.1 Biotic interactions

Predation helps to maintain balance among organisms and greatly affects community structures in habitats. One important example of predation in microbial communities is that of protozoan grazing, which can alter both the morphological and taxonomic structure of microbial communities [62]. Another mechanism contributing to the maintenance of diversity is hierarchical, and especially, nontransitive competition network formation. Nontransitive competition networks are the equivalent of rock–paper–scissors, as no single species out-competes the others. Therefore, local extinctions are avoided and species coexistence is fostered [63].

2.3.3.1.2 Physical parameters

Comparing the effects of different environmental factors (temperature, pH, and salinity) on microbial community composition, salinity is one of the greatest factors that shapes bacterial community composition, species richness, and diversity [64,65]. This is not to say that saline environments necessarily have lower diversity in microbes as is usually seen with plant and animal life, but species, genera, and even families of microorganisms become increasingly different with an increase in salinity [66].

Temperature fluctuations naturally occur with seasonal and diurnal patterns. Temperature influences nearly every other water quality parameter, such as solubility of gases and solids, pH, and metabolic rates of aquatic organisms. For example, ice-cold water can hold twice as much dissolved oxygen as warm water [67]. In lakes with an extreme pH, diversity also differs greatly. Soda lakes, such as Lake Magadi and Bogoria in Kenya, have a high pH, which supports a high diversity of prokaryotes, especially alkaliphiles. Some uncultured species that have been found in these lakes seem to have no phylogenetic ties with known microbes. They appear to be from separate evolutionary lines unique to the soda lake environment [23,68]. In most African lakes, Proteobacteria are abundant biological entities, regardless of whether it is a soda lake, freshwater, or even a meromictic lake [5,69,70].

2.3.3.1.3 Lake stratification

The water column of lakes is divided into three layers characterized by gradients of temperature and oxygen. These are, from top to bottom, the epilimnion, metalimnion, and hypolimnion. Stratification occurs in many deep tropical African lakes, such as Albert, Cabora Bassa, Chad, Kariba,

Malawi, Niger, and Turkana [71]. Lakes are categorized on how often, and how completely, these layers mix annually. Some lakes are classified as meromictic, which means only partial mixing occurs, and this could occur only once every few decades, or even millennia [72]. The cold bottom layer of meromictic lakes (termed the monimolimnion) usually contains high concentrations of dissolved salt and CO_2 and is permanently anoxic. This layer is much denser than the warmer, oxygen-rich, less saline top layer (mixolimnion), creating a barrier against mixing. Several studies, including one on Lake Kivu in East Africa, have found that the monimolimnion layer has an elevated microbial diversity compared to the mixolimnion [70,73,74]. Thus, total lake microbial diversity depends heavily on depth and subsequent stratification and mixing. An example of bacterial diversity can be found in Table 2.1.

Table 2.1 Bacterial diversity in different zones of three stratified African lakes.

Bacteria	Lake Kivu	Lake Tanganyika	Lake Nyos
Alphaproteobacteria	Oxic zone	n.d.	Oxic zone
Betaproteobacteria	Transition zone	n.d.	Oxic/transition zone
Deltaproteobacteria	Anoxic zone	Anoxic zone	Anoxic zone
Epsilonproteobacteria	Anoxic zone	n.d.	n.d.
Gammaproteobacteria	Anoxic zone	Anoxic/oxic zone	Oxic zone
Actinobacteria	Oxic zone	Oxic zone	Oxic/anoxic zone
Armatimonadetes	Anoxic zone	n.d.	n.d.
Bacteroidetes	Oxic zone	n.d.	Anoxic/transition zone
Chloroflexi	Anoxic zone	n.d.	n.d.
Cyanobacteria	Oxic zone	Oxic zone	n.d.
Planctomycetes	Oxic/ transition zone	n.d.	n.d.
Nitrospirae	n.d.	Anoxic/ transition zone	Anoxic zone
Firmicutes	n.d.	Anoxic/ transition zone	Oxic/transitional/ anoxic zone

2.3.3.2 Extrinsic factors

2.3.3.2.1 Land-use change

Land-use change refers to the process by which natural landscapes are transformed due to human activity, especially for economic activities [75]. Examples of land-use change include settlement, agriculture, industries, and aquaculture. Human activity along lake shorelines usually results in run-offs of polluted water into the lake, altering the biogeochemical cycles and microbial ecology. This results in drastic changes in the physical properties of the water and can lead to the introduction of new microbes and the dying-off of existing microbes adapted to the natural conditions of the lake. An example of this is algal bloom, and especially harmful algal bloom, which releases toxins into the water. An algal bloom is caused by nutrient-rich run-off from, for example, agricultural fertilizers, resulting in an increase of autotrophic algae and some heterotrophic protists [76]. Algal bloom also causes depletion of oxygen in the water and blocks sunlight from entering the water. Lake Victoria has recently faced challenges of algal bloom due to an increase in nitrogen and phosphorous [77]. Similarly, Lake Malawi has seen a 50% increase in nutrient and sediment loading due to agricultural practices and associated soil erosion [78]. This increase in nutrients might cause an increase in phytoplankton biomass as well as a species shift to nitrogen-fixing Cyanobacteria. This would be disastrous for the lake's diversity since it is considered to be the most species-rich lake in the world [79].

2.3.3.2.2 Global warming

Temperature affects a number of the properties of water. Environments, where greenhouse gases are increasing, are favorable for specific species of microbes, but detrimental to others and can lead to their extinction from that environment. Carbon dioxide can lead to acidification of water, and stratification of lakes rises due to temperature changes, leading to the expansion of anoxic zones [80]. Freshwater bodies such as lakes are likely to experience a rise of 1°C−7°C in the surface temperature [81]. Climate changes usually reflect inter-annual variations in phytoplankton composition and biomass, and there will be a shift in species diversification, toward more heat-tolerant organisms, such as phytoplankton species Chlorophyceae to Cyanophyceae [71,82]. Epilimnions are becoming less light transparent, in response to elevated temperatures, which could adversely affect primary producers in deep African lakes such as Kariba, Malawi, Tanganyika, and Victoria [82]. For example, changes in

planktonic diatom composition were observed in Lake Tanganyika between 1970 and 2005. In the 1970s, there was an abundance of *Cyclostephanos*., *Nitzschia* spp., and *Aulacoseira granulate*, whereas a recent study showed mostly dominance of *Nitzschia asterionelloides* and an absence of other planktonic taxa [83]. This can be explained by global warming which strengthened the stratification of the lake, reducing phosphorous supply to the euphotic layer, in turn, reducing primary production. Vertical mixing may also be affected by global warming because a warmer lake will have a shallower and more stable thermocline. This will restrict nutrient flux from the hypolimnion to the epilimnion [84]. East African lakes are potentially very sensitive to global warming. Small temperature variations cause large fluctuations in the thermocline. Stratification isolates nutrients from the euphotic zone and disruption of this can lead to eutrophication of the lakes [85]. Increased temperatures also mean increased evaporation. Lake Chad is an excellent example of how destructive droughts and high temperatures are. This lake was once the sixth largest lake but has shrunk by 90% over the last 60 years [86].

2.4 Exploring archaea in African lakes

.Archaea have a cellular morphology identical to that of bacteria; however, they have unique cells (ameboid type) [87]. In addition, Archaea have ether-linked membrane lipids whereas Eukarya and bacteria have membrane lipids with ester bonds [88]. Taxonomical studies of organisms in African lakes revealed higher archaeal diversity containing at least five different phyla [5,9,10] (Table 2.2). The taxonomical classification is based on phenotypic characteristics of cultivated strains as well as non-cultivated strains [11]. In the archaeal domain, most of the phyla belong to *Crenarchaeota* and *Euryarchaeota*. Each of the phyla is composed of a single dominant class. For example, *Crenarchaeota* has "*Thermoprotei*" as its dominant class (Table 2.2), as reported by [89]. *Euryarchaeota* is a phylum that is represented by various species, which mostly belong to the class *Halobacteria*. Phylum *Korarchaeota* is strictly anaerobic and hyperthermophilic and represented by the species *Korarchaeum cryptophylum* [90]. The *Nanoarchaeota* phylum only contains the species called *Nanoarchaeum equitans*. This phylum was described for the first time by Huber and coworkers in 2002 [90]. Finally, the phylum *Thaumarchaeota* contains the genus *Cenarchaeum*. Species of this phylum have been found in soils and also in marine systems worldwide [91]. Notably, Lake Magadi and Lake Kivu

Table 2.2 Archaea recorded in African lakes.

Phylum	Class	Order	Family	Genus	African lakes	References
Crenarchaeota	Thermoprotei	Desulfurococales	Desulfurococcaceae	*Desulfurococcus* *Staphylothermus* *Sulfophobococcus* *Thermodiscus*	Lake Magadi, Kenya	[9]
		Sulfolobals	Sulfolobaceae	*Acidianus* *Metallosphaera* *Stygiolobus* *Sulfolobus* *Sulfurisphaera*	Lake Magadi, Kenya	[9]
Euryarchaeota	Halobacteria	Halobacterials	Halobacteriaceae	*Haladaptatus* *Halarchaeum* *Halobacterium* *Halodesulfurarchaeum* *Halomarin* *Halorussus* *Halovenus* *Natronoarchaeum*	Lake Magadi, Kenya	[9]
		Natrialbals	Natrialbaceae	*Natrialba* *Natronobacterium* *Natronolimnobius* *Natronococcus* *Natronorubrum*		
	Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermobacter* *Methanobacterium* *Methanosphaera* *Methanobrevibacter*	Lake Kivu, Rwanda-Democratic Republic of the Congo	[46,70,92–94]

(*Continued*)

Table 2.2 (Continued)

Phylum	Class	Order	Family	Genus	African lakes	References
	Methanomicrobial	Methanosarcinales	Methanosarcinaceae	*Methanosalsum* *Methanococcoides* *Methanimicrococcus* *Methanosarcina* *Methanohalobium* *Methanohalophilus* *Methanolobus* *Methanomethylovorans*	Lake Nasser, Egypt Lake Sonachi, Central Kenya	
	Thermoplasmata	Thermoplasmatal	Ferroplasmaceae	*Acidiplasma* *Ferroplasm*	Lake Magadi, Kenya	[9]
Korarchaeota	Korarchea	Korarchaeales		*Korarchaeum*	Lake Tanganyika, Central Africa	[10]
Nanoarchaeota		Nanoarchaeales	Nanoarchaeaceae	*Nanoarchaeum*	Soda Lake Magadi, East African Rift Valley	[9]
Thaumarchaeota	Thaumarchae	Nitrosopimulales	Nitrosopumilaceae	*Candidatus nitrosomarinus*	Lake Nyos, Cameroon, Central Africa	[95]
	Nitrososphaeria	Nitrosopumilales	Nitrosopumilaceae	*Candidatus nitrosopumilus*		

contain the most diverse *Crenarchaeota* and *Euryarchaeota* phyla (Table 2.2), compared to the other African lakes such as Lake Nasser, Lake Sonachi, Lake Tanganyika, and Lake Nyos. Therefore, in Lake Nasser and Lake Sonachi, *Euryarchaeota* are the most abundant archaeal phylum. The typical archaeal diversity of the *Korarchaeota* phylum has been recorded in Lake Tanganyika. Lake Nyos has been characterized by the dominance of the *Thaumarchaeota* phylum. It is worth noting that another phylum such as *Nanoarchaeota* was also found in the Soda Lake Magadi, being the lake with the greatest archaeal diversity. However, it can be concluded that African lakes contain huge archaeal diversity yet to be explored.

2.4.1 Case study in revealing the archaeal community structure of Lake Nyos, Cameroon

Lake Nykos is a crater lake located in the Northwest region of Cameroon with a depth of 210 m [96,97]. The lake is characterized by its permanent stratified nature and layers of water separated by vertical gradients of temperature [96–98]. The lake is marked by the presence of CO_2 that reaches the bottom and dissolves in the water creating an anoxic condition. In 1986, a sudden limnic eruption of CO_2 in the atmosphere killed almost 1800 people and 3000 livestock in the villages and towns that were in its close vicinity. Since this catastrophe, various studies have been conducted to understand the lake's geological and physiochemical characteristics. The dissolved chemical species mainly consist of CO_2 and HCO_3, followed by Fe^{2+}. In the sediments, there are small amounts of endogenic siderite, and traces of pyrite have also been observed [99,100]. It could be possible that microbes present in this environment may be responsible to drive the geochemical processes.

Likewise, a metagenomic study, by implementing the polymerized chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE) of the 16S rRNA gene, has been conducted to profile the archaeal communities of Lake Nykos. The archaeal communities exhibited that the closest relatives belonged to phylum Thaumacheota (53.3%), Euryarchaeota (33.3%), and Crenarcheota (13.3%). The Thaumacheota chiefly contains the *Candidatus Nitrosopumilus koreensis* AR1 while Euryarchaeota and Crenarcheota comprise *Methanolobus psychrophilus*, *Natronolimnobius baerhuensis*, *Salinarchaeum* sp., and *Vulcanisaeta distribute*, respectively [100].

2.5 Exploring bacterial communities in African lakes

The implementation of molecular tools to study the aquatic bacterial community composition has led to a new era in the research of aquatic ecosystems, ranging from shallow to deep lakes, coastal seas, and oceans. Some of the tools used in the research include polymerized chain reaction-restriction fragment length polymorphism, denaturing gradient gel electrophoresis/temperature gradient gel electrophoresis (DGGE/TGGE), automated ribosomal intergenic spacer analysis, next generation sequencing, single single-strand conformational polymorphism, DNA-DNA hybridization, and fluorescence in situ hybridization [101–105]. Studies have elucidated 34 putative phylogenetic clusters that typically constitute the freshwater bacterial consortia, which include phyla predominantly from Proteobacteria, Bacteroidetes, Verrucomicrobia, Cyanobacteria, Actinobacteria, and green nonsulfur bacteria [106,107]. However, one study indicated the dominance of γ-Proteobacteria in the freshwater environment. Notably, a few studies have concentrated on large, ancient lakes of the world or tropical lakes [83], and therefore, the bacterial diversity of the Great African Lakes has been tabulated (Table 2.3) to give an idea of this scarcely studied topic.

Table 2.3 Recorded bacterial diversity of African lakes.

Lake	Bacterial diversity	Techniques used for identification	Location	References
Nasser	Cyanobacteria, total Coliforms	Visualization of bacterial cell morphology, viability, and their abundance, biochemical tests, and microscopy	Egypt	[108]
Wadi An Natrun	α-Proteobacteria, -γ-Proteobacteria, δ Proteobacteria, Bacteroidetes, Firmicutes, Bacillales, Actinobacteria, Spirochaetes, Verrucomicrobia	16S rRNA clone libraries followed by 16S rRNA gene sequencing	Egypt	[109]
Zeiton	α-Proteobacteria, Bacteroidetes, *Lewinella agarilytica*	PCR-DGGE, followed by 16S rRNA gene sequencing	Egypt	[110]

(*Continued*)

Table 2.3 (Continued)

Lake	Bacterial diversity	Techniques used for identification	Location	References
Siwa	Bacteroidetes	PCR-DGGE, followed by sequencing of 16S rRNA gene	Egypt	[110]
Maraqi	α-Proteobacteria, Bacteroidetes	PCR-DGGE, followed by sequencing of 16S rRNA gene	Egypt	[110]
Aghormy	Bacteroidetes, single spirochete-like phylotypes, *Lewinella agarilytica*	PCR-DGGE, followed by sequencing of 16S rRNA gene	Egypt	[110]
Mariout	*Escherichia coli, Vibrio cholera, Mycobacterium tuberculosis, Pseudomonas*	Visualization of bacterial cell morphology, viability and their abundance, biochemical tests	Egypt	[111]
Elementaita	Cyanobacteria, Firmicutes, β-Proteobacteria	Cultivation of pure bacterial colonies and PCR-amplification of 16S rRNA genes and sequencing	Kenya	[112]
Malawi	Cyanobacteria (*Planktolyngbya* spp.)	Visualization of bacterial cell morphology, viability and their abundance	Between Malawi, Mozambique and Tanzania	[61]
Victoria	Cyanobacteria taxa (*Cylindrospermopsis* and *Anabaena*)	Visualization of bacterial cell morphology, viability and their abundance	Between Tanzania and Uganda but bordering on Kenya	[61]
Kivu	Cyanobacteria—chlorophyte dominated phytoplankton	Visualization of bacterial cell morphology, viability and their abundance	Bordering between Rwanda and the Democratic Republic of the Congo	[61]
Edward	High biomass, dominated by Cyanobacteria (*Microcystis* spp., *Chroococcus* spp. And *Merismopedia*)	Visualization of bacterial cell morphology, viability and their abundance	Bordering between Uganda and the Democratic Republic of Congo	[61]
Albert	Cyanobacteria, abundance of *Anabaena flos-aquae* (Bréb.)	Visualization of bacterial cell morphology, viability and their abundance	Bordering between Uganda and the Democratic Republic of Congo	[61]

2.5.1 Case study exploring bacterial diversity and composition of equatorial Lakes Olbolosat and Oloiden in Kenya

Lake Olbolosat (Olobolosat means marshy land in the Maasai language), is a freshwater lake and drainage wetland lake in Central Kenya, Africa, which has been regarded as one of the endangered freshwater lakes [5,113,114]. The lake has been formed by down warping and is located outside the rift valley. The lake undoubtedly supports the livelihood of communities, wildlife, and livestock and forms the chief source of water for the Ewaso Nyiro river from Thompsons falls in Nyahururu town, although it is facing massive shrinking due to anthropogenic activities [114]. On the other hand, Lake Oloiden (Oloiden means salty in the Maasai language) lacks water inflow and evaporation leads to water loss. The only source of water is rainfall via the peninsula from Lake Naivasha [5,113,115]. These two lakes harbor rich organic sources, and therefore, provide suitable conditions for microbial growth [113]. Studies have shown huge microbial diversities in both the Olbolosat and Oloiden lakes. For instance, a cultivation-based study conducted on the sediments and water samples collected from the Olbolosat and Oloiden lakes has recorded 35 and 25 isolates, respectively, with a microbial count ranging from 0 to 1.75×105 CFU/mL [116]. Morphologically, the isolates are mostly rod-shaped followed by cocci and filamentous; 58 isolates were gram-positive and the rest gram-negative. The growth condition of the isolates has shown to grow maximally at pH 6−10, with a temperature range of 25°C−30°C and a salinity range of 0%−5%. The sequences of the 16S rRNA gene of the isolates showed an abundance of *Firmicutes* (77%), followed by *Actinobacteria* (15%), and followed by 4% for each of *Proteobacteria* and *Bacteroidetes*. Notably, the isolates, *Pseudomonas aeruginosa*, *Bacillus subtilis*, *Escherichia coli*, *Staphylococcus aureus*, and *Candida albicans*, have been found to exhibit enzymatic (hydrolases) and antimicrobial activities [113]. Another study on the microorganisms sampled from the two lakes, using high throughput Illumina Miseq sequencing of V3-V4 hyper variable region of the 16S rRNA gene, has revealed *Proteobacteria* as the most abundant phylum (33.8%) followed by *Firmicutes* (27.3%), *Actinobacteriota* (21.2%), *Chloroflexi* (6.8%), *Cyanobacteria* (3.8%), *Acidobacteriota* (2.8%), *Planctomycetota* (1.9%), and *Bacteroidota* (1.1%) [5].

2.5.2 Case study exploring bacterial community composition of Lake Tanganyika in Burundi: vertical and horizontal heterogeneity

Lake Tanganyika in Burundi is the third largest lake by volume and the second deepest lake after the massive ancient Lake Baikal, which is located

in the mountainous Russian region of Siberia [83]. Lake Tanganyika is a meromictic, permanently temperature-stratified lake with robust vertical oxygen concentration gradients. Notably, it contains the largest volume of anoxic freshwater in the world at a depth of 100–200 m. On a large scale, these typical conditions may affect the bacterial community structure [83,117,118]. Particularly, during the dry season, Lake Tanganyika also shows differences in the thermocline that eventually affects the nutrient concentration in the epilimnion, and consequently, the differences in phytoplankton biomass between the north and south lake, which may, in due course, lead to variation in biological community composition. For instance, DGGE of the PCR-amplified 16S rRNA gene from water samples collected from Lake Tanganyika during the dry season has detected gel bands belonging to members of Cyanobacteria, Actinobacteria, Nitrospirae, green nonsulfur bacteria, Firmicutes, and Proteobacteria (γ and δ) [83].

2.5.3 Case study exploring bacterial community composition of Lake Quran in Egypt

Lake Quran in Egypt is a historic lake that has supported human civilization for over 7000 years but is severely polluted due to the intense disposal practices of solid/liquid household and industrial wastes. Additionally, there is pesticide contamination and a lack of long-term and efficient sewage treatment. The salt production company located on the lake's southern shore enhances the salinity with possible effects on human health and aquatic life, including microbial diversity. For instance, a high throughput Ion Torrent 16 rRNA gene amplicon study on Lake Quran water samples has recorded five phyla, including Firmicutes (with an abundance of 53%), Proteobacteria (33%), Bacteroidetes (7%), Actinobacteria (5%), and Thermi (1%). Taxonomic classification at the family level has indicated that Streptococcaceae (14%) was the most abundant, followed by Bacteroidaceae (7%), Listeriaceae (7%), Clostridiaceae (7%), Moraxellaceae (7%), Helicobacteraceae (6%), Lactobacillaceae (6%), Enterobacteriaceae (6%), and unclassified (5%). *Streptococcus* (10%), *Bacteroides* (7%), and *Lactobacillus* (6%) have been recorded as abundant genera [116].

2.5.4 Case study exploring bacterial community composition of Lake Manzala in Egypt

Lake Manzala is a brackish lake located in northeastern Egypt on the Nile Delta and is considered to be the largest deltaic lake in Egypt, between 31°00 and 31°35′N latitude and 31°45′ and 32°15′E longitudes [119].

The lake is bounded by the Suez Canal in the east, the Mediterranean Sea in the north, Damietta province in the Northwest, and the Dakahlia province in the southwest. Lake Manzala has been recognized as the most productive fishery ground and in the 1970s has contributed to nearly 50% of the total country's yield that has significantly decreased to 35% during the 1980s due to the increased rate of water pollution in the lake [119]. Therefore, this lake provides rich organic sources suitable for microbial growth. A bacterial diversity study, using the 16S rRNA gene as the phylogenetic marker, has been conducted on the metagenomes extracted from the water and sediment samples at the two sampling sites, namely Bashtir and Genka sites of the Manzala Lake [120]. The 16S rRNA gene-cloned library revealed 8 bacterial phylotypes from the Genka water and 20 phylotypes in each of the sediment samples. Notably, it has been observed that both sediment and water samples are dominated by the phylotypes of Proteobacteria, however, the water samples collected from both sites exhibit phyla from Cyanobacteria, Proteobacteria, and Bacteroidetes. The Genka and Bashtir water have been differentiated by the presence of the phyla in the former while it is absent in the later. The sediment samples from both the sites are identified with the phyla Proteobacteria, Chloroflexi, Bacteroidetes, and Planctomycetes. Further, the Genka sediment samples exhibit two phylotypes associated with Actinobacteria. Concurrently, some of the other unique phylogenetic lineages have also been observed, proposing new bacterial phyla. This culture-independent PCR-dependent investigation in Lake Manzala has been conducted for the first time, and revealed some of the phyla that could not be identified in the conventional culture-dependent techniques [120].

2.5.5 Case study on phylogenetic characterization of the bacterial communities present in Lake Aghormy, Siwa Oasis, Egypt

In the western dessert of Egypt, lies the Siwa Oasis which is a depression between latitudes 29°05′N and 29°05′N and longitudes 25°05′E and 265° 06′E encompassing an area of about 1200 km^2. The climate prevailing is arid to semi-arid with rare rainfall. The salty lakes are bounded by salt marches that lodge the deepest parts of the oasis. The abundant artesian wells, springs, and cultivated areas drain water into the lakes in Siwa Oasis that contain mostly Na-Cl-SO_4-type formation [121]. One of the Siwa lakes is Lake Aghormy which is located 18 m below sea level and is fed by the spring openings inside the lake which is characterized by the total

dissolved solids of 220.03 g/L with a pH of 7.83 [122]. Additionally, the Lake Aghormy chemical composition is predominated by Na^+, Ca^{2+}, K^+, and Mg^{2+} cations with a concentration of 55, 10, 10.4, and 52 g/L, respectively, while the anions such as Cl^- (246.8 g/L) and SO_4^{-2} (10.7 g/L) are being observed. The lake's sediment is significantly enriched by metals such as Cu, Cd, Se, Co, Pb, Mn, and Zn [122]. Several studies were conducted that reported the seasonal blooming of microbial mats along the Lake Aghormy margins in spring and early summer [122].

Similarly, another lagoon named the Bardawil Lagoon is a flat low-lying plain, bordered from the north by the Sinai Mediterranean coast and covers about 600 km^2, largely linked to the Mediterranean Sea through one natural inlet and two artificial ones, with the pH value constantly fluctuating within the alkaline side at a narrow range of 7.94–8.79 [123]. Notably, the lagoon water salinity value increases from southward to northward with an amount of 40–75 g/L, respectively [124]. The increase of salinity is often aided by the rapid evaporation of the water that simultaneously leads to the deposition of gypsum and halite minerals that eventually cover the southern and eastern parts of the lagoon and are generally described as "Sabkhas", and therefore, it is named as the "Sabeaka Sabkha." The increased level of NaCl (300 g/mL) also leads to the increased concentration of Mg, K, Cl, and sulfate ions, resulting in pH ranges from 7.5 to 8.3 [125]. Studies have supported the growth of bacterial halophiles in these high salt concentrations [126].

Likewise, a culture-independent, PCR-dependent 16S rRNA gene metagenomic study was conducted on athalassohaline Lake Aghormy and also on the thalassohaline saltern, "Sebeaka Sabkha" that generated a total of 488,828 reads from both sites, grouped into 17,741 OTUs. Three thousand thirty OTUs are shared between both sites, while 2255 and 9426 OTUs were unique to the Aghormy Lake and Sebeaka Sabkha, respectively. Aghormy brine is characterized by the presence of phylotypes such as Deinococcus-Thermus, Spirochaetes, Rhodovibrio, Piscirickettsiaceae, and GMD14H09 (Deltaproteobacteria), while phylotypes such as AT12OctB3 (Bacteroidetes), Rhodobacteriaceae, Ectothiorhodospiraceae, and Xanthomonadaceae constituted the Sebeaka Sabkha bacterial community. Notably, a Cyanobacteria-like phylotype was assigned to the genus Dactylococcopsis in both the brines [127].

2.6 Exploring fungi in African Lakes

Despite the interesting biodiversity of fungi and their important role in the aquatic environment, there is very little information about the fungal

species in aquatic environments, especially in Africa [128]. The studies which were carried out on African aquatic systems recorded that most of the common fungal species belong to Hyphomycetes [129]. They were found attached to submerged plants as their conidia are transported from the water streams to the plants, and thus, exist in water and on submerged plants [130]. Studies in Nigerian and South African water supported previous findings, whereas the most abundant aquatic Hyphomycetes in Nigeria are *Flagellospora curvula* [131]. There was, however, remarkable variation between aquatic Hyphomycetes in Nigerian and South African water.

Microbial diversity in water has been studied more in Egypt than in other African countries. The majority of studies were done on brackish and saline lakes such as Manzalla, Marriott, Edku, Burullus, and Quaron [128]. The minor studies were for saline lakes due to their high salinity, decreasing the fungal diversity. The abundance of fungal species in Egyptian aquatic life belongs to Ascomycetes, Basidiomycetes, and Anamorphic fungi [128].

Some terrestrial and zoosporic fungal species contaminate the Egyptian lakes through the animals, plants, and soil. The most frequently recorded species of zoosporic fungi were *Ditcyuchus sterile* and *Aphanomyces laevis* [132]. Also, a limited number of fungal species has been discovered on hyacinth plant leaves such as Eichhornia, *Alatospora acuminate*, *Triscelophorus monosporus*, and *Tetracladium marchalianum* [133].

Edku and Marriott are the most popular brackish lakes in Egypt, while Burullus and Qarun lakes are saline. Lakes Edku, Burullus, and Marriott are located in the north of Egypt, near the Mediterranean coast [134]. The water of Edku is characterized by the salinity of 1.6 g/L, pH 6.55, and temperature of 24°C; while Marriott's water salinity average is 2.9 g/L, pH 6.7, and temperature of 24°C. Burullus lake possesses a salinity of 16 g/L, pH 7.4, and water temperature of 26°C, while Qarun is the most saline Egyptian lake, recording 35 g/L, pH 7.5, and water surface temperature of 25°C [135].

El-Sharouny et al. [135] studied the occurrence and frequency of fungi in lakes Edku, Marriott, Burullus, and Qarun [135]. The diversity of fungi in Edku was the highest among the four lakes with 62 taxa in the collected samples, 26 Ascomycetes, and 36 Anamorphic fungi [135]. The lowest fungal diversity has been reported in samples from Lake Qarun, with only 21 taxa (6 Ascomycetes, 13 Anamorphic fungi, and 2 basidiomycetes), suggesting high salinity reduces the abundance of fungi [135].

Forty-four taxa (14 Ascomycetes and 30 Anamorphic fungi) and 30 taxa (10 Ascomycetes and 20 Anamorphic fungi) have been recorded for Lakes Marriott and Burullus, respectively, [135].

In terms of species abundance, *Panorbis viscosus* (20.8%), *Zopfiella leucotricha* (20%), and *Cirrenalia basiminuta* (45.6%) have been observed as the most frequent species in Edku, Marriott, and Burullus, respectively, [135]. Some species, such as *Periconia prolifica*, have been recorded as dominant fungi in Qarun, but rare in Edku [135]. *Microthelia heterospora*, *Podospora carpinicola*, *Microthelia triseptata*, and *Halocyphina villosa* have been observed in Marriott, Burullus, and Qarun samples, respectively [135]. Seventeen unique fungal species have been discovered and characterized the fungi community in Lake Qarun, among which three species, *M. triseptata*, *Hypocline penniseti*, and *Westerdykella dispersa* [135]. The most common fungal species in the four Egyptian lakes were *Periconia prolifica* and *C. basiminuta* [135]. However, *P. prolifica* occurrence has increased with increasing salinity from Edku to Marriott, Burullus and Qarun. *C. basiminuta* was isolated from the host *Arthrocnemon glaucum*'s decayed stems within lake waters [135].

Fungal biodiversity is always shaped by variation in environmental factors and this is evident in extreme environments [136]. The hot Soda lake springs in Kenya are an example of an extreme environment for fungal communities. Fungal communities have been studied in Kenyan soda lakes of Bogoria, Magadi, Elementaita, and Little Magadi [137]. The most common phyla, which have been recorded in these lakes were Ascomycota, Basidiomycota, Glomeromycota, and unclassified fungi [138,139]. Lake Elementaita has been characterized by water temperature between 30°C and 40°C, pH 9, and a high concentration of chlorides, sulfates, and carbonates [140]. Lake Bogoria's water has high salinity (100 g/L) and alkalinity (pH 10.5). In addition, there are about 200 hot springs around the Bogoria lake (water temperature ranges from 39°C to 98.5°C). Lake Magadi situated in the north of Tanzania's Lake Natron has water temperatures up to 86°C because of hot spring discharge [141]. Little Magadi is located about 40 km south of Lake Magadi with temperatures between 81°C and 83.6°C. Water and sediment samples were collected from the four Kenyan soda lakes and it was found that the most predominant fungal phylum was Ascomycota. Under Ascomycota, there were seven classes: Dothideomycetes, Eurotiomycetes, Saccharomycetes, Sordariomycetes, Pezizomycetes, Leotiomycetes, and Lichinomycetes [137]. These seven classes presented in the four soda lakes Bogoria,

Magadi, Elementaita, and Little Magadi, with different frequencies, and among them, the most abundant were Dothideomycetes and Eurotiomycetes [137,142]. Sixty-two genera belonged to the phylum Ascomycota were molecularly identified and the highly recorded genera were *Cladosporium*, *Epicoccum*, and *Aspergillus* in Lake Bogoria; *Aurobasidium* and *Auxarthron* in Lake Magadi; *Cladosporium*, *Penicillium*, and *Debaryomyces* in Little Magadi; and *Westerdykella* in Lake Elementaita [137,143,144].

The phylum Basidiomycota has been also detected in the soda lakes of Kenya [145,146]. The most diverse classes belonging to this phylum are Agaricomycetes, Exobasidiomycetes, Tremellomycetes, and Ustilaginomycetes. The two classes with high frequency in the collected samples were Tremellomycetes (69.9% up to 70.6% in Lake Elementaita) and Agaricomycetes (100% in Lake Magadi). The genera *Termitomyces*, *Dioszegia hungarica*, and *Malassezia globosa* have been discovered in Lake Magadi. The genera *Rhodotorula* and *Malassezia* have been recorded in Lake Bogori [133]. *Tremella* has been observed as the most frequent genus in Little Magadi [137,147]. The phylum Glomeromycota and unclassified fungi have been found only in the samples of Lake Elementaita with frequencies of 0.1 to 0.4% and 4% to 13%, respectively [137,147].

2.7 Exploring microbial functional diversity in African lakes

2.7.1 Exploring carbon cycle-related microbes

The carbon cycle is the conversion of carbon dioxide into chains made up of sugars with the structure CH_2O.

2.7.1.1 Diversity of autotrophic microorganisms

Some of the chemolithoautotrophs, oxygenic and anoxygenic haloalkaliphilic phototrophs can fix inorganic CO_2 into organic polymers [148]. African lakes, especially tropical soda lakes in Kenya and Ethiopia, are rich in haloalkaliphilic Cyanobacteria [145]. Consequently, the primary production of organic matter in these lakes is very high. Oxygenic haloalkaliphilic Cyanobacteria such as *Euhalothece natronophila*, *Arthrospira*, *Anabaenopsis*, and *Cyanospira* species have been found as dominants in the moderately saline lakes such as Nakuru, Elmenteita, and Manyara [149–151], while salt-tolerant unicellular green algae, such as *Dunaliella viridis* and *Picocystis salinarium* have been recorded in high salinity lakes such as Lake Bogoria [152]. Furthermore, anoxygenic phototrophs such as *Ectothiorhodo spiracea* can thrive in high salt concentrations and

Chromatiales inhabit moderately saline lakes such as Magadi and Natron [153]. Moreover, aerobic chemolithoautotrophic bacteria such as *Natronobacterium gregoryi*, *Natrialba magadii*, and *Natronococcus occultus* also have a role in inorganic carbon fixation in African soda lakes [148].

2.7.1.2 Diversity of heterotrophic carbon-relating microorganisms

The organic polymers produced by autotrophs are degraded by heterotrophic bacteria. These heterotrophs include aerobes and fermentative anaerobes, and are classified into both, hydrolytic (degrade polymers) and secondary heterotrophs (utilize monomers such as amino acids, sugars, alcohols, and organic acids) [148]. Aerobic hydrolytics include various species of *Bacillus* (*B. subtilis*, *Bacillus licheniformis*, *Bacillus pumilus*), *Alkalimonas* Gammaproteobacteria, *Cellulomonas*, and *Dietzia* actinobacteria, which produce hydrolases that play an essential role in breaking down polymers [154]. The anaerobic bacterium *Clostridium alkalicellum* isolated from low salinity African lakes such as the lakes of the African Great Rift plays a role in carbon fixation in these lakes [155]. Interestingly, pectin can be used as a substrate by two newly described fermentative anaerobic haloalkaliphiles from soda African lakes such as Wadi El Natrun, Lake Basaka, Lake Turkana, Lake Natron, and Lake Ngami with high concentration like *Natronovirga*; Clostridiales, or moderate salt concentrations, such as *Natronoflexus pectinovorans*; Bacteriodetes. The high saline-tolerant *Chitinivibrio alkaliphilus* utilizes chitin as a substrate [148]. Among the aerobic secondary heterotrophs, Actinobacteria are the most abundant [156]. Members of the genera *Anaerovirgula*, *Anoxynatronum*, *Alkaliphilus*, *Natranaerobaculum*, *Natranaerobius*, *Spirochaeta*, *Anaerobranca*, and *Anaerobacillus* are common fermentative anaerobic secondary heterotrophs recorded from some African soda lakes such as Wadi El Natrun [156,157]. Amino acids and alcohols are utilized as substrates by *Natronincola*, *Tindallia*, and *Natroniella* [34]. Notably, *Fuchsiella alkaliacetigena* thrives under high salt concentrations in African soda lakes such as Wadi El Natrun, Lake Basaka, Lake Turkana, Lake Natron, and Lake Ngami [155].

2.7.1.3 Diversity of methane cycle-related microbes

Methanogenic (CH_4-producing) archaea are the primary biological source of CH_4 in natural systems, landfills, and agriculture. They are active in anaerobic settings and produce CH_4 as a metabolic by-product. Methanotrophic (CH_4-consuming) bacteria (also known as CH_4-oxidizing

bacteria or MOB) are aerobic bacteria that obtain energy and carbon from the oxidation of CH_4 [148]. Recent studies estimated that 64% of methane is emitted by methanogenic archaea in tropical areas, from which 10% is released by tropical freshwater [158]. Although this percentage seems high, a large portion is aerobically or anaerobically oxidized in these ecosystems [159,160]. Some haloalkaliphilic methylotrophs such as *Methanolobus taylorii* (moderate salinity), *Methanosalsum zhilinae* (high salinity), and *Methanocalculus natronophilus* (extremely high salinity) have been isolated from soda lakes such as Wadi El Natrun in Egypt, Lake Basaka in Ethiopia, Lake Turkana in Kenya and Lake Ngami in Botswana north of the Kalahari Desert [148]. Lake Kivu is characterized by a high amount of methane. However, a very low concentration of CH_4 is emitted into the atmosphere due to intense CH_4 oxidation processes in the lake [160]. Compared to temperate and boreal lakes, the high temperature in tropical lakes promotes bacterial activity. In addition, the water column of Lake Kivu permits high CH_4 concentrations to accumulate in anoxic waters, which can then slowly flow to the oxic layer, allowing both aerobic and anaerobic CH_4 oxidation to occur [160]. The high concentrations of the favorable electron acceptors such as Fe, Mn, and SO_4^{2-} can also accelerate the process [161].

2.7.2 Exploring nitrogen cycle-related microbes

Prokaryotes play an effective role in the nitrogen cycle in African lakes. Nitrogen-fixing bacteria fix nitrogen gas in the atmosphere to ammonia, the form that can be utilized by different microorganisms in the ecosystem. Ammonia is oxidized to nitrites or nitrates by nitrifying bacteria [148]. Heterotrophs have the most important role in the denitrification process. This process is dominated by the extremely salt-tolerant alkaliphilic *Halomonas*, the anaerobic lithotroph *Thioalkalivibrio* and *Alkalilimnicola–Alkalispirillum* group of the Gammaproteobacteria [144]. Moreover, heterotrophic anaerobic fermentative haloalkaliphiles such as cyanobacterial genera *Anabaenopsis* and *Nodularia* (low salinity tolerant), *Anaerobacillus diazotrophicus* (moderate salinity tolerant), *Natronobacillus azotifigans* (high salinity tolerant), the iron-reducing *Geoalkalibacter ferrihydriticus*, and the cellulolytic *C. alkalicellulosi* fix nitrogen efficiently in soda African lakes [148]. Remarkably, haloalkaliphilic nitrifiers such as *Nitrosomonas halophila* and *Nitrobacter alkalicus* can convert ammonium generated during nitrogen fixation to nitrate via nitrite [162]. As a consequence, the nitrogen cycle

in African lakes, particularly the hypersaline ones, is reliant on an external source of NO_x^- [148].

2.7.3 Exploring sulfur cycle-related microbes

Sulphidogenesis is the process of sulfide formation after the reduction of sulfur compounds such as sulfate, sulfite, thiosulphate, and sulfur [148]. These reactions can be carried out by a variety of obligatory anaerobic and haloalkaliphilic bacteria such as the genera *Desulfonatronum*, *Desulfonatronovibrio*, *Desulfonatronospira, Desulfobulbus*, and *Desulfobotulus* [163]. Further, both *Dethiobacter alkaliphilus* and *Desulfurivibrio alkaliphilus* can reduce sulfur and thiosulphate through polysulphide disproportionation [164].

Phototrophic and chemotrophic sulfur-oxidizing bacteria have a role in oxidizing sulfide to elemental sulfur. The most abundant genera are *Ectothiorhodospira* and *Halorhodospira* (high salinity tolerant); *Thiorhodospira*, *Thioalkalicoccus* and *Ectothiorhodosinus* (low salinity tolerant); *Thioalkalimicrobium* and *Thioalkalispira* (moderate salinity tolerant) [165]. They are obligate autotrophs that use reduced sulfur compounds as an electron donor, such as sulfide, polysulphide, thiosulphate, polythionates, and elemental sulfur [166]. Recent research revealed that Desulfobacteraceae such as *Desulfotomaculum carboxydivorans*, *Desulfurispora thermophile*, *Desulfosalsimonas propionica*, *Desulfatibacillum alkenivorans*, and *Desulfotomaculum alkaliphilum* are related with the sulfur cycle from African lakes [144].

2.7.4 Exploring microbes related to biostabilization of sediments

Microbial mats that grow in siliciclastic sediments play a vital role in diagenesis and accretion [167,168]. Microbial-induced sedimentary structures form as a result of the biotic physical interaction of microbial mats with the geological dynamics of aquatic lakes [169]. Cyanobacteria are the most dominant microbial mat builders.

In Lake Aghormi, Siwa Oasis, Egypt, coccoid Cyanobacteria form on the surface of sand grains, and fill the pore space between them [168]. Thus, extracellular polymeric substances secretion, cohesive effects, and network formation bind and stabilize sediments. Interestingly, Siwa's climate is hot and dry almost all year, and solar radiation is intense. These conditions favor the deposition of halite, which acts as a good conduit for light, reduces the effect of intense harmful solar radiation, and protects

microbial mats from high cosmic radiation, allowing them to survive and thrive [168].

Furthermore, microbial cocci biofilms play a role in the formation of Mg silicate minerals and crust depositional processes of lacustrine carbonate towers in Lake Abhe, Djibouti [170]. In conclusion, microbes play a fascinating role in African lakes. Thus, intensive studies on exploring the diversity of microorganisms in African lakes are needed to address many gaps in the sustainability of the lakes.

2.8 Current threats to microbial diversity in African lakes

Microbial diversity in the lakes is key to creating sustainability and healthy microbial ecosystems [171]. Therefore, it is important to study and understand the factors that affect microbial diversity and the threats that may occur. Microbial diversity is characterized by different microbes that contain more than one kind of organism including archaea, protists, bacteria, and fungi with varied distribution [12,13]. There are many threats affecting microbial diversity including the planting industry, fish aquaculture, and stock farming [14]. These activities can change the biological characteristics of freshwater lakes such as microbial biodiversity [14]. Among the other threats affecting microbial diversity in the African lakes are agricultural and aquaculture activities that use drugs, such as antibiotics, and organic matter to promote growth [14]. Sengupta et al. [168] elucidated that antibiotics would trigger the inhibition of microbial activities and influence biogeochemical processes in these ecosystems, especially in the lakes [172]. Following an analysis of the microbial community in the lakes, Sengupta et al. [168] demonstrated that *Bacillus flexus* is strongly affected by TN, NH_4^+-N, PO_4^{3-}-P, and oxytetracycline antibiotics [14,172]. Furthermore, some strains of *B. flexus* can solubilize phosphorus and are resistant to oxytetracycline [172].

Pesticide waste can shape the microbial composition in contaminated lakes [16]. It may be beneficial for some microbes, especially bacteria that utilize pesticides as a source of nutrients facilitating their growth and survival. Other microbes may, however, be sensitive to pesticides and have impaired growth, which leads to dramatic shifts in microbial community concentrations [16]. Pesticides can induce a cascade of indirect effects by eliminating a particular microbial population and then releasing pesticide-tolerant microbes to compete for shared resources [16]. Also, pesticides trigger changes in microbial diversity and community structure disrupting

ecosystem functions if microorganisms are unable to utilize pesticides or lose microbial function in utilizing them [16]. These changes affect the bacterial and archaeal community diversity [16].

In addition, there are other factors affecting microbial diversity in lake environments such as exposure to heavy metals, hydrobiological waste, and overconsumption of lake water [171]. Heavy metals such as Cd, Pb, Hg, and Ni are considered to be the most dangerous stressors because of their toxicity, accumulation tendency, persistence, and low degradability [173,174]. Releasing of heavy metals into the lake water influences microbial abundance [171,174]. Following the release of the heavy metal, significant changes occur in the structures and functions of lake microbial communities, which affect the ecological functionalities of aquatic ecosystems [174]. Studies performed by [175–177] show that there is a strong correlation between environmental factors and community structure.

Cumulative factors, including Cr, organic matter, and pH, have been found to change bacterial community structure in the lakes [17]. However, members of Proteobacteria, which constitute the main phylum in the lake environments, are resistant to heavy metal contamination [17]. *Verrucomicrobia* and *Planctomycetes* are found in normal soil but not in polluted soil contaminated with heavy metals such as uranium and chromium [17].

Microbial interaction is another factor that influences microbial diversity and eventually poses a threat to community structure and affects microbial population dynamics. Certain microbial interactions are observed in matrixes such as metabolite exchange, physiochemical changes, metabolite conversion, signaling, and genetic exchange resulting in a genotype selection [178], but no studies have reported their interactions in lake ecosystems. Braga et al. [178] clarified that microorganism–microorganism interaction depends on more than one factor; species diversity and microbial population have a high level of functional redundancy [178]. Microbial interaction occurs by the transmission of molecular and genetic information. Also, the function of microbial interaction includes secondary metabolite transfer, biofilm formation for adaptation to environmental stress factors, and cellular transduction signaling [178]. The result of microbial interaction is adaptation and specialization, which allow the occupation of different niches by reducing factors such as biotic and abiotic stress or exchanging growth factors and signaling [178]. Therefore, understanding these threats and taking suitable measures to mitigate them will be required to restore microbial diversity, human health, and ecological balance.

2.9 Future prospective

- It is necessary to study the microbial biodiversity of the microbial communities of the African lakes on a larger scale.
- It is important to involve DNA metabarcoding and metagenomics to solve the problems of microbial community compositions in the African lakes through exploring uncultured microbes and their ecological role in the lakes.
- It is important to clarify the mechanisms of microorganisms in the African lakes and how they adapt to severe future stresses at the molecular level.
- Based on this information, the African lakes can be monitored and maintained.
- Finding solutions to address future threats to microbial diversity in the African lakes.

2.10 Conclusion

The microbiomes of the African lakes are one of the most important factors affecting natural ecosystem functioning. The microbial content of the lakes comprises bacteria, archaea, unicellular eukaryotic organisms, protozoa, fungi, and viruses. Thus, it is important to study the microbial diversity, taxonomical classification, and factors that may change the diversity. The factors that influence the composition of microbial communities may be extrinsic or intrinsic. The intrinsic factors in the lakes include biotic interactions (predation, parasitism, competition, and symbiosis), salinity, pH, nutrients available in the water, and barriers caused by lake stratification. The extrinsic factors include land-use change, water pollution due to anthropogenic activity, and global warming. Of the intrinsic factors, salinity seems to be the principal factor determining microbial diversity. The threats affecting microbial diversity include the planting industry, pesticides, heavy metals, fish aquaculture, and stock-farming activity. Changes affect bacterial and archaeal communities' growth, survival, and reproduction, which subsequently change population and community growth.

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CHAPTER 3

Genomics of microbial communities in African lakes

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3.1 Introduction

Extreme habitats are described as having conditions that make it difficult for typical living things to survive, and microorganisms that live in these environments are referred to as extremophiles. Although certain extremophiles may survive in extremely harsh environments, for the most part, they require these conditions for optimum growth. Our knowledge of microbial diversity and ecology has been greatly influenced by molecular methods for characterizing microbial species and assemblages. Comparing the sequences of the ribosomal RNA (rRNA) gene, in particular, has revolutionized the way that microbial evolutionary links are understood. A logical extension of this method was the direct extraction of phylogenetically relevant genes (like rRNAs) from naturally existing microorganisms, which marked a significant advancement in microbial biology and allowed for a closer examination of the natural microbial environment [1], similar to how advances in genome sequencing technologies have greatly impacted microbial research. This chapter provides an overview of the results of the lake's molecular microbial community investigations, microbial ecology study, and diversity analysis.

Genomic technologies are now also extending their influence on microbial ecology and environmental science. Advances in genome sequencing technologies have similarly had a great impact on microbial biology, providing new insights into microbial evolution, biochemistry, physiology, and diversity. A unique geochemical characteristic of soda lakes induces the presence of several ecologically and commercially significant bacteria. The most significant soda lakes in Africa are located in

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Kenya, Lake Bogoria, Lake Nakuru, Lake Elmenteita, and Lake Magadi; Ethiopia, Lakes Beseka and Arenguadi. The dominant microbiota in a lake is directly determined by its geological and chemical characteristics; however, the preexisting microbial population may also contribute to the development of these characteristics.

As suggested by the name, these lakes are rich in soda (sodium carbonate, Na_2CO_3, or complexes of this salt), which is a product of evaporative concentration. There are some characteristics that all of these soda lakes have in common, and it appears that everyone agrees that the absence of alkaline earth cations, Ca^{2+} and Mg^{2+}, in the rocks of the water catchment region is the most significant aspect. The bacteria are obligatory alkaliphilic or alkali-tolerant, according to systematic investigations, and many of them appear to represent distinct alkaliphilic lineages within recognized species, suggesting they may evolve independently within the alkaline environment. Chloride ions (Cl^{-1}) continue to dominate in the solution as evaporative concentration increases. Because of this, the trona beds and concentrated lagoon brines of the Magadi-Natron basin have a very distinct population of prokaryotes than lakes in the East African Rift Valley which have more dilute lakes [1].

The habitats that are harmful to living things are referred to as extreme environments. Physicochemical characteristics of these environments include salinity, pressure (0.1 MPa), nutrient content, pH (acidic pH 5.0, alkaline pH 9.0), temperature ($>40°C$ and $<5°C$), salinity (35‰), as well as radiation. The species that are thriving beneath these extremes are known as extremophiles. Another crucial characteristic of alkaline lakes is salinity. The microbial community composition of the hypersaline, alkaline lakes differs significantly from that of the more diluted lakes. The ability to cultivate microorganisms is undoubtedly a significant barrier to a thorough understanding of the microbial communities in soda lakes. The remoteness of these extremely severe environments does not help this business.

The preliminary research shows that more has to be learned about the soda lake's microbial diversity, community structure, and individual organisms' functions. Soda lakes are highly alkaline aquatic environments. Their terrestrial analogs, soda deserts, are their dried-out remains and are frequently transient. Although soda lakes are found throughout the world, they are primarily restricted to (sub)tropical latitudes in the interiors of continents or areas in the rain shadow. Due to their hostile nature, they are frequently away from the major hubs of human activity, and possibly

as a result, they have been little researched. Lakes and solonchaks in the Central Asian (Siberia) steppes and the Rift Valley in eastern Africa have received the most research.

Latest metagenomics investigations collectively shed fresh light on the metabolic adaptability of microbes in aquatic sediments, as well as their functions in carbon and nitrogen metabolism, the biogeochemical cycles of sulfur, and how they have been changed to fit each unique environment. Hardly any freshwater lake sediment surfaces have undergone metagenomics research. Researchers have only focused on the taxonomic reconstruction of ecological time series from preserved lake sediments and developing methods to target microbial subpopulations. Metagenomics is now being used in an increasing number of environmental investigations to overcome these constraints [2–4]. Through the use of a molecular technique called metagenomics, hundreds of genes from many individual species can be characterized in a sample [5,6]. It generates information on functional potential and offers a comparatively objective assessment of community organizations.

The metagenomic analysis is an extremely difficult process as shown in Fig. 3.1. Not all of the gene sequences may be present in the current metagenomic sequence database [7]. Because they need phylogenetic ancestral connectivity between their functional gene and taxonomic classification, researchers approach metagenomic libraries.

In targeted metagenomics, ambient DNA is first extracted, and then, the gene of interest is amplified using PCR-amplified primers. With the aid of next-generation sequencing technology, these amplified genes are further sequenced. The effectiveness of reading thousands of small rRNAs per sample and simultaneously probing hundreds of samples make next-generation sequencing popular [8–11]. Targeted metagenomics has advantages of its own since it enables detailed comparisons of changes in microbial diversity before and after a disturbance and offers a better understanding of the microbial taxa present in the sample sets [12]. The shotgun metagenomic approach, which uses genomic sequencing to probe an ecosystem's entire genetic complement, is another form of metagenomics. This technique involves extracting DNA from the sample,

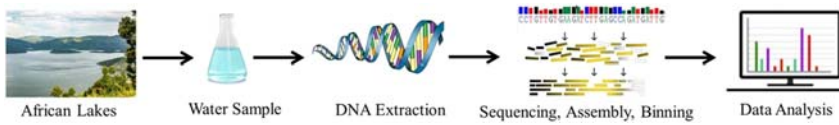

Figure 3.1 Basic metagenomics protocol.

fragmenting it to create genomic sequencing libraries, and then determining the genomic composition of the sample.

Shotgun metagenomics identifies a microbial community's functional potential but is frequently constrained by the depth of the sequencing. To obtain entire genes, environmental samples must undergo deep sequencing. This is additionally necessary for the thorough evaluation of an environmental sample's functional potential. But the shotgun metagenomics method's primary flaw is that it primarily analyzes the genomes of microorganisms that are abundant in the environment while excluding the least abundant members of that community.

Limited research has been done on the microbiological quality of the sediments in developing nations and how this relates to various land uses, even though numerous studies have been done to evaluate the quality of environmental waters in many countries. To determine how diverse land uses impacted bacterial diversity and to confirm the functional classes of the bacterial communities that are associated with human diseases, a proper study must be assessed the diversity of bacteria in water and sediments in some heavily used South African rivers. The biggest anoxic freshwater body on Earth's surface, Lake Tanganyika (LT), is a tropical freshwater lake. Rich animal richness can be found in the mixed oxygenated surface waters of LT, which float above a constantly anoxic stratum. Very little information is available about the microorganisms that live in the 1470 m deep water column of LT and how they contribute to the cycling of nutrients, which has an impact on the production and operation of ecosystems. A model for incorporating aquatic microbial genomics in the representation of tropical freshwater lakes is thus provided by using genome-resolved metagenomics and environmental analyses to link specific taxa to important biogeochemical processes across a vertical gradient in LT. This is especially true in the light of climate change and is predicted to rise in stratification and anoxia in freshwater lakes [13].

The use of molecular-based approaches has the prospective to advance our understanding of how anthropogenic stresses affect lake ecosystems. Numerous geochemical cycling processes in lakes involve microbial populations, and a better knowledge of their roles could help direct more focused remedial activities. The functional efficiency of whole microbial communities can now be determined thanks to recent developments in metagenomics. Functional variations in communities across land use, eutrophication, and pollution gradients have been demonstrated by metagenomic research. The microbial communities' potential for a function was examined using metagenomics.

3.2 Molecular ecology as an efficient tool for studying lake microbes

A lake ecology depends on the unique microbial communities of prokaryotic taxon groupings known as bacteria and archaea. To learn more about bacterial/archaeal diversity, the makeup of microbial genetic resources, patterns of microorganisms, the functional significance of microbial diversity, and the regulation of microbial diversity, studies on bacterial/archaeal communities within endorheic lake ecosystems are crucial. Prokaryotes are crucial for the breakdown of organic matter into nutrients that are used as food by other species and for regulating the lake's water quality. They are crucial for maintaining equilibrium between respiration and photosynthesis in the oxygen, carbon, sulfur, and metal cycles that occur naturally.

The variety, abundance, composition, distribution, dynamics, and the existence of microbial communities within these ecosystems are all impacted by a wide range of abiotic and biotic variables. According to reports, environmental conditions encourage the diversity of microorganisms. The hydrogeology of tropical endorheic lakes varies significantly as a result of climate change. These lakes go through phases where they are filled with freshwater, turn salty, or even completely dry out due to evaporation and human activity. Within saline–alkaline lakes, prokaryotic communities derived from water and dry sediments play a significant role. However, only a small number of prokaryotes have been thoroughly examined because of the intricacy of the culture-dependent approaches.

In East Africa, the Great Lakes are the largest and most amazing freshwater system on the planet. Much of the amazing biological diversity found in the lakes was able to emerge with evolutionary radiation and explosive speciation due to intrinsic biological variables and external ecological conditions [14]. World distribution of surface freshwater (wetlands, lakes, and rivers), by highlighting the high proportion found on the African continent, is shown in Fig. 3.2.

A significant component of the biosphere is made up of microorganisms. They make up around 60% of the earth's biomass, are at least two to three orders of magnitude more numerous than all of the plant and animal cells put together, and are also incredibly diverse. Due to their important roles in biogeochemical cycles and food webs, this considerable representation enables them to be seen as the planet's controllers.

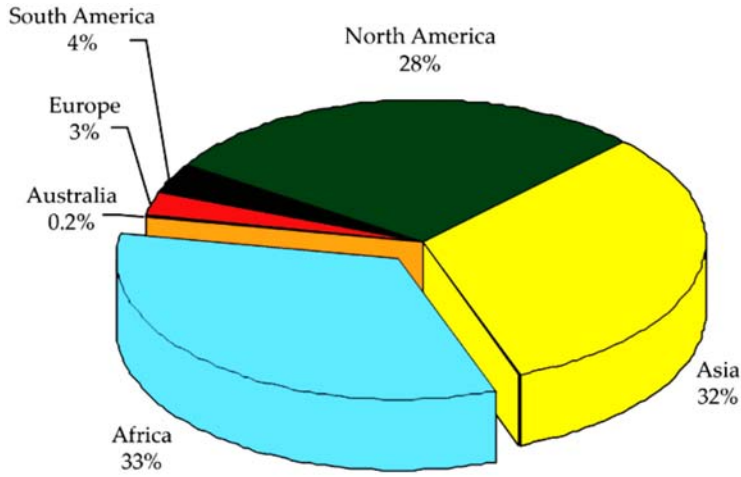

Figure 3.2 World distribution of surface freshwater (wetlands, lakes, and rivers) highlights the high proportion found on the African continent [15].

Microorganisms belonging to the three distinct phylogenetic domains, Archaea, Bacteria, and Eukarya, descended from the same progenitor. They fall under the so-called "three-domain system" genetically. These three categories of microbes have been utilized by researchers to examine aquatic environments over the years. Modern molecular biology techniques have replaced traditional culture techniques as the primary techniques employed in microbial ecology. These molecular biological techniques, which are based on the 16S and 18S rRNA genes, showed that several potential divisions were not amenable to study using conventional culture methods [16]. Concerning a thorough characterization of microbial communities in a given environment, this statement highlights the importance of molecular approaches in microbial ecology. The cultivable fraction only accounts for around 1% of the total number of prokaryotic species present in a given sample; therefore culture techniques would not be able to examine microbial communities. Denaturing gradient gel electrophoresis (DGGE) is one of the many fingerprinting techniques that have been developed to address this issue.

Although essential for studying microbial communities, genetic fingerprinting techniques cannot directly demonstrate how functioning a community is. Only research-based RNA analysis or culture techniques might provide assurances on the functionality of genes encoded in a microorganism's genome. However, based on the activities encoded in genomes of

closely related organisms, the functioning of a detected organism's genome may be predicted [17]. Several genotypes that may be active in the sulfur cycle have been found in the anoxic strata of soda lake. The distribution of microbial activity in anoxic sediments is mostly influenced by the sulfate ion. Through cellular enumeration, using flow cytometry, chlorophyll quantification (photosynthetic microorganisms), and microscopic analysis, the vertical distribution of heterotrophic and photosynthetic microorganisms has been evaluated (unicellular and filamentous photosynthetic microorganisms) [18]. To comprehend microbial diversity, microbial genetic resources, patterns of microorganisms, and the regulating function of microbial diversity, a study on bacterial and archaeal communities within endorheic lake ecosystems is essential [19]. Microorganisms are the largest source of untapped biodiversity, and despite several studies as shown in Table 3.1 of soda lakes and prokaryotic communities in Kenya, exploitable microbial diversity is not exhaustive [21].

Table 3.1 Previous researches to elucidate microbiology of soda lakes [20].

Major studies	Soda lake
Cultivation of alkaliphilic bacteria and archaea	Rift Valley soda lakes
Molecular survey of bacterial and/or archaeal diversity	Rift Valley soda lakes, Mono Lake
Investigations on methanogenesis and methanotrophy	Big Soda Lake, Mono Lake, Transbaikal soda lakes
Characterization of microbes associated with an arsenic cycle	Mono Lake, Searles Lake
Characterization of microbes associated with a sulfur cycle	Several African lakes
Characterization of microbes associated with C1, cycle	Tuva and Transbaikal soda lakes, Rift Valley soda lakes, Lake Hotontyn, Mono Lake, Lonar Lake
Identification of active microbes associated with C1, cycle	Transbaikal soda lakes, Lonar Lake
Investigations on the nitrogen cycle and the characterization of microbes or photoautotrophic bacteria associated with this cycle	Big Soda Lake, Mono Lake, Siberian soda lake, Mongolian soda lake, Rift Valley soda Lake
Characterization of the diversity of chemo or photoautotrophic bacteria	Mono Lake, Kulunda, Soap Lake

3.3 Genome size and GC content

The amount of same-strand guanine + cytosine sites divided by the length of DNA sequence, known as the "GC content," varies significantly between different bacterial species, ranging from less than 13% to more than 75% [22]. Even within a single genome, nucleotide composition can vary significantly [23]. Although the precise reasons for these GC differences, both within and in between species, are unknown, several elements are connected to evolutionary history. Genome size, oxygen, and nitrogen abundance, also the uptake of foreign DNA, including conjugation, transformation, and transduction, are factors that have some correlation with the genomic base composition of bacteria. Although this is a topic of discussion, there are few indications for a function of growth temperature in influencing the GC content of specific genes. Optimal growth temperature may also affect the composition of genomic DNA [24]. The elements that might affect the G + C content have been analyzed using a variety of methods, including traditional microbiology and in silico analysis employing evolutionary studies to try and find similarities between organisms with different G + C contents. The probable association between an organism's genome size and genomic G + C concentration was one of the simplest anticipated relationships. Initial studies that relied on measuring genome size had issues since DNA was sheared during the extraction procedure, potentially resulting in underestimations of the true size. This issue persisted despite the development of pulsed-field gel electrophoresis, which significantly eliminated the possibility of DNA fragmentation [25].

3.4 Diversity in the microbial genome in relation to the lake environment

The polymerase chain reaction (PCR) and DNA sequencing methods have gained popularity in recent years for analyzing the composition of an ambient microbial community without the requirement for or bias of culture. These methods use variations in rDNA molecules to distinguish between the microbes that belong to a specific niche or community. Microbial DNA from the sample can be isolated for the phylogenetic study of the microbial communities found in environmental samples. The 16S rDNA can then be amplified using the appropriate primers, PCR, and clonal libraries can be created. Genomes from single-cell sequencing,

metagenomic assembly, and isolate sequencing are all being produced more quickly and, as a result, are becoming more readily accessible through public resources.

In microbial genomics, phylogenetic and associated taxonomic categorization is essential for placing genomes in context without prior phenotypic knowledge, as well as for figuring out their genetic uniqueness and genotype–phenotype correlations. Reconstructing the entire microbial tree of life is essential for comprehending evolutionary relationships at the broadest scale, and in studies of microbial communities, such a reference can be a key link between novel sequences and bacteria that are important for human health or the environment. The necessity to classify newly sequenced genomes and metagenomic assembled genomes into the microbial taxonomy and phylogenetically characterize them about the nearest relatives is thus a requirement for many contemporary microbial genomic projects, regardless of scale. As cultivation and sequencing grow more affordable and acquiring metagenome-assembled genomes (MAGs) gets more efficient, microbial genomes are becoming more and more accessible. Thus, phylogenetic placement algorithms must be effective and sensitive from closely related strains to divergent phyla to contextualize thousands of genomes [26].

Various natural and artificial influences, such as changes in temperature and light, have an impact on the microbial communities within lakes, especially shifts in nutrient concentrations commonly associated with diffuse pollution related to land use change [27,28]. Bacteria are prevalent in lakes and play a vital role in the cycling of nutrients, breaking down both organic and inorganic substances [29–31]. These substances can build up in lake sediments, as environmental stress on microbial communities, and, consequently, modify the microbial composition of the lake [32]. It has been difficult to assess the activities of microbial communities up until recently, and the majority of molecular research has concentrated on characterizing their composition using methods like metabarcoding [33]. Although metabarcoding is a very effective technique, it has drawbacks such as taxonomic biases that can be introduced by PCR primers [34] and the fact that it does not reveal what metabolic processes can organisms carry out [6].

Lake Olbolosat is an endangered freshwater lake in Central Kenya, Africa. It is a drainage lake that was formed by downwarping in Kenya outside the Rift Valley. The freshwater lake supports wildlife and livestock. Even in the salterns at Magadi, the most extreme environment in

terms of alkalinity and salinity, unexpected variety was found when the sequences of PCR-amplified 16S rRNA genes from DNA taken on-site were examined. Sequence signals from microorganisms that are phylogenetically related to the cultured haloalkaliphilic archaea but different from it have been discovered. With only 76% identity to known archaea, two of the 16S rRNA clones showed low relatedness to published species, designating them as belonging to a highly branched clade of the *Euryarchaeota*. The extreme halophilic archaea and methanogens share several characteristics, according to signature sequence analysis, but there is no clear connection to any of the three main methanogen groups [35].

Using a culture-dependent methodology, Kiama et al. [36] investigated the isolation and characterization of bacteria from Lakes Olbolosat and Oloiden, where there is still an undiscovered resource of microorganisms from lake sediments. The diversity of bacteria in Lake Oloiden, a saline–alkaline lake, and Lake Olbolosat, a freshwater lake, has been studied. Thirty-five isolates have been recovered from Lake Olbolosat and 25 isolates from Lake Oloiden, out of the 60 that were found in sediment and water samples. Both lakes had microbial counts, with a maximum value of 1.75×10^5 CFU/mL. Fifty-eight isolates were gram-positive and two were gram-negative, with a significant difference between bacterial density and sample locations ($P < .001$, $F = 6.667$). Fifty-five isolates, of which three were cocci and two were filamentous, had a rod shape. Optimal growing conditions for isolates included a pH range of 6–10, a temperature range of 25°C–30°C, and a salinity range of 0%–5%.

The distribution of bacteria and archaea in the meromictic tropical Lake Kivu, East Africa, was investigated by İnceoğlu et al. [37]. In contrast to its deep waters, which contain enormous concentrations of dissolved CO_2 and CH_4, Lake Kivu's surface waters have unexpectedly low levels of CH_4. To gain knowledge of the ecology of the microbes in Lake Kivu, the compositions of the bacterial and archaeal communities (BCC and ACC, respectively) were studied using 454 pyrosequencing of 16S rRNA gene fragments. The stratified distribution of microbial communities may be caused by the vertical distribution of electron donors and acceptors in the chemically stratified water column, which suggests well-defined functional specialization. The anoxic zone of Lake Kivu, which had significant concentrations of bacterial sequences linked to uncultured and inadequately characterized phyla, showed the greatest microbial richness. Consequently, anoxic settings have been represented in databases, and unknown taxa have been presented. The diversity of microbes is

divided into two fractions: abundant species and rare species. Over time, abundant species remained more stable than rare species. Anoxic waters may have interactions in carbon and sulfur cycles when rare candidate divisions (e.g., OP3, WS3, GN02) co-occur with sulfur-oxidizing *Epsilonproteobacteria*, sulfate-reducing *Deltaproteobacteria*, and hydrogen-oxidizing *Dehalococcoidetes*.

Four tropical East African Great Lakes were the subject of research by Fermani et al. [38] on microbial eukaryote assemblages and possibly new diversity. Natural resources in the East African Great Lakes are heavily utilized by the countries that surround them. Pelagic processes, in which microorganisms play a crucial role, are what drive ecosystem functioning in those lakes; nevertheless, little is known about the diversity of Protista. By sequencing the 18S rRNA gene, small eukaryotes (<10 μm) communities have been screened in the surface waters of four African Lakes, Kivu, Edward, Albert, and Victoria. Additionally, two sites in the meromictic Lake Kivu were vertically examined. In 779 operational taxonomic units (OTUs) spanning 11 high-rank lineages, a high Protista diversity, with *Alveolata* (31%), *Opisthokonta* (20%), and *Stramenopiles* (17%), has been represented as supergroups. While depth had a significant impact on the Protista community in Kivu, with a higher contribution of heterotrophic organisms, surface Protista assemblages were related to conductivity and productivity gradients. It has been found that approximately 40% of OTUs have low similarity ($<90\%$) to sequences reported in public databases. These are mostly found in the deep anoxic waters of Kivu, suggesting a high level of novel diversity. Surface sediments from three lakes with various trophic levels have been studied by Laura et al. [39] for the presence of microbial communities and their potential for use. Metabarcoding and metagenomics have been used to analyze the nutritional and elemental makeup of surface sediments. The lack of a clear gradient in the number of nutrients in the surface sediments compared to the results from water chemistry monitoring likely reflects the influence of other lake parameters, particularly depth. Different bacterial community compositions and functional potentials have been recorded among lakes, according to metabarcoding and metagenomics. The energy metabolism pathways of oxidative phosphorylation and photosynthesis differ from one another. The presence of cyanobacteria in two of the three lakes and changes in the community composition were most likely responsible for this. The lakes have the largest concentration of xenobiotic routes, such as those involving polycyclic aromatic hydrocarbons. Based on these

findings, microbial metagenomics can be used to gain insight into lake trophic status differences.

Deep-discrete metagenomics in Lake Tanganyika has been applied to study microbes' roles in biogeochemical cycling. The researchers collected 523 metagenome-assembled genomes (MAGs) from 34 bacterial and archaeal phyla, including several rare freshwater species. In the oxygenated mixed upper layers, they found predominantly freshwater species, while in the deep anoxic waters, archaea and uncultured candidate phyla were prevalent. Nitrogen and sulfur cycling were significant in MAGs from anoxic environments, which suggest microbial recycling of nutrients and greenhouse gases in the productive surface layers [13]. The study provides a model for incorporating aquatic microbial genomes into tropical freshwater lakes in the light of climate change-induced stratification and anoxia. Jones and Grant [40] studied the microbial diversity and ecology of the Soda Lakes of East Africa. Soda lakes are highly alkaline aquatic environments where evaporative concentration results in carbonate as a major dissolved anion. Prokaryotic photosynthetic primary production is presumably the main driver of all nutrient recycling in these lakes because it occurs in such highly productive conditions. In general, the main trophic groups involved in the carbon and sulfur cycles have now been recognized. Even though there are many similarities to athalassohaline salt lake systems, the microbes are obligatory alkaliphilic or alkali-tolerant, and many seem to represent different alkaliphilic lineages within recognized taxa. Microbes are also obligatory alkaline-tolerant, according to systematic studies. Chloride ions take over in solution as evaporative concentration keeps going. As a result, compared to more diluted lakes elsewhere in the East African Rift Valley, a very distinct community of prokaryotes is present in the trona (sodium sesquicarbonate) beds and concentrated lagoon brines of hypersaline lakes (Magadi-Natron basin) [40].

To determine the functional classes of bacterial populations representing human diseases, Abia et al. [41] evaluated the diversity of bacteria in the water and sediments of a highly used South African river to learn how varied land uses have affected bacterial diversity. The Apies River's informal settlement had the greatest impact on the bacterial variety in the water and sediments, according to the study of metagenomic data, which showed that there was a large diversity in the microbial communities connected with the varied land uses. The most prevalent phyla were the *Proteobacteria* (69.8%), *Bacteroidetes* (2.7%), *Cyanobacteria* (4.3%), and *Actinobacteria* (2.7%); the most often observed classes were

the *Alphaproteobacteria, Betaproteobacteria*, and *Anaerolineae*. Additionally, compared to the water column, the bacterial populations in the sediments were more diverse and abundant. The bacterial communities' functional profiles showed a correlation with several human diseases, including cancer pathways. In South Africa's Limpopo Province, a dolomite stone mine was alleged to have severely contaminated the groundwater. Metagenomic techniques have been applied for monitoring the microbial treatment of water contaminated with hexavalent chromium. An environmentally friendly method of groundwater treatment was used to remove chromium pollution to stop the contamination from the site from spreading and causing environmental issues. Up to 6.49 mg/L of Cr61 may be effectively extracted from groundwater using this method. The metal-reducing microbial communities used in the study were *Enterobacter cloacae, Flavobacterium* sp., and *Ralstonia* sp., and they achieved a 100% reduction. This study demonstrates that the use of microorganisms in bioremediation can successfully remove heavy metals like chromium (VI) [42].

Egypt's Lake Qarun (Moeris) is currently suffering from significant water contamination. Major issues include the growing water resource contamination of Lake Qarun and its impact on both human and aquatic health. Water is essential for the survival of animals, including humans and aquatic life; hence, it is crucial to study the microbial communities of Lake Qarun. The tools for amplicon and shotgun genome sequencing allowed for a clearer comprehension of the interaction between the microbiota and the host. Using 16S rRNA high-throughput amplicon sequencing, it was possible to analyze bacterial diversity and abundance in Lake Qarun under various pollution conditions [43]. To understand the microbial dynamics in the lake under diverse pollution scenarios, the study introduced uncultured microbial diversity profiles [43].

Various proportions of five bacterial phyla dominated the bacterial communities in Lake Qarun. Furthermore, the metagenomes of bacterial communities predicted by PICRUSt revealed significant functional gene families involved in metabolic, environmental, genetic, and cellular processes. Among the 18 specific KEGG pathways involved in xenobiotic biodegradation and metabolism, benzoate degradation had the highest average relative abundance, followed by aminobenzoate degradation. As a result of the collected data, different sources of pollution in Qarun Lake affect bacterial populations and biota, which could negatively affect human health [43].

Researchers in Egypt studied the diversity of bacterial communities in the water and sediments of the three main lakes of the Wadi El Natrun [44]. New cellulose sequences can be carefully chosen for high-throughput expression via metagenomic sequencing. Microorganisms from Wadi El Natrun are known to produce cutting-edge natural chemicals. As a consequence, a new cellulose gene was cloned utilizing a functional metagenomic method employing ambient soil samples from Wadi El Natrun. Samples under extremely saline and alkaline conditions have been chosen to search for a prospective enzyme that can withstand the demanding conditions. A metagenomic technique has been applied to clone useful recombinant cellulose(s) from the Wadi El Natrun soil in Egypt. To build a library, the extracted DNA was cloned into competent *Escherichia coli* DH5. The molecular and functional properties of the cloned gene have been examined. Metagenomics software has been used to help in screening the range of uncultured bacterial genomes for various types of gene coding catalysts that have not yet been recognized. This approach gives immediate access to bioactive candidates and comprehensive microbial research genomes [44].

The phylogenetic makeup of the intestinal flora of tilapia fish living in Lake Nasser, Egypt, encompasses all domains, eukaryotes, bacteria, and archaea, using high-throughput rRNA gene metabarcoding. Metagenomic DNA was extracted from fish gut contents and used in PCR and next-generation sequencing to determine the eukaryotic 18S and prokaryotic 16S rRNA genes [45].

3.5 Metagenomics of microbial communities

The Great Lakes of Africa are a collection of lakes that are located in and close to the Great Rift Valley. One of the most endangered water systems in the world is the Great Lakes. Large African rift lakes have historically been home to a vast amount of wildlife. Freshwater lakes in the Western Rift Valley are home to a staggering variety of unique species. The majority of lake bacteria composition, 99% of total bacterial content, has yet to be discovered, with only about 1% of them having been recognized. Metagenomics is the only way to comprehend the genetics of bacteria that cannot be grown. Understanding the genomes of bacteria that cannot be cultured is theoretically challenging, but metagenomics helps to overcome this and allows for the complete disclosure of the microbiota's information [46].

Targeted metagenomics and shotgun metagenomics are two different types of metagenomic methods. Targeted metagenomics, also known as microbiomics, makes use of a single gene diversity to identify the whole complement of a particular gene in the environment. It is mostly utilized for the in-depth examination of phylogenetic analysis and the relative abundance of a particular gene in an environmental sample.

The sequenced metagenomes were acquired, according to Vavourakis et al. [47], from four surface sediments in Siberian soda lakes with a pH of 10 and a salt content varying from 70 to 400 g/L. The majority of the retrieved 16S rRNA gene sequences contained bacteria, even in salt-filled lakes. The majority of OTUs were assigned to uncultured families. A total of 871 metagenome-assembled genomes (MAGs) representing more than 45 phyla have been reconstructed, and the first extremophilic members of the candidate phyla radiation (CPR) have been identified. Novel dominant lineages were found within previously well-characterized functional groups involved in carbon, sulfur, and nitrogen cycling [47].

A metagenomic sequencing technique was used to compare the composition and functional patterns of microbial communities from two soda lakes in the subregion Nhecolandia, in the state of Mato Grosso do Sul, Brazil. There is a difference between these two lakes in that Salina Verde has permanent cyanobacterial blooms and Salina Preta has no record of cyanobacterial blooms. Anabaenopsis elenkinii dominated the Salina Verde bloom. Abiotic parameters such as pH, turbidity, and dissolved oxygen were altered by this cyanobacterium, which, in turn, altered the structure of the microbial community [48].

3.6 Application of microbial genetics

Microbial genetics has historically been a field of study in fundamental science due to the many properties that bacteria have that allow the study of evolutionary processes. Their fast generation time, haploid genome, ease of culture, and abundance make this kind of research conceivable. They do, however, come with some complications; clonal and asexual reproduction, recombination, and gene conversion often make it difficult to conclude evolution. Microbes are perfectly suited for biochemistry and genetics research, and they have greatly advanced these fields of knowledge as shown in Fig. 3.3. As microbial agents are involved in many human diseases, implications of both microbial and human genetic variations have also been productive areas for research. Numerous molecular

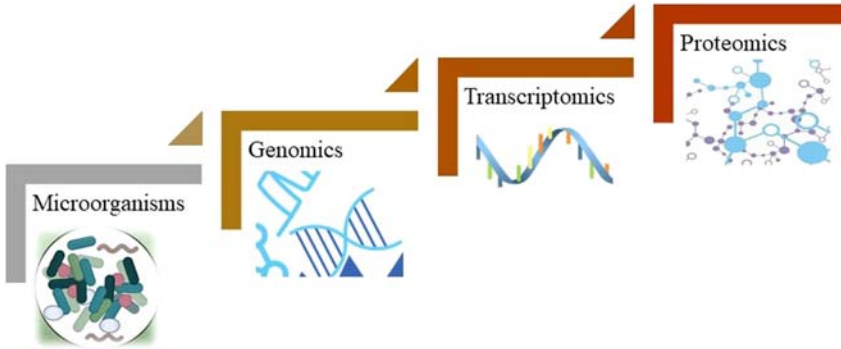

Figure 3.3 Microbial genomics analysis.

biological techniques that are also employed for research have emerged from microbial studies due to the impact of the disease.

Methods were developed to put genes onto bacterial plasmids and take advantage of their quick replication to build biofactories for the target gene. These genetically altered bacteria can produce interferons, human growth hormone, insulin, and blood clotting agents, among other medications. These biofactories are frequently much less expensive to operate and maintain than conventional methods of producing pharmaceuticals. With just a few basic raw materials and the right conditions, they can produce large quantities of products, like millions of little pharmaceutical machines. The usage of the human insulin gene alone has had a huge impact on the medical field. It is thought that biofactories may hold the key to dramatically reducing the price of expensive yet vitally important pharmaceutical chemicals.

Microbiology and genetic engineering both include the field of microbial genetics. Microorganisms are studied in microbial genetics for a variety of reasons. Bacteria and archaea are the microbes that are seen. Additionally, several protozoa and fungi are used as research subjects in this area. Studies of genotype and expression systems are part of the study of microorganisms. The study of processes and pathways that are similar to those in humans, such as drug metabolism, is another use of microbial genetics. The transfer of hereditary traits in microbes is the focus of microbial genetics. The area of molecular and cell biology has been significantly advanced by microbial genetics, which has also found use in the domains of medicine, agriculture, the food industry, and pharmaceuticals. Microbes are ideally suited for combined biochemical and genetic studies

and have been successful in providing information on the genetic code and the regulation of gene activity. The majority of the ecosystem is made up of microbes, which can be found in any location with a temperature that is conducive to their growth and survival [49]. Previous studies indicated that the Antarctic and Greenland glaciers have a massive reservoir of microbial variety. However, $\approx 99\%$ of these are not cultivable in a lab setting using conventional techniques like agar plate medium or broth, which are used to culture bacteria [50].

Genomes of uncultivated microorganisms are a useful resource for discovering novel enzymes with commercial potential. Metagenomics has been proposed to discover new cellulase and hemicellulases from bacteria, particularly inventive bacteria. This approach gives us immediate access to bioactive candidates and comprehensive microbial research genomes [51]. Without the requirement for separation or microbial cultivation, metagenomics is the study of uncultivable bacteria through the direct isolation of DNA from their habitats [52]. Metagenomic gene banks (libraries) are created by cloning the metagenomic DNA directly isolated from environmental samples in suitable hosts with the aid of cloning vectors to analyze the ecology and metabolic profiling of the microbes and identify novel bioactive molecules encoded by their genes [53]. Therefore, metagenomics can be referred to as a technique that is independent of culture and examines the functional and/or sequence-driven assessments of the whole genome of the microbial diversity present in that particular environmental niche. An emerging technology is shotgun metagenomics.

Studies on bacterial/archaeal communities within endorheic lake ecosystems are essential to understanding bacterial/archaeal diversity, the composition of microbial genetic resources, patterns of microorganisms, the functional significance of microbial diversity, and the management of microbial diversity [19]. Identifying the steps that must be taken to safeguard and restore each lake and underlining the current situation of each lake are essential tasks. These vast lakes all have the same characteristics, even though each of them is unique. These lakes are among the largest and/or deepest on the planet; some of them are quite old, and their sediments offer priceless repositories for paleolimnology and opportunities for the reconstruction of past climates. The deepest lakes remain stratified all year since they are in the tropics and enjoy year-round summer, albeit there is a large seasonal fluctuation in the depth of the mixed layer (surface temperature, winds). They support a large amount of biodiversity.

During the past decades, the largest lakes of the Rift (Victoria, Tanganyika, and Malawi) have been the focus of science, both for their outstanding characteristics and also for their many problems. The need for their conservation has been highlighted. In contrast, the smaller Rift lakes have been almost entirely ignored, except Lake Kivu, whose results are available. It is still lacking complete and up-to-date studies of the limnological and plankton systems of some lakes (Edward and Albert), which are vital to the local environment [54].

Five "soda" or alkali lakes can be found in Kenya: Bogoria, Elementaita, Magadi, Nakuru, and Turkana. A Global Environment Facility (GEF)-funded pilot project that focuses on Lake Bogoria and Lake Magadi (the most alkaline lake in Kenya) and is run by UN Environment in collaboration with the Kenya Wildlife Service and several academic and research institutions in Kenya runs from 2014 to 2018. It aims to ensure equitable benefit sharing with local communities. The project's focus on scientific research with practical applications is important. Partners in the project are creating and producing industrial enzymes with the help of microorganisms from the two lakes [55].

Over 6 months in 2010, bacteria in Lake Nakuru with industrial potential were identified and characterized. The ability of 30 isolates to break down casein, cellulose, starch, and lipid substrates was tested to look into the enzymatic activities of these macromolecules. The ability to hydrolyze two or more macromolecules was demonstrated by 15 isolates, including 8 that could break down starch, 6 that could break down proteins, 5 that could break down cellulose, and 5 that could break down lipids. The genomic DNA of the isolates with the highest potential to break down macromolecules, including LNS08, LNC09, LNC11, and LNC06, was examined. Their identity was found to be closely related to that of the known bacteria *Nesterenkonia lacusekhoensis* (LNS08), *Bacillus agaradhaerens* (LNC06), and *Bacillus* sp. accession no. AB043860.1 (LNC09 and LNC11). As a lipid degrader, *N. lacusekhoensis*, *B. agaradhaerens*, and *Bacillus* sp. accession no. AB043860.1 are all useful. Additionally, *B. agaradhaerens* can be utilized to break down proteins. As a result, Lake Nakuru is a plentiful supply of industrially useful alkaliphilic bacteria [56].

Since the discovery of alkaliphilic bacteria, more than 1000 papers have been published on a range of subjects relating to alkaliphiles and alkaliphilic. The unique bacteria known as alkaliphiles hold a lot of promise for usage in microbiology and biotechnology. The topics that have received the most attention recently are the taxonomy of alkaliphilic

microorganisms, techniques of membrane transport and pH regulation, and extracellular enzymes and their genetic studies. Alkaline enzymes should find new applications in several industrial sectors, including the manufacture of chiral molecules, biological wood pulping, and the increased production of complex enzyme detergents. Alkaliphiles may also make excellent universal genetic resources for uses like the production of signal peptides for secretion and promoters for the hyperproduction of enzymes [57].

3.7 Conclusion

Genomic research of microbial communities can reveal the metabolic capacity of uncultivated microorganisms. Community genomics places a strong emphasis on employing environmental genome sequencing, which is independent of agriculture, to study populations of naturally coexisting species. The technique enables post-genomic functional experiments to be carried out to study the ecology and evolution of microbial consortia. It is possible to directly reconstruct entire or nearly complete genome sequences from environmental components, such as water samples from a lake. It is fundamentally challenging to reconstruct genomes from mixed populations due to population genomic rearrangements, heterogeneity in gene content and sequence similarity, and variability in gene content. The reduction of genetic heterogeneity at the strain level is one of the main goals of community genomic analysis. Comparative genome assembly is an efficient and rapid method to study the relevant environmental population using a sequenced strain as a scaffold. Proteomic and gene expression array-based approaches can be utilized to examine metabolic activity using genomic data from populations. The timing of genetic and environmental change must be synchronized to fully comprehend how adaptation and evolution function.

Metagenomics research has uncovered functional variants, neighborhoods impacted by pollution levels, land usage, or eutrophication. The microbial communities in nutrient cycling water cycles and biochemical degradation habitats have been highlighted in studies on metagenomics. Marker gene sequencing is rapid, and it can be used to determine a community's or taxonomic distribution profile or an organism's fingerprint by using PCR amplification and the sequencing of evolutionarily conserved marker genes. It is possible to link the taxonomic distribution to the metadata gathered from the study's sampling sites. High-throughput

sequencing is used in numerous studies of the diversity and composition of bacterial populations. The potential of these approaches to be applied to study the internal working mechanisms in the lake ecosystem is demonstrated by this small-scale metagenomics study of lake surface sediments. The ability of bacterial colonies to function throughout time can be affected by changes in the paleolimnological setting, which makes it possible to evaluate how changes in the catchment (such as increased agricultural intensification) have affected the functional potential of the lake system.

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CHAPTER 4

From benthic to floating: phytoplankton dynamics in African freshwater lakes and reservoirs

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4.1 Introduction

Freshwater ecosystems are among the most biologically diverse systems per unit habitat volume on Earth, with more than 140,000 species compressed into just 2% of the world's surface area [1–3]. They have inestimable economic, cultural, health, scientific, and educational values [4]. Beyond these ecosystem services, understanding the resident species of an ecological system and how they are being exploited and threatened is vital to conserve important and rare species [5].

Among the biotic components of aquatic systems are phytoplankton (i.e., algae) which are ubiquitous, unicellular autotrophic microorganisms adapted to live partly or continuously in open water and are major primary producers of organic carbon [6]. Phytoplankton species are grouped into 15 legitimate phyla, covering both bacterial and eukaryotic protist domains consisting of a wide diversity of size, morphology, and colony formations [6]. The various phytoplankton groups which are well described in John et al. [7] and Reynolds [6] include Bacillariophyta (diatoms), Chlorophyta (green algae), Chrysophyta (golden algae), Cryptophyta (cyptomonads), Cyanophyta (Cyanobacteria), Euglenophyta (euglenoids), Eustigmatophyta, Glaucophyta, Haptophyta (Prymnesiophyta), Prasinophyta, Pyrrophyta (dinoflagellates), Phaeophyta (brown algae), Raphidophyta, Rhodophyta (red algae), and Xanthophyta (yellow-green algae), with the Chlorophyta and Bacillariophyta being the most diverse groups [8]. These seemingly

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inconspicuous primary producers are extremely abundant and are found throughout the ~1 billion km^3 of living space in aquatic ecosystems [9], and form the base of aquatic food webs, on which almost all aquatic fauna directly or indirectly rely on [10]. In addition, as part of the photosynthetic process of converting light into energy and oxygen which is released into the environment, it is thought that phytoplankton are responsible for more oxygen production than tropical rainforests such as the Amazon (see [11]). Phytoplankton growth depends on the availability of light, carbon dioxide, and nutrients. They, like terrestrial plants, require nutrients such as nitrate, phosphate, calcium, and silicate at various growth levels depending on the species [6]. Phytoplankton help in water purification by taking up nutrients and pollutants [8,12], and transforming nutrients from inorganic to organic forms, for example, converting atmospheric nitrogen into ammonium [13].

Given their basal role in the food web of aquatic systems and their importance in atmospheric processes, phytoplankton are among the most important aquatic biotic group, although their role is often overlooked by the public [8]. The importance of phytoplankton can be seen in fisheries, with African lakes being havens for diverse endemic fish fauna of immense ecological and scientific importance that are dependent on sustained phytoplankton growth [14]. Most African livelihoods are dependent directly on fish and their products for both food and nutritional security, as well as many social, cultural, and economic benefits gained from the biodiverse freshwater resources [15,16]. Any stressor that affects phytoplankton cascades through the trophic chain affecting zooplankton (that graze on phytoplankton) and fish production and ultimately threatening fisheries that sustain the livelihoods of riparian communities [14]. Unfortunately, the poor communities are at the most risk as they depend on the natural resources provided by many African lakes, yet policies around these resources do not benefit them much [14].

Although phytoplankton are integral biotic components of aquatic ecosystems, they can cause serious adverse effects [6,17]. When present in high densities, they can produce "*blooms*" that, on decomposition, deoxygenate the aquatic systems causing fish deaths. This increases the costs of water purification and reduces biodiversity. Some phytoplankton are harmful or toxic as a result of their biotoxins, physical damage they cause, anoxia, irradiance reduction, and nutritional unsuitability [6,17]. Harmful phytoplankton species (e.g., Cyanobacteria) can produce toxins that may alter the physiology of both invertebrates and vertebrates [17]. Dinophyta and Cyanophyta stand out among the particularly problematic phytoplankton

groups in forming harmful blooms and having noxious properties [18]. The proliferation of harmful phytoplankton is mainly caused by changes in local environmental factors, especially nutrients (nitrogen and phosphorous) and temperature which have been shown to regulate phytoplankton community structure ([19,20]; see Box 4.1).

Since phytoplankton are primary producers living in dispersive environments, abiotic and biotic factors exert strong controls on their composition and dynamics [22]. In the African continent with different climatic conditions, phytoplankton assemblages are likely to vary across geographic regions, and species richness has been shown to increase from the poles to the Equator according to the latitudinal diversity gradient (LDG) [23,24]. To date, very little is known about the geographic diversity and structuring of phytoplankton. Although many species of phytoplankton have been identified, the question of where they occur is largely unexplored; in light of the current biodiversity crisis, this represents a serious knowledge gap [25]. As the world's biological diversity faces unprecedented threats, the urgent challenge facing the concerned biologists is to understand ecological processes and biotic components well enough to maintain their functioning in the face of the pressures resulting from human population growth.

This chapter summarizes phytoplankton communities in African freshwater lakes and reservoirs and further assesses the LDG which has been used to explain species variations in other higher taxonomic groups. Current knowledge of phytoplankton species diversity, distribution, and ecology is still too limited to make far-going conclusions on geographical patterns of richness and levels of endemicity among African regions. Knowledge of phytoplankton composition is vital for evaluating the ecological status of freshwater ecosystems and is essential for understanding the structure and dynamics of aquatic ecosystems [26,27]. This chapter also identifies freshwater lakes and reservoirs on the continent that have been heavily impacted by anthropogenic impacts and assesses how these have led to variation and/or changes in phytoplankton communities. Lastly, the chapter assesses how environmental managers and policymakers are addressing eutrophication and climate-based problems as a result of human anthropogenic impacts.

4.2 Phytoplankton studies in Africa

The earliest paper was published in 1879 describing the phytoplankton from Lake Malawi. Since then, the number of articles studying

BOX 4.1 The annual cycle of stratification and phytoplankton growth in Lake Victoria [21].

Lake Victoria although relatively shallow is the second largest lake in the world and the largest in the equatorial regions. Its stratification shows pronounced seasonal changes and can vary between inshore (bay and gulfs) and offshore (open lake) regions. This stratification is important for the seasonal cycles in phytoplankton growth. The pH values range from 7 to 8.9. Distributions of three nutrients, that is, nitrate, phosphate, and dissolved silicone (expressed as silica) had several features in common. High concentrations were generally present near the mud surface and low concentrations in the uppermost 20 m or photosynthetic zone. An appreciable increase in PO_4^{3-} did not occur during the mixing associated with temporary isothermal conditions in January and March 1961. However, there was a pronounced increase during the almost isothermal conditions of August 1961. During most of the year, the exceptionally low concentrations of nitrate ($<10\ \mu g/L\ NO_3$-N) and phosphate ($<7\ \mu g/L\ PO_4$-P) in the surface layers were undetectable. By contrast, dissolved silica was present in relatively large and rather uniform concentrations (4.0−4.5 mg/L) during most of the year. During most of the year, a large part of the offshore plankton was composed of colonial coccoid Myxophyceae. In total, 24 species were counted and these included 5 diatoms, 4 blue-green algae, 7 desmids, 7 chlorococcalean and other green algae, and 1 dinoflagellate. The taxonomy of other algae was not clear, but they resembled *Aphanocapsa elachista* and *Aphanocapsa delicatissima*. These algae and another *Microcystis* sp. were present in July 1961 but could not be readily counted. Diatoms were most abundant in the offshore open lake during the periods of isothermal mixing of the water column. *Aulacoseira agassizii, Aulacoseira nyassensis*, *Surirella nyassae*, and *Nitzschia acicularis* were the most important diatom species. Cyanophyta dominated during periods of thermal stratification with *Anabaenopsis tanganyikae, Anabaena flos-aquae, Planktolyngbya circumcreta*, and *Microcystis wesenbergii* as the most abundant. The green algae were present in low numbers throughout the year as well as the dinoflagellate *Ceratium brachyceros*. Inshore, longer periods of vertical mixing were associated with a more prolonged abundance of diatoms particularly *Melosira* sp. and *N. acicularis*. Although the temperature is an important indirect factor, a direct effect in limiting algal growth is unlikely given the small annual temperature range (approx. 23°C−26°C) in Lake Victoria and the widespread geographical occurrence of most of the species. Another consequence of the equatorial position is the small seasonal variation of solar radiation which is very unlikely to affect algal growth directly. The production of phytoplankton is, however, related to the stratification cycle. The patterns of seasonal occurrence of individual species differ chiefly in the amplitude of variation and the response to increased vertical mixing. Of the nutrients measured, nitrates were the most likely to limit algal growth.

phytoplankton in African lakes and reservoirs has been increasing, with a steady increase, especially after 1997, and with most papers being published in 2004–09 (Fig. 4.1).

Phytoplankton information is available for 51 reservoirs in Africa (Table 4.1). While the number of reservoirs analyzed in this study is minimal, when compared to the number of reservoirs on the African continent, phytoplankton information for major reservoirs is available. Concerning the spatial distribution of the reservoirs, phytoplankton information is available for 19 reservoirs in the northern region; 13 reservoirs in the Equator region; and 20 reservoirs in the southern region (Table 4.1; Fig. 4.2).

4.2.1 Latitudinal diversity gradient of phytoplankton species

Lakes and reservoirs on the African continent are estimated to contain a total of 1633 freshwater phytoplankton species belonging to nine taxonomic groups (Bacillariophyta, Chlorophyta, Chrysophyta, Cryptophyta, Cyanophyta, Dinophyta, Euglenophyta, Synurophyta, and Xanthophyta) (Table 4.2). Bacillariophyta (642 species) are the most abundant taxonomic group while Synurophyta were the least abundant (1 species). However, it is important to note that this might be a huge underestimation of the phytoplankton species diversity as some of the taxa are only identified to genus level making the counts unreliable. There is strong

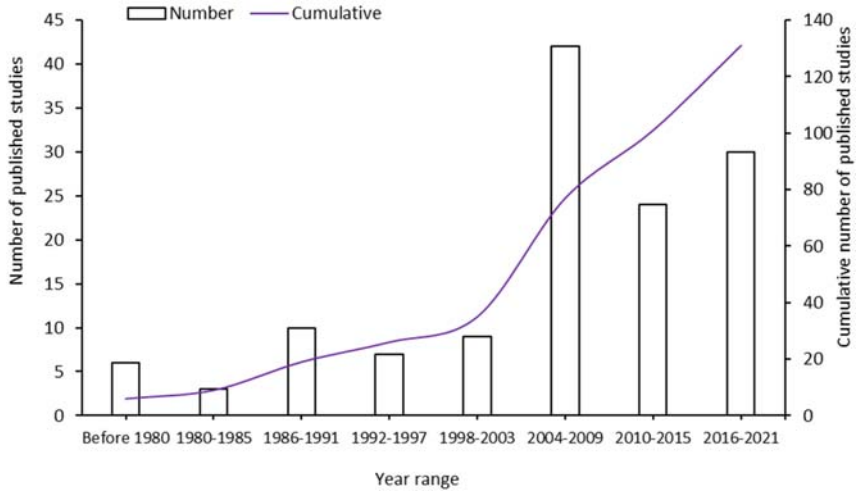

Figure 4.1 The number of papers (and the cumulative number of papers) referring to phytoplankton in African lakes and reservoirs between 1879 and 2021.

Table 4.1 List of reservoirs per geographical location reviewed in the current study chapter. References in this Table are listed in the Supplementary material.

System	Region	References
Lake Mefou	Northern	Ndjouondo et al. [28]
Lake Ahémé	Northern	Olodo et al. [29]
Awba Reservoir	Northern	Akin-Oriola [30]
Lake Ehoma	Northern	Okogwu and Ugwumba [31]
Lake Iyieke	Northern	Okogwu and Ugwumba [31]
Lake Guiers	Northern	Bouvy et al. [32]; Berger et al. [33]; Ka et al. [34]
Lake Qarun	Northern	Fathi and Flower [35]
Lake Lago Biao	Northern	Schabetsberger et al. [36]
Lake Lago Loreto	Northern	Schabetsberger et al. [36]
Lake Tana	Northern	Wondie and Mengistu [37]; Wondie et al. [38]
Lake Chitu	Northern	Ogato and Kifle [39]
Lake Shala	Northern	Ogato and Kifle [39]
Lake Volta	Northern	Karikari et al. [40]
Lake Arenguade	Northern	Belachew [41]
Sennar Reservoir	Northern	Sinada and Abdelrahman [42]
Roseires reservoir	Northern	Sinada and Abdelrahman [42]
Lake Nasser	Northern	Goher et al. [43]
Lake Chala	Equator	Cocquyt and Ryken [44]
Lake Edward	Equator	Stoyneva-Gartner and Descy [45]
Lake Victoria	Equator	Nozaki et al. [46]; Gikuma-Njuru et al. [47]; Sekadende et al. [48]; Lung'Ayia et al. [49]; Gophen et al. [50]
Lake Kivu	Equator	Rugema et al. [51]; Sarmento et al. [52]; Sarmento et al. [53]
Lake Chad	Equator	Toyosi et al. [54]; Carcea et al. [55]; Compere and litis [56]
Lake Kyaninga	Equator	Cocquyt et al. [57]
Lake Nakuru	Equator	Kaggwa et al. [58]; Okoth [59]
Lake Bukoni	Equator	Nyakoojo [60]
Lake Naivasha	Equator	Ballot et al. [61]
Lake Oloidien	Equator	Ballot et al. [61]
Lake Baringo	Equator	Schagerl and Oduor [62]
Lake Albert	Equator	Evans [63]
Lake Kyoga	Equator	Evans [64]
Lake Turkana	Equator	Kallqvist et al. [65]

(*Continued*)

Table 4.1 (Continued)

System	Region	References
Malilangwe Reservoir	Southern	Dalu et al. [66]; Dalu and Wasserman [19]
Mazvikadei Reservoir	Southern	Mhlanga et al. [67]
Tugwi-Mukosi Reservoir	Southern	Mhlanga et al. [68]
Swakoppoort Reservoir	Southern	Sirunda et al. [69]
Von Bach Reservoir	Southern	Sirunda et al. [69]
Vaalkop Reservoir	Southern	Swanepoel et al. [70]
Lake Loskop	Southern	Oberholster et al. [71]; Oberholster and Botha [72]
Lake Tanganyika	Southern	Stoyneva et al. [73]; Cocquyt and Vyverman [74]
Lake Tswaing	Southern	Oberholster et al. [71]
Loch Logan Reservoir	Southern	Vos and Roos [75]
Lake Chivero	Southern	Tendaupenyu [76]
Wagendrift Reservoir	Southern	Hart and Bychek [77]
Lake Malawi	Southern	Higgins et al. [78]; Haberyran and Mhone [79]
Hartbeespoort Reservoir	Southern	Zohary et al. [80]
Lake Kariba	Southern	Cronberg et al. [81]; Ndebele-Murisa et al. [82]
Lake Gariep	Southern	Venter [83]
Lake Manyame	Southern	Tendaupenyu [76]
Lake Zeekoevlei	Southern	Harding and Paxton [84]
Lake Rukwa	Southern	Moto and Maghembe [85]
Lake Liambezi	Southern	Seaman et al. [86]

evidence that supports LDG for phytoplankton species richness. The number of taxa, species richness, and abundances increased from the poles toward the Equator region. A high number of species (i.e., 813 taxa) was recorded from lakes and reservoirs in the Equator region, while the low species richness (i.e., 354 taxa) was recorded from the southern region (Table 4.2). Nine phytoplankton taxonomic groups were recorded from reservoirs in the Equator region while eight and seven phytoplankton

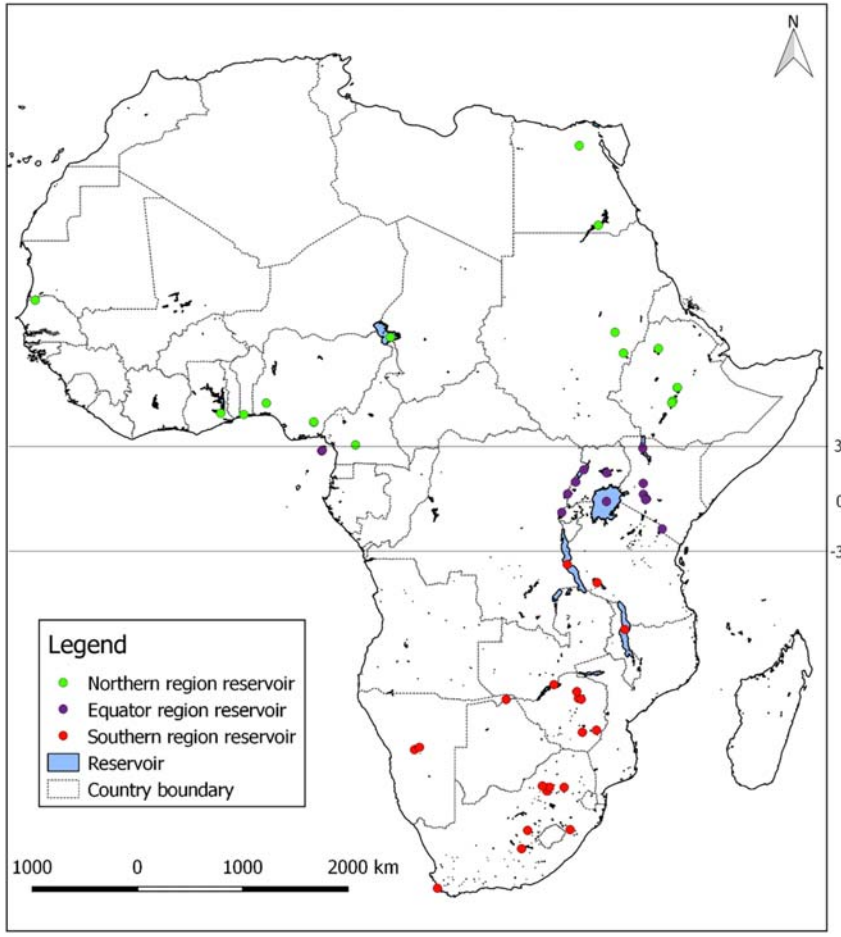

Figure 4.2 Spatial distribution of African reservoirs studied in this chapter.

taxonomic groups were recorded from the northern and southern regions, respectively. The most abundant and dominant phytoplankton groups: Bacillariophyta, Chlorophyta, and Cyanophyta (in order of abundance) also supported the LDG hypothesis as their abundance decreases from the Equator region (Table 4.2). Like other taxonomic groups, three explanations have been proposed for LDGs: (1) ecological hypotheses that focus on the mechanisms of species coexistence and maintenance of species diversity; (2) evolutionary hypotheses that focus on diversification rates; and (3) historical hypotheses that focus on the period and extent of tropical environments in Earth's history [24]. The taxonomic group Bacillariophyta is abundant

Table 4.2 Total number (N) of phytoplankton species recorded from different African study regions.

Group	Northern region	Equator region	Southern region	Total N
Bacillariophyta	213	330	89	632
Chlorophyta	123	215	157	495
Chrysophyta	6	6	9	21
Cryptophyta	8	5	4	17
Cyanophyta	83	198	69	350
Dinophyta	11	10	11	32
Euglenophyta	21	30	15	66
Synurophyta	0	1	0	1
Xanthophyta	1	18	0	19
Total N	466	813	354	1633

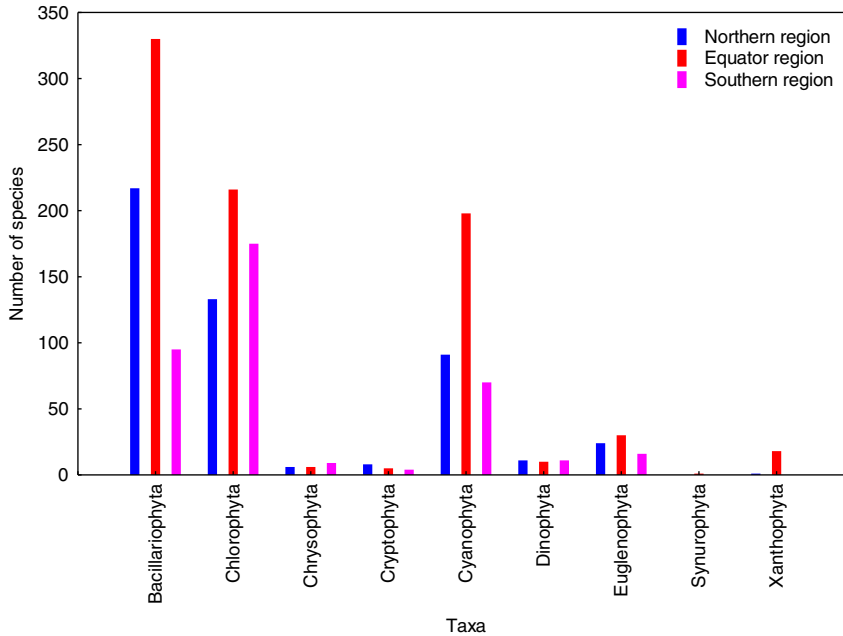

Figure 4.3 Phytoplankton taxonomic richness between reservoirs in regions on the African continent.

in the northern and Equator regions, while, Chlorophyta is the abundant group in the southern region (Fig. 4.3). Only one taxonomic group, Synurophyta, was unique in the Equator region and absent in the other regions (Fig. 4.3).

4.2.2 Highly occurring phytoplankton species

The occurrence of phytoplankton species in the reservoirs was detected when an individual species was present, thereby, indicating the number of reservoirs with that particular species.

The Cyanophyta *Merismopedia tranquilla* and *Anabaena* sp. highly occurred in lakes and reservoirs from the Equator (62%) and southern regions (60%), respectively, while, the Bacillariophyta *Cyclotella meneghiniana* highly occurred in the northern lakes and reservoirs (58%) (Table 4.3). Species that highly occurred in reservoirs from the three regions include *Microcystis aeruginosa*, *C. meneghiniana*, *M. tranquilla*, and *Aulacoseira granulata*.

As few species were common between the regions, the Jaccard similarity index was low (Fig. 4.4). The northern versus the Equator, northern versus southern, and southern versus Equator regions had a similarity index of 0.12, 0.25, and 0.20, respectively (Fig. 4.4).

Table 4.3 Phytoplankton species that highly occurred in different reservoirs in the northern, Equator, and southern regions analyzed using the Frequency of Occurrence (% F.O) index.

Northern region	% FO	Equator region	% FO	Southern region	% FO
Cyclotella meneghiniana	57.89	*Merismopedia tranquilla*	61.54	*Anabaena* sp.	60.00
Microcystis aeruginosa	54.34	*Cosmarium subtumidum*	46.15	*Microcystis aeruginosa*	59.00
Navicula sp.	47.37	*Aulacoseira granulate*	38.46	*Ankistrodesmus falcatus*	55.00
Merismopedia tenuissima	42.11	*Anabaenopsis cunningtonii*	38.46	*Aulacoseira granulata*	50.00
Oscillatoria sp.	42.11	*Aphanothece microscopica*	38.46	*Merismopedia* sp.	50.00
Nitzschia sp.	36.84	*Merismopedia convoluta*	38.46	*Cyclotella meneghiniana*	50.00
Aulacoseira granulata	31.58	*Cyclotella meneghiniana*	30.77	*Amscottia* sp.	45.00
Pleurosigma sp.	31.58	*Ankistrodesmus falcatus*	30.77	*Micrasterias furcate*	45.00
Fragilaria sp.	31.58	*Microcystis aeruginosa*	30.77	*Oscillatoria* sp.	45.00
Gyrosigma acuminatum	26.32	*Coelastrum astroideum*	30.77	*Melosira* sp.	40.00

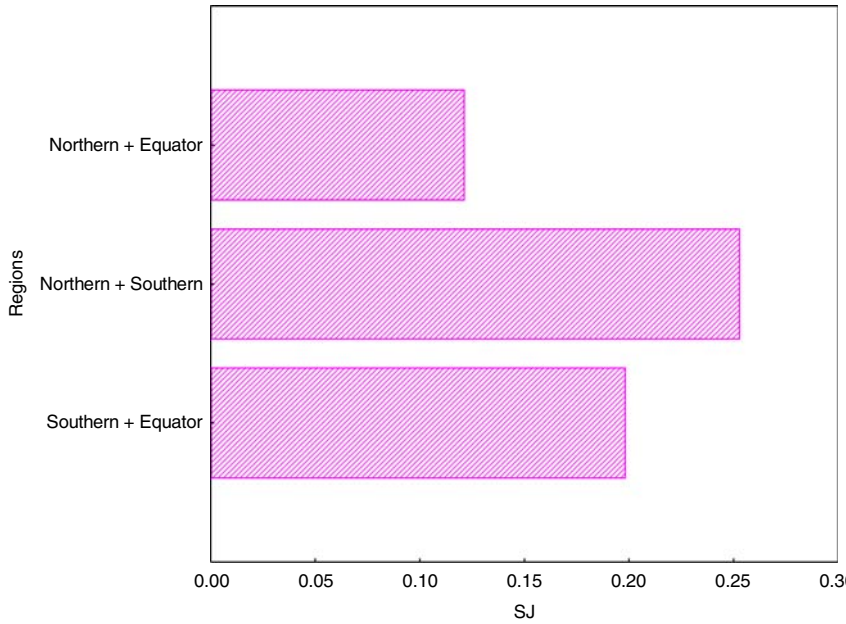

Figure 4.4 The Jaccard index of similarity between regions of Africa concerning phytoplankton species.

4.2.3 Phytoplankton importance in African reservoirs

A highly diverse system is more productive, stable, and resilient to anthropogenic stressors. Different phytoplankton taxa are specialized to perform several functions that are important for the functioning of an ecosystem. Cyanophyta, for example, can take up toxic nitrogenous compounds in reservoirs such as nitrite, nitrate, ammonium, and urea, which they can directly assimilate [87]. Cyanophyta are the only photosynthetic microorganisms capable of fixing and utilizing atmospheric nitrogen (N_2) in the free-living state and symbiosis [88]. Nitrogen fixation occurs inside special transformed, vegetative cells, the heterocytes, which are thick-walled [89], formed in some filamentous Cyanobacteria, but the process is also observed in nonheterocystous filamentous and unicellular forms [90]. Examples of N_2-fixing Cyanophyta include *Calothrix* sp., *Fischerella* sp., *Nodularia* sp., *Anabaena* sp., *Trichodesmium* sp., *Nostoc* sp., *Rivularia* sp., *Symploca* sp., *Lyngbya* sp., sp., *Crocosphaera* sp., *Cyanothece* sp., and *Gloeothece* sp [91]. Most of these N_2-fixing Cyanophyta species are present in African lakes and reservoirs, except for Cyanophyta *Fischerella* sp. and *Symploca* sp., which have been recorded in Brazil and Australia. The presence of these N_2-fixing

Cyanophyta species in African freshwater lakes and reservoirs facilitates the functioning of ecosystems and production [89].

Lakes and reservoirs' pelagic food webs are mainly based on phytoplankton primary production. Herbivorous zooplankton diet consists of various phytoplankton species, which differ in nutritional quality and their grazing resistance (e.g., armor, size, shape, toxins) [92–94]. The phytoplankton composition and abundance are vital in defining secondary and primary production since phytoplankton synthesizes many essential biomolecules (e.g., amino acids, fatty acids, sterols), which consumers are not able to synthesize de novo [95–99]. The relative carbon (C) and nitrogen (N) contents are similar in all phytoplankton species, and therefore, are not often considered limiting nutrients for zooplankton [100]. Phytoplankton are often assumed to be a homogenous group and a uniform food source for higher trophic levels [101]. The dietary quality of distinct phytoplankton classes for consumers is known to vary primarily due to the different availability of omega-3 (ω-3) and omega-6 (ω-6) fatty acids as they are the only source of long-chain polyunsaturated fatty acids (PUFAs) in pelagic food webs [92,102,103]. Thus, the availability of essential fatty acids in aquatic food webs depends on phytoplankton community composition [92,104,105]. The availability and quality of the ω-3 and ω-6 fatty acids affect the somatic growth of consumer species, which is important since the consumer body size is directly reflected in its fitness and reproductive output [77]. This is ecologically important for consumers, particularly zooplankton, which have a key position in pelagic food webs by linking the flow of dietary energy and essential fatty acids from phytoplankton (primary producers) to fish (upper trophic levels) [106].

Fatty acid composition, particularly PUFAs, and the long-chain ω-3 fatty acids like eicosapentaenoic acid (EPA, 20:5 w3) and docosahexaenoic acid (DHA, 22:6 ω3) of freshwater taxa are strongly related to that of their phytoplankton diets. These are vital for growth and reproduction (see [98,99,104,105,107–110]). However, only certain phytoplankton taxa can synthesize EPA and DHA fatty acids, whereas all phytoplankton taxa can synthesize shorter-chain ω-3 and ω-6 PUFA. Further, it has been shown that high ω-3 compared to ω-6 PUFA (ω-3:6 ratio) is beneficial for *Daphnia* [92,102]. Among freshwater phytoplankton, Cryptophyta, Dinophyta, Chrysophyta, Bacillariophyta, and Raphidophyta have been identified as EPA-synthesizing taxa, and Cryptophyta, Dinophyta, Chrysophyta, and Euglenophyta as DHA-synthesizing taxa [92,93,106]. Even though Cyanophyta and Chlorophyta cannot synthesize EPA or

DHA, some Cyanophyta species and all Chlorophyta can synthesize alpha-linolenic acid and stearidonic acid (18:4ω3) [106,111] and can contribute much or all to their fatty acids. In addition to long-chain and medium-chain PUFA, Chlorophyta and Bacillariophyta can synthesize 16 PUFA, which does not have physiological importance for aquatic consumers [112].

It is with no doubt, that phytoplankton play a major role in food security and human health in Africa through the consumption of fish and other aquatic products which will be high in essential fatty acids that will have come mostly from phytoplankton and transferred along the food chain up to humans [113]. Fish are one of the cheapest sources of quality animal protein and play an important role in quenching the protein requirements within the developing world [114,115].

4.2.4 Phytoplankton problems in African reservoirs

Several aquatic ecosystems have undergone substantial changes over the last five decades due to the introduction of exotic species, eutrophication, and climate change (see [116–118]). Eutrophication can occur naturally over centuries as reservoirs age and are filled in with sediments [119]. However, human activities (e.g., agriculture, industry, and municipal sewage disposal) have accelerated the rates and extent of eutrophication through both point-source discharges and nonpoint loadings of limiting nutrients, such as nitrogen (N) and phosphorus (P), into aquatic ecosystems, with dramatic consequences for drinking water sources, fisheries, and recreational water bodies [120].

High nutrient loading results in the overall increase in phytoplankton biomass (e.g., recorded in Lake Chivero, Lake Victoria, Lake Nasser, Hartbeespoort Reservoir, see Ndebele-Murisa et al. [82]) in the inshore and offshore areas, and a notable decrease in water transparency [118]. The classic sign of eutrophication in reservoirs is blooms of Cyanophyta such as *Microcystis* sp., *Cylindrospermopsis* sp., *Anabaena* sp., *Planktothrix* sp., *Aphanizomenon* sp., and *Nodularia* sp. [121] which cause notable decreases in water transparency ([122]; see Box 4.2). Cyanophyta species have all been recorded from African reservoirs and are anticipated to increase with climate change [76]. Increased phytoplankton biomass as a result of Cyanophyta blooms in the epilimnion also results in increased phytoplankton decomposition rates which ultimately depress dissolved oxygen (DO) concentration to ≤ 1 mg/L, similar to the observation in Lake

BOX 4.2 Cyanobacteria dynamics in a small tropical reservoir: Understanding spatio-temporal variability and influence of environmental variables [19].

Malilangwe reservoir is in the south-eastern lowveld of Zimbabwe. Rainfall occurs between November and March and the area is prone to droughts due to the erratic rainfall patterns. Summer temperatures are high, with a daily maximum of >32°C and peak temperatures of >45°C. Thermal stratification was established during the hot-wet season. In the cool and hot dry seasons, the reservoir was not stratified but was completely mixed. The reactive and total phosphorus, ammonium and total nitrogen were generally high at the bottom (<8 m depth) during the hot-wet season. During the cool-dry season when the reservoir mixed, the nutrient concentrations were generally low. A total of 15 Cyanobacteria taxa belonging to 9 families were recorded from the Malilangwe Reservoir over three seasons. The most abundant species during the hot-wet season when the reservoir was well stratified were *Cylindrospermopsis raciborskii* (Woloszynska) Seenayya and Subbaraju, *Merismopedia* sp., *Chroococcus* sp. and unidentified filamentous Cyanophyta. Three species dominated the cyanobacterial blooms in the cool-dry season when the reservoir was weakly stratified, and these were *Anabaena circinalis* Rabenhorst ex Bornet and Flahault, *M. aeruginosa* (Kützing) Kützing and *Chroococcus* sp. Macrophyte cover, DO, water transparency, reactive phosphorus, water level depth, chemical oxygen demand were found to have a significant effect on the Cyanobacteria community structure. The Malilangwe Reservoir as a model of a small reservoir shows that certain conditions are conducive for key Cyanobacteria proliferation in semiarid subtropical environments. Cyanobacteria blooms in the cool-dry season came after an increase in phosphorus in May which likely drove the increase in nitrogen-fixing species such as *Chroococcus* sp., *M. aeruginosa*, and *A. circinalis*. This could also have been partially attributed to the decrease in the destabilizing effects of river inflows and increased reservoir mixing. Overall, the high pH, low nitrogen and nitrate concentration, and low transparency in the reservoir were associated with increased Cyanobacteria abundance. However, the period associated with the most animal and human risk was the cool-dry season as Cyanobacteria were the most abundant taxa, and known cyanotoxin producers, such as *Anabaena*, *Microcystis*, and *Cylindrospermopsis*, were among the most prevalent bloom-forming taxa found. Their high occurrence suggests a high risk of potential exposure to toxigenic Cyanobacteria and associated cyanotoxins to animals and humans through recreational activities and drinking with serious socio-economic costs.

Victoria [123]. The impact of hypoxia (i.e., lack of oxygen) can be two-fold: on a macro-scale in the environment hypoxia constrains the distribution of species in the water column and forces them to depart from their normal behavior; and on a micro-scale, it causes physiological changes and shifts, and thus, alters lifecycle performance, reproductive capacity, growth capacity, and the vulnerability to diseases [124]. Hypoxic conditions in the hypolimnion of reservoirs fundamentally affect the community structure and diel vertical migration patterns of zooplankton [124].

Zooplankton play a vital role in regulating water quality in reservoirs because of their crucial position in the food chain. They are the dominant phytoplankton grazers and are in turn consumed by fish [125]. Zooplankton commonly exhibit diel vertical migration in which most populations reside in the hypolimnion during the day to avoid visual predation from fish [126,127]) or damaging ultraviolet (UV) radiation from the sun [128,129], at the cost of reduced growth and reproduction in the colder hypolimnion [130]. Furthermore, zooplankton need oxygen for respiration and exhibit decreased growth rates, fecundity, and increased mortality under low-oxygen conditions (e.g., [131]). Hypoxic conditions in the hypolimnion because of high phytoplankton decomposition rates result in zooplankton experiencing a trade-off during the day between experiencing increased metabolic stress and mortality due to low hypolimnion DO versus mortality and increased zooplankton cellular damage due to increased fish predation and UV radiation exposure in the oxic epilimnion. Low zooplankton densities result in increases in phytoplankton blooms as zooplankton regulate phytoplankton by grazing on them [132].

Under eutrophic conditions, Cyanophyta dominate the phytoplankton community and disrupts food web processes due to their high abundance, toxicity, and reduced food quality for grazers [133–135]. For example, the zooplankton in Lake Chivero were drastically reduced by eutrophication which promoted the proliferation of the inedible Cyanophyta *M. aeruginosa* which are currently dominating the phytoplankton composition in the reservoir [20]. The failure of zooplankton to regulate Cyanophyta blooms lies within key attributes that can reduce zooplankton growth and abundance [121]. The production of water-soluble toxic metabolites, including hepato- or neurotoxins, and various other less known metabolites cause lethal and sublethal effects when ingested by the zooplankton [136]. The Cyanophyta species release toxins as their defense mechanism, when disturbed, grazed, and/or in competition with other phytoplankton [137]. *Cylindrospermopsis raciboskii*, which dominates in Lake Kariba [20],

can affect the aquatic ecosystem in three ways. (1) Its toxicity to zooplankton and vertebrates [138,139]. *C. raciboskii* produces hepatotoxins and nephrotoxins and is among the most commonly recognized toxigenic Cyanophyta associated with harmful algal blooms (HAB) in freshwater systems, being specifically associated with multiple water-soluble toxins [140]; (2) allelopathy, in which it suppresses the growth of other phytoplankton and macrophytes [141,142], and (3) inducing teratogenic effects to the fish embryos as recorded on zebrafish *Danio rerio* [143], which could also be happening in other African lakes and reservoirs dominated by *C. raciboskii*. Although Cyanophyta dominate most phytoplankton blooms globally, other species in other taxonomic groupings (e.g., Dinophyta) have also been shown to produce HAB (see the complete list in [144]). Cyanophyta also limit zooplankton fitness because they are deficient in sterols and PUFAs, vital for regulating cell function in animals [102,145]. Finally, the aggregation of Cyanophyta cells into large, inedible filaments or colonies provides a grazer refuge, and the filaments can inhibit grazing by large daphniids by clogging the filtration apparatus [146,147].

It is clear from several studies globally that phytoplankton blooms often have devastating effects on fisheries [144]. Reduced zooplankton affects fisheries as zooplankton provide the crucial trophic link between phytoplankton and fish. Harmful phytoplankton have caused considerable damage by depleting fish stocks, restricting harvests resulting in great losses to the fishing industry, and having significant economic impacts [144]. Phytoplankton blooms cause the sudden and unexpected death of several fish over a short time and often within a particular area in the wild, often referred to as "fish kills" [148]. Fish kills are attributed in some cases to hypoxic conditions when blooms decay, while in others, there is clear evidence of the involvement of water-soluble toxic metabolites [144]. There is either a direct action of the phytoplankton on the fish itself, especially on sensitive organs such as the gills, liver, and tissue of the nervous system causing asphyxiation and eventually death, or indirect death of predators which have consumed herbivores by feeding on blooms [144,149]. Fish kills in Lake Chivero resulted from hypoxic conditions caused by the high oxygen demand from the massive algal die-off and released algal toxins [67]. Lake Chivero is hypereutrophic with sewage and industrial effluent discharged into the reservoir through the Mukuvisi and Marimba rivers [150]), with *M. aeruginosa* being the dominant algal group [67,151]. Approximately 100 tons of greenhead tilapia *Oreochromis*

macrochir in Lake Chivero in March/April 1996 were lost to deoxygenation that was compounded by ammonia toxicity which was unacceptably high at 3.5 mg/L [67]. Depressed DO levels (< 1.9 mg/L) are lethal for cichlid fish species that dominate fisheries catches in Africa [150]). In the Nyanza Gulf of Lake Victoria, Cyanophyta blooms have been observed since 1980 which are associated with massive fish kills [149,152,153]. In South Africa, fish kills (as well as the death of mammals) attributed to Cyanophyta toxins have been recorded from several reservoirs [84]. It is therefore important to distinguish between natural events and anthropogenic activities so that remedial measures are implemented to address the cause and prevent future fish kills. This is particularly important for other human activities (e.g., agriculture, mining, urban expansion) which could be the first to be blamed when a fish kill occurs.

4.2.5 Impact of phytoplankton on human health

Human exposure to cyanotoxins is likely to occur through direct consumption of toxin-contaminated drinking water [144]. In Lake Victoria, cylindrospermopsin and microcystin were detected in the lakeshore sites although none were detected in wells or treated drinking water samples [154]. The existence of multiple toxins in the lake may lead to synergistic effects and increase the toxicological risk to humans [154]. In South Africa, water used for domestic purposes (including drinking) by communities around the Hartbeespoort reservoir had microcystins averaging 4.3 μg/L in communal tap water and 4.8 μg/L in the water stored in tanks [155]. This is of concern as the Hartbeespoort reservoir is a major water source in the northwest province of South Africa. The decaying of Cyanophyta emits a strong septic odor; this has also been reported in areas around the Hartbeespoort reservoir [155]. In Lake Embu, Kenya, there are unconfirmed reports of hundreds of deaths attributable to cyanotoxin exposure in 2001 [156]. In Zimbabwe, circumstantial evidence linked the seasonal increase of gastroenteritis cases in Harare to algal blooms in Lake Chivero [157,158]. Between 1991 and 2001, gastrointestinal infections and liver cancer cases in Harare rose by over 300% [151]. Documented cases of gastroenteritis rose from <100 to 300 per 1000 people, whereas, liver cancers rose from 30 to 130 per 1000 people [151]. Microcystin concentrations in Lake Chivero were ≤13.9 μg/L and were also detected in the city of Harare's drinking water [151]. This observation is a matter of concern, mainly because microcystin has been linked to hepatocellular carcinomas, a

major type of primary liver cancer [159]. The high incidences of cancer in Africa could, therefore, also be attributed to the consumption of fish and water with high microcystin levels. Despite the dangers of cyanotoxins to human health, the risks posed by exposure to cyanobacterial toxins through water and fish consumption remain poorly described [160].

Consumption of agricultural plants following irrigation with toxin-contaminated water is also another route of cyanotoxin intake by humans [161]. The uptake and accumulation of three different hepatoxic cyanotoxins in lettuce *Lactuca sativa*, ryegrass *Loliumperenne*, clover *Trifoliumrepens*, and rape *Brassica napa* were demonstrated (see [161]) which poses a serious health concern, especially in Africa, where agricultural production is highly reliant on irrigation water from Cyanophyta-dominated lakes and reservoirs. Although oral exposure is the main route of human cyanotoxin intake, dermal exposure may occur [162]. Dermal exposure can be through recreational, sport, and water activities (e.g., fishing, swimming) in infested waters, or through the domestic use of cyanotoxin-containing water (in the case of showering) [162], causing dermatitis and mild to severe allergic reactions or maybe a systemic toxic effect [161]. Case reports and anecdotal references dating from as early as 1949 describe a range of illnesses associated with recreational exposure to Cyanophyta: hay fever-like symptoms and pruritic skin rashes are most frequently reported, while others describe more serious acute illnesses, with symptoms such as severe headache, fever, pneumonia, myalgia, vertigo, and blistering in the mouth [163]. Although not much has been documented in Africa with regards to cyanotoxin dermal exposure, communities living around reservoirs who often come in contact with the water might be experiencing these symptoms, hence, further studies are warranted.

The quality of fish meat is defined based on the sensory characteristics, chemical composition, and physical properties which influence how the fish are perceived by the consumer [164]. Fish quality also involves safety aspects such as being free from parasites, harmful bacteria, pesticides, heavy metals, biotoxins, and many other substances [165]. Accumulation of biotoxins in fish muscle and viscera render the fish unsafe for human consumption [144] as toxins produced by Cyanophyta can be biomagnified along the food chain from lower to higher trophic levels [166]. For instance, the potent microcystins, which are hepatotoxins, may cause liver damage and promote tumor growth in animals as well as humans through the inhibition of protein phosphatase 1 and 2A [167,168]. These toxins are highly water-soluble and are also resistant to boiling, thus, posing a huge threat to water and food quality if not properly monitored [168].

In the Loskop reservoir in South Africa, extremely high microcystin levels were observed in the liver and muscles of *Labeo rosae* and *Oreochromis mossambicus*, indicating that the consumption of high fish biomass might cause severe adverse effects in humans [166]. Microcystins were also detected in *Rastrineobola argentea*, a small planktivorous fish in Lake Victoria [160]. In the Koka reservoir, Ethiopia, the liver and muscle tissues of *Oreochromis niloticus*, *Cyprinus carpio*, and *Clarias gariepinus* had high levels of microcystins [169]. Most studies in Africa, however, have only looked at the presence of Cyanophyta in the fish guts, and not the presence of cyanotoxins in fish tissues. Some studies on tilapia diets in Lake Victoria demonstrated that Cyanophyta (especially *Microcystis* sp.) constitute about 30% of the phytoplankton community [170,171]. The few examples we have of the presence of cyanotoxins in fish tissues are of concern as globally more than 2000 cases of human poisoning through either fish or shellfish consumption are reported every year with a mortality rate of 15% [172].

4.2.6 Impact of phytoplankton on other animals

The impact of Cyanophyta blooms on piscivorous birds as well as terrestrial mammals has been well documented [144]. This observation was first reported over a century ago, when dogs, horses, pigs, and sheep were seen to die within hours of drinking from a waterbody contaminated and dominated by Cyanophyta *Nodularia spumigena* [163]. Cyanotoxins have frequently been the suspected cause of mass deaths of medium- and large-sized terrestrial mammals in Africa, including livestock (i.e., cattle, goats, sheep) as well as nonwading wild mammals (i.e., rhinoceros, wildebeests, giraffes, zebras, impalas) [173]. Interestingly, due to the vigilance against predators, many of these wild mammals drink at the downwind edge of waters where dense Cyanophyta scum tends to accumulate, thus, exposing them to high levels of cyanotoxins [173]. In Kruger National Park, South Africa, several clustered, multispecies, wildlife mortality events occurred in the vicinity of two reservoirs [174]. On investigation, heavy Cyanophyta blooms were visible in these reservoirs and microscopic analysis of water samples showed the dominance of *M. aeruginosa*. Laboratory toxicity tests confirmed the presence of significant levels of microcystins in water from the two reservoirs. The postmortem of the dead animals showed macroscopic lesions and histopathological lesions which were compatible with a diagnosis of Cyanophyta intoxication. The recent mass mortality event of 350 African elephants in Botswana was attributed to biotoxins produced

by Cyanophyta [173]. Cyanotoxins were indeed the most likely cause of this tragic event, which would be the first confirmed case of cyanotoxin-induced elephant mass mortality. Thus, increasing exposure to cyanotoxins in polluted reservoirs will inevitably be harmful to the health and livelihoods of humans who consume livestock and wildlife [173].

4.3 Phytoplankton and climate change

In moderate emission scenarios that feature little change from present global-development patterns, for instance, average global temperatures are projected to rise by 2.1°C–3.5°C [175], which is way above the 1.5°C–2°C limit laid out as a goal by signatories that signed the 2015 Paris climate agreement. The most obvious and easily measured indicator of warming in aquatic systems is a change in water temperature with the thermal cycle being the ecological driver which is most likely to be directly affected by changing temperatures [176]. African reservoirs are known to be sensitive and vulnerable to climate change, as small variations can cause wide fluctuations in their thermal dynamics and their aquatic environment [14,177–179]. Surface temperatures in the Hartbeespoort and Roodeplaat reservoirs in South Africa rose by about 0.14°C/year between 1980 and 2000, rose by about 5°C between 1962 and 1995 in Lake Albert, and the epilimnion temperature of Lake Kivu increased by about 0.5°C–1.0°C since the mid-1970s, and by about 0.5°C at the depth of the temperature inversion. Deeper water temperatures in Lake Malawi increased by about 0.7°C over six decades and the surface temperatures of Lake Victoria increased by 0.05°C per decade between 1927 and 2000, and 0.92°C between 2000 and 2009, while its deep waters warmed by 0.08°C and 1.09°C over the same period [176], and Lake Kariba increased by 2.0°C in the 50 years since its creation [82,150].

Increased water temperatures associated with climate warming are likely to cause a shift in phytoplankton species composition from a balanced ecosystem to a Cyanophyta-dominated ecosystem, which is competitively superior at high temperatures [82]. The growth rate of Chlorophyta declined at temperatures above 24°C, becoming negative after 28°C [180]. In contrast, Cyanophyta increased almost exponentially up to 34°C [180]. As water temperatures increase, phytoplankton succession follows a progression from Bacillariophyta to Chlorophyta to Cyanophyta [181]. The results corroborated several reports from various lakes and reservoirs globally where Cyanophyta is the dominant

phytoplankton group thriving under the changing climate. For example, in a study of 188 lakes and reservoirs exhibiting a wide range of trophic status, it was concluded that lake warming strongly favors phytoplankton species such as Cyanophyta [182]. The same scenario is happening in African lakes and reservoirs that are already experiencing the impacts of climate change such as Lake Kariba (with average temperatures of the epilimnion > 25°C), where *C. raciboskii* is now dominating the phytoplankton community (see [20]). In Lake Victoria, the phytoplankton blooms observed during February and August comprised over 90% *Microcystis* sp. at concentrations of 34,000 colonies/mL. The blooms corresponded with high temperatures, discharge of nutrients, nutrient upwelling, and nutrient release from sediments [153].

Besides the effects of climate warming on phytoplankton communities in African lakes and reservoirs as described above, warming also affects the thermal stratification of lakes [14]. Stratification is the tendency of reservoirs to form separate and distinct thermal layers during warm weather [14]. Stratification is prevalent in many deep African lakes and reservoirs such as Albert, Cahora Bassa, Chad, Kariba, Malawi, Niger, Tanganyika, and Turkana. A fairly stable stratification is established during the wet season, characterized by increased water temperatures and diminished wind intensities, however, currents and internal waves, as well as coastal jets and return flows, can cause localized upwelling, which may partly disrupt this stratification [14]. Global warming is likely to cause many reservoirs to exhibit prolonged stratification with decreased nutrient concentrations in the epilimnion and prolonged hypoxia in hypolimnion [183] leading to overall productivity reductions in lakes and reservoirs [150]. There is evidence that global warming is already affecting African lakes and reservoirs [184]. Lakes Malawi [185], Kivu, [186] and Tanganyika [179] appear to have strengthened stratifications. Lake Kariba still becomes isothermal in winter, and mixing occurs despite its warming [184]. This mixing releases nutrients from the hypolimnion to the epilimnion, indicated by a general increase in primary production and nutrients during the winter season. It is essential that regular monitoring be carried out in African lakes and reservoirs as all systems might not respond to climate change in the same way [184].

4.4 Management of reservoirs in Africa

Africa is exceptionally well endowed with river basins and large inland lakes and reservoirs that extend over the territories of several countries

with both crisis-prone hotspots and a good number of promising approaches to transboundary water management [187]. In Africa, there are international agreements in effect for 20 of the continent's 63 river basins. There are institutionalized forums that have the task of coordinating national initiatives in 16 river basins. Despite this limited number of formal coordination forums on the African continent, transboundary water management has made considerable progress, especially in southern Africa. The Southern African Development Community provides an overarching political framework in southern Africa conducive to efforts aimed at transboundary cooperation with regard to the management of water basins in the region. Other transboundary river basin organizations in Africa include the Lake Chad Basin Commission, Organization pour la mise en valeur du fleuve Sénégal, the Niger Basin Authority, Zambezi Watercourse Commission, and the new initiatives for cooperation being undertaken on Lake Victoria. The founding of the African Ministers' Council on Water also established a continent-wide cooperation context that has placed transboundary water cooperation on its agenda and is receiving external support and funding for the purpose [187]. These organizations have put in frameworks that work to promote cooperation, security, social and economic development, and poverty eradication among the member states through the effective management of the continent's water resources and provision of water supply services. As lakes and reservoirs in Africa have been subjected to various anthropogenic pressures, the frameworks aid in management as usage of the lakes and reservoirs are governed by the national, regional as well as international frameworks although it is proving to be difficult to manage threats to biodiversity like pollution of aquatic ecosystems and climate change, both of which have negative impacts on phytoplankton communities.

Wastewater disposal is becoming a problem in African countries as large quantities of municipal waste and industrial effluent (both containing extremely high nutrients) are being produced due to increased industrialization and urbanization [188]. In the Kisumu District in Kenya, all three of the existing pump stations are broken down resulting in the overflow of sewage at manholes upstream of the pump stations and direct discharge of raw sewage into Lake Victoria [188]. The hypereutrophic Lake Chivero receives raw sewage from the City of Harare which contains alarmingly high nutrients, more than the applicable Zimbabwean nutrient limits for effluents discharged into sensitive waters (which are 10 mg/L total N and 0.5 mg/L total P) (Government of Zimbabwe Statutory

Instrument 274 of 2000). Population growth, frequent breakdowns, and no maintenance of wastewater treatment plants contribute to untreated wastewater discharged into receiving aquatic ecosystems [189].

The deteriorating state of sewage and wastewater treatment facilities or infrastructure management in Africa is one of the largest factors contributing to the numerous pollution problems experienced in most parts of the continent and a major contributor to human and environmental problems [190]. Of the 824 treatment plants in South Africa, it is estimated that only 60 release water within the recommended limits. Raw or partially treated sewage flows directly into rivers and reservoirs throughout the country, turning reservoirs green, laying waste to sensitive aquatic ecosystems, and harming people who drink the polluted water. From large cities, such as Johannesburg, to smaller rural towns, wastewater from domestic industries frequently either escapes out of broken pipes or from the wastewater treatment plants into the natural environment [190].

The Nkolbisson reservoir in Cameroon receives untreated wastewater from the Abiergue and Mintotomo rivers of the Mefou watershed flowing across Cité Verte which has gradually degraded its quality and environment [191]. Not only is wastewater the only contributor of high nutrients into reservoirs, but other human activities such as agriculture equally contribute [192]. Excessive use of various agrochemicals in the nearby lands around watersheds, lack of well-planned development on the riverbanks, and population growth are increasingly polluting lakes and reservoirs. Areas surrounding Lake Edward are used for agricultural activities and water from the reservoir is generally used for irrigation purposes, washing clothes, bathing, and for the domestic animals which lead to the degradation of water quality [192]. This is also being experienced in several reservoirs across the continent. This results in a massive proliferation of undesirable phytoplankton, and this coupled with other anthropogenic stressors (e.g., climate change), further strains our lakes and reservoirs.

4.4.1 Controlling phytoplankton blooms

Nitrogen and phosphorous are the major nutrients governing phytoplankton primary production and biomass in African lakes and reservoirs with warm temperatures playing a huge role in the proliferation of phytoplankton blooms [193,194]. Theoretically, to prevent eutrophication and phytoplankton blooms, environmental managers must control the three factors (N, P, and temperature). This, however, has been difficult for

various African states besides having sound regulations for anthropogenic stressors. Policymakers and principal government service providers who are supposed to be spearheading the prevention of pollution are neglecting their oversight role, resulting in the local municipalities and governments being the largest polluters of aquatic ecosystems [190]. As discussed in the previous section, most local municipalities in African states are disposing of untreated sewage into aquatic ecosystems resulting in increased nutrient levels which promote algal blooms. Local municipalities should invest in sound sewage treatment systems that efficiently reduce nutrient loads to aquatic ecosystems. Constructed wetlands can also be used which consist of a shallow depression in the ground with a level bottom designed and built like natural wetlands to treat wastewater [195,196]. The flow is controlled so the water is spread evenly among the wetland plants, thereby, allowing natural processes to occur and clean the wastewater more efficiently [195–198]. Constructed wetlands provide a simple and effective option and have proven to be effective in the treatment of domestic, industrial, agricultural, and municipal wastewater [195–198]. Constructed wetlands, a promising green technology, are also very effective in treating toxic metal-contaminated water, pharmaceuticals and personal care products contaminated waters, oil refinery wastewater, diesel, and agricultural drainage water (see [199]). Their construction and operational costs are much less than conventional systems. Some statistics show that the cost of subsurface constructed wetlands in Africa for wastewater treatment is approximately US$ 5 per person compared to mechanical wastewater treatment (i.e., activated sludge system used by municipalities), which costs approximately US$ 50 per person [200]. Constructed wetlands also provide scenery, are pleasant to look at, attract desired wildlife, and provide environmental education opportunities [196]. Natural wetlands are more desirable to perform the treatment of wastewater, but these are being developed as well as being affected by agriculture which affects the water cycle. Constructed wetlands, therefore, could be a better option that offers a low-cost and low-maintenance treatment alternative for wastewater to prevent African lakes and reservoirs from receiving high nutrient loads which affect phytoplankton communities.

Climate change experts have been researching ways to counter the increasing global temperatures which are presently being reflected in the proliferation of undesirable phytoplankton in some reservoirs. A holistic approach is required when dealing with the issues of climate change. The emission of greenhouse gases from anthropogenic activities must decline

substantially by greatly reducing our dependency on fossil fuels, which is the largest challenge of our time [175]. Reducing deforestation and massive planting of trees is something citizens can easily get involved with which could help in mitigating the effects of climate change.

4.5 Remote sensing in the monitoring of phytoplankton: key research strides, challenges, and opportunities

Although, the use of in situ methods for phytoplankton assessment and monitoring is considered to be accurate, limited financial resources for routine monitoring and malfunctioning equipment, restricted aerial coverage, and the existing data gaps have resulted in the lack of proper understanding of phytoplankton distribution and occurrence in most African lakes and reservoirs. This has prompted the need to integrate in situ and remote sensed datasets to achieve a holistic understanding of the phytoplankton taxonomic richness in African lakes and reservoirs. As such, the remote sensing of phytoplankton has increased drastically over the years since the emergence of Earth observation satellite platforms over the past four decades. This has been largely motivated by the need for lake-scale spatial explicit information on phytoplankton distribution and occurrence.

To date, various remotely sensed datasets have been used ranging from Advanced Very-High-Resolution Radiometer, Hyperspectral, Landsat Series, MERIS, MODIS, SPOT, and Sentinel data [201–204]. However, the results varied significantly depending on the trade-offs between the sensor type and lake size variations. For instance, some of the lakes or reservoirs are small in size which makes the use of broadband and course multispectral satellite datasets challenging due to spectral mixing [202]. In addition, the return time (temporal scale) for the majority of these satellite data sensors ranges between 10 and 20 days [205–207], except for MERIS and MODIS data which have a daily coverage. It is important to note that because of these limitations, the use of MERIS and MODIS data remains largely restricted to big lakes such as Kariba in Zimbabwe, Lake Malawi, and Lake Naivasha, Kenya, although several attempts have been observed in Lake Chivero among others. Despite the limitations, numerous remotely sensed models (e.g., the maximum peak-height algorithm after Matthews and Bernard [204] and the Fluorescence Line Height algorithms [208]) have been developed for estimating and predicting phytoplankton concentrations or presence in freshwater ecosystems and these have proved to be accurate based on the validation results

conducted in some lakes and reservoirs in Africa. The majority of these models focused on the chl-a estimation and high accuracies have been reported [207,209].

Overall, the use of remotely sensed data in monitoring and assessing phytoplankton is gaining significant traction in Africa. This is further motivated by the development of new generation sensors with unique strategically positioned spectral bands such as the 10 m Sentinel 2 data with a repeated temporal coverage of 5 days [210]. The introduction of these data has opened new avenues for data fusion with other readily available remotely sensed datasets such as Sentinel 3 (OLCI), Landsat 8, the newly introduced Landsat 9 using machine learning and artificial intelligence, and Google Earth Engine clouding computing techniques [211]. New research breakthroughs have been reported in southeast Asia [212], Europe [213,214], and America [215]. There is, therefore, a need to test the transferability of some of these research advancements and methodologies on inland freshwater ecosystems (lakes and reservoirs) in Africa.

4.6 Conclusions

The absence of information on phytoplankton from hundreds of reservoirs on the African continent clearly shows there is considerable limited research and necessary infrastructure to enable and/or facilitate research (see [216]). The LDG is supported as more species are found in the Equator region, with diversity decreasing toward the poles, with the Bacillariophyta group being the most dominant in terms of species. Of concern is the highly occurring *M. aeruginosa* among other Cyanophyta species in almost all the lakes and reservoirs, which form blooms that affect various levels of aquatic ecosystem structure. Apart from its negative impacts on the trophic structure of aquatic ecosystems, cyanotoxins produced by *M. aeruginosa* have been detected in the water and fish of the lakes and reservoir that are consumed by humans, with significant detrimental impacts on the indigenous local communities' livelihoods and health.

Nutrient enrichment is the primary water quality issue that is leading to nuisance Cyanophyta blooms, with many African lakes and reservoirs being recipients of untreated wastewater which is causing nutrient enrichment and proliferation of bloom formations. To control algal blooms, this review calls on municipalities in respective states to ensure that wastewater is adequately treated before being discharged into reservoirs to prevent biodiversity loss as well as serious human health issues. This chapter

further makes recommendations for local municipalities to construct wetlands as a cost-effective and environmentally friendly option for treating wastewater. Climate change is predicted to cause further increases in Cyanophyta blooms as they have a competitive advantage compared to other phytoplankton groups at elevated temperatures (see [76]). For this, a holistic approach is required when dealing with the issues of climate change to reduce the emission of greenhouse gases from human activities.

Management of reservoirs against eutrophication and associated cascading impacts promotes the attainment of Sustainable Development Goals:

1. SDG 1 No poverty
   Productive reservoirs are beneficial to livelihoods when they harvest ecosystem services that can generate income (e.g., selling fish).
2. SDG 2 Zero hunger
   Similar to SDG 1. Productive reservoirs are beneficial to livelihoods when they harvest ecosystem services that they use for family consumption or can generate income (e.g., selling fish), which they will use to buy food for family consumption.
3. SDG 3 Good health and well being
   When a reservoir is well managed (including the watershed), the reservoir will have nutrients within acceptable ranges, with diverse phytoplankton composition and less cyanotoxic phytoplankton which can cause serious health issues.
4. SDG 6 Clean water and sanitation
   Similar to SDG 3. When a reservoir is well managed (including the watershed), the water can be consumed in households without causing serious health issues.
5. SDG 14 Life below water
   Managing reservoirs promotes the conservation of biotic components below water to maintain biodiverse aquatic systems.

Periodic phytoplankton biodiversity monitoring and assessments should be carried out in African aquatic systems to provide insights into the changes (biotic, physical, or chemical) of aquatic ecosystems over time. The assessments indicate the status of these ecosystems. Monitoring and assessment also provide evidence-based documentation of the state of these reservoirs as a result of human disturbances and interventions. Furthermore, monitoring and assessment programs provide insights into whether management actions and/or strategies are effective in reducing or preventing further aquatic ecosystem degradation. Overall, monitoring and assessment facilitate decision-making, supports policy development, and provide information to stakeholders which

may encourage their participation in decision-making and implementation processes. Lastly, monitoring and assessment programs are essential for the sustainable development and management of water resources.

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CHAPTER 5

Plankton and fish nutrition in African lakes

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5.1 Introduction

Plankton and fish are inextricably linked; in fact, the predation relationship is a crucial element in fish recruiting. Understanding the trophic and dynamic actions among various groups of aquatic organisms and the ecosystem provided may raise awareness of the need for preserving lake environments. Zooplankton play an important part in the food web since they represent food resource to higher groups in the food chain. Malfunctions at each trophic level influence the predator–prey interaction, causing catastrophic ecological damage. To prevent the food chain from collapsing, it is crucial to keep zooplankton alive since they are necessary for the maintenance of ecosystems [1].

Plankton is a broad term that refers to organisms with limited locomotive ability concerning the bodies of water in which they live. Plankton consist of a wide range of organisms, from viruses (femtoplankton) as the smallest plankton size to large species (megazooplankton). Plankton communities in African lakes, especially tropical ones, are extremely diverse, containing organisms from nearly every kingdom, phylum, class, and family. These organisms interact with their environment, their resources, and one another in a variety of ways. The most common method of classifying planktonic organisms is by size, which influences their sinking and floating, light utilization, movement, and trophic status. Planktonic organisms with specific functional characters in the ecosystem (e.g., grazers, predators, and nitrogen-fixers) come in a variety of sizes, however, in general, primary producers are smaller than grazers, which are smaller than predators.

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5.2 Importance of plankton to fish larvae

One of the many critical possible factors affecting the survival of fish larvae is food availability [2]. Because of the larvae's incapacity to manage larger food, newly born individuals of many fish species feed mostly on tiny zooplankters and phytoplankton (Fig. 5.1). Furthermore, the majority of fish larvae have undeveloped and nascent alimentary tracts, which are often characterized by short length, simple structure, narrow breadth, a weak digestive enzyme secretion, and consequently, low digestive ability. Interspecific interactions, furthermore, can have a significant impact on fish development, survival, and recruitment success, in the presence of competition for food sources among species, for instance, fish may adjust their diets and develop at a slower rate [3].

Experts in limnology discovered a horizontal and vertical distribution of zooplankton that is applicable in every circumstance when studying the physical structure of lakes, and Hutchinson established distinct patterns of distribution in the 1950s: clumps, swarms, or aggregation [4]. Because zooplankton is inextricably linked to higher trophic levels, comprehending the effects of its dispersal on the broader ecosystem and relationships with other planktonic organisms may be beneficial in comprehending ecological models including other planktonic groupings [5]. No doubt that there is a relationship between zooplankton diurnal vertical movement and fish-feeding habits where the existence of the euphausiid *Euphausia vallentini*, and the copepod *Rhincalanus gigas* was discovered in the stomach material of *Kreffrichthys anderssoni*, a native fish in the Prince Edward Archipelago (South Africa), where the presence of this type of

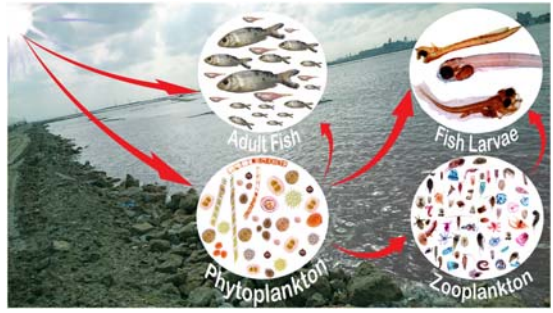

Figure 5.1 Plankton-fish relationship within the lakes, which include plankton (phytoplankton and zooplankton) and the different life stages of the fish, where the arrows indicate the direction of energy transfer.

fish for feeding in the water column is related to the depth at which these types of plankton reside. *Kreffrichthys anderssoni* spends its daytime at 300–400 m below the surface and migrates to the surface at night for eating zooplankton [6]. Zooplankton vertical movement has repercussions on fish movement and the availability of food.

Zooplankton has a significant impact on other planktonic groups' biomass stocks (such as phytoplankton and chromista); in particular, as well as, it may have an impact on the prey populations through consumption as well as the predatory populations themselves, hence, affecting fish biomass [7]. Lake deepening or bottom trawling is the most common anthropogenic disturbance for fish and has a significant influence on the biogeochemical cycle of nutrients and carbon. Nutrients, both particulate and dissolved, can be transported from pelagic to benthic ecosystems and back, promoting algal blooming, and thus, feeding larvae and mature herbivorous fish [8]. This increase in primary production may have a significant impact on water column zooplankton communities as part of this ecosystem [9]. Because it is critical, zooplankton is frequently collected from lakes and used as a live feed for cultured fish, although it is one of the most expensive in fish production [10]. It is also one of the most important criteria because the amount and quality of feed directly impact fish development and, indirectly, mortality and maturation [11]. As a result, using live food can help to reduce this expense. Traditional live food diet includes rotifers (e.g., *Brachionus* spp.) and brine shrimp (*Artemia* spp.) [12].

It has been shown that zooplankton are necessary as a nutrient source for fish larvae in lakes that will later grow into mature forms to constitute an important component of the human diet in Africa [13]. Long-term, time-series research on zooplankton and their relationships with fish larvae can be used to analyze or predict the existence of fish stocks that contribute to fisheries management [14]. Several zooplankton species have been identified as bioindicators sensitive to changes in natural habitats. As a result, they are frequently referred to as "sentinels of environmental changes and stresses" [15–17]. The presence of zooplankton influences ecosystem dynamics. Herbivorous zooplankton graze on algae and bacteria, influencing the surrounding aquatic communities [18], and because they feed on phytoplankton, which contains nitrogen and phosphorus [19], they create a complete nutrient recycling cycle.

Zooplankton are used as environmental indicators since they reflect the quality of the ecosystem as well as the living components, providing

in-lighting information on the quality and quantity of aquatic organisms including fish communities [20]. Zooplankton have direct impact on fish populations and recruitment. Variations in zooplankton biomass abundance might set off a chain reaction that has an impact on fish stocks in African lakes.

Furthermore, plankton is important as food for fish larvae in the aquatic environment because docosahexaenoic acid (DHA) and eicosapentaenoic acid (EPA) are necessary for development, eye, and brain growth, and immune system function in young fish as well as humans and aquatic birds [21]. Because the omega-3 fatty acids EPA and DHA are exclusively generated by a few phytoplankton species, including golden algae, dinoflagellates, diatoms, and cryptomonads [22,23], fish absorb such biomolecules via consuming zooplankton that relies on phytoplankton or synthesizing the fatty acid precursor linolenic acid [24]. Feeding preferences and metabolism differ among zooplankton groups; for example, cladocerans prefer EPA-rich phytoplankton species (e.g., *Daphnia magna*), copepods, on the other hand, prefer DHA-rich phytoplankton organisms (e.g., *Eudiaptomus*) [24]. Because of copepods' high presumption and fish feeding, DHA is abundant in many aquatic food webs [25].

Metamorphosis is a critical step in the development of fish larvae into juveniles. Several elements, including hormones, impact this process. Every physiological change that happens in the development process of fish at every stage of their life cycle is influenced by hormonal regulation [26]. The thyroid hormone is recognized to have an essential function in fish larval metamorphosis. That hormone is thought to be obtained from zooplankton as live food. Copepods and rotifers, which are eaten by fish larvae, have a considerable influence on thyroid hormone activity. Copepods have higher iodine content than rotifers, and hence, have a greater potential for speeding the metamorphosis of fish larvae [27].

Fish predation on zooplankton controls the quantity of herbivorous zooplankton, which, in turn, regulates phytoplankton levels in any water body [28]. Sarvala [28] has discovered that variations in the population of planktivorous fish affected both phytoplankton and zooplankton abundance and diversity. However, the majority of existing data originates from experimental enclosures and considerably less is known about trophic interactions in huge bodies of water [29].

In Egypt and elsewhere in Africa, fishery resources have been exploited in the absence of an appropriate ecological understanding of the plankton-feeding organisms [13] and a shortage of detailed information

about the nature of different food webs in the natural lakes. There is a large proportion of global fish species in freshwater bodies, with African lakes constituting a vast proportion as well as the ability of many of these species to produce very high yields of fish. The majority of those larval and mature stages rely heavily on plankton for nutrition, indicating that natural feeding patterns on plankton are very successful [30]. Zooplankton are regarded as the primary prey group for fish fry in southern African estuaries and lakes with low or high zooplankton biomass production. Understanding the reasons for plankton selectivity, the benefits of fry feeding on zooplankton, and the suggested causes of any ontogenetic changes in fish nutrition will aid in the management of freshwater lake fisheries [31].

5.3 Plankton and productivity of African lakes

Measurements of primary production can help enhance estimates of tropical lake fish yields. Commercial fish production in tropical African lakes grows logarithmically when primary productivity improves arithmetically [32]. Understanding ecosystem dynamics requires an understanding of the geographic changes in primary output, nutrient content, and community structure [33]. It is hard to construct a reliable estimate of all African lakes' primary production due to a lack of basic data on several lakes such as thorough data on seasonal and local variations in big tropical lakes like Lake Tanganyika [34]. Biological differences in aquatic systems can be qualitatively and quantitatively expressed as the abundance of composite biomass, diversity, or the rate of production of new organic matter. However, the rate of primary productivity is known to provide a more dynamic view of an aquatic system's evolution representing the immediate results of the interaction between physicochemical and biological variables, and a quicker response to trophic changes than biomass. It provides a more valuable record of changes in the trophic state of an aquatic system, while a measure of the standing crop provides only a static picture of the system [35]. Hence, the factor of the greatest importance in freshwater systems is often the assessment of the rate at which organic matter is formed from inorganic matter and accumulated. The fundamental process involved is photosynthesis, which is primarily carried out by the phytoplankton in the lacustrine environments of the lakes [32].

The primary productivity of a water body provides an index of potential energy support at the bottom of the food chain, and therefore, the

system's capacity to support the ecosystem is considered a sensitive and relatively accurate indicator of eutrophication and its measure is often mandatory in the monitoring and assessment of the ecological status of aquatic ecosystems [36]. Phytoplankton production is also important for element cycling and food supply to heterotrophs [37]. Consequently, information on the extent, variability, and regulation of photosynthetic productivity of phytoplankton have been and still are some of the main objectives in phytoplankton ecology [38]. On the other hand, zooplankton are one of the most significant biotic constituents in aquatic ecosystems, influencing all functional aspects such as food chains and trophic networks, energy flow, and water quality, as well as the circulation of matter as asserted by Paturej et al. [39]. A variety of physical, chemical, and biological variables can impact the species composition and abundance of zooplankton populations as demonstrated by Sampaio et al. [40]. The trophic condition of reservoirs has been shown to have a substantial influence on the composition and quantity of zooplankton [41–43].

To fulfill the world's expanding food demand, considerable efforts are required to create and use biological resources in the aquatic ecosystem. Energy flow in lakes and reservoirs is essential to determine the phytoplankton primary production and the environmental conditions that restrict or alter this productivity. The primary production of aquatic habitats is mostly determined by autotrophic organisms' photosynthetic activities [44]. Phytoplankton have a significant source of human food [45].

Melack and Kilham [46] hypothesized that in natural ponds that have not been affected by humans, gross in the rate of photosynthetic oxygen 30 g $O_2/m^2/d$ (c. 11 g $C/m^2/d$) or greater are seldom encountered. Phytoplankton's primary production and biomass are influenced by several chemical, physical, and biological factors. The more frequently the wind stirs the bottom of a lake, the faster nutrients are recycled from the mud into the photosynthetic domain, and more production may occur [47]. It has been found that changes in water level have a direct impact on the phytoplankton standing dynamics stock and African lake productivities [32,48]. Melack [32] discovered a favorable relationship between primary production and fluctuations in water level. To replicate, algal cells require a generally set number of components [49]. The nutrients needed by algal for development and proliferation are not always present in the proportions required by the phytoplankton [49]. Phosphorus and nitrogen, as well as silicon in diatoms, are thought to be growth-restraining nutrients.

A few but widely distributed species dominate the East African Rift lakes [50], making them an ideal location for studying previous changes in the production of algae and the organization of the community. Diatoms (Bacillariophyta) currently dominate primary productivity in Lake Malawi afterward, donations from Cyanobacteria (Cyanophyta) and green algae (Chlorophyta), with quite minor contributions from dinoflagellates (Pyrrophyta) [51]. The succession and composition of phytoplankton in Malawi Lake are primarily determined by the intensity of stratification density [52], which is influenced by temperature and dissolved solids gradients in the water column [53].

Lake Tanganyika's north-south rift valley is regarded as a key source of nourishment and trade for neighboring countries like Zambia, and Burundi. Throughout the year, the lake is oligotrophic and thermally stratified, with an anoxic hypolimnion. Strong southerly breezes shift the thermocline through the cold season, resulting in the upwelling of deeper nutrient-rich surrounding waters at the lake's southern margin [54,55]. Overall, these mixing episodes serve as the primary origin of many limiting nutrients to the surface of the water and are considered very critical in the maintenance of the pelagic food web [55,56].

The rates of phytoplankton primary productivity in tropical African lakes in general range from 0.8 in Lake Tanganyika to 30.90 g/Cm^2/d in Hartbeespoort Dam [57]. The productivity of phytoplankton in African tropical lakes varies significantly, reflecting their trophic condition. Lake Kainji is a model of an African poor nutrient lake (oligotrophic), with a low phytoplankton output of 0.3 gCm^2/h [58]. Lake Nasser the nutrient-rich lake (eutrophic), whose phytoplankton productivity has been mentioned to obtain 4.48 gCm^2/h, is at the upper end of the production range [59]. Expanding nutrient imports due to improved urbanization and agriculture have increased the production of primary productivity in numerous African lakes. Lake Chivero is an excellent example, where primary production levels have grown by more than 10 orders of magnitude from their own previously recorded span of 1.64 to 6.03 gCm^2/h in 1979 to their present range of 18.5 to 140 gCm^2/h [60,61]. Similarly, in the physio-nomically comparable Hartbeespoort Dam, primary production levels have surged to as high as 185 gCm^2/h, from a usual range of 0.40 to 30.90 gCm^2/h. These increased levels of primary production are linked to algae blooms and are the result of excessive nutrient inputs that overwhelm the lakes' natural purification mechanisms [62,63].

The imports of nutrients have a considerable influence on primary production in Africa's deeper lakes. Lake Malawi, for example, has seen primary production degrees climb from 0.24 to 1.14 gCm^2/h in recent years, to between 14.04 and 26.20 gCm^2/h [64], and Lake Victoria, where primary output has increased from 3.30 to 13.50 gCm^2/h, reaching 234 gCm^2/h [65]. Because of photo-inhibition, primary production in African tropical lakes is generally near or low at the water's surface. Phytoplankton thrive in the first 3–5 m of the water column. Below the euphotic depth, light becomes the restricting factor, while productivity tends to decline as depth increases. In Lake Chivero, which has been considered a reservoir on Zimbabwe's Manyame River, light is the most important limiting element for phytoplankton development [66], while conductivity and trophic state (as assessed by chlorophyll-*a* [Chl-*a*]) are the most significant environmental variables determining ciliate species distribution in this and other African fresh body waters [67]. These properties match a categorization of 17 East African lakes relating to water conductivity and phytoplankton diversity [68].

The Ethiopian Rift Valley features seven big lakes with a total size of around 2500 km^2. Zwei, Abiata, and Awassa Lakes have moderate to high primary production and phytoplankton crops, but Langano and Shala Lakes exhibit extremely poor productivity. The most and least productive lakes have the largest and lowest dissolved solids concentration, respectively, Lake Shala, although being the least prolific, has gross chemistry that is extremely close to one of the most productive [69].

On the other hand, Lake Hora-Kilole is tiny, shallow (7.8 m) some 50 kms southeast of Addis Ababa. The phytoplankton primary production and species composition in Lake Hora-Kilole vary significantly over time. Some photosynthetic indicators were also extraordinarily high, indicating that primary productivity was five times lower than before the river has been diverted off, however, the levels reported in 1994 were 6–57 times lower [69] following the river's diversion into the lake [70].

Diatoms, Cyanobacteria, and cryptophytes dominate at Lake Kivu (African Rift), with significant seasonal fluctuations caused by varying the depth of the mixed layer, as a result of varying light exposure and availability of nutrition. In terms of the productivity of phytoplankton, the phytoplankton ecology of Lake Kivu is analogous to that of other rift lakes. Despite its greater mean Chl-*a* content, Lake Kivu is comparable to the other rift valley lakes in terms of mean Chl-*a* concentration. As seen

in Lakes Tanganyika and Malawi, phytoplankton productivity can be N or P restricted, or N and P co-limited [71].

A comprehensive review of phytoplankton composition indicates a one-of-a-kind assemblage with few chlorophytes but long, thin *Nitzschia* and *Fragilaria* species, filaments Cyanobacteria (e.g., *Planktolyngbya limnetica*), pico-Cyanobacteria, and a large number of cryptophytes. At times, relatively considerable biomass of *Urosolenia* sp. may be found in the surface waters, and colonies of Microcystis migrate vertically, becoming evident at the surface of the Kivu Lake. Thus, phytoplankton diversity suggests functional group links in more fertile East African lakes like Lakes Victoria and Edward [71,72].

The type and diversity of phytoplankton in lakes typically reflect their nutritional status. Lake Ogelube with low Euglenophyceae biomass indicates minimal organic contamination and the dominance of desmids, representing an oligotrophic state [73]. Nutrient concentrations in the generally oligotrophic Lakes, Kivu, Kariba, and Malawi are relatively low. African lakes have seen significant increases in primary productivity (PP) as a result of human activity in their catchments, but they are still vulnerable to eutrophication due to high nutrient imports.

Phytoplankton photosynthetic characteristics in the Kenyan Rift Valley lakes (West Africa), which are famous saline-alkaline lake systems, have the light attenuation coefficients average of 13/m, displaying the massive phytoplankton bloom in the PP field measures, and no photoinhibition was detected. As a result of acclimatization to limited light supply, the curve initial slope (a) of photosynthesis–irradiance increased to 0.85 (mg O_2 mg Chl-a^{-1}/h) (mol photons/m^2/s) and the start of productive saturation (Ek) decreased to 11.4 μmol photons/m^2/s. In terms of the trophogenic zone, Bogoria, Nakuru, and Elmentaita lakes in Great Rift Valley, Kenya, all had high average net primary production (NPP) rates of 6.8, 10.7, and 8.5 g O_2/m^2/day, respectively. For the whole water column, NPP decreased to 21.4, 1.6, and 7.2 g O_2/m^2/day due to the high level of communal respiration. Modeling of gross primary production (GPP, Chl-*a*, initial slope a, light supply, maximum production rates considered) yielded annual values of 4.9, 6.8, and 4.2 kg O_2/m^2/year for Bogoria, Nakuru, and Elmentaita, respectively. Annual NPP values have been calculated down to the compensation depth to be 70%, 65%, and 55% of the GPP, respectively [74].

The phytoplankton production in the Kainji Lake (West Africa, Nigeria) is characterized by a relatively low pelagic photosynthetic

activity. The water temperature and hydrogen ion concentration do not limit the primary production in the lake. Low nutrient content and restricted transparency of the water caused by inorganic turbidity are believed to be the main factors limiting primary production. The lake has reached a dynamic equilibrium as regards the primary production level. Decomposition of the excess organic matter in the lake may lead to oxygen deficiency with an effect on fish production [75]. While in closed-basin lakes, like Lake Bosomtwe in West Africa, which is relatively deep compared to their surface area, with steep bathymetry, the dependence of phytoplankton primary production is even greater [76]. Because of restricted littoral areas and watershed inflows, such lakes typically have modest macrophyte development with a modest intake of allochthonous organic carbon [76]. Knowledge about the phytoplankton of Lake Bosomtwe is limited, with mentions by Whyte [76] of phytoplankton as food organisms for the zooplankton and fish of the lake and phytoplankton in relation to mercury biomagnification in a phytoplanktivorous cichlid, *Sarotherodon multifasciatus*, and other fishes in Lake Bosomtwe [77].

Lake Victoria is the second largest freshwater lake in the world. Its surface area is estimated to be 68,000 km^2 and a catchment that extends up to 193,000 km^2, with an average depth of 40 m. The lake is surrounded by five countries, three of which share most of the catchment (Kenya, Uganda, and Tanzania) and two share the drainage basin of the lakes (Rwanda and Burundi) [78,79]. Lake Victoria's eutrophication is driven by anthropogenic activities and climatic conditions in and around the lake basin. Variations in nutrient concentrations cause a substantial rate of primary production. The lake's organic matter in the basin is mostly derived from algae. The three nutrients, carbon, nitrogen, and phosphorus, are important for plant growth as well as algal production. Its excess amounts would cause permanent irreversible impacts to the lake and its fish catch, considering the excess amounts is through nonpoint sources [80]. The specific details chronostratigraphies for these cores' sediment have demonstrated significant changes in the lake's trophic structure state that happened before the transition in the fish population structure, and that the lake's higher productivity contributed more likely to an increase in fish captures after 1980 [81].

Phytoplankton diversity and biomass in the African tropical lakes show well-established seasonality [82,83]. Naturally, oligotrophic lakes, like Kivu, Edward, Malawi, and Kariba, have poor phytoplankton biomass and species variety, as well as a seasonal transition of major phytoplankton

species similar to that seen in Lake Tanganyika, where Chlorophyceae and Cyanophyceae dominate when phytoplankton biomass peaks during the rainy season, and Bacillariophyceae dominate during turnover in the dry season [83]. There is already evidence that Africa's tropical lakes are very productive [84]. Tropical lakes are often more productive than temperate lakes. However, the processes underlying high productivity in the tropics remain unknown due to a lack of published extensive seasonal studies on tropical lakes other than Lake Victoria [84]. Natural lakes in the tropics are uncommon, Africa being the sole exception, where they are predominantly found in the rift valley as well as the huge Congo River basin [85,86]. PP studies in aquatic environments are prevalent in the Northern Hemisphere, but in Africa, they have mostly focused on east African lakes and Egypt's subtropical waters [87].

Blooms of Cyanophyceae have also been seen in various nutrient-rich reservoirs, including the Erfenis, Hartbeespoort, and Allemanskraal Dams in South Africa [88,89], Cameroon's shallow tropical Yaounde' Municipal Lake [90], and the South African Orange River [91], within which nutrient-rich inflows have led to significantly increased phytoplankton biomass dominated by Euglenophyceae and where eutrophication has a greater impact on shallow lake ecosystems than on deeper tropical lakes such as Malawi, Victoria, and Kariba. Localized contamination is unusual in Lake Malawi, Lake Kariba, and Lake Victoria, for example [92,93]. The body water in Lake Kariba has progressed from an early eutrophic state to the current oligotrophic one, with phosphorus limiting its PP [94–96]. The large levels of fecal coliform bacteria observed in Zambezi waters above Victoria Falls, on the other side, along Lake Kariba's northern boundary, imply that the lake's waters are transitioning to a mesotrophic state [97–99].

Following the construction of the Aswan High Dam in Egypt's Southeast region. The El Nubaria Canal and El-Umoum Drain emerged as one of the mainland-based sources that regularly discharged their waters into the Mediterranean Sea via the Mariout Lake, west of Alexandria at the El Max Bay. Because of the discharge of home and industrial wastewaters, the drain water is somewhat brackish, does not extend above 5 psu, and has DO levels ranging from 0.5 to 3.58 mL/L. The nutrient salts had high quantities of phosphate, silicate, ammonia, and nitrites of up to 28, 346, 42, and 22 μM, respectively; the pH values ranged between 7.25 and 7.93 [100–102]. Previous studies on the water characteristics, phytoplankton, and zooplankton community in El-Mex Bay and the El-

Umoum Drain [103,104] indicated that the continual flow of contaminated water into the lake resulted in massive algal blooms and a chronic worsening of water quality. Furthermore, the consequence salinity variations affected the abundance and community structure of zooplankton in Lake Mariout was investigated.

Edku Lake, Egypt, is one of the northern African lakes which is subjected to daily industrial, domestic, and agricultural pollution. The lake is divided into different water masses according to the water sources. The lake is polluted, highly eutrophic, and subjected to severe conditions. These facts are confirmed by the domination of rotifers species, the extreme eutrophication conditions, and the declivity of water quality [105].

Few ecosystems in the world can match the high primary production of African lake wetland habitats. The nutrient-rich waters of wetlands provide critical feeding, breeding, and nursery grounds for fish without significant contributions from their floodplains which trap a large amount of nutrient material [106]. The high levels of primary production in the wetlands, coupled with their characteristic habitat complexity, provide the support base for some of the world's highest levels of biodiversity. Many wetlands support important populations of wildlife and plants, including endangered species, terrestrial mammals such as primates, and often a spectacular concentration of birds. Many mangrove regions are part of international flyways used by migrating birds [107]. Furthermore, there is significant fluctuation in phytoplankton production seasonally in African lakes [108], although comprehending these changes in connection to community structure and nutrient concentrations is lacking in comparison to temperate lakes [109]. The African continent has the greatest rates of carbon fixation in the Southern Hemisphere [110].

5.4 How eutrophication affects fish nutrition?

Phytoplankton are vitally important in tropical lake and reservoir ecosystems as they can be used to estimate expected fish production [111], productivity [112], and management [113]. When assessing the ecological status of lakes, plankton components (phytoplankton and zooplankton) should be considered. Researchers can examine patterns of response to cyclical changes and episodic disturbances by studying the shape and functioning of planktonic communities in reservoir ecosystems, as proposed by Nogueira [114]. According to the OECD [115], biomass, taxonomic

makeup, and phytoplankton variety are among the factors used to determine a water body's health.

Eutrophication is characterized by increased algal growth, which causes water quality to deteriorate through the appearance of abnormal color, decreased clarity, bad odor and taste, loss of dissolved oxygen, and changes in the aquatic food web [116]. Furthermore, Cyanobacteria (blue-green algae) can produce cyanotoxins, which can be harmful to people and animals who come into contact with or consume polluted water [117].

The energy passes from phytoplankton, the main producers, to zooplankton, the consumers, via traditional food chains and microbial food webs in pelagic environments [118]. Models that employ phytoplankton primary production as the key controlling variable for forecasting fish output in lakes and reservoirs have outperformed many other techniques [119].

The Municipal Lake of Yaounde (Central Africa), was formerly a well-known aquatic sport and leisure facility, but it has been deteriorating since the 1980s due to wastewater pollution from the "Grand-Messa" construction estate and ministerial and hotel compounds erected on pond shorelines. For many years, the pond has been threatened by phytoplankton blooms and thick, floating macrophyte growths, both of which indicate poor ecosystem health [90].

The form and transparency of the Great Lakes, Lake Malawi, and Lake Tanganyika are comparable, and they are all meromictic. Lake Victoria is shallower than Lakes Malawi and Tanganyika, yet they differ significantly in terms of hydrology, dynamics of nutrients [120], the composition of plankton [121], and trophic dynamics [122]. Hecky and Bugenyi [120] discuss this phenomenon, as well as the tropical Great Lakes' expected sensitivity to eutrophication due to their "endless summer," warm deep water, and reliance on direct precipitation in their water budget. Lake Victoria, in particular, got more deoxygenated as a result of eutrophication, resulting in a loss of acceptable habitat for fish and even fish deaths [123]. Lake Victoria as a whole is presently suffering from eutrophication, and many once-common species are no longer present or may have become extinct. Except for Lakes Malawi and Tanganyika, this is not yet the case. This demonstrates that the hydrology of the water body affects biodiversity vulnerability in addition to eutrophication, pollution, and other variables [124].

Phytoplankton communities go through numerous unique successions during their yearly evolution, with abundant, dominating, and

uncommon species coexisting [125]. The majority of phytoplankton species compete in their ecosystem for the same scarce resources, notably light and nutrients. Sommer [126] claims that the yearly fluctuation of dominant species can be anticipated, although the taxa that dominate communities are influenced by complicated variables like retention duration, nutritional load, and grazing stress. In most shallow tropical lakes, Cyanobacteria outweigh other species of algae and are significant competitors in high turbidity conditions [127].

Algal successions in tropical aquatic systems are often marked by a dramatic difference between the two main seasons (dry/wet-flood season): Lake Victoria Cyanobacteria/diatoms [128], Cyanobacteria (blue-green algae)/chlorophytes (green algae)−Chroococcales (blue-green algae) in Lake Tanganyika [129], and Cyanobacteria/diatoms−chlorophytes−Chroococcales in numerous reservoirs in northeast Brazil [130,131].

Lake Guiers in Senegal, in West Africa, is experiencing increasing eutrophication, particularly in the center zone close to the pumping station (N'Gnith) [132−134]. In comparison to pelagic responses, benthic population responses to eutrophication of the lake are poorly studied [135].

One of the most significant water quality issues is eutrophication in lakes across the world. To counterbalance the long-term consequences of eutrophication in human-dominated settings, long-term ecosystem management is required due to phosphorus accumulation in sediments, from agricultural regions [136,137]. A key component of Lake Ecosystem theory is the correlation between total phytoplankton chlorophyll and phosphorus in the water column. The capacity of competitive interactions among macrophytes and phytoplankton to change the clarity of shallow lakes from clear to turbid demonstrates that primary producer functional groups other than phytoplankton influence the ecosystem structure [138].

According to Gupta [139], high fertilizer inputs, eutrophication, acidification, heavy metal contamination, organic pollutants, and unpleasant fishing techniques all contribute to the deterioration of reservoir water quality. Monitoring reservoir water quality is crucial because it aids in the control of eutrophication and water body production. Eutrophication has a significant influence on the two main components of plankton communities (phytoplankton and zooplankton), causing various changes in their abundance and species composition in addition to influencing their linkages. Changes in the organization of the plankton communities with physicochemical parameters may be the first symptom of degradation in

water quality [140]. Bloom conditions are frequently associated with significant water quality disturbances, such as undesirable taste and odor.

5.5 Plankton and fisheries of African lakes

The state of productivity of each African lake, as well as the extent of diversity and abundance of plankton in it, has a direct impact on the survival and development of fish larvae in it, and thus, the abundance of its fish stocks and catches.

Year-to-year variability is a major productivity feature of African fisheries making it have the potential for improvement. Lake swamps that are surface-area systems with considerable seasonal and interannual changes, shallow lakes, floodplains, and reservoirs account for 57% of all water surface area [141], although climate-driven productivity fluctuations are also prevalent in larger and more stable systems [142–144].

Most African wetlands are rich in terms of species diversity and endemism, as evidenced by the presence of over 2000 identified indigenous freshwater fish species. With over 700 recognized species, 560 of which are indigenous to the Zaire River Basin, the Zaire River Basin is perhaps Africa's most diverse place for fish. There are at least 18 groups of indigenous freshwater fish fauna, many of which are located in East and Central Africa's large lakes [145].

The majority of countries with substantial inland fish caught are in Africa and Asia, with 5.8 and 2.1 million tons produced, respectively. The top 20 nations in inland capture fisheries output account for 84% of worldwide production, with 10 in Asia and 7 in Africa. However, the importance of inland catches changes from Asia to Africa on a per capita basis. The top 20 thus includes 13 African nations and just 4 from Asia. Even though Cambodia has the greatest inland capture fishery per capita, with 28.2 kg, outweighing Chad by a factor of more than three. In Africa's landlocked countries (Chad, Zambia, Uganda, Central African Republic, Mali, and Malawi), inland fisheries are especially significant, with a per capita catch ranging from 3.3 to 9.7 kg [146]. Inland capture data are not broken down by waterbody type, but rather apply to all rivers, lakes, and reservoirs. Despite the continent's massive river systems such as the Nile, Niger, and Congo, tropical lake fisheries remain the most important in Africa. Because many lakes and reservoirs are linked to larger river systems, accurate data are difficult to get. Zambia, Tanzania, Zimbabwe, and Malawi, all of which have significant lake fisheries, account for 60%–80% of total catch estimates [142].

As we mentioned before, throughout the year, Lake Tanganyika is oligotrophic and thermally stratified. Strong southerly breezes shift the thermocline through the cold season, resulting in the upwelling of deeper nutrient-rich surrounding waters at the lake's southern margin [54,55], and this results in high diversity and abundance in phytoplankton and zooplankton communities and maintenance of the pelagic food web which provides ideal feeding conditions for fish larvae in that lake. Lake Tanganyika has long been considered one of the world's most prolific pelagic fisheries, with a yearly catch estimated to be between 165,000 and 200,000 metric tons, worth tens of millions of US dollars [147]. The diversity of plankton communities declined significantly in the North Africa Edku Lake, Egypt, as a result of the decline in Lake Idku's natural characteristics, where rotifers and protozoans predominated, copepods and cladoserans were severely reduced, extreme eutrophication conditions prevailed, and water quality deteriorated [105], which was reflected in the diversity and subsistence of fish larvae, bringing the total number of recorded species to five.

Fisheries on Lake Victoria (LV) are particularly productive, contributing about one percent to global capture fisheries [148,149]. In Uganda, lake-based fisheries account for half of the total fish output and are economically significant. The LV fisheries contribute to the GDP in the following ways: food, income, employment, and foreign exchange earnings. Kenya has 0.5%, Tanzania has 2.5%, and Uganda has 2.8% [150,151]. Since the peak production of Nile perch in the early 1990s, LV has maintained high fish productivity, albeit the proportion contribution of the key commercial species to the overall production and the total value has changed over time. From 2011 to 2014, the anticipated total fish landings from Catch Assessment Surveys were over 1 million tons, with a beach value increasing from around US$ 550 million in 2011 to around US$ 840 million in 2014. The Dagaa output was predicted to be 456,721.20 tons in 2011 and climbed to 509,598 tons in 2014, while Nile perch production was 198,624 tons with a little increase to 251,063 tons. In 2014, the beach value of Dagaa remained relatively modest (US $ 135 million) as compared to previous years [152].

5.6 The impact of changes in plankton productivity on fish production

The East African Rift Valley contains a large number of lakes that have warmed throughout the twentieth century, including Lakes Tanganyika

[153,154], Victoria [155], Albert [156], and Malawi [156,157]. The surface-water temperature in Lake Tanganyika has risen by 0.9°C since 1913, meanwhile, deep-water temperatures have risen by 0.31°C [154]. Previous climate change has already had an impact on Lake Tanganyika's operation. This is observable as an increase in water level, surface-water temperature, and greater water column stability, which reduces layer mixing. Historical data indicate a 30% drop in fish productivity as a result of climate change and its consequences [153]. A comparable rise in surface-water temperatures has been seen in Lake Malawi throughout the twentieth century [156]. In comparison to Lake Tanganyika, Lake Malawi saw significant warming in the deep water of 0.7 °C between 1940 and 2000 AD [157]. It has been claimed that Lake Malawi's deep-water warming, attributed to milder winters reducing the amount of cold-water incursions into the lake's deep waters, may have lowered the lake's density stratification [157]. Significant storage gains in LV demonstrate that the lake's water level climbed by 1.4 m, resulting in a volume increase of around 1750 Giga tons. Multiple positive trends in the lake's water storage increase have been observed in the last 2 years, with two major events in April–May 2019 and December 2019–January 2020, with rainfall occurring during the short rainy season of September to November (SON) having a dominant effect on the lake's rise due to climate change [155].

Aside from climate changes that happened throughout the twentieth century, the lakes of the East African Rift Valley have also witnessed the consequences of anthropogenic activity in their watersheds, such as land-use change caused by fast-expanding populations. In Malawi, it was estimated that landscape-wide deforestation rates during 2000–09 were 42,961 ha/year and increased during 2009–15 recording 71,878 ha/year [158].

Because the maximum rate of photosynthesis per unit of biomass (photosynthetic capacity) changes with temperature, warm tropical lakes have two to three times the PP of temperate lakes [47,159].

Furthermore, interannual variations in phytoplankton composition and biomass are known to be affected by climate change [160]. The impact of climate change models' predicted global warming is unknown [161,162]. The phytoplankton production in tropical African lakes has received little attention [163]. Previous phytoplankton research in tropical African lakes such as Lake Volta, Lakes Malawi, Tanganyika, and Victoria [84,111,164], as well as other African lakes [165–167], did not focus on climate-related changes. The lakes of East Africa, on the other hand, may be especially

sensitive to climate change [168,169], as a result of climate change and global warming, large-scale changes in the plankton ecosystem occur in terms of plankton biodiversity, production, and species distribution, which have had an impact on other aquatic life. For example, the biomass of the dominant and important zooplankton species, such as *Calanus finmarchicus*, has decreased. Additionally, Warmer-water affinities species (e.g., *Calanus helgolandicus*) substitute the other species that are not as abundant or nutritious important (e.g., less lipid-rich). Many plankton and fish species' distributions shift as a result. In response to recent climate changes, the seasonal alternation and production of some plankton species have altered [17]. This has implications for plankton feeder organisms, such as fish, whose life cycles are synchronized to take advantage of specific prey species' seasonal production.

Tropical African lakes are particularly vulnerable to climate change because of significant changes in the thermocline throughout a small range of high-water temperatures. Lake phytoplankton's biomass and productivity have been diminished as a result of recent global warming. A drop in attractive chlorophyte development, along with a rise in Cyanobacteria, has resulted in a decrease in zooplankton production and, as a result, a decrease in fish populations, both of which may be attributed to rising water temperatures. This demonstrates that even little climate change may affect phytoplankton dynamics in tropical African lakes, lowering water quality and food availability for planktivorous fish, with major consequences for human life [108].

Plankton response and mitigate eutrophication and climate change, resulting in a consequent impact on lake fish stocks and human livelihoods. As water temperatures rise, algal succession proceeds from diatoms to chlorophytes and then Cyanobacteria [24]. The prevalence of Cyanobacteria (especially *Microcystis*) in LV as a result of rising water temperatures (over 25°C) has raised concerns that rising water temperatures caused by global warming can indeed lead to a decline in the yield of palatable chlorophytes, resulting in a reduction in zooplankton production and a consequent significant drop in fish stocks [142]. Over the last decades, fisheries data from Lake Tanganyika have shown significant correlations with climatic (ENSO) data. This assumes that even minor warming could disrupt plankton dynamics, lowering water quality and potentially reducing food resource availability for higher trophic levels like planktivorous fish [34]. Furthermore, as reported in Lake Chivero, oxygen depletion (3.9 mg/L at water surface and 2 mg/L at 5 m depth), lesser

than in the Nyanza Gulf of LV, and the release of toxins caused by the die-off of algal bloom result in massive fish mortality of *Oreochromis niloticus* [63,94]. Algal toxins resulting from algal bloom die-off have previously been found in Lake Chivero and the drinking tap water regenerating from the lake. Furthermore, Microcystis strains that are toxic have been found in other African lakes as well as in freshwater bodies around the world [63,94].

In a changing climate, the future of African lakes appears gloomy, posing many challenges that must be overcome, the most significant of which is gaining a better understanding of how climate change will affect aquatic habitats and human livelihoods. The impact of climate change and global warming on the lakes' water temperature and lakes' hydrology (through stratification destabilization) could have an impact on phytoplankton production by reducing both their diversity and abundance in African lakes. The resulting cascade through a longer trophic chain, caused by the domination of smaller phytoplankton, might significantly influence zooplankton availability and fish production, threatening the viability of riparian communities' fishery industries that sustain their livelihood [162,163].

African lakes are essential because they provide a significant source of inexpensive protein (fish) as well as drinking water for humans, farm animals, and agricultural irrigation. Lakes Victoria, Tanganyika, Malawi, and Kariba, as well as Lake Chilwa, provide more than 60% of dietary protein for neighboring rural societies. Nowadays, many African lakes are experiencing drops in fish diversity and abundance as well as a decline in water quality. The lakes also play an important role in the transport of goods both locally and internationally, and they are regarded as a means of hydroelectric power generation as well as a source of income from eco-tourism and fishing. Furthermore, many African lakes, especially Victoria, Tanganyika, and Malawi, are havens for various endemic fish species of enormous ecological, economic, and scientific importance, which rely on the sustained seasonality of the plankton and their stratification [83]. Although policies have been established to mitigate such threats, there is still an immediate need to continuously monitor the environmental status of African lakes to avoid the negative effects of anthropogenic impacts and climate change.

Increased water temperatures caused by climate change may favor a shift in phytoplankton species' composition from Chlorophyceae to Cyanophyceae, which are more competitive at higher temperatures [170]. Although total phytoplankton biomass is often unaffected by high

temperatures, microcosm experiments have revealed that high temperatures diminish overall zooplankton biomass by changing phytoplankton community composition toward high-temperature-tolerant species [171]. These findings are consistent with changes in phytoplankton composition observed in temperature-controlled experiments on phytoplankton cultured in Lake Chivero water samples, where water temperatures where Cyanophyceae predominated were several degrees higher than those where Chlorophyceae predominated [172]. As water temperatures rise, algal succession proceeds from Bacillariophyceae through Chlorophyceae to Cyanophyceae [173]. Concerns have been raised that rising water temperatures caused by global warming may impair the production of edible Chlorophyceae, resulting in decreased zooplankton production and, as a result, a loss of fish supply. Indeed, Lake Tanganyika fisheries' harvest statistics have demonstrated substantial negative associations with climate (ENSO) data during the previous 40 years [174]. Mild warming has been proven to influence plankton dynamics in shallow cold-water situations, lowering water quality and food options for higher trophic levels such as planktivorous fish [175].

On the other hand, the examination of climate data for the middle Zambezi Valley suggests that warming near Lake Kariba is occurring quicker than regional models expected [176]. These changes in the thermal characteristics of the lake have already resulted in upward migration of the thermocline [96], pointing to future changes in phytoplankton species' richness and productivity, which could have a negative impact on fish populations and human livelihoods.

5.7 Plankton in fish guts in African lakes

Cells of phytoplankton and zooplankton might be utilized as natural fish food [165,166], as they provide a lot of vitamin precursors, growth boosters, and vital fatty acids [167]. Fish, in general, may consume several morphological types of phytoplankton and zooplankton, such as filamentous, colonial, and single-celled forms [177]. Fish that feed on phytoplankton and zooplankton can reduce phytoplankton biomass in tropical lakes and reservoirs by eating on bigger algal and cyanobacterial forms rather than tiny ones [178].

The cichlid is an example of the most abundant and widespread fish species in African lakes where it accounts for the majority of fish production and is economically significant. It thrives in the shallow and stagnant

waters and vegetation areas of these lakes [179]. Many scientists have investigated these organisms' feeding habits. Based on a study of the feeding habits of Nile tilapia fish in the lakes of South-Benin, West Africa, Houehanou et al. [180] confirmed that these fish rely on a variety of food sources, including plankton; they can utilize different types of food, making them omnivorous.

Tesfahun [181] conducted a review of biological evidence in some Ethiopian lakes, as well as the results of stomach contents and feeding habits of *O. niloticus*, in 2018, and concluded that these fish are heavily dependent on plankton abundance, as they primarily contribute to accelerating growth rates.

The feeding habits, food contents, and stomach contents of adult and juvenile Nile tilapia fish in Lake Chamom, Ethiopia, were studied, and it was concluded that plankton components in the stomachs of such planktivorous fish varied seasonally [182]. They feed by capturing plankton in a plankton-rich bulk with mucus produced by their gills [183]. This is also confirmed by the studies of Ali et al. [184] on fish of Lake Alau, Nigeria, and Abidemi-Iromini [185] on the Lagos Lakes, Nigeria, which confirmed the importance of plankton as one of the main food sources for fish in such African lakes, forming the main bulk of food items (representing 62.32% of stomach contents) as most of these fish are filter and benthic feeders, and they consume plankton and its detritus in considerable proportion.

According to Kamanyi et al. [186], analysis of the stomach content of *O. niloticus* samples collected from Lake Edward and Lake George, Uganda, found that blue-green algae were the most abundant (44% of total plankton in stomach content in the fish of Lake Edward, 62% in Lake George), followed by diatoms (40% and 25%, respectively, for the two lakes) and green algae (16% and 13%). Furthermore, there was diatom domination (49.2% of total plankton content) in the stomach content of *O. niloticus* collected from Egypt's Abu-Zabal lakes [187].

Turker et al. [177] mentioned that Nile tilapia is more effective in filtering green algae and Cyanobacteria from African water sources. Salazar Torres et al. [188] studied the tilapia stomach contents in a tropical eutrophic reservoir and found that Cyanobacteria formed a significant part of its diet. The number of these species in the fish gut appears to be influenced by the density of these species in the African lakes' habitat as well as the health of the fish [189]. Potentially poisonous Cyanobacteria, such as *Microcystis* and *Anabaena*, have been identified as the most prevalent phytoplankton consumed by Nile tilapia in several African lakes [190].

Tilapia may provide options for Cyanobacteria management in eutrophic lakes. The phytoplankton species in the stomach and feces of tilapia fish (*O. niloticus*) in Egyptian fishponds were studied by Mohamed et al. [191], and phytoplankton in bulk were detected in the gut of Nile tilapia (36%–50%) and Chlorophyta (27%–38%). Other groups such as diatoms, Euglenophyta, and Dinophyta were also discovered, albeit at a lesser rate (19%). The potentially hazardous Cyanobacteria *Anabaena*, *Anabaenopsis*, *Cylindrospermopsis*, *Microcystis*, and *Planktothrix* were the most important and prevalent phytoplankton species discovered in the tilapia gut. Only diatoms were found in the tilapia feces, demonstrating that tilapia can digest all phytoplankton except diatoms.

Food items in the stomachs of *O. niloticus* in Lake Baringo, Kenya, included algae (26%–88% of diet depending on size classes of the fish), detritus, zooplankton, plant materials, fish, and insects; however, the dependence on zooplankton decreased as fish growth accelerated and the size increased [192]. The cladocerans *Daphnia barbata*, *Diaphanosoma excisum*, and *Moina micrura* are among the zooplankton species that compose the major food of *O. niloticus* while *Brachionus patulus*, *Keratella tropica*, and *Filinia opoliensis* were the most abundant rotifer species. On the other hand, Copepod nauplii were the most abundant among all copepod species and expressed in a small proportion of the total zooplankton species. *D. excisum* and *M. micrura* were the most commonly consumed prey by the fish. While the African catfish *Clarias gariepinus* fed mostly on fish, with fish accounting for 75% of stomach content. *C. gariepinus* consumes zooplankton as well, particularly the cladoceran *D. barbata*.

In addition, several previous studies reported that *O. niloticus* feeds on bottom sediments formed from plankton rain and other origins, and derives its nutrients from organic molecules and microorganisms [193–195]. They are fed on plankton that is shaped and mainly driven by the habitat's nutrient dynamics [183]. The fish-feeding habits and stomach contents are dependent on the presence and abundance of plankton in their environment, which contributes to the fish's growth rate [181].

5.8 Future perspectives of plankton and fish nutrition in African lakes

To summarize, not all African lakes received equal attention in research studies, particularly those related to their PP and its impact on the subsistence and abundance of fish larvae, which is ultimately reflected in the

catches of those lakes, however, the findings of previous studies confirm that the state of any African lake's fish productivity is directly correlated to its PP. The level of interest in developing and sustaining those lakes, as well as dealing with the effects of climate change, has a significant impact on their PP and subsequent fish catches.

In a changing climate, the status of plankton in tropical African lakes is gloomy. This comes with several challenges, the most important of which is determining how climate change will affect aquatic ecosystems and human livelihoods [162,163].

The effects of climate change on lake hydrology, such as stratification instability and lake temperature, may have an impact on phytoplankton production by lowering both quantity and composition in many tropical African lakes. Because of the dominance of smaller phytoplankton, the subsequent cascade down a longer trophic chain might disrupt zooplankton and fish productivity, ultimately threatening the viable fisheries sectors that maintain the lives of riparian communities [196].

African lakes have a high value because they contribute greatly to poverty reduction and food security. They are an inexpensive source of dietary protein, with lakes such as Chilwa, Kariba, Malawi, Tanganyika, and Victoria delivering more than 60% of dietary protein to neighboring rural people. The lakes also serve as a supply for drinking water for humans and cattle, irrigation water for agriculture, a mode of transit for products, a source of hydroelectric power, and a source of money from fishing and eco-tourism. Lakes Malawi, Tanganyika, and Victoria, in particular, provide a home for rich indigenous fish species of enormous ecological and scientific significance. Many tropical African lakes are experiencing decreases in fish population and variety as well as deterioration in water quality. Although laws have been put in place to counteract these concerns, there is still an urgent need to constantly monitor the health of tropical African lakes to avoid the negative consequences of anthropogenic pressures and a changing climate [197].

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CHAPTER 6

Diversity and importance of zooplankton in the African lakes

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6.1 Introduction

In 1957, Hutchinson [1] published a monograph titled *A Treatise on Limnology* which is regarded as a landmark discussion and classification of all major lake types, their origin, morphometric characteristics, and distribution. The African lakes were divided into three classes according to their conductivity by Talling and Talling [2]. The first class has conductivity less than 600 μS. These lakes draw their water from direct surface runoff or low-salinity rivers. These include Lakes Nasser, Malawi, Malombe, Victoria, Tana, and George. The second-class lakes have higher total ion concentrations and conductivity between 600 and 6000 μS. This class includes Lakes Tanganyika, Edward, Albert, Turkana (Rudolf), and the Egyptian North Lakes. The third class has a conductivity of 6000−160,000 μS. These lakes, which often include accumulates of hard minerals like trona, include Nakuru, Magadi, Natron, Manyara, and Katwe.

Africa has five major basins occupying the center of the continent (Fig. 6.1). The flow of most rivers toward the ocean occurs through canyons and cataracts, which have a major impact on the distribution of aquatic taxa in the Congo, Zambezi, Nile, or Niger basins. Some lakes have no outlet to the sea (endorheic lakes), in semiarid regions [3]. With an area of 65,000 km^2, Lake Victoria occupies a depression located in the center of the two divisions of the Rift Valley. The volcanic activity associated with these various rifts resulted in the formation of hundreds of crater lakes, mostly along the Western Rift.

Africa has about 30,000 km^3 of water in large lakes and reservoirs [5,6], both natural (Lake Victoria) and artificial (Lake Nasser). Many lakes have had great attention, including Lakes Nasser, Victoria, Volta, and Tanganyika. Human impacts in the lakes that cause many problems to water quality in the African lakes include pollution, eutrophication, and

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Figure 6.1 The main hydrographic basins in Africa with altitudinal zones above 1000 m and distribution of Africa's major lakes [3,4]. *From D. Paugy, C. Levêque, O. Otero (Eds.), The Inland Water Fishes of Africa Diversity, Ecology and Human Use, IRD Editions, Mrac Editions, Marseilles, 2018, p. 680. EAN (Print Edition): 9789492669100, Electronic EAN: 9782709924016, https://doi.org/10.4000/books.irdeditions.25130; L.C. Beadle, The Inland Waters of Tropical Africa, Longman Group Limited, England, 1981.*

increasing salinity of lake water. These changes will alter the species composition of phytoplankton, zooplankton, and fish in these African lakes. The significance of African lakes is great because they make a significant contribution to poverty reduction as the main source for fish production [7] as shown in Fig. 6.1 and Table 6.1.

Zooplankton are small, about 0.1 to 13 mm in length, free-swimming organisms, floating, and lack the ability to move horizontally against water currents. Zooplankton organisms are classified according to the time they spend in the plankton into two groups; holoplankton (true plankton) have a full life cycle in the water column. Other animals, namely, meroplankton, spend a portion of their early life cycle as free-living plankton,

Table 6.1 Important lakes in Africa [8].

Country	Important lakes
Algeria	Lake Rhaba, Lake Bokka E, Lake Edku
Cameroon	Lake Chad, Lake Monoun, Lake Nyos
Chad	Lake Chad
Egypt	Lake Nasser, Northern Lakes (Burullus, Maruit, Manzala, Edku, Bardawil)
Ethiopia	Lake Tana
Ghana	Songor Lagoon
Kenya	Lake Nakuru, Lake Tana, Lake Victoria
Madagascar	Lake Alaotra
Malawi	Lake Malawi
Mali	Lake Manantali
Morocco	Reservoir of Yacoub El Mansour
Nigeria	Challawa Gorge Reservoirs
Niger	Lake Chad
Rwanda	Lake Kivu
South Africa	Lake Sibaya, Lake St. Lucia
Tunisia	Lake Zerga, Lake Chitane, Lake Ichkeul, Lake Korba
Tanzania	Lake Malawi, Lake Tanganyika, Lake Victoria
Uganda	Lake Victoria

Source: Modified from World Lakes Network, Protecting and reshaping the health of lakes throughout the world, 2004. Available at http://www.worldlakes.org/.

and the other portion is either benthic organisms or swim against currents like a fish.

The main groups of zooplankton are Protozoa, Rotifera, and Crustacea. Although rotifers are abundant, Cladocera and Copepoda constitute the majority of the biomass. Some zooplankton feed on phytoplankton or bacteria (herbivorous), while others feed on other zooplankton (predatory). The abundance and diversity of zooplankton taxa vary spatially at any water body due to both abiotic and biotic factors.

All fish feed on phytoplankton and zooplankton as the main source of energy. The search for food by these fish is therefore a key activity. Bowen [9] pointed out that the majority of African fish rely on phytoplankton for food in addition to zooplankton or benthic invertebrates. The most important zooplankton groups in the African lakes are crustaceans and rotifers. The role of zooplankton in food webs is shaped by a variety of different interacting factors. The most important ones relate to the catchment area, water chemistry, climate, and ecosystem characteristics [10–12].

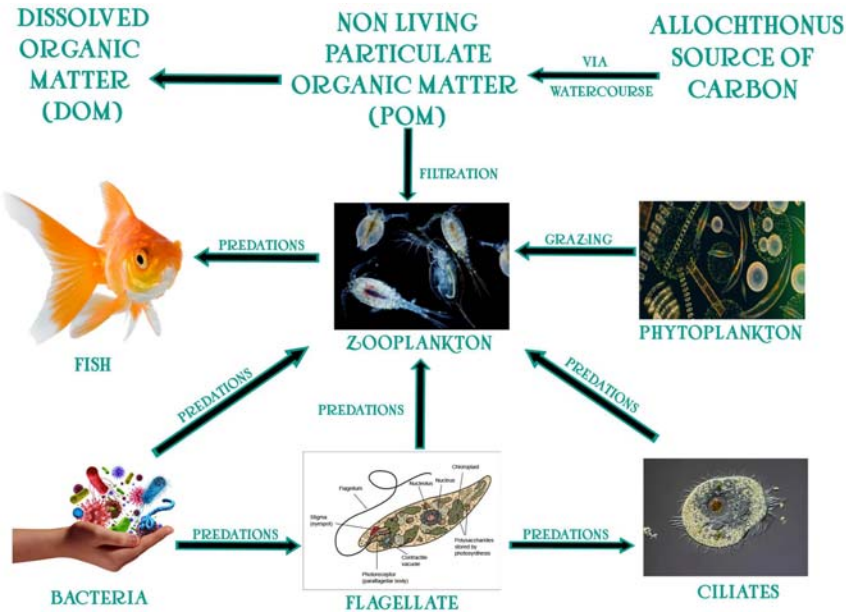

Figure 6.2 Sketch showing the importance of zooplankton in the aquatic food web of a lake in Africa. All organisms are in the DOM pool after death [17]. *Modified after A.S.M. AL-Budeiri, The Role of Zooplankton in the Pelagic Food Webs of Tropical Lakes, M.Sc. University of Leicester, United Kingdom, 2021, 231 pp.*

Zooplankton are central to the aquatic food web [13] (Fig. 6.2). They consume bacteria, flagellates, ciliates, phytoplankton, particulate organic matter (POM) and are themselves a major food source for fish [14]. Zooplankton can also reduce eutrophication from phytoplankton grazing [15]. In addition, zooplankton can feed directly on POM derived from autochthonous sources, including algal debris [16]. The aim of this chapter is to comprehend the diversity and distribution of zooplankton organisms and their function in some African lakes.

6.2 Population and distribution of zooplankton in African lakes

Zooplankton play major role in maintaining the quality of aquatic ecosystems in African lakes. They are distributed in the different African lakes according to their physicochemical parameters, predators, and food availability.

6.2.1 Zooplankton of North African lakes

18,19 studied nine northern African lakes (Megene Chitane, Merja Sidi Bou Rhaba, Merja Bokka, Merja Zerga, Lac de Korba, Garaet El Ichkeul, and three Egyptian northern lakes) during 1997/99. The total zooplanktonic taxa recorded were 88 taxa characterized by broad tolerance to water quality. However, some recorded species were very rare for North African freshwater lakes, like *Alonella excisa*, *Leydigia quadrangularis*, and *Ilyocryptus sordidus*. North African lakes typically show high variations in salinity due to stagnant waters in these lakes, and some groups are good indicators of large varying characteristics. The zooplankton communities (Table 6.2) identified in northern African lakes included crustaceans (Cladocera, Copepoda, Ostracoda, and Diptera larvae) in addition to Rotifera [20–23].

Chakir and Saadi [24] studied the spatiotemporal distribution of crustacean zooplankton in relation to environmental factors in the Yacoub El Mansour Reservoir in Oued N'fis, located at 65 km south of Marrakech (Morocco). The samples are taken during two annual cycles, 2012 and 2013. In this study, six species of crustacean zooplankton are divided into two groups: copepods and cladocerans were identified. *Daphnia lumholtzi* is the most dominant species, accounting for 58.26% of the total zooplankton.

All zooplankters of Lake Edku have a distinct freshwater character. This indicates that despite the sea connection, the diversity is currently not strongly influenced by seawater. However, as *halophobes*, *Bosmina longirostris* and *Brachyurum excisum*, were only distributed in the freshwater areas to Edku, El Hawary [23] recorded *Diaphanosoma excisum* in a few locations beside the freshwater Edku drain. Cladocera dominated Lake Edku during the 1970s and 1980s, followed by copepods, while Rotifera were a rare group or even absent as indicated by Ref. [25]. The zooplankton assemblage has changed from the dominance of Cladocera and large zooplankters to rotifers and tiny zooplankters over the past 50 years as a result of increasing eutrophication due to drainage water. The zooplankton community in Lake Edku consists of 72 taxa, rotifers accounted for 90.35% of all zooplankton counts [26]. Rotifers were dominated by the *Brachionus* as an indicator of organic pollution and eutrophication. The dominance of rotifers may be due to favorable ecological parameters, excessive food requirements, and lack of invertebrate predators [27]. Hassan et al. [26] concluded that the species *Brachionus calyciflorus* and

Table 6.2 Species of copepods and rotifers taxa from nine northern African lakes.

Taxa	Morocco		Tunisia				Egypt		
	R	B	Z	C	I	K	E	BU	M
Copepoda									
Acanthocyclops robustus	×	–	×	–	×	–	–	–	–
A. vernalis	–	–	–	–	–	–	×	×	×
Acartia clausi	–	–	×	–	–	–	–	–	–
Attheyella trispinosa	–	–	–	–	×	–	–	–	–
Calanipeda aquae-dulcis	–	–	×	–	×	–	–	–	–
Canthocamptus microstaphylinus	–	–	–	×	–	–	–	–	–
Cletocamptus confluens	×	–	–	–	–	×	–	–	–
Diacyclops bicudpidatus	–	–	×	–	–	–	×	×	×
Diaptomus cyaneus cyaneus	–	–	–	×	–	–	–	–	–
Eucyclops serrulatus	–	–	–	×	×	–	–	–	–
E. speratus	×	–	×	–	–	–	×	×	×
Halicyclops neglectus	–	–	–	–	–	×	–	–	–
Mesocyclops leukarti	–	–	–	–	–	–	×	×	×
Metacyclops minutus	–	–	–	×	–	–	–	–	–
M. planus	–	×	–	–	–	–	–	–	–
Neolovenula alluaudi	–	×	–	–	–	–	–	–	–
Oithona heloglandica	–	–	×	–	–	–	–	–	–
Tropocyclops prasinus	×	–	×	–	–	–	–	–	–
Rorifera				–	–	–	–	–	–
Brachionus plicatilis	×	–	–	–	–	–	–	–	×
B. urceolaris	–	×	–	×	–	–	–	–	×
Brachionus calyciflorus	–	–	–	–	–	–	×	×	×
Colurella uncinata	×	–	–	–	–	–	×	–	×
Keratella quadrata	–	–	–	–	–	–	×	–	×
Notholca marina	–	–	–	–	–	×	–	–	–
N. salina	–	–	–	–	×	–	–	–	–
N. squamula	–	–	–	–	–	–	×	–	×
Species number	**6**	**3**	**7**	**5**	**5**	**3**	**9**	**5**	**9**

Note: *R*, Lake Rhaba; *B*, Lake Bokka; *Z*, Lake Zerga; *C*, Lake Chitane; *I*, Lake Ichkeul; *K*, Lake Korba; *E*, Lake Edku; *BU*, Lake Burullus; and *M*, Lake Manzala. × = Present, – = Absent.
Source: Adapted from M. Ramdani, N. Elkhiati, R.J. Flower, H.H. Birks, M.M. Kraïem, A.A. Fathi, et al., Open water zooplankton communities in North African wetland lakes: the CASSARINA project, Aquat. Ecol. 35 (2001) 319–333.

Brachionus angularis together contributed about 60% of the total zooplankton density. Fourteen species of Copepoda were represented with *Acanthocyclops tragani* dominating. Cladocera were represented by eight species: *Moina micrura* and *B. longirostris* dominating. Hassan et al. [26] surveyed zooplankton in Lake Edku during 2004. They identified 72 species

of zooplankton, including Rotifera, Copepoda, and Cladocera, with the dominance of rotifers (90.35% of the total number of zooplankton).

The community of zooplankton in Lake Burullus contained 12 zooplankters with low species abundance, and four species were dominant [28]. They were *B. calyciflorus*, the ostracods *Limnocythere inopinata*, *Loxoconcha elliptica*, and *Cyprideis torosa littoralis*. The dominant Ostracoda species indicate that brackish water conditions prevailed in the lake. Saad [28] identified 48 species of zooplankton community in Lake Burullus during 2001–02 (34 Rotifera, 7 Copepoda, and 7 Cladocera). Rotifera was the highly predominant group representing 73.5% of the total zooplankton, with high densities in the western section of the lake.

Lake Manzala had higher biodiversity with 19 taxa of zooplankton. All the identified taxa indicate the prevalence of freshwater characters. However, the presence of *L. inopinata* with low abundances reflected the effect of some brackish water [19].

Galal [29] collected monthly zooplankton, particularly protozoan organisms, from Lake Manzala at 30 cm depth of the water surface. Regarding the numerical abundance of the major zooplankton groups in Lake Manzala, protozoa represented the most dominant type of zooplankton where ciliates predominate flagellates than sarcodines. The numerical densities of the total protozoa and their three differential superclasses (Sarcodina, Mastigophora, and Ciliophora) showed their lowest values in winter (7.99, 0.32, 1.87, 5.8, and 103/L), while their highest ones were achieved during autumn for sarcodines and ciliates (0.64 and 7.9 10^3/L) besides those of flagellates and total protozoa which were obtained in summer (4.9 and 12.86 10^3/L).

6.2.2 Zooplankton in Lake Nasser (Egypt)

Lake Nasser is one of the largest artificial lakes in Africa. It is located in Aswan (Egypt), next to the Sudanese borders. The lake was created between 1958 and 1970 by damming the Aswan High Dam over the Nile. Lake Nasser extends about 300 km and has an area of about 5250 km^2 [30]. Rzoska [31] checked the Nile zooplankton in the River Nile and Lake Nasser. He found that the species diversity has been more or less stable over time (Table 6.3). Many studies have addressed the zooplankton community in the main channel and khors of Lake Nasser [32–34]. El-Shabrawy [35] found that the density of zooplankton in the main channel varied between 25 and 120×10^3 ind. m^3. El-Shabrawy and Dumont [36] surveyed the zooplankton of some khors and the littoral

Table 6.3 Species of zooplankton recorded from Lake Nasser between 1981 and 2015.

Taxa	1989/90	1993/94	1996/98	2003	2009	2015
Protozoa						
Arcella discoides	–	×	×	–	×	×
A. dentate	–	–	–	–	×	×
Centropyxis aculeata	–	×	×	–	×	×
Epistylis bimarginata	–	×	–	–	×	×
Euplotes patella	–	×	–	–	–	–
Vorticella campanula	–	–	–	–	×	×
Rotifera						
Anuraeopsis fissa	–	×	×	–	–	
Ascomorpha ecaudis	–	×	–	–	×	×
Asplanchna girodi	–	–	×	–	×	×
Brachionus angularis	×	×	×	–	–	
B. calyciflorus	×	×	×	×	×	×
B. caudatus	×	×	–	–	×	×
B. falcatus	×	×	×	×	×	×
B. patulus	–	×	×	×	×	×
B. plicatilis	×	×	–	–	×	×
Cephalodella catellina	–	–	–	–	×	×
Collotheca balatonica	–	–	–	–	×	×
Conochilus sp.	–	–	–	–	–	×
C. hippocrepis	–	×	–	–	×	×
C. unicornis	–	×	–	×	–	–
Conocholodies sp.	–	–	–	–	×	×
Epiphanous sp.	–	–	–	–	×	×
Euchlanis dilatata	×	×	×	–	×	×
Filinia opoliensis	×	×	×	×	×	×
F. longiseta	×	×	×	–	×	×
Hexarthra mira	×	×	×	–	×	×
Keratella cochlearis	×	×	×	×	×	×
K. quadrata	–	×	–	×	–	–
K. tropica	×	×	×	×	×	×
Lecane arcula	–	–	×	–	–	–
L. bulla	×	×	×	–	×	×
L. closterocerca	–	–	×	–	–	–
L. luna	×	×	×	–	×	×
L. lunaris	×	×	×	–	–	–
Mytelina ventralis	–	–	–	–	–	×
Phylodina sp.	–	–	–	–	×	×
Polyarthra vulgaris	×	–	×	×	–	–
Pompholyx complanata	–	×	–	–	–	–

(*Continued*)

Table 6.3 (Continued)

Taxa	1989/90	1993/94	1996/98	2003	2009	2015
Proalides sp.	–	–	×	–	–	–
Scaridium longicaudum	×	–	–	–	–	–
Synchaeta sp.	–	–	–	–	×	×
Trichocerca sp.	–	–	–	–	–	×
T. similis	×	×	×	×	×	×
T. pusilla	–	×	–	–	–	–
T. porcellus	–	×	×	–	–	–
T. longiseta	–	–	×	×	×	×
Trichotria tetractis	–	–	–	–	×	×
Testudinella patina	–	×	–	–	–	–
Copepoda						
Thermodiaptomus galebi	×	×	×	×	×	×
Thermocyclops neglectus	×	×	×	×	×	×
Mesocyclops ogunnus	×	×	×	×	×	×
Ergasilus sieboldi	–	–	–	–	–	–
Halicyclops magniceps	–	–	–	–	–	–
Harpacticoida sp.	–	–	–	–	×	×
Cladocera						
Alona rectangula	–	–	×	×	–	–
A. intermedia	×	–	–	–	–	–
A. affinis	–	–	–	–	–	–
A. quadrangularis	–	–	–	–	×	×
Bosmina longirostris	–	–	×	×	×	×
Chydorus sphaericus	–	×	×	×	×	×
Ceriodaphnia dubia	–	–	×	×	×	×
C. quadrangula	×	–	×	–	–	–
C. cornuta	×	×	–	×	–	–
Daphnia barbata	×	–	×	×	–	–
D. longispina	–	×	×	×	×	×
Diaphanosoma excisum	×	×	×	×	–	–
D. mongolianum	–	–	×	–	×	×
Macrothrix laticornis	×	–	×	–	–	–
M. spinosa	–	–	–	–	×	×
Simocephalus vetulus	–	–	×	×	–	–
Number of species	26	36	38	23	41	44

Note: 1998/90: after [32], 1993/94: after [37], 1996/98: after [35], 2003: after [38], 2015: after [39].
× = Present, – = Absent.

area of Lake Nasser and found that taxa of Rotifera, Cladocera, and Copepoda were the main taxa. El-Shabrawy and Dumont [36] recorded 27 species of zooplankton taxa. Copepods were represented by the

cyclopoids, *Thermocyclops neglectus* and *Mesocyclops ogunnus*, and the calanoid, *Thermodiaptomus galebi*. Ten cladoceran species were identified, contributing 17% of the total zooplankton density, with *B. longirostris*, *Ceriodaphnia dubia*, *Daphnia longispina*, and *Diaphanosoma mongolianum* being the most common species.

Fourteen rotifers species, accounting for 16% of the total zooplankton, were recorded [35]. *Keratella cochlearis* dominated (76% of the total rotifers count), followed by *B. calyciflorus*. El-Shabrawy [35] recorded the assemblage of zooplankton in Lake Nasser, consisting of Copepoda, Cladocera, and Rotifera in addition to Protozoa and meroplankton. Copepoda were the most dominant group (>65% in number) and was represented by *T. neglectus*, *M. ogunnus*, and *T. galebi*. Cladocera is next in dominance (about 20% of the total number), while rotifers are less. Khalifa et al. [39] surveyed zooplankton of Lake Nasser and recorded 38 species at the main channel (4 Copepoda, 6 Cladocera, 24 Rotifera, and 4 Protozoa). They identified 31 species at Khor Tushka, and the smallest number (24) was counted in Khor Wadi Abyad. Copepoda were the most dominant group, and *T. galebi* recorded the highest number of copepods; however, the greatest diversity was observed among Rotifera with the dominance of *Keratella* and *Collotheca*.

Goher et al. [40] investigated zooplankton groups, 3 Copepoda, 7 Cladocera, and 10 Rotifera in Lake Nasser, and concluded that the percentage of average number of zooplankton during the post-flood period represented 83%, 10%, and 7%, respectively, while in the pre-flood period, they were 63%, 26%, and 11%, respectively. Copepoda were mainly represented by *T. galebi*, *M. ogunnus*. The Cladocera were dominated by *D. mongolianum* and *C. reticulate*. Rotifera were more common with *K. cochlearis*, *K. quadrata*, *K. tropica*, *B. calyciflorus*, and *Asplanchna* sp.

6.2.3 Zooplankton of Lake Kariba (Zambia and Zimbabwe)

Lake Kariba is the world's largest artificial lake, which was filled between 1958 and 1963 after the completion of the Kariba Dam. It lies between Zambia and Zimbabwe, with 223 km long, an area of 5580 km^2, and capacity of around 185 km^3. The diversity of zooplankton at Lake Kariba was described by Ndebele-Murisa [41]. He identified 77 species, including 48 species of Rotifera, of which *K. cochlearis* was the most dominant, 15 species of Copepoda, with the dominance of *Thermocyclops albidus*, 14 species of Cladocera, with the dominance of *B. longirostris*. Zooplankton density varied in Lake Kariba with phytoplankton biomass, and zooplankton

production is determined to a greater extent by phytoplankton availability than by fishing pressure and predation [42]. After the introduction of the Tanganyika sardine, the Cladocera species has declined, while that of Copepoda has remained relatively stable [43].

6.2.4 Zooplankton of Lake Victoria (Kenya, Tanzania, and Uganda)

Lake Victoria is one of the African Great Lakes, the largest tropical lake in the world (68,800 $km^{2)}$. It is divided into three areas: Kenya (6%), Uganda (45%), and Tanzania (49%). It has an area of about 59,947 km^2 [44]. Lake Victoria used to be very rich in fish, comprising many endemics, but a high percentage of these have become extinct in the last 50 years [45]. The main fish group in the lake is the haplochromine cichlids with more than 500 species, almost all endemic [45]. As a consequence, result of predation by the introduced Nile perch, eutrophication, and other ecosystem changes. Lake Victoria has received exceptional attention due to its altered limnological conditions caused by nutrient inputs and regional climate changes [46]. These nutrients enter the lake through the inlets due to runoff and agricultural activities with high nutrient levels from urban/industrial causing eutrophication and pollution [47].

Worthington [48] collected plankton from Lake Victoria in 1927 and reported Calanoids and Cladocera were the dominant (50% and 39% of the total count). Goudswaard et al. [49] estimated that predation pressure on the juvenile shrimp decreased with haplochromine breakdown, but that predation on the adult shrimp continued. Zooplankton community of Lake Victoria consists of three main groups (Copepoda, Cladocera, and Rotifera) while other groups of minor importance are the Diptera larvae and the Acarid mites [50]. Field studies by Wakwabia et al. [50], carried out in Kenya, Uganda, and the southern part of Lake Victoria between 2000 and 2002, showed that over 80% of the community consists of cyclopoid copepods. The species composition of the zooplankton is almost uniform across the lake. For example, among the cyclopoid copepods, 6 of the 8 species are distributed in the three parts of the lake. The only two exceptions are *T. oblongatus*, absent from Tanzanian waters, and *T. decipiens*, absent from Ugandan and Tanzanian waters. The two species *T. galeboides* and *T. stuhlmanni* are widespread across the lake. Seven of the ten cladoceran species occur in all three parts, as *D. barbata* only occurs in the Kenya part, while *Chydorus sphaericus* and *Alona* sp. are not found in the waters of Tanzania. A total of 16 out of 24 Rotifera species are

distributed throughout the lake. The remaining 8 species are absent from the southern part of the lake.

A total of 41 zooplankton species were identified from Lake Victoria. Copepoda were the most dominant group (94%), with *T. neglectus* and *T. emini* being the most common species [51]. Rotifera and Cladocera were with the least frequency (4.6% and 1.4%, respectively). Cyclopoid copepods contributed more to the copepod biomass, followed by calanoids and then harpacticoids. In general, Rotifera had the highest diversity among the dominant groups [50,51] (Table 6.4).

6.2.5 Zooplankton of Lake Tana (Ethiopia)

Lake Tana is the largest lake in Ethiopia and starts from the Blue Nile, located in the northwestern Ethiopian highlands, extending about 84 km and at an altitude of 1788 m. Water sources of Lake Tana are the Gilgel Abay, Reb and Rivers fed Gumara. Its area extends from 3000 to 3500 km^2 [55]. Zooplankton dynamics were studied by Dejen et al. [56]. Of the limnetic species, four copepods and nine cladocerans were identified, 11 of which together accounted for more than 99% of all individuals collected. About half of the numbers encountered were copepods, and the other half were cladocerans. The calanoid copepod *T. galebi* dominated the zooplankton community and is endemic to Lake Tana. Of the three cyclopoid copepod species, *Thermocyclops ethiopiensis* was the most common. *B. longirostris*, *D. hyalina*, *D. lumholtzi*, and *D. sarsi* were the most common cladoceran species. Of the two rarely encountered species, *Microcyclops varicans* and *C. sphaericus*, the latter species is probably predominantly littoral and associated with macrophytes [56].

Community structure zooplankton in Lake Tana's is unique due to its relatively high proportion of temperate species, i.e., *D. hyalina* and *C. dubia*. Most likely, this effect is due to its altitude, which results in relatively low water temperatures in the lake [56]. The addition of temperate species to its zooplankton assemblage resulted in relatively high biodiversity of limnetic microcrustacean zooplankton in the lake. Significant temporal differences in copepod and cladoceran abundance were observed, with the highest densities during the dry season. Cladocera showed a significantly higher density in the subtidal zone, but copepods showed similar densities in the littoral, sublittoral, and offshore.

Krylova et al. [57] found in their study of zooplankton in the coastal zone (Ethiopia) at the beginning of the dry season in Lake Tana Rotifera

Table 6.4 A checklist of zooplankton taxa recorded in Kenyan (K), Ugandan (U), and southern part (SP) of Lake Victoria.

Taxa Crustaceans	K	SP	U	Taxa Insecta	K	SP	U
Cyclopoida				*Chaoborus* larvae/ pupae	×	×	×
Thermocyclops neglectu	×	×	×	**Rotifera**			
T. emini	×	×	×	*Brachionus calyciflorus*	×	×	×
T. incisus	×	×	×	*B. caudatus*	×	×	×
T. oblongatus	×	–	×	*B. patulus*	–	–	×
T. decipiens	×	–	–	*B. falcatus*	×	×	×
Mesocyclops spp.	×	×	×	*B. angularis*	×	×	×
Tropocyclops confinnis	×	×	×	*Filinia longiseta*	×	×	×
T. tenellus	×	×	×	*F. opoliensis*	×	×	×
Calanoida				*Keratella cochlearis*	×	×	×
Thermodiaptomus galeboides	×	×	×	*K. quadrata*	×	×	×
Tropodiaptomus stuhlmanni	×	×	×	*K. tropica*	×	×	×
Cladocera				*Polyarthra vulgaris*	×	×	×
Daphnia lumholtzi		×	×	Sychaeta sp.	×	×	×
D. lumholtzi var. monacha	×	×	×	Lecane spp.	×	×	×
D. longispina	×	×	×	*Monostyla* sp.	×	–	×
D. barbata P	×	–	–	*Collotheca* sp.	×	–	×
Ceriodaphnia cornuta	×	×	×	*Asplanchna brightwelli*	×	×	×
Diaphanosoma excisum	×	×	×	*Ascomorpha* sp.	×	×	×
Bosmina longirostris	×	×	×	*Trichocerca cylindrica*	×	×	×
Chydorus sphaericum	×	–	×	*Aneuropsis* sp.	×	–	×
Alona sp.	×	–	×	*Epiphanes*	×	–	×
Moina micrura	×	×	×	*Euchlanis* sp.	×	×	×
Decapoda				*Hexathra mira*	×	–	×
Caridina nilotica	×	×	×	*Platyias patulus*	×	–	–
				Pompholyx sp.	×	–	×

× = Present, – = Absent.
Source: [50–54].

as the dominant group (34.2%) tended to increase and the proportion of Cladocera (2.2%) tended to decrease at the boundary of macrophyte thickets in comparison to the open water zones (22.3% and 6.3%, respectively). The species composition of the dominant species in terms of biomass varied significantly in different zones. Representatives of Calanoida

(Copepoda) predominated at most stations in the open water zones and near the boundary of macrophyte thickets, and representatives of the family Chydoridae (Cladocera) dominated in the zone of macrophyte thickets. The average percentage of dominant Copepoda in the thicket was 36.4%. Their relative abundance was higher in the open water zone and at the thicket boundary (46.4% and 56.9%, respectively). At the same time, the boundary of the macrophyte thickets was marked by the minimal proportion of dominant Cladocera (8.5%). Their highest proportion was recorded in macrophyte thickets (43.3%). The average proportion of dominant Cladocera in the open water zone was 22.0%.

6.3 Importance of zooplankton as food for fish in the African lakes

Zooplankton is an important food source for all fish larvae. Inland fishing in the African lakes provides nutrition, food security, and income and reduces unemployment. Many studies have referred to the importance of zooplankton as food for African fish. As a result of Wakwabia et al. [50] in their study in Lake Victoria, the survival of fish larvae and the eventual recruitment of fish to the fishery largely depend on the availability of zooplankton. Trophic relationships between zooplankton and fish have demonstrated the importance of certain taxa of zooplankton as important feeders for commercially valuable fish such as *Rastrineobola argentea*, *Oreochromis niloticus*, and *Lates niloticus* larvae. *R. argentea* obtains over 70% of its diet from copepods (particularly cyclopoid copepods), which are the most common and abundant group in Lake Victoria [52]. Fish larvae prefer rotifers, which are abundant in the shallow coastal areas of the lake. Juvenile fish of the commercially important Nile perch *L. niloticus* feed mainly on the shrimp *Caridina nilotica* [7]. Adult Nile perch indirectly depends on zooplankton by feeding on the zooplanktivor *R. argentea* and haplochromines. *Mesocyclops* spp. and *Chaoborus* sp. are important food for fish [58]. The zooplankton assemblage is therefore an important link in the energy flow that integrates carnivorous invertebrates and pelagic fish for the production of important commercial fish such as the Nile perch.

Yongo et al. [59] studied food and feeding habits and diet regarding the size and season of six *Synodontis* species in the African freshwaters. They found variety of different kinds present in the stomach of *Synodontis* species, as omnivorous feeders. The importance of zooplankton and insects declined steadily with the size of fish. Zooplankton (Copepoda and

Cladocera) had the highest occurrence in the diet of the stomachs of *Synodontis* fish species (35.9%), indicating wide adaptability to the food and feeding habit in the water bodies in which they live. For *Synodontis* victoriae in Lake Victoria [59], the most ingested food items included *C. nilotica* (57.1%), insects (22.3%), fish remains (19.3%), *R. argentea* (17.9%), and detritus (13.9%). For *Synodontis schall* from Lake Chamo in Ethiopia [59], the importance of zooplankton and insects declined as the size of fish increased, while that of scales increased with increase in fish size. Zooplankton contributed 68.1% of the food consumed by *S. schall* of size 10.0–14.49 cm, but they contributed only 12.5% of the total volume of food consumed in 35.0–39.9 cm. In Lake Albert, Waya et al. [51] and Yongo et al. [59] found Caridina forms a major part of the diet of the Tiger Fish, *Hydrocynus forskalii*. Waya et al. [51] studied gut content of *O. niloticus*, *L. niloticus*, Haplochromine, and *T. zillii* in Lake Victoria. They found *Haplochromine* feed primarily on zooplankton organisms (Table 6.5).

Table 6.5 Gut contents of juvenile planktivorous fish from Lake Victoria (2005–06) [51].

Food item	*L.n.*	*O.n*	H.	*T.z.*
Rotifera				
Asplanchna spp.	×	–	×	–
Filinia opoliensis	–	–	×	–
Lecane spp.	–	–	×	×
Macrothrix spp.	–	–	×	–
Cladocera				
Ceriodaphnia cornuta	–	–	×	–
Moina micrura	–	–	×	–
Copepoda				
Nauplii	–	–	×	×
Cyclopoid copepodite	×	×	×	×
Adult cyclopoids	×	×	×	×
Adult calanoids	×	×	×	×
Insects				
Chaobrid larvae	–	–	×	–
Chironomid larvae	–	–	×	×
Others				
Caridina nilotica	×	–	–	–
Ostracods	–	–	×	–
Phytoplankton	–	×	×	×

O.n., *Oreochromis niloticus*; L.n., *Lates niloticus*; H., Haplochromine; and T.z., *Tilapia zillii*. Key, × = Present, – = Absent.

Shalloof et al. [60] examined the gut contents of the three tilapia species in Lake Nasser. They revealed that there are 37 food items belonging to 14 food taxa, rotifers (2 species), copepods (2 species), cladocerans (4 species), worm (1 species), animal derivatives (1), and miscellaneous invertebrates (2 taxa). They found the food of animal origin (copepods, ostracods, worms, and miscellaneous invertebrates) was higher in autumn than in spring (Fig. 6.3).

6.4 Zooplankton as bioindicators in African lakes

Bioindicators are now used and promoted by various organizations (World Conservation Union, International Union for Conservation of Nature (IUCN)) as a method of managing biomonitoring and assessing human impacts. Zooplankton are used in a variety of ways as an indicator of water quality. Zooplankton are mainly used as a species indicator of saprobity (atrophic state). For a long time, the use of zooplankton community characteristics as a bio-indication tool was considered to be of little value use. Zooplankton indices based on, e.g., taxonomic composition, size distribution, trophic levels, spatial patterns, and functional characteristics as well as quantitative data, can have high informative potential and should not be overlooked in surveillance studies [60] as shown in Fig. 6.4. They also play an essential function as bioindicators

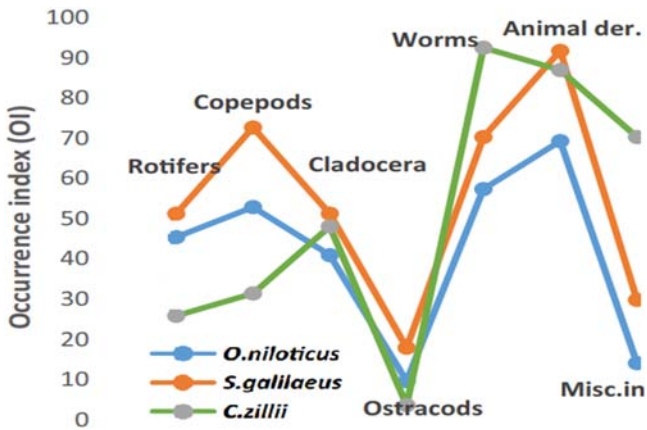

Figure 6.3 Occurrence index of various zooplankton groups in the gut of cichlid species in Lake Nasser in the period 2015–16. *Modified from K. Shalloof, A. El-Far, W. Aly, Feeding habits and trophic levels of cichlid species in tropical reservoir, Lake Nasser, Egypt, Egypt. J. Aquat. Res. 46 (2020) 159–165.*

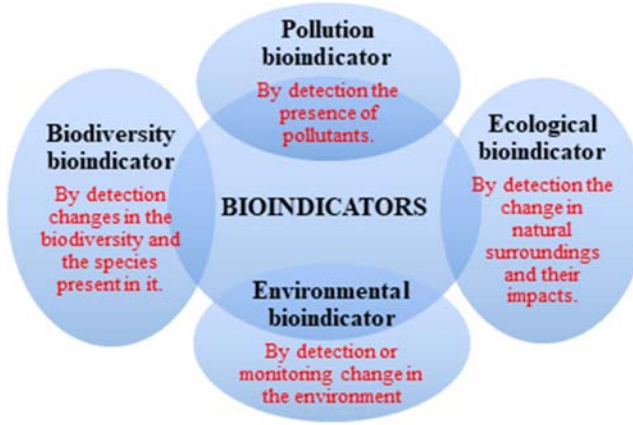

Figure 6.4 Types of bioindicators as zooplankton tool. *According to T.K. Parmar, D. Rawtani, Y.K. Agrawal, Bioindicators: the natural indicator of environmental pollution, Front. Life Sci. 9 (2) (2016) 110–118. https://doi.org/10.1080/21553769.2016.1162753.*

and help to assess water pollution. Differences in species richness, biomass diversity, and abundance of zooplankton groups can be applied to determine the intensity of a biological system. The capability of zooplankton as a bioindicator species is documented [61].

Rotifers are an important group of zooplankton that can be considered as a valuable part of the freshwater ecosystem. The abundance of rotifers depends strongly on the trophic state of the water bodies. They have a higher ability to tolerate pollution-induced stress than their predators and have been used to some extent as bioindicators of aquatic trace metal pollution [62,63]. The rotifers, *Conochilus dossuarius* and *Synchaeta longipes*, which are typical for oligotrophic to mesotrophic systems, were absent in the Ovia River (Nigeria). Worse *Keratella tropica, K. quadrata, Brachionus angularis, Trichocerca pusilla, Filinia longiseta, Pompholyx sulcata*, and *Proales* sp. that are generally most predominant species in West African freshwater ecosystems which are indicator species of high trophic levels [64] were also not recorded in the river [65] (Table 6.6). The lack of these vital species in the river indicates poor trophic status, evident in the spatiotemporal profiles of nitrates and phosphates. The occurrence of *Tropodiaptomus incognitus, T. processifer*, and *T. galebi*, *T. neglectus, M. varicans*, and *Halicyclops korondiensis* confirms the work of Imoobe and Adeyinka [64] and was facilitated by Isibor [65].

Mohamed et al. [74] indicated the response of zooplankton to deteriorating water quality in Tungan Kawo Reservoir (Nigeria). Some of the

Table 6.6 Types of zooplankton and their indications.

Names of zooplanktons	Indications	References
Rotifers	Trophic status	[66]
Keratella tropica, *Hexarthra mira*	High turbidity due to sediments	[67]
Brachionus calyciflorus	Eutrophic conditions and organic pollution	[68]
Cladocerans group (unspecified)	Low concentration of contaminants	[69]
Trichotria tetractis	Pollution due to accumulation of phosphorous and heavy metals	[70]
Brachionus angularis, Rotatoria, Thermocyclops, Argyrodiaptomus	Eutrophic conditions	[71]
Leeches	Indicates contamination because of the presence of polychlorinated biphenyl	[72]
B. dolabrotus	High turbidity due to sediments	[73]

zooplankton like *Megacyclops viridis*, *Leptodiaptomus minutus*, *Leptodiaptomus ashlandi*, and *Harpacticoida* sp. were clearly correlated with BOD_5 and turbidity. *Ceriodaphnia cornuta* is correlated with pH while *Cyclops scutiser* is weakly associated with conductivity.

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CHAPTER 7

Geomicrobiology of African lakes

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7.1 Introduction

Africa, particularly East Africa, has large lakes that support important fisheries that provide a living for millions of people contributing significantly to food security. Although Africa's lakes are restricted and delicate resources that require proper care and management, they are among the continent's most exploited natural resources [1]. Indeed, Africa's Great Lakes are among the world's largest and most ecologically diversified freshwater systems. Because of their size and depth, 8 of the region's 15 lakes are classified as "Great Lakes," which include Lake Tanganyika, the world's second largest freshwater lake by volume and depth. Great Lakes are part of the Rift Valley lakes in and around the East African Rift. In general, the major African Great Lakes are listed as Lake Victoria, Lake Albert, Lake Edward, Lake Tanganyika, Lake Kivu, Lake Malawi, and Lake Turkana [2].

On the other side, the combination of sodium and carbonates comes about in alkaline conditions, and such environments are "soda lakes." They have saline waters with Na^+ and carbonate species ($HCO_3^- + CO_3^{2-}$) as the dominant ions and ordinarily surpass a pH of 9. Their waters commonly have high concentrations of chloride, and variable concentrations of sulfate and potassium, but these lakes have exceptionally low concentrations of alkaline soils, because of the equilibrium state with carbonate minerals. Indeed, soda lakes represent the most stable high-pH environments on Earth, due to their formation depending on low levels of dissolved calcium and magnesium, and dominance of bicarbonate ($HCO_3^- >> Ca^{2+} + Mg^{2+}$) [3]. Meromictic lakes are ecosystems where microbial geochemical activity is most commonly achieved. The microbial processes occur in the area where anoxic and oxic (sulfide-

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enriched, euxinic, O_2-free) water layers contact. Thus, meromictic lakes are used as models for the screening of biogeochemical-microbial processes taking place at the oxic–anoxic interface [4].

Freshwater and saline-alkaline lakes are ecologically and economically important environments due to their nutrient recycling capacities and high productivity. The fast recycling and the input of nutrients are due to active aerobic and anaerobic microorganisms, which are important to the biogeochemical and major functioning cycles within lakes [5].

Knowingly, both carbon and nutrient cycles, as well as the global food web, rely on microorganisms which were on Earth from the beginning of life, at least 3.8 billion years ago [6]. More specifically, geomicrobiology studies the microorganisms that drive the Earth's biological–geochemical cycles, and mediate precipitation of minerals, dissolution, and mineral concentration and uptake. Clearly, geomicrobiology also explains the different cycles of carbon, nitrogen, sulfur, and methane. It inv[1]olves methanogenesis and photoferrotrophy significantly [7].

On the other side, there are valuable biotechnological applications for geomicrobes isolated from African lakes. Preliminarily, many of these microbes are used to reduce pollution from polluted sites via biological bleaching that uses geomicrobes to extract minerals from waste of mine. In addition, geomicrobes can improve the quality of oil and gas deposition by metabolic processes. Moreover, several enzymes including lipases, proteinases, cellulases, and xylanases can be applied in various mechanical, pharmaceutical, and waste treatment fields [8].

7.2 African lakes

Africa is endowed with hundreds of lakes, both natural and artificial (e.g., Bosumtwi and Nasser lakes). Africa also has some of the world's largest lakes, many of which are surrounded by two or more countries. Lake Victoria, for example, is the largest of all African lakes and the world's second largest freshwater body. There are 677 lakes in Africa, according to the WORLDLAKE database. Eighty-eight of them are listed as principal lakes. It's worth noting that Africa's lakes are changing dramatically as a result of a mix of human activity and climate change, with potentially dire consequences for people's livelihoods and aquatic biodiversity [9]. In addition, human causes, in combination with natural climate and

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geological circumstances, may have a significant impact on water quality in Africa. Pollution induced by land-use changes, environmental modification, and other practices linked with rapid population growth, on the other hand, has caused or exacerbated many changes in the continent's lakes [10].

7.2.1 African great lakes

The majority of Africa's big lakes are located along a continental fault line called the East African Rift Valley, which also provides the continent's most beautiful mountains, including Africa's highest mountain Kilimanjaro (Fig. 7.1). The Great Lakes of Africa are a system of deep lakes located in the Rift Valley in the continent's southeast corner. Collectively, the Great Lakes contain more water than either Lake Baikal or the North American Great Lakes combined. This amount accounts for a quarter of the planet's unfrozen surface fresh water. Africa's vast rift lakes are the historic home of immense biodiversity, with 10% of the world's fish species found there. In addition, countries in the African Great Lakes region include the Democratic Republic of Congo, Burundi, Kenya, Ethiopia, Mozambique, Malawi, Rwanda, Zambia, Uganda, and Tanzania. However, the most important and famous lakes in such manner are Lake Kyoga, Lake Victoria, Lake Albert, Lake Edward, Lake Tanganyika, Lake Kivu, Lake Malawi, and Lake Turkana [2].

7.2.2 General characteristics of the African great lakes

The highlands have a cool climate, with average temperatures ranging from 17°C to 19°C and plenty of rain. The Congo-Zaire, Nile, and Zambezi rivers all have major drainage basins that drain into the Atlantic, Mediterranean, and Indian Oceans, respectively. The Congo-Zaire Basin's lowlands are dominated by forests, while the southern and eastern highlands are dominated by grasslands and savannas. The lowlands have an average temperature of 35°C [2,9]. The Western Rift Valley lakes are naturally freshwater, and they are home to a large variety of unique species. The lakes are home to about 1500 cichlid fish species, as well as other fish families. Several amphibian species use the lakes as a breeding ground [11].

Geologically, the bountiful waters of the equatorial plateau either flowed west into the Congo River system or east to the Indian Ocean, until 12 million years ago. A rift is a weak spot in the Earth's crust caused by the separation of two tectonic plates, which is usually followed by a

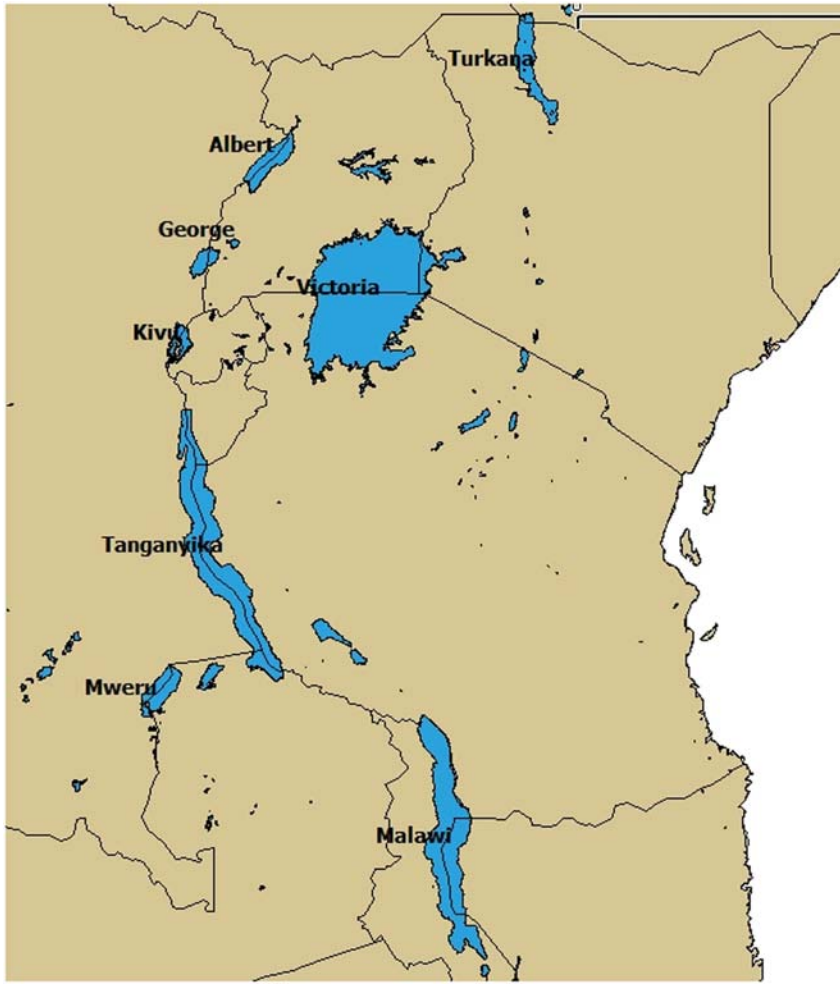

Figure 7.1 Distribution of major lakes in Africa (*left*). Satellite image for the Great Lakes of Africa showing the major lakes of eastern Africa (*right*).

graben, or trough, where lake water can accumulate. This rift formed when East Africa began to separate from the rest of Africa and move northeast, propelled by mantle currents. The basins created by geological uplifts were filled with water that is now flowing north [11].

7.2.3 African soda lakes

Soda lakes are hypersaline and alkaline environments, which are accepted to have existed all through the geographical record of Earth. They have

high levels of sodium carbonates and are characterized by salinity (up to saturation) and raised pH (9–12). Such biological systems are found in Africa, Asia, Europe, Australia, North, Central, and South America. They are colonized by a different haloalkaliphilic microbial community. However, the most famous soda lakes are Wadi El Natrun lakes (Egypt), Malha Crater Lake (Sudan), Lake Chitu (Ethiopia), Lake Magadi (Kenya), Lake Turkana (Kenya), Rombou Lake (Chad), and many others [12,13].

Although soda lakes are all over the world, they are exceedingly inexhaustible in earthbound biomes such as deserts and steppes and in geographically curious districts like the East African Rift Valley. The abnormal geochemistry of these lakes confirms the development of an amazing cluster of microorganisms that are of environmental and financial significance. Haloalkaliphilic microscopic organisms such as archaea and bacteria having a place in all major trophic groups have been depicted in numerous soda lakes, involving lakes with outstandingly high levels of heavy metals. Incredibly, the existence of differing functional groups of microbes, like syntrophs, phototrophs, methanotrophs, methanogens, denitrifiers, sulfur oxidizers, and sulfate reducers in soda lakes, recommends these environments harbor complex microbial food webs. This complexity interconnects different organic cycles through redox coupling and affects the generation and utilization of greenhouse gases (GHGs) [14].

Later investigations that the anoxic deep zone of lakes harbor more assorted microbial communities than the oxic zones contradict past reports and the common desire that organisms flourish in cruel conditions [15]. In soda lakes, decreased substances may be collected within the bottom water, and basic nutrients may be missing within the surface layer. Sulfide toxicity may result from the prohibition of grazers from the anoxic zone of the water column, and this may lead to the aggregation of microbial biomass [16].

Dead natural things that sink and collect at the foot (anoxic zones) parts of these lakes make also perfect substrates for assorted haloalkaliphilic fermentative organisms, sulfate reducers, and methanogens, which in turn play a part in carbon, hydrogen, and methane cycling. Methanogenesis is one of the common forms carried out by a few anaerobic communities of soda lakes. Anaerobic fermentation of organic substances beginning from the degradation of the biomass of primary producers produces, for illustration, one-carbon compounds such as methanol and methylamine. Within the anoxic zone of lakes, methanogens

utilize these compounds to derive vitality and energy via yielding methane through methanogenesis. When the coming methane arrives to the O_2 consuming zone of a soda lake, methane-oxidizing bacteria (methanotrophs) return the carbon within the methane into the common pool of organic matter (OM) [17].

A few fermentative anaerobes carry out ammonification, acetogenesis, and saccharolysis at high pH, and play a part in C and N cycling. Acetogens create acetate anaerobically from an assortment of substrates (such as H_2 and CO_2). Organic nitrogen from dead organisms is changed back into ammonium by ammonification making the N accessible to other living beings. A few other saccharolytic bacteria deliver isobutyric acid, acetic acid, and H_2 from the cellulose substrate [18]. Other organisms like anoxygenic phototrophs, cellulose acetogenic microbes, and sulfate-diminishing microbes utilize these products resulting from the fermentation process. Furthermore, there are alkali-tolerant sulfate-diminishing, and oxidizing bacteria special to the soda lakes. These anaerobic communities in soda lakes, hence, have different microbial communities with different metabolic capabilities [19].

Professional microbiologists have broadly examined saline and soda lakes, where they are facilitating microbial communities characterized by extraordinary alkaliphilic and halophilic phenotypes. These ecosystems show up to be much more particular than other aquatic environments, and the individuals of the archaeal and eubacterial communities found in soda lakes are agents of the ordinary phylogenetic groups of life forms that flourish in extraordinary environments [13]. Significant biodiversity of alkaliphilic prokaryotes, included in the major taxonomic groups, has been isolated. Later, other groups including phototrophs, spirochetes, lithotrophs, and many anaerobes have been isolated. This has allowed the identification of the major tropic groups responsible for the cycling of carbon, nitrogen, and sulfur within the lakes. Furthermore, many microbes providing industrially critical enzymes have been isolated and characterized [20].

Taxonomically, individuals of the assorted prokaryotes having a place to the phyla Cyanobacteria, Actinobacteria, Firmicutes, Bacteroides, Proteobacteria, Verrucomicrobia, Verrucomicrobia, Spirochetes, Thermotogae, Chloroflexi, and the diverse candidate divisions of bacteria are well presented in African soda lakes [21]. Comprehensive records of prokaryotes isolated from alkaline saline lakes are reported in the previous works as well as investigations have appeared that the microbial

communities in soda lakes are dominated by prokaryotes as extreme systems [18]. In addition, studies carried out on the soda lakes of the Wadi al Natrun in Egypt have given new data on the diversity of anaerobes from these locations, counting the new genera of *Natrananaerobius* and *Natronovirga* inside a recently named family Natranaerobiaceae [21]. Six genera: *Natronobacterium*, *Natronococcus*, *Natrialba*, *Natronorubrum*, *Halorubrum*, and *Natronomonas*, have moreover been isolated from human-made or natural hyperhaloalkaline systems in the East Africa Rift Valley [22].

On the other hand, the microbes of these lakes harbor a few biotechnologically pertinent enzymes and biomolecules (e.g., cellulases, amylases, ectoine) and ought to expand bioprospecting endeavors in soda lake environments with modern coordinates approaches. These biological systems of the world are critical characteristic resources with impressive esthetic, social, financial, recreational, logical, conservation, and ecological value. Significantly, a few saline and soluble lake environments around the world have to be ensured from anthropogenic pressures that undermine their long-term presence [23].

7.2.4 African meromictic lakes

Lakes of meromictic are formulations in which microbial geochemical activity is most evident. The highest microbial processes take place in the area where anoxic and oxic (sulfide-enriched, euxinic, and O_2-free) water layers contact. This area is termed a pycnocline, chemocline, an oxic–anoxic interface, or a transitory zone. Oxygen is the most useful electron acceptor for heterotrophic microorganisms and acts as an oxidant that consumes OM. Microorganisms oxidize reduced compounds of manganese, sulfur, and iron, as well as methane, mainly using O_2 [24]. However, the most famous meromictic lakes are Lake Nyos (Cameroon), Lake Kivu (Rwanda and The DRC), Lake Tanganyika (Burundi, The DRC, Tanzania, and Zambia), and Lake Malawi (Malawi, Mozambique, and Tanzania).

Respiration of O_2 for chemolithotrophic and heterotrophic microorganisms may occur at minimum levels of ambient O_2, which are below 120 nM, the threshold for conventional O_2 sensors. The occurrence of processes at micromolar O_2 concentrations has not been reported until recently [25]. Among organisms in aquatic ecosystems, prokaryotes are the only organisms that can oxidate CH_4 under both anoxic and oxic

conditions. In the presence of sulfate and absence of O_2 in aquatic environments, CH_4 is mainly consumed because of sulfate-dependent anaerobic CH_4 oxidation. This is responsible for the oxidation of more than 90% of CH_4 in anoxic areas. The microbial CH_4 oxidation in the water column of meromictic lakes is known to occur, aside from the anoxic area, also at the oxic–anoxic interface, as well as in the oxic area, where O_2 cannot be discovered [26].

Lakes of meromictic may be used as models for the screening of biogeochemical-microbial processes occurring at the oxic–anoxic interface. Moreover, screening of the function and composition of microbial communities involved in the CH_4 biogeochemical–microbial cycle is also useful for the knowledge of climatic changes [27]. The microbial process patterns in lakes of meromictic rely on their genesis and topographic location. The functional activity and composition of microbial communities rely on several parameters: salt composition, temperature, depth of light penetration, trophic status, etc. In East Africa, Lake Kivu is a meromictic lake with a low amount of dissolved CH_4 in its surface waters and high amounts of CO_2 and CH_4 in the deep waters [28].

7.3 Microbial diversity of African lakes

7.3.1 Microbial composition in African lakes

The extremophiles are creatures that have adapted so effectively to their severe conditions that they can easily thrive and multiply. Kenya's haloalkaline soda lakes have extraordinarily high productivity rates due to high light intensities, high ambient temperatures, phosphates availability, and limitless access to CO_2. In Lake Magadi, salinity levels can reach 30% saturation, while pH levels range from 9 to 11.5. Solutes are primarily supplied by a series of alkaline springs in Lake Magadi, with temperatures ranging from 33°C to 86°C. Within the three hot springs, there were significant differences in microbial community structure at the 95% confidence level for both total diversity and active microbial diversity [29].

Microbes are critical to the ecological functioning of aquatic systems because of their crucial roles in the production, decomposition, and conversions of OM, besides nutrient intake and regeneration. So, they control many stages of biogeochemical transformations.

In watery habitats, prokaryotes are responsible for biological, geological, and chemical activities [30]. Microorganisms are essential to all organisms in an ecosystem. Increased phytoplankton levels, such as algae, are

often accompanied by an increase in heterotrophic bacterium activity and production in many aquatic environments. Bacterial activities have a significant impact on ecosystem function and metabolism because bacteria account for a large amount of planktonic biomass. The active bacterial community helps with substrate uptake, metabolism, growth, and reproduction. In freshwater samples, 36% of total bacterial populations were involved in respiration, but in the marine environment, they only account for 12% [31].

In aquatic habitats, dissolved organic matter (DOM) is decomposed by more than 50 phyla of bacteria and archaea. The identification of prominent ones in freshwater environments is critical because these bacteria take up and control DOM, while also contributing to other processes such as matter and energy cycles [32]. Bacterial alpha diversity has been shown to change across environmental gradients, including cross-productivity gradients. Because the link between diversity and productivity is not consistent across all bacterial taxa, patterns of alpha diversity may not be universal across all bacterial taxonomic groups. The great diversity could be attributed to the complicated and fine-scale chemical gradients seen in saline sediments, which provide an unusually large number of ecological niches for bacterial variety. Compared to sediment environments, watery habitats are thought to support fewer bacterial species, owing to a lower level of variety. The mechanisms that generate and maintain bacterial alpha diversity are forming patterns of variation. Bacterial taxa with novel morphological and/or ecological functions are fast evolving as a result of rapid mutation and lateral gene transfer, enhancing bacterial biodiversity. Microbial ecologists have become interested in unraveling the patterns of bacterial success over location and time because of the importance of bacterial alpha diversity [33].

The elements responsible for the turnover of community composition in place and time include both intrinsic (e.g., dispersal rate, trophic factors) and extrinsic factors (e.g., latitude, ecosystem, ecosystem size, and habitat isolation). Across vast geographical gradients, the importance of each element varies. Temperature, ultraviolet radiation, quality, and quantity of DOM; nutrient concentrations; and grazing pressure are some of the most important factors that regulate prokaryotic assemblages, which can vary depending on the geographic location, watershed, and surrounding landscape of the lakes. Seasonal patterns in bacterial community structure recur in freshwater ecosystems according to recent reports based on high-frequency multiyear datasets of site-specific studies, and these seasonal

patterns indicate that some microbial communities change directionally according to environmental conditions [34].

The primary productivity of aquatic habitats is mostly determined by autotrophic organisms' photosynthetic activities [35]. Descy and Sarmento [36] examined phytoplankton composition and succession in the East African Great Lakes as well as their responses to environmental changes and microbial food web communities. Information indicating that phytoplankton composition in Lakes Tanganyika and Kivu may reflect recent changes as a result of global warming or species introduction was presented in particular as well as confirming the importance of microbes in these systems and suggesting that the microbial food web, which has been largely ignored until recently, may play a very important role in these systems. Effectively, bacteria can be found in a variety of freshwater habitats, including lakes, bogs, mudflats, sulfur springs, and rivers, where they form large pelagic and benthic populations. Different kinds of pelagic bacteria in lake habitats arrange themselves in the water column based on local variables such as light intensity, oxygen level, and nutrient concentration. As a result, the bacterial community composition of lakes fluctuates depending on many environmental factors. Varied bacterial community compositions result from different intrinsic environmental circumstances in lake water and sediments, and these differences explain different microbial biogeographies in lake environments. These microorganisms have been employed as an indication of the adequacy of water quality in practically all lakes since they are well adaptable and diverse [37,38].

Llirós et al. [39] found that sequences belonging to the Euryarchaeota kingdom were largely retrieved from anoxic water compartments and classified into methanogenic lineages (Methanocellales and Methanosarcinales). Crenarchaeal species were found across the tested epipelagic waters (0−100 m depth), with clear phylogenetic separation along the transition between oxic and anoxic water masses. According to current research, some members may acquire energy from anaerobic methane oxidation (AOM)—a proposal that corresponds with the physicochemical circumstances in Lake Kivu's monimolimnion. *Methanosaeta concilii* and uncultured Methanosarcinales or hydrogenotrophic (*Methanocellula paludicola*) representatives, which agree with the biological origin of methane in the lake as well as the methanogenic archaeal groups were observed in other stratified lakes [40].

Finlay et al. [41] emphasized the relevance of bacteria in the food web in Lakes Tanganyika and Kivu systems implying that the microbial food

web, which has been largely ignored until recently, could play a significant role in determining productivity and nutrient cycling in these enormous lakes. Lake Simbi, Kenya, is a volcanic crater lake with a depth of 23 m. The littoral region of Lake Nakuru, Kenya, is extensive and shallow (less than 2 m). The main ions in both lakes include Na^+ and HCO_3-CO_3^{2-}, and the pH is around 10. High plankton biomass has been recorded in both lakes (206 mg particulate carbon/L in Lake Nakuru and 46 mg/L in Lake Simbi).

Early, Finlay et al. [42] observed that Lake Nakuru has extensive cyanobacterial populations with short filaments (*Anabaenopsis magna* and *Spirulina fusiformis*) as well as high concentrations of bacteria (2.7×10^8/mL) and flagellates (8.4×10^4/mL). All of them provided food to build a ciliate colony that was both plentiful (> 1000/mL) and diverse (21 species). The large quantities of excretory waste products deposited by large numbers of flamingos are likely contributing to the high number of bacteria and protozoa in Lake Nakuru.

The study of bacterial/archaeal communities in endorheic lake ecosystems is critical for learning about archaeal/bacterial diversity and the composition of their genetic sources, microorganism patterns, the functional importance of microbial diversity, and microbial diversity regulation [43]. Although several studies of prokaryotic communities have been conducted in Kenya's various natural settings, exploitable microbial diversity is not exhaustive, and microorganisms constitute the largest reserve of untapped biodiversity [44,45]. Recently, bacteria discovered by Kiama et al. [46] from Lakes Olbolosat and Oloiden were found to be predominantly of the Proteobacteria phylum in the collected samples. Furthermore, the interaction network of bacterial communities inside both Lakes Olbolosat and Oloiden has revealed that Proteobacteria are very positively related to other microbes. This could be related to a variety of metabolic pathways that promote microbial community expansion [47]. When the composition of Amplicon Sequence Variants (ASVs) was investigated in both lakes, the indicator species with the highest indicative value in the microbial mat was *Exiguobacterium*, while *Clostridium sensustricto* had the highest indication frequency in sediments. Phyla; Proteobacteria, Actinobacteriota, *Pseudarthrobacter*, *Paracoccus*, *Micromonospa*, and *Methylosistis* were the most prevalent ASVs. The planktonic assemblage of Lake Kivu closely resembles that of the other East African lakes, that is, dominated by chlorophytes and Cyanobacteria, with lower abundances of diatoms [48,49].

In the main basin of Lake Kivu at >100 m depth, there is an unusual geochemical feature characterized by high P concentrations, refereeing to massive OM decomposition. This is supported by the strong correlation between P and NH_4. This may suggest the relatively high N_2 concentrations in the deep water of a lake due to bacterial activity [50].

7.3.2 Microbial feature of African soda lakes

Primary production is the major source of OM in closed soda lakes. Protein materials are one of the principal components of this OM in these lakes in which *Arthrospira* is the main primary producer. The uniqueness of soda lakes features has encouraged the presence of typical bioprocesses within the cycling of this OM. For instance, the unusually high pH forces many chemical changes essential for microbial nutrient cycling, especially in connection to sulfur metabolism [51].

Moreover, primary production in these frameworks is based primarily on phytoplankton photosynthesis, frequently ruled by Cyanobacteria instead of eukaryotic essential makers. High photosynthetic rates are kept by highly dissolved inorganic carbon concentrations, though the shortage or absence of zooplankton grazers diminishes the topdown control of phytoplankton biomass. On the other hand, marine salterns are regular hosts to eukaryotic microalgae, such as *Dunaliella salina*, with bigger, herbivorous metazoan organisms such as brine shrimps *Artemia* spp. [13].

In freshwaters, exceptionally high microbial densities and metabolic rates are more often than not transitory and connected to bloom occasions, sometimes related to supplement inputs, though saline and alkaline lakes have high biomass and generation rates [52]. Subsequently, soda lakes are considered to be among the most beneficial aquatic frameworks on Earth. For instance, the saline lakes within the Rift Valley harbor high biomass of *Arthrospira* cyanobacterium, with a temporal dominance of diatoms or chlorophytes (e.g., *Picocystis salinarum*) besides sharp changes in chlorophyll biomass over a long time. Soda lakes are interesting biological systems harboring profits [53].

Besides the primary producers, the presence of physiological types such as lipolytic, proteolytic, cellulolytic, acetogenic, and sulfate-reducing bacteria as well as methanogenic and halophilic archaea have been shown in soda lakes [51]. Observably, Cyanobacteria are known for primary production in soda lakes of anoxygenic photosynthetic bacteria to a significant extent. Many of their species (notably *Arthrospira*, *Cyanospira*,

Synechococcus, and *Chorococcus*) are abundant in such habitats contributing to a major portion of primary production. Therefore, these habitats are observed to amend a huge OM for the diverse groups of heterotrophs (chemo-organotrophic bacteria) [54].

Additionally, some haloalkaliphilic eukaryotic algae may constitute an essential portion of the microbial community in some less saline-alkaline lakes, such as Lake Arenguade, Ethiopia. The huge primary production in such lakes may be contributed by these algae. In productive soda lakes, oxygen depletion is a common phenomenon because aerobic chemoorganotrophic bacteria, which are known to be abundant in such habitats, could consume oxygen for the oxidation of huge OM. Consequently, anoxygenic phototrophic bacteria including *Halorhodospira*, *Ectothiorhodospira*, *Roseinatronobacter*, *Rhodobacter*, *Alkalispirillum*, and *Heliorestis* spp. have been documented from alkaline soda lakes and probably contribute to primary productivity in such lakes [55].

Further, credited to high primary production in soda lakes, there is high OM from the biomass of primary producers and likely from bird's feathers in the case of some lakes, such as Lake Bogoria, Lake Nakuru, Kenya, and Lake Chitu, Ethiopia. There must be an important role played by various heterotrophic organisms in the soda lakes in the usage and reusing of this huge biomass. The family Halomonadaceae of moderately halophilic bacteria are abundant in soda lakes of East Africa, which are moreover frequently isolated from environments such as the wastewater from the olive oil industry, alkaline soils, and tannery waste, appearing in a clear role in the reduction of biological oxygen demand (BOD) and chemical oxygen demand (COD) in the system [18]. Other Proteobacteria related to pseudomonas and enterics have been isolated. Also, novel streptomycetes, species of *Dietzia, Bogoriella*, and *Nesterenkonia* have been observed in soda lakes' aerobic zones. All these communities are likely key players in the cycling of OM within the oxic region of soda lakes [18].

7.3.3 Microbial features of African meromictic lakes

In general, the meromictic lakes have high microbial biodiversity. Inceoglu et al. [28] studied the archaeal and bacterial community compositions to give insight into the diversity of the microbes in Lake Kivu as a good example of a meromictic lake. The stratified diversity of microbial communities may be caused by the vertical distribution of acceptors,

donors, and electrons in the stratified water column, which may be a clearly defined functional specialty. The highest microbial diversity has been presented in the anoxic area, which provided uncultured bacterial phylotypes uncovering previously undescribed taxa [28]. Microbial diversity consists of two parts: rare species and abundant species. Rare species were less stable than abundant species over time. The discovery of rare candidate divisions simultaneously with sulfur-oxidizing Epsilonproteobacteria, sulfate-reducing Deltaproteobacteria, hydrogen-oxidizing Dehalococcoidetes, and methanogens suggested involvement in the sulfur and carbon cycles in the anoxic waters.

Pirlot et al. [56] elaborated on bacterial mortality using two complementary procedures between 2002 and 2004 in the two main basins (South and North) of Lake Tanganyika. They concluded that, in terms of evaluating the nutritional role of bacteria, it was estimated that 5%–8% of the organic carbon (OC) absorbed by the bacteria was converted to primary protozoan biomass and thus became available for metazoan. Meromictic Lake Tanganyika is permanently stratified, but the depth of the upper mixed layer varies according to temporal and spatial scales. Especially, during the summer season, deeper vertical mixing occurs in the oxic layer and a rising takes place in the southern end. The tilted of the thermal line and north-south water movements generate internal waves with the return of the rainy season in October [57]. All of these water events favor the introduction of nutrients from the water below the thermal line. Observations mention that primary producers benefit from these movements and increase the biomass of phytoplankton, whereas bacterial biomass does not differ significantly despite the provision of large amounts of nutrients to surface waters during upwelling water events [56].

In Lake Tanganyika, there is no relationship between bacterial production and primary particle production, where Pirlot et al. [58] observed high biomass of bacteria and heterotrophic nanoflagellates. The forms of resistant heterotrophic bacteria were not shown in the 0–100 m water layer, although filamentous forms have been observed at a depth of 200 m [59]. Kiama et al. [46] studied the comparison of bacterial diversity within a freshwater Lake Olbolosat and a saline-alkaline Lake Oloiden, which obtained 60 bacterial isolates from water and sediments samples, 25 from Lake Oloiden and 35 from Lake Olbolosat. Four different phyla have been obtained from partial sequences of BLAST analysis: Firmicutes (20 phylotypes), Actinobacteria (4 phylotypes), Proteobacteria (1 phylotype), and Bacteroidetes (1 phylotype).

Lake Oloiden, in the Maasai language meaning salty, was also considered for its saline-alkaline. The lake poverty is a water influx leading to saline-alkaline conditions and is disconnected from its west beach by a peninsula [60]. Lake Olbolosat, Kenya, in the Maasai language means a marshy zone and is seriously at risk of extinction may be due to human activities [61]. More studies in Kenya have focused on salty lakes, such as Lake Elementaita, Lake Magadi, scanty fresh, Lake Nakuru, and saline-alkaline lakes in which the microbes are ubiquitous [62].

There are still undiscovered microorganisms from water and sediments within Lakes Oloiden and Olbolosat. Although the culture-dependent technique is very essential for industrial application in understanding the physiology of microorganisms, however, very few microorganisms can be isolated from both saline-alkaline and fresh lakes during the study of microbial communities due to the use of culture-dependent techniques and also due to the uncultivability of most microbes [63]. However, bacteria of the genera *Arthrobacter*, *Pseudomonas*, *Paenibacillus*, *Bacillus*, *Acinetobacter*, and *Fictibacillus*, have been isolated from Lake Olbolosat [61].

7.4 Impact of climate change on microbial composition in African lakes

Many anthropogenic influences are threatening the littoral and pelagic ecosystems of Lake Tanganyika and Lake Malawi, including global warming, fisheries overexploitation, crisis erosion, and wastewater discharge. In addition to these constraints, alien species introduction has accelerated ecosystem changes in Lake Victoria and Lake Kivu, with dramatic effects on ecosystem function, geochemistry, biodiversity, fisheries, and socioeconomics [64].

Current assessments have endeavored to assess the current state of each lake and have emphasized the steps that must be taken to preserve and restore these bodies of water [65]. Many writers have underlined the tremendous importance of phytoplankton in ecological processes in large lakes [66], but tropical lake phytoplankton has received comparatively less attention. Recent research in some of East Africa's Great Lakes, focusing mostly on smaller size compartments of the food web, may have introduced new notions to tropical limnology. To comprehend the functioning of these systems and their response to the environmental changes projected, or already occurring, in this century, new hurdles must be

addressed. In most parts of Africa, the simple problem of sample preservation remains an insurmountable barrier to good research production [36].

The largest lakes of the rift (Victoria, Malawi, and Tanganyika) have provided very exciting chances, in recent decades, for scientists because of their unique qualities and because of the myriad issues they have encountered. The importance of their preservation has been highlighted. The smaller rift lakes, on the other hand, have almost entirely been overlooked, except Lake Kivu, for which contemporary results are abundant. Lakes Albert and Edward still lack complete and current limnological and plankton investigations. On the other hand, there is essentially no biological research on microbes in this portion of the world, with the significant possible exceptions of Lake Tanganyika and the ongoing, unreported work on photosynthetic and heterotrophic picoplankton. [59].

Microbial primary generation contributes significantly to CO_2 sequestration in aquatic environments. In addition to recycling nutrients for use in the food web, aquatic microbes emit CO_2 into the atmosphere. Microorganisms are the primary decomposers of OM in a wide range of terrestrial habitats, releasing nutrients into the soil as well as CO_2 and CH_4 into the atmosphere. Over millions of years, microbial, biomass, and other organic materials (plant and animal remains) have been transformed into fossil fuels. As a consequence, cellular respiration has become significantly out of balance, and CO_2 levels in the atmosphere will continue to rise as long as fossil fuels are burned. Anthropogenic activities, such as agriculture, industry, transportation, population growth, and human consumption, have a significant impact on the complex network of microbial interactions with other microbes, plants, and animals, as well as local environmental factors, such as soil type and light. These interactions determine how microorganisms influence climate change, besides how climate change affects microbial responses [6]. However, Fig. 7.2 illustrates the microorganisms and climate change in the aquatic ecosystem.

7.5 Geomicrobiology of African lakes

Geomicrobiology is the domain of science dealing with the intersection of geology and microbiology, so it is a subfield of geobiology. It examines the role of microorganisms in geochemical and geological processes and the effects of metals and minerals on microbial activity, survival, and growth. These interactions occur in the geospheres (minerals, rocks, sediments, soil), the hydrosphere, and the atmosphere. Some microorganisms

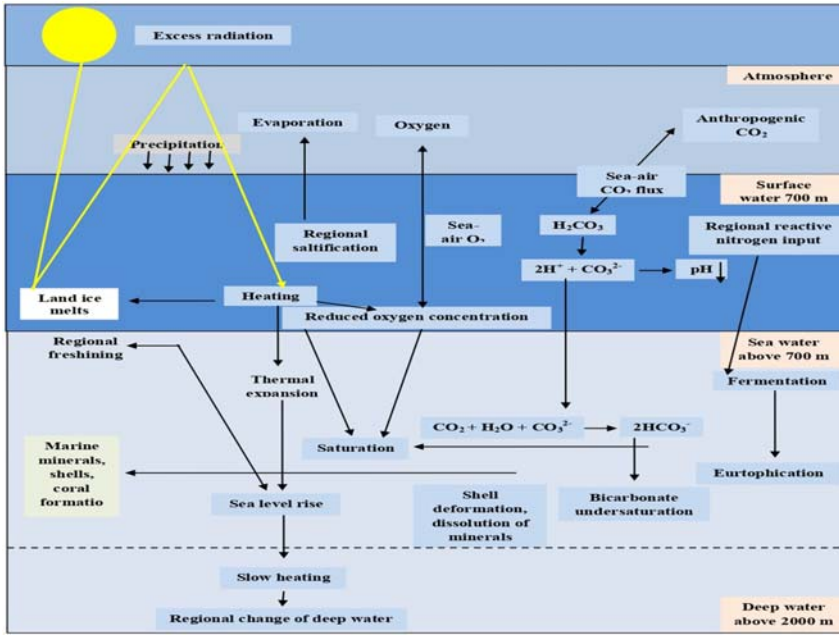

Figure 7.2 Microorganisms and climate change in the aquatic ecosystem.

use metal ions as a source of energy that converts (or chemically reduces) dissolved metal ions from one electrical state to the next. This reduction releases energy that bacteria can use and, as a byproduct, concentrates minerals into what ultimately becomes an ore deposit. Bio-hydrometallurgy or on-site extraction is the place where low-grade minerals can be attacked by well-designed microbial processes under controlled conditions of mineral extraction. It is believed that some gold, uranium, copper, and even iron ores were formed as a result of the action of microbes [67].

7.5.1 Biogeochemical processes in aquatic ecosystems

The microorganisms oxidize and reduce N compounds to gain energy. In any case, this energy may also be released by redox processes linked to other biogeochemical cycles, such as those of C, Fe, or S, and control of the microbial activity destroys DOM utilized as electron donors. Many prokaryotes may grow in the absence of oxygen, either as facultative or stringent anaerobes, depending on their oxic tolerance. As a result, these bacteria may thrive in anoxic conditions such as lacustrine sediments or

the bottom layer of meromictic lakes. The metabolism of heterotrophic microbes, based on the mineralization of OM via oxidation of organic C to the reduction of terminal electron acceptors, is one of the most effective techniques (e.g., NO^{3-}). While OM is the most common electron donor in redox reactions, microbes employ the terminal electron acceptors with the greatest tendency to be reduced (i.e., reduction potential) after a redox reaction sequence. Fig. 7.3 shows the principle for understanding the transformations of energy and matter within ecosystems. The thermodynamic sequence starts using O_2 as an electron acceptor, followed by NO_3^-, Mn oxides, Fe oxides, SO_4^{2-}, and CO_2 in the different redox zones [68].

When OC flow adds energy to the system, it causes thermodynamic imbalance, fueling biogeochemical turnover. Then, beyond oxic–anoxic barriers, microbial respiration drives a vertical series of redox processes (e.g., water–sediment interface). The oxic zone is the source of the majority of terminal electron acceptors. Some of them (NO_3^-, O_2, SO_4^{2-}) can permeate into the anoxic zone from the water column, while others (e.g., NH_4^+) are replenished by oxidation at the oxic–anoxic boundary. As previously noted, salinity may increase the availability of N. However, S is also important in saline lakes, where large quantities of SO_4^{2-} are common. The cycle of S is visible in these ecosystems at the

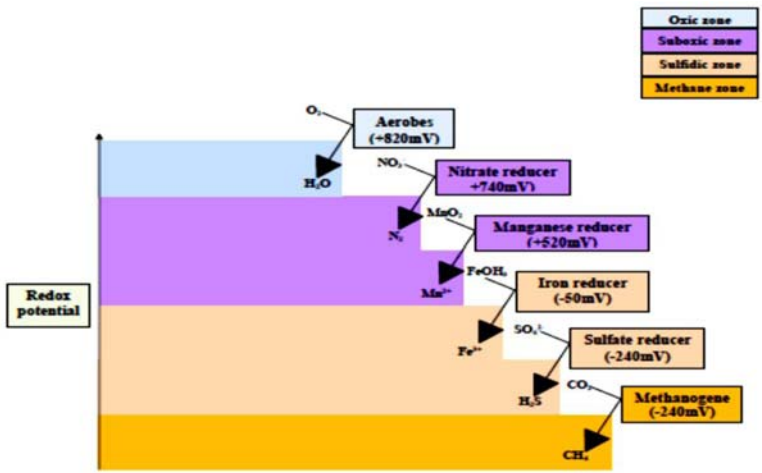

Figure 7.3 In natural systems, sequence of microbially mediated redox processes. The greater the redox potential, the greater the amount of energy released per electron transferred.

outline layer of the water-sediment interface, where S compounds interact with the biogeochemical cycling of other elements like N, O, Fe, and C. The biogeochemical cycle of S in sediment is dominated by dissimilatory sulfate reduction. SO_4^{2-} functions as an electron acceptor during sulfate reduction, producing H_2S, which is often linked to the oxidation of organic components. Hydrocarbons, organic acids, sugars, alcohols, and aromatic compounds are among the many electron donors found in these molecules. As a result, the S cycle is critical for removing organic contaminants in salty aquatic environments. Redox reactions are important in aquatic interfaces, which are hubs of biodiversity, nutrient turnover, and pollutant removal [68].

Biogeochemical cycling is linked with steep gradients between compartments of aquatic habitats, such as those observed in salty lakes where brine waters meet freshwater from the underlying aquifer (saltwater—freshwater interface). In addition, an oxic—anoxic interface within the sediment characterizes both saltwater and freshwater environments (water—sediment interface). The depth of this interface is determined by the amount of degradable organic materials introduced into the sediment. In systems with highly primary productivity (e.g., eutrophic lakes), O_2 transport is governed by molecular diffusion, and oxygen can only reach a few millimeters into the sediment, where prokaryotes (archaea and bacteria) are common. Because they are at the bottom of the food chain, these bacteria are critical to the ecosystem's functioning. Those living in saline lakes have acclimated to high salt concentrations and strong osmotic pressure due to extreme salinity. These microorganisms can range from halotolerant (nonhalophile but tolerate salt) to severe halophiles, depending on their interaction with salt (grow best in hypersaline media). Furthermore, saline lakes are frequently found in dry environments and/or have alkaline characteristics. As a result, poly-extremophiles with halophilic, alkaliphilic, and/or thermophilic characteristics are frequent in such systems [69].

In high saline environments, halophilic and halotolerant prokaryotes have two major mechanisms to deal with their osmotic stress. First, they accumulate large concentrations of inorganic ions in their cytoplasm. Second, they prevent high salt concentrations to reach their cytoplasm. the first technique necessitates adaptation of the entire intracellular machinery to the presence of high ionic concentrations. The second includes the usage of organic compatible solutes created by the cells to maintain osmotic equilibrium. As a result, many metabolic processes

described in freshwater lakes can also occur in saltwater lakes, whereas others cannot exist due to their high energy cost (e.g., autotrophic nitrification). As a result, studying microbial activities in saline lakes is critical to find metabolic pathways not characterized in freshwater environments [70].

Moreover, within the field of geochemistry, "alkaline" is related to high pH values (pH > 7), whereas "alkalinity" is calculated as the summation of bicarbonates and carbonates in water ($mHCO_3^- + 2\,m\,CO_3^{2-}$). The lack of accuracy within the utilization of these chemical terms can lead to the erroneous chemical distinguishing proof of saline waters as soda brine, particularly when the pH is taken into consideration [71]. In general, saline water around the world is dominated by eight major solutes such as Mg^{2+}, Ca^{2+}, Na^+, K^+, HCO_3^-, CO_3^{2-}, SO_4^{2-}, and Cl^-, but many cation–anion incompatibilities are found in concentrated brines (high $HCO_3^- + CO_3^{2-}$ concentrations are coupled with low amounts of Mg^{2+} and Ca^{2+}; low Ca^{2+} concentrations are combined with high SO_4^{2-}; Ca^{2+} as a dominant ion often correlates with high concentrations of Cl^-). Hence, the number of major brine types is restricted, but the chemical types of lakes are in an unexpected way classified, and likely no classification is completely satisfactory, particularly not in the case of soda lakes. Besides, most workers recognize four or five major saline water types employing a minimum of 25 mol or proportionate rate limit for ions. These major types can be subdivided to provide a few subtypes based on the rank of major ions with an identical rate surpassing 25% [72].

Although there is a prove of major soda brine are not utilized enough by limnologists , different combinations of ions exist for the classification of soda brine are explained in numerous comprehensive studies, such as $Na\text{-}CO_3$, $Na\text{-}HCO_3\text{-}CO_3$, $Na\text{-}CO_3\text{-}Cl\text{-}SO_4$, and $Na\text{-}HCO_3\text{-}CO_3\text{-}Cl$. Consequently, the prevalence of Na as the most overwhelming cation is adequate, but this simple criterion is misleading since sodium is by far the most common dominant cation in saline lakes around the world. The Kurlov equation, which incorporates pH, total dissolved solids, and equivalent percentage of ions, can be applied for the visual interpretation of ion composition [73].

7.5.2 Biogeochemical cycles in African lakes

Dissolved gases and water collected along vertical profiles in the five basins (Bukavu Main, Kalehe, Ichungu, and Kabuno Bay) that make up the

485 m depth of Lake Kivu (Congo) were analyzed to provide a geochemical conceptual model for the multiple processes that control the chemistry of the lake. The measured vertical and horizontal variations of the water and gas compositions indicate that each basin has distinct chemical features resulting from (1) a different contribution from the long-circulating fluid system containing magmatic CO_2 responsible for the huge CO_2-(CH_4) reservoir hosted within the deep waters; (2) spatial variations of biomass speciation and/or distribution; and (3) solutes from water–rock interactions. The Kapuno Bay Basin has the highest rate of the inlet of rock fluid. Accordingly, this basin should be considered the most dangerous site for a possible explosion of gas that could result from the activity of the volcanoes Nyamulagira and Nyiragongo, located a few kilometers north of the lake [50].

Kivu is a large tropical meromictic lake located between Congo and Rwanda [74]. As first reported by Damas [75], this lake is characterized by the presence of a large gas reservoir at a depth of $>50-80$ m, which has a CO_2(CH_4)-rich composition. In 2004, the calculated total amounts of CO_2 and CH_4 in the deep waters of Lake Kivu have been estimated as 300 and 55 km^3 STP (gas volume at 0°C and 1 atm), respectively [76,77].

7.5.2.1 Carbon cycle

Primary autotrophic producers in soda lakes are capable of fixing inorganic CO_2 in organic polymers including anoxygenic and oxygenated haloalkaline phototrophs and certain chemolithoautotrophs (Fig. 7.4). Primary production in most soda lakes is high because of dense haloalkaliphilic cyanobacterial communities [78]. They include filamentous heterocystous, nonheterocystous, and unicellular groups. Forms of planktonic Cyanobacteria include prevalence in tropical soda lakes in Kenya and Ethiopia of genera *Anabaenopsis*, *Cyanospira*, and *Arthrospira* (Spirulina) [79]. The extremely unicellular haloalkaliphilic cyanobacterium *Euhalothece natronophila* dominates in hypersaline soda lakes [80]. At moderate salinity, haloalkaliphilic Cyanobacteria predominate, however, at greater salt concentrations, only exceptionally salt-tolerant unicellular green algae, such as *Dunaliella viridis* and *P. salinarium*, may grow [81]. The most prevalent oxygenic phototrophic communities in an East African soda lake, at low salinity, have been presented by the mass growth of *heterocystous Anabaenopsis* [79].

Cyanobacteria have long been thought to be the only diazotrophic component of the oxygenic phototrophic community (Fig. 7.5).

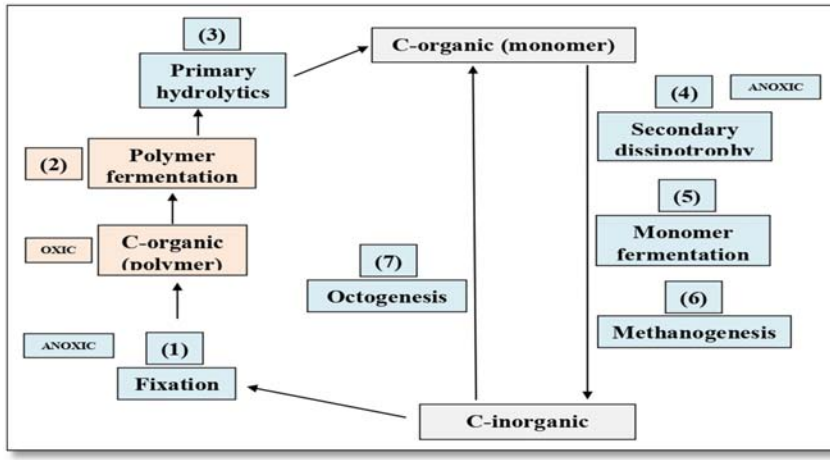

Figure 7.4 Microbially mediated biogeochemical carbon cycle in soda lakes.

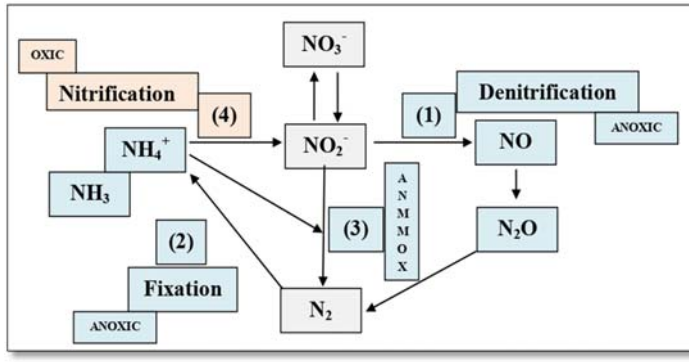

Figure 7.5 Microbially mediated biogeochemical nitrogen cycle in soda lakes.

However, because hypersaline soda lakes are only modestly salt-tolerant, the identification and processes of primary nitrogen fixation remain unknown. Anoxygenic phototrophs, such as haloalkaliphilic *Chromatiales* (*Thiorhodovibrio, Thiorhodospira*) at moderate salinity and *Ectothiorhodospiracea* (*Halorhodospira/Ectothiorhodospira*) at high salinity, also contribute to primary production in soda lakes [78]. Aerobic chemolithoautotrophic bacteria, which are secondary primary producers, also contribute to inorganic carbon fixation in soda lakes. Recently, haloalkaliphilic representatives of nitrifying, sulfur-oxidizing, H_2-oxidizing, and carboxydotrophic bacteria have been described and isolated from soda lakes [18].

Aerobic hydrolytic enzymes, which break down polymers by creating alkali-stable hydrolases, have previously been the subject of several investigations due to the significant application potential of their enzymes in the industry [20]. Only a handful of the known isolates have been obtained from soda lakes. Aerobic Firmicutes, such as *Bacillus* species with diverse glycosidase activities and numerous Actinobacteria, such as *Cellulomonas* and *Dietzia*, as well as Gammaproteobacteria, such as the amylolytic *Alkalimonas*, are among them [18].

It was recently discovered that aerobic haloalkaliphilic Gammaproteobacteria and Actinobacteria of the genus *Marinimicrobium* from soda lakes and soda soils may use chitin as a growth substrate [82]. To date, only one pure culture of the low-salt-tolerant cellulolytic anaerobic bacterium, *Clostridium alkalicellum*, has been recovered from a soda lake [83]. Two newly identified fermentative anaerobic haloalkaliphiles from soda lakes may utilize pectin as a substrate at either high (*Natronovirga* from the *Clostridiales*) or low salt concentrations (*Natronoflexus pectinovorans* of the *Bacteriodetes*) (Fig. 7.4; step 3). In addition, two deep lineages of fermentative haloalkaliphilic bacteria adapted to thrive solely on chitin have been recovered from soda lakes. Both groupings are members of the phylum TG3, which previously solely featured uncultured bacteria. *Chitinivibrio alkaliphilus* is the name given to the highly salt-tolerant group [84].

Secondary heterotrophs, or those that use monomeric organic molecules including alcohols, sugars, amino acids, and organic acids, are among the most abundant types of haloalkaliphiles recovered from soda lakes thus far (Fig. 7.4; step 4). The most numerous aerobes are haloalkaliphilic species of the genera *Halomonas* from the Gammaproteobacteria, *Bacillus* from the Actinobacteria, and Firmicutes [18]. Members of the Clostridia genera *Anaerovirgula*, *Anoxynatronum*, *Alkaliphilus*, *Natranaerobaculum, Natranaerobius*, and some species of *Anaerobacillus, Spirochaeta*, and *Anaerobranca* dominate as soda lake fermentative anaerobes [85] (Fig. 7.4; step 5). The least researched functional categories of soda lake microbial communities are homoacetogens (Fig. 7.4; step 7) and methanogens (Fig. 7.4; step 6), which function during the last step of OC breakdown. *Natroniella acetogena* (Halanaerobiales) and *Tindallia, Natronincola* (Clostridiales) are heterotrophic fermentative haloalkaliphilic acetogens that feed on amino acids and alcohols [86]. *Hydrogenotrophic acetogens* have just lately been detected in soda lakes. *Fuchsiella alkaliacetigena*, a new,

exceptionally salt-tolerant haloalkaliphilic member of the Halanaerobiales, is the sole culturable organism [87].

7.5.2.2 Nitrogen cycle

In soda lakes (such as Wadi El Natrun, Malha Crater, Chitu, Magadi, and Turkana), the denitrification process is achieved by heterotrophs, which dominates through, exceptionally salt-tolerant alkaliphilic *Halomonas* representatives and various facultative anaerobic lithotrophs, such as *Alkalilimnicola–Alkalispirillum*, and the genus *Thioalkalivibrio* of Gammaproteobacteria [88] (Fig. 7.5; step 1). It is unclear if dissimilatory ammonification competes with denitrification in soda lakes. So far, the alkaliphiles exhibiting this metabolism have only been discovered in high-pH bioreactors, namely *Sulfurospirillum alkalitolerans* from the Epsilonproteobacteria and *Desulfurispirillum alkaliphilum* from the phylum Chrysiogenetes [89].

In soda lakes and soda soils, heterotrophic anaerobic fermentative haloalkaliphiles actively fix nitrogen (Fig. 7.5; step 2), and two Firmicutes groups represent these organisms: a moderate salt-tolerant *Bacillus alkalidiazotrophicus* and a very salt-tolerant *Natronobacillus azotifigans* [90]. Furthermore, the presence of the *nifH* gene, which codes for a nitrogenase, has been found in two different soda lake anaerobes: the cellulolytic *Clostridium alkalicellulosi* [83] and the iron-reducing *Geoalkalibacter ferrihydriticus* [91]. Furthermore, the *nifH* gene has been found in numerous soda lake anoxygenic phototroph representatives, suggesting that anoxygenic phototrophs may potentially contribute to N_2 fixation. Nitrogen fixation in soda lakes under oxic circumstances has rarely been studied. However, a group of low salt-tolerant alkaliphilic Cyanobacteria (e.g., *Nodularia* and *Anabaenopsis*) is a key suspect [92].

Haloalkaliphilic nitrifiers may convert ammonium generated during nitrogen fixation in soda lakes to nitrate via nitrite (Fig. 7.5; step 4). *Nitrosomonas halophila*, a very alkali-tolerant subpopulation, oxidizes ammonium to nitrite in soda soils and soda lakes, whereas *Nitrobacter alkalicus*, a moderately alkali-tolerant subpopulation, oxidizes nitrite. The nitrogen cycle is impeded in hypersaline soda lakes because the maximal salt concentration for nitrification in soda lakes is 1 M of total Na^+. Furthermore, at high pH, the NH_3/NH_4^+ balance promotes the generation of hazardous NH_3, resulting in possible N-loss from the environment. As a result, the nitrogen cycle in soda lakes, particularly hypersaline ones, may be dependent on an external source of NOx^- [93].

On the other hand, several individuals of the sort *Methylomicrobium* (Gammaproteobacteria) are known to be alkaliphiles methane-oxidizing and have been detected to oxidize ammonia to nitrite within the existence of CH_4 or methanol exceptionally at alkaline pH between 10 and 11 [94]. Additionally, this might keep the existence of N_2 within the NH_3 from soda lakes. However, many isolates of lithotrophic and alkaliphilic ammonia or nitrite oxidizers are known in the Ethiopian and Kenyan pop lakes [17].

Fermentative anaerobe, chemoorganotrophic alkaliphilic bacteria, are also found in the anoxic zone of some African lakes [17]. Members of these bacteria carry out acetogenesis and ammonification at high pH. Members of thermophilic acetogens have been recorded within the hot spring regions that commonly encompass the soda lakes [17]. Other alkaliphilic thermophiles that are likely thermotogas have also been detected in these springs. Saccharolytic bacteria such as spirochetes and the species related to the Haloanaerobiales and Clostridial taxa are described too [17]. Enhancement of soda lake specimens with cellulose as a substrate taken after investigations of the end products of a few of these anaerobes shows the yield of isobutyric corrosive, acetic acid, ethanol, and H_2. Some of these products are expended by anoxygenic phototrophs, acetogenic bacteria, sulfate-reducing bacteria, or methanogens [18].

7.5.2.3 Sulfur cycle

Within soda lakes, the dissimilatory reduction of oxidized sulfur compounds like sulfur, sulfate, thiosulfate, and sulfite, resulting in sulfide production is essential biogeochemical processes [95] (Fig. 7.6; step 1). These reactions can be carried out by a variety of obligatory anaerobic and obligatory haloalkaliphilic microorganisms. *Desulfonatronospira, Desulfonatronovibrio*, and *Desulfonatronum* are deltaproteobacterial taxa that represent lithotrophic sulfate-reducing bacteria in soda lakes [19]. They can either grow as sulfate-reducing typical bacteria by oxidizing hydrogen, formate, or short-chain organic compounds, as electron donors, with thiosulfate, and sulfate, or sulfite, as electron acceptors, or by sulfite or thiosulfate disproportionation [95]. Heterotrophic sulfate-reducing bacteria in soda lakes are incomplete oxidizers that use butyrate (*Desulfobotulus alkaliphilus*) or propionate (*Desulfobulbus alkaliphilus*) as an e-donor/C-source, sulfate or thiosulfate as an e-acceptor, and acetate as a final product [96].

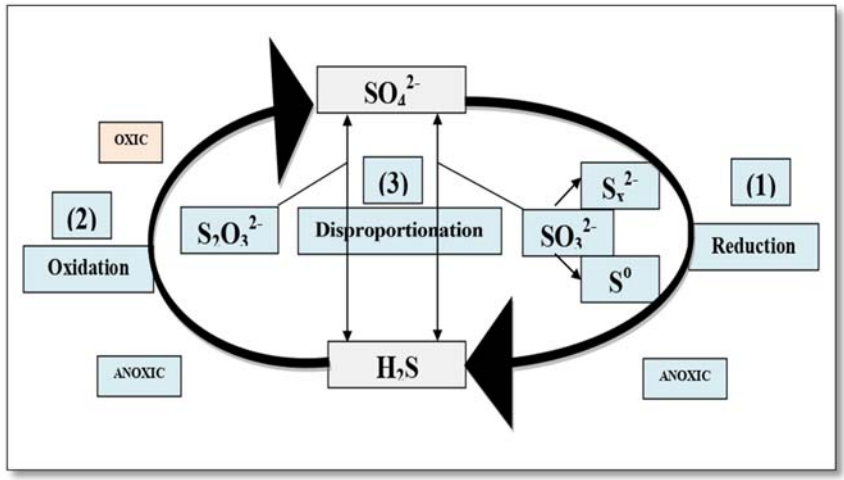

Figure 7.6 Microbially mediated biogeochemical sulfur cycle in soda lakes.

Up to this point, only one haloalkaliphilic sulfate-reducing bacterium, *Desulfonatronobacter acidivorans*, has been discovered in soda lakes and is classified as a full oxidizer [97]. It can oxidize numerous volatile fatty acids to CO_2 using sulfate or thiosulfate as an e-acceptor, but it cannot use externally supplied acetate. Under sulfate-reducing circumstances, haloalkaliphilic syntrophic partnerships of reverse acetogenic Clostridiales members and lithotrophic sulfate-reducing bacteria drive acetate oxidation in soda lakes. The relationship at low salt concentrations includes "*Candidatus Contubernalis alkalaceticum*" and "*Desulfonatronum cooperativum*" [98]. The association comprised "*Candidatus Syntrophonatronum acetioxidans*" and *Desulfonatronospira* sp. at exceptionally high salt concentrations [84].

Elemental sulfur reduction in soda lakes is most likely not carried out by sulfate-reducing bacteria, because no pure cultures of haloalkaliphilic sulfate-reducing bacteria can grow with sulfur as an e-acceptor. Instead, the sulfur reduction is mediated by three distinct lineages of obligate anaerobic haloalkaliphiles. The real e-acceptor in all three is polysulfide (Sx^{2-}), which forms abiotically at high pH from sulfur and sulfide. *Desulfurispira natronophila* is a member of the phylum Chrysiogenetes. The Firmicutes are the second group of sulfur/polysulfide-respiring haloalkaliphiles identified from soda lakes using formate as an e-donor. *Desulfuribacillus alkaliarsenatis* is a relatively salt-tolerant representative [82]. In addition to sulfur, it may utilize arsenate and thiosulfate as e-acceptors.

Natroniella sulfidigena, a *Halanaerobiales* member, may execute microbial-mediated sulfur reduction at saturated soda concentrations. For sulfur/polysulfide-dependent respiration, it can utilize formate, H_2, and acetate as e-donors [99].

On the other hand, phototrophic and chemotrophic sulfur-oxidizing bacteria may oxidize sulfide generated by sulfidogens to elemental sulfur or sulfate (Fig. 7.6; step 2). Anoxygenic purple sulfur bacteria dominate in soda lakes, including haloalkaliphilic species of the genera *Halorhodospira* and *Ectothiorhodospira* at high salinity and members of the genera *Thiorhodospira, Thioalkalicoccus*, and *Ectothiorhodosinus* at low salinity. The chemotrophic sulfur-oxidizing bacteria in soda lakes are members of four haloalkaliphilic Gammaproteobacteria genera: *Thioalkalimicrobium, Thioalkalispira, Thioalkalivibrio*, and *Thioalkalibacter* [89]. They are obligate autotrophs that use reduced sulfur compounds as e-donors, such as sulfide, elemental sulfur, thiosulfate, polythionates, and polysulfide [100].

Other types of *Thioalkalivibrio* such as *Tv. Thiocyanodenitrificans*, *Tv. paradoxus*, and *Tv. thiocyanoxidans* can grow using thiocyanate as the sole source of energy, nitrogen, and sulfur. The first two bacterial species degrade thiocyanate preferentially to cyanate and were the first sulfur-oxidizing bacteria cultures to identify the cyanate route for primary thiocyanate degradation [101].

The high salinity of soda lakes produces osmotic stress in haloalkaliphilic microbes, making them synthesize osmoprotectants. Halophilic microorganisms may synthesize and/or accumulate compatible solutes by which high concentrations of neutral soluble organic molecules are stored in their cytoplasm [102]. Glycine betaine, glutamine, proline, ectoine, and hydroxyectoine have been discovered to perform important functions as compatible solutes in bacteria [103]. Extremely haloalkaliphilic Euryarchaeota primarily use K^+ as an osmotic regulator. These osmolytes do not participate in cell metabolism, but are critical to cellular volume and homeostasis, and have been demonstrated to maintain membrane protein structures [104]. Although the "salt out" osmotic control technique is more energy expensive than the "salt in" strategy, it permits microorganisms with extremely efficient energy metabolism to live over wider salinity gradients [105].

The cell membrane of haloalkaliphilic prokaryotes has structural changes that include an increase in the levels of the neutral lipid squalene and the polar lipid cardiolipin in the phospholipid bilayer [106]. Squalene, first discovered in *Thioalkalivibrio versutus*, works with cyclopropane fatty

acids to maintain their cellular membranes, which may help to avoid proton leakage. Squalene is physically located in the middle of the membrane, perpendicular to the membrane's two lipid layers. Cardiolipins are another kind of lipid found in bacterial membranes (*Thioalkalivibrio*) [107] and their negative charge inhibits protons from migrating out from the cells [108]. Diacidic phospholipids are abundant in the membrane lipids of the very halophilic Euryarchaea. Some very halophilic prokaryotes, such as Halobacteriaceae and *Salinibacter* members, have membrane surface layers that are rich in acidic amino acids [69].

Furthermore, in Lake Chitu, as specific soda lake, sulfur is among the most components for OM primary production. Hence, the sulfur cycle controlled by certain microbes is believed to be among the most dynamic forms in soda lakes. Sulfur-reducing bacteria are dominant in anoxic layers of soda lakes and they discount sulfate and organic sulfur resulting from decaying cells into sulfide (S^{2-}). This is the reason why anoxic layers of soda lakes are frequently wealthy in harmful and toxic sulfide too. A high pH encourages converting the H_2S to its ionic form (HS^-) [51].

In soda lakes, the genera of alkaliphilic sulfur-reducers present involve *Desulfonatronovibrio* and *Desulfonatronum* and are likely favored by this process [51]. These expend H_2 coming about from the OM fermentation for creating H_2S. Amazingly, *Desulfonatronovibrio* utilizes formate and desulfonatr onumuseformate and ethanol/lactate [83].

A curious interaction between methanogens and sulfate reducer happens under anaerobic conditions in the presence of a considerable amount of adequate sulfate. This can be a competition for substrates, since reducers of sulfate ordinarily outcompete methanogens for the majority of fermentation byproducts utilized by methanogens via oxidizing them to CO_2, whereas lessening sulfate to H_2S. In other terms, the sulfate comes about in inhibition of CH_4 union from CO_2/H_2 as well as acetate. However, reducers of sulfate show partial ability for methanol or trimethylamines, and certain genera of methanogens (e.g., *Methanosarcina*, *Methanolobus*, and *Methanococcoides*) can utilize them for methanogenesis [109].

On the other hand, sulfur-oxidizing bacteria instead obtain their vitality from the oxidation of the sulfide coming to the oxygenated layers of soda lakes. A few of these are photosynthetic sulfur phototrophs, which implies that they require light to get vitality too. Examples of alkaliphilic sulfur-oxidizing microbes are the genera of *Thiorhodospira, Thioalkalivibrio, Thioalkalimicrobium*, and *Natronhydrogenobacter* [93].

7.5.2.4 Methane cycle

Initially, methane was considered to be the second most long-living greenhouse gas in the atmosphere, with critical worldwide emissions. Although this emission is significantly smaller than human-made CO_2 emissions, the impact of CH_4 on global warming is 34 times greater than CO_2 over 100 years. Because methane has a short residence period in the atmosphere (about 10 years), reducing CH_4 emissions might be an effective method of mitigating climate change. Methane concentrations in the atmosphere grew from 722 parts per billion in 1750 to 1803 parts per billion in 2011, most likely as a result of human activity [110,111]. There are three types of CH_4 sources for the atmosphere: biogenic (due to microbial activity: termites, wetlands, oceans, rice fields, ruminants, sewage treatment, and landfills), thermogenic (fossil fuel), and pyrogenic (biomass burning). Natural emissions account for approximately 53% of total CH_4 emissions, whereas anthropogenic emissions account for 47%. For the decade 2003–2012, the total anthropogenic CH_4 emissions were previously calculated to be 346 Tg CH_4/year [112].

Both production and consumption of fossil fuels, the usage of agriculture, landfills, etc., and incomplete biomass burning are all human activities that contribute to CH_4 emissions. Domestic ruminants and the production and consumption of fossil fuels (oil, coal, shale gas, and natural gas) account for 31% and 23% of anthropogenic sources, respectively. Wetlands are the primary natural producers of CH_4 in the atmosphere, emitting an estimated 185 Tg of CH_4/year, or 25% of total CH_4 emissions. Wetland methane generation is biogenic, meaning it is caused by microbial activity. More than 70% of total CH_4 production (anthropogenic and natural) is biogenic. Methane generation, commonly known as methanogenesis, is a biogeochemical process mostly carried out by methanogenic archaea in anoxic habitats. Methanopyrales, Methanosarcinales, Methanomicrobiales, Methanocellales, Methanococcales, and Methanobacteriales are the current orders of methanogenic archaea. To digest organic materials and create CH_4, they adopt one of the three metabolic pathways: acetoclastic (acetate fermentation), hydrogenotrophic (CO_2 reduction), or methylotrophic (methyl group reduction). The most common process in the oceans is hydrogenotrophic methanogenesis (performed by the six orders of methanogenic archaea), whereas acetoclastic methanogenesis (performed solely by the Methanosarcinales) is primarily found in freshwater sediments [113].

For a long time, it was widely considered that methanogenesis was entirely anaerobic, but the well-known "oceanic CH_4 conundrum" prompted different theories. Although it is unknown that CH_4 is created in anoxic sediments and waters, it has been proposed that CH_4 is formed in anoxic micro-environments within anaerobic particles (fecal pellets and aggregates). Later, Karl et al. [114] proposed that CH_4 was created as a byproduct of methylphosphonate decomposition in phosphate-depleted waters, and Metcalf et al. [115] corroborated that hypothesis by identifying archaea capable of producing considerable amounts of methylphosphonate in marine environments.

The researchers hypothesized that phytoplankton may create methylated products such as dimethyl sulfoniopro prionate (DMSP) or dimethyl sulfide (DMS), which aerobic methanogens employ to generate CH_4. Numerous pieces of research have focused on synthesizing CH_4 from DMS [116] or DMSP [117]. They discovered that CH_4 and DMS or DMSP concentrations were negatively connected.

In the aquatic systems, methanogenesis, in the anoxic bottom layers of water columns or sediments, can create AOM in fluids and biogeochemical processes related to CH_4. Methane enters the atmosphere by diffusion, ebullition, or plant-mediated transport when it is generated. Methanotrophs can oxidize CH_4 either aerobically or anaerobically during this transport. The electron acceptor in aerobic CH_4 oxidation is O_2. It is carried out by methanotrophic bacteria and is an extremely efficient CH_4 consumer. Oxygen is the most efficient electron acceptor in terms of thermodynamics. However, anoxic CH_4 oxidation may be accomplished with various electron acceptors such as nitrate (NO_3^-), nitrite (NO_2^-), iron (Fe), manganese (Mn), and sulfate (SO_4^{2-}) [112]. The methane cycle has been researched in soda lakes as an important component of the microbial carbon cycle. Significant efforts have been made in Central Asia and North America to detect methanogenic activity in anaerobic sediments from soda lakes. The results clearly showed that methylotrophic methanogenesis predominated and that acetoclastic processes were absent, but the results for hydrogenotrophic methanogenesis were equivocal [118]. Some of the major haloalkaliphilic factors influencing methanogenesis production in soda lakes have been isolated and described in pure culture, including two groups of methylotrophs, *Methanosalsum zhilinae* (high salinity) and, *Methanolobus taylorii* (moderate salinity) as well as a highly salt-tolerant lithotroph, *Methanocalculus natronophilus* [87].

Generally, CH_4 is oxidized by methanotrophs (methylotrophs that use only methane) when they come to the oxic zones and become a portion of the organic pool. Different methanogens counting the archaeal genera, *Methanolobus, Methanocalculus, Methanosalsus, Methanosaeta*, and *Methanoculleus*, have existed within the anoxic zones of soda lakes. Methane-oxidizing bacteria like *Methylobacter* or *Methylomicrobium* are displayed within the oxic zones too. Hence, methanotrophy returns CH_4 carbon into the common pool of OM and avoids the loss of C to the environment as CH_4. Typically, it is also an ecologically vital process for worldwide warming as the action of CH_4-oxidizers could be an impressive sink of CH_4. Moreover, alkali-tolerant *Methanobacterium* spp. are documented as H_2 utilizing organisms. In such a manner, both methanogenesis and methylotrophs are vital microbial mechanisms in the ecological as well as application sectors [17].

7.5.2.4.1 Pathways of methanogenesis

Methanogenesis can occur in a variety of ways, including the hydrogenotrophic, acetoclastic, and methylotrophic routes. The substrates used to make methane are classified, but they all have the same end step of reducing methyl-coenzyme M to methane, making the gene encoding methyl-coenzyme M reductase an excellent biomarker for detecting methanogens. However, each pathway's contribution to methanogenesis varies depending on the environment, and little is known about the influencing elements. Numerous studies have related certain genera to the substrates used in methanogenesis, allowing researchers to examine potential methanogenic routes based on methanogen community composition [119].

Methanogenesis activity and emissions differ greatly among lakes. The rate of methanogenesis was found to be linked to lake productivity. Ebullition allows the majority of the methane produced in anoxic sediments to reach the atmosphere in shallow lakes. As more than just an outcome, eutrophic and shallow lakes emit far more methane to the atmosphere than oligotrophic and deep lakes. Methanogenesis activity and/or associated microbial populations have been discovered in various lakes in recent investigations. Methanogenesis and/or methanogen vertical patterns in a few eutrophic freshwater lakes [76], however, have not addressed the seasonality effect on methanogenesis and methanogens. While phytoplankton growth is seasonal, nutrient intake in conjunction with primary production is a key contributor to lake methanogenesis. The sampling season and the trophic condition of the lake may have an impact

on methanogenesis activity and the related methanogens. Principally, purple nonsulfur bacteria use nitrogenase to convert CO_2 to CH_4, while fungi make it via methionine as a potential carbon precursor. Furthermore, cyanobacterial species can generate methane by attributing demethylation of methyl phosphonates using methylated sulfur compounds as carbon precursors [120].

7.5.2.4.2 Source of methane hydrogen

In a variety of geological contexts, including continental hyperalkaline springs and dry gas seeps, submarine hydrothermal vents, and mud volcanoes, CH_4 is frequently found in hydrogen-rich (H_2) fluids associated with serpentinized ultramafic rocks. At hydrothermal vents, serpentinization events can provide strongly reducing conditions that encourage the reduction of CO_2 to CH_4. Previous research has suggested that the H_2 utilized to reduce CO_2 comes from OM breakdown or free geogenic H_2. In Lake Kivu, Pasche et al. [121] found that below 260 m, about 35% of CH_4 has been derived from acetoclastic methanogenesis.

The bottom water δ^2H_{CH4} values of −220% are in the range that is typical for carbonate reduction (−250% to 150%), supporting the idea that CO_2 reduction is a major process in deep water. To account for the remaining 65% (PCH_4 - $CO_{2red_geo} = 44 \pm 18$ g C/m^2/year) of CH_4 synthesis via CO_2 reduction, a significant amount of H_2 is required. To explain these findings, another source of H_2 is needed. The same authors [121] theorized on the origin of this extra H_2. The source of these gases is unknown. However, this might imply that groundwater inflows that have been in touch with juvenile gases could be a substantial source of H_2. Chemical reactions, such as pyrite precipitation, might potentially produce H_2. Another possibility is a direct influx of geogenic CH_4, generated during the cooling of magmatic gases at depth in the absence of oxygen, which would also have a dead ^{14}C signal and a high δ^2H_{CH4}.

7.5.2.4.3 Methane fluxes

Practically, the discharge of CH_4 was estimated from the Gisenyi sediment core as between 60 and 100 g C_{CH4}/m^2/year. Observably, the low productivity was corrected during the 2 years of sediment trap deployment. So, the upper flux estimate was too high to be explained by the available OC in sediment layers. On the other hand, the lower estimate was calculated and ranged from net sedimentation and OC gross ($P_{CH4_sed} = 49 \pm 14$ g C_{CH4}/m^2/year [122].

Pasche et al. [121] also reported that numerous concurrent environmental changes may have boosted OC sedimentation. First, an increase in subaquatic inflows, possibly induced by heavier rainfall in eastern Africa from 1961 to 1990, might have resulted in stronger uplift and, as a result, a bigger supply of nutrients. Second, recent external P and N inputs may have grown as a result of the rapidly rising population. Third, the introduction of *Limnothrissa miodon* significantly impacted the food chain, perhaps altering the exporting OC 9. Because a considerable fraction of CH_4 appears to be created by geogenic H_2, Pasche et al. [121] cannot rule out the possibility that geogenic inputs have also grown, particularly in this geologically active region. Incubation trials, the existence of heavier ^{13}C-CH_4 in water layers over 90 m deep, and the presence of certain microbial communities all indicated methane oxidation. Ebullition releases the bulk of the methane generated in many anoxic strata. The difficulty in quantifying bubble sizes across large geographical or temporal dimensions limits the current understanding of natural methane bubble size distributions. Even in very small regions of comparable flow, bubble size distributions were spatially diverse, indicating that localized sediment conditions are crucial in influencing bubble size. Over the 3-month sample period, there was no change in bubble size distributions, although mean bubble size was positively linked with daily ebullition flux. Bubble data were used to validate the performance of a widely used bubble dissolution model, which was then used to estimate that bubble dissolution accounts for about 15% of the diffusive air-water-methane flux from the epilimnion and no more than 10% of the methane accumulated in the hypolimnion during summer stratification [123].

7.5.2.4.4 Methanogenesis in African Lakes

Methane has historically been thought of as a byproduct of microbial methanogenesis of organic materials—a potent greenhouse gas of worldwide significance. Surprisingly, evidence is mounting that certain microbes, including Cyanobacteria, algae, fungi, purple nonsulfur bacteria, and cryptogamic coverings, create methane in oxygen-saturated aquatic and terrestrial habitats. The nonmethanogenesis process has the potential to contribute significantly to methane emissions [120].

Microbial methanogenesis occurs largely in anoxic conditions according to the current paradigm in aquatic science. To achieve the observed methane accumulation in the presence of oxygen, methane production must be uncoupled from methane oxidation. Methane is also a significant

substrate for microbial development in aquatic environments. Microbial methanogenesis is thought to occur largely in anoxic conditions according to popular belief. Methane accumulation in well-oxygenated waters is a common occurrence, which is typically considered to be the result of physical transfer from anoxic soil and water or in situ generation inside micro-anoxic zones [124].

In oxygenated environments, several processes for methanogenesis have been postulated [125]. The UV-induced methyl-ester cleavage, hypoxia-induced methane generation in mitochondria, methane release by organisms under oxidative stress, and microbial degradation of methylated substances are all examples of processes that produce methane. The UV penetration in oligotrophic lakes is restricted to 2.0 m, substantially lower than the reported methane peak. Although methanogenic archaea can benefit from the conversion of methylation molecules like methanethiol to methane, neither methanethiol nor other methylated compounds are usually found in high concentrations in oxygenated epilimnion in lakes [126,127].

According to Selley [128], methane is produced in three different ways: (1) from the mantle, (2) from the thermal maturation of OM, and (3) through bacterial decomposition of OM at shallow depths. The major methane-forming mechanism in Lake Kivu's water column is bacterial-mediated methanogenesis of CO_2, which is the most abundant natural gas in volcanically active locations. Other gases, ions, and anions, such as silica, phosphate, iron, sulfide, and ammonia, are present in lower amounts.

In hypersaline circumstances, methanogenesis occurs via a noncompetitive (methylotrophic) pathway, while at moderate salinity, sulfate depletion prohibits hydrogen or acetate oxidation via sulfate reducers [129]. Even in the absence of sulfidogen competition, lithotrophic methanogenesis in NaCl brines has never been demonstrated at salinities more than 2 M NaCl, and the acetate-dependent pathway is unknown for salt concentrations above marine conditions (3.5%). Although the absence of hydrogenotrophic methanogenesis at extreme salinity may have more complex explanations (for example, the absence of hydrogenotrophic lifestyle in extremely halophilic lineages of "Methanomicrobia"), the former has plausible thermodynamic grounds [105].

There is little evidence of methanogenesis in soda lakes, especially those with high salinity. Direct incubation experiments revealed no methane synthesis from competitive substrates (H_2 or acetate), implying that the noncompetitive methylotrophic route is the only one in operation

(with MeOH and DMS). Methane generation in sediment incubations with ^{14}C-bicarbonate, on the other hand, was linked to the presence of hydrogenotrophic methanogenesis. Even though it is unknown how ^{14}C-bicarbonate is exchanged with the huge pool of bicarbonate/carbonate in hypersaline soda lakes, using it as a source for methanogenesis or primary sector estimation in soda lakes is challenging. A perspective emerges that this could lead to a significant overestimation of actual activity and that only direct stimulation of methanogenesis with noncompetitive substrates should be considered evidence [130].

Members of Methanomicrobiales appear to be the only lithotrophic methanogens active at high salt levels both in NaCl and KCl and in soda brines. Furthermore, *Methanobacterium alcaliphilus*, a member of the "Methanobacteria," appears to be able to endure diluted alkaline lake conditions (i.e., salinity below seawater conditions and pH 8.5–9) [131]. Two Methanosarcinales members represented specialized methylotrophic methanogens cultivated so far from haloalkaline lakes. Both are obligate alkaliphilic and slightly salt-tolerant, with *M. zhilinae* being more salt- and alkali-tolerant than *Methanolobus oregonense* [132].

Lake Kivu is unique in the world in that it accumulates massive volumes of CO_2 and methane. According to recent research, methane concentrations in the lake have grown by up to 15% in the previous 30 years, and buildup at this rate might result in catastrophic outgassing by ~2100. Analyses of ^{13}C and ^{14}C in CH_4 and possible carbon sources found that below 260 m, an extremely high ~65% of the CH_4 derives either from direct inflows of geogenic CH_4 or from geogenic CO_2 reduction with primarily geogenic H_2. Aerobic methane oxidation, which is carried out by near relatives of methane-oxidizing bacteria, is the primary activity that keeps methane from escaping into the atmosphere. Anaerobic CH_4 oxidation was also identified in the SO_4^{2-} reducing area by CH_4-oxidizing archaea, although it is restricted by the availability of sulfate. Changes in ^{14}C-CH_4 and ^{13}C-CH_4 during the 1970s indicate that the quantity of CH_4 generated by decomposing organic material has risen due to increasing OM buildup. This, along with the quick commencement of carbonates in the 1960s, was previously explained by three environmental changes: (1) the introduction of nonnative fish, (2) amplified subaquatic inflows due to hydrological changes, and (3) increased external inputs due to the rapidly growing population. As a result of the increased primary production and OM sedimentation, CH_4 levels are projected to rise, however, due to the high concentration of ancient CH_4 carbon [121].

The two major CH_4-producing mechanisms in lacustrine sediments are CO_2 reduction and acetoclastic methanogenesis [133].

Based on the availability of oxidants, CH_4 can be oxidized in the sediment, at the sediment-water interface, or in open water. Currently, two distinct biological processes are thought to be the primary contributors to CH_4 oxidation in aquatic systems: aerobic methanotrophic bacterial oxidation and anaerobic CH_4 oxidation by syntrophic consortia of CH_4-oxidizing archaea and SO_4^{2-}-reducing bacteria. Unconsumed CH_4 is ultimately carried to shallower seas and released into the atmosphere, where it functions as a powerful greenhouse gas. Lakes are estimated to provide 6 to 16% of worldwide CH_4 emissions to the atmosphere. As a result, CH_4 oxidation is critical in regulating lacustrine CH_4 emissions [134].

Lake Kivu is a Rift Valley lake in Africa with a constantly stratified hypolimnion that holds an estimated 300 km^3 of CO_2 (gas volume at 0°C and 1 atm) and 60 km^3 of CH_4 [76]. The concentration of CH_4 in the lake raises the possibility of catastrophic outgassing, akin to the limnic eruptions in Lakes Monoun and Nyos. In contrast, extracting the lake's CH_4 might generate enough energy to power the lake's neighboring countries for a decade. However, the origin of these gases has been a source of contention. Most scholars believe that CO_2 is largely geogenic, whereas CH_4 is biogenic. According to reports, two-thirds of CH_4 is created by geogenic CO_2 reduction and one-third by acetoclastic methanogenesis of sedimentary organic or biogenic material [121].

A recent study found that since the 1960s, Lake Kivu has experienced an increase in gross and OC sedimentation due to a modified internal food web caused by the introduction of the nonnative Tanganyika sardine (*L. miodon*) and hydrological changes that enhanced internal upwelling. They may be increased also due to external nutrient inputs generated by the rapidly growing human population [122].

The generation of active CH_4 in the waters of an oxygenated lake defies the long-held belief that microbial CH_4 production happens only in anoxic environments. The production of CH_4 in the upper oxic water layers brings the source of CH_4 closer to the air–water interface, since convective mixing and microbubble detrainment can result in a larger methane efflux than previously thought. Microorganisms can create CH_4 in oxic settings if they have enzymes that mitigate the effects of molecular O_2 during methanogenesis or if they use alternate pathways that do not use oxygen-sensitive enzymes. Modifications in lake ecology due to global

warming will modify CH_4 creation in oxic lakes with far-reaching ramifications for CH_4 flux and climate feedback [119].

Methane could be created in African lakes (such as Kivu) by acetoclastic methanogenesis, which uses acetate produced by OC, or CO_2 reduction, which uses either geogenic or OC-derived CO_2. OM fermentation produces a little amount of CO_2 compared to the overall upward flux of DIC across the anoxic water column or CO_2. Geogenic CO_2 ($F_{CO2_geo} = 138 \pm 30$ g C/m^2/year) is thus far more abundant than CO_2 from mineralization of OC and will be the main substrate for CO_2 reduction. Furthermore, the OC flux observed in sediment traps did not decrease with depth, indicating that mineralization in the anoxic water column is minor [122]. Although examination of the *mcrA* gene revealed the presence of a methanogenic population in the water column, Pasche et al. [121] conclude that acetoclastic methanogenesis in the anoxic water column is limited.

Lake Kivu has become one of the world's largest methane reservoirs, as well as a unique habitat for geomicrobiologists interested in the methane cycle and risk assessment and management [76]. There is extensive research on the diversity and activity of planktonic populations of big and tiny eukaryotes, as well as their trophic interplay, in the lake's epilimnetic waters. Recent surveys have also revealed more information about photosynthetic and heterotrophic picoplankton seasonal variations, although very few data exist on the composition, diversity, and spatial distribution of bacterial and archaeal communities [49].

Roland et al. [135] studied methane oxidation in Lake Kivu's water column—a deep meromictic tropical lake with huge amounts of methane in the anoxic deep waters—between June 2011 and August 2014. Depth profiles of dissolved gases (N_2O and CH_4) and possible electron acceptors for AOM (sulfate, iron, manganese, and nitrate) were measured. Significant CH_4 oxidation activity was identified in both oxic and anoxic waters, and CH_4 is a primary electron donor to support anaerobic metabolic activities connected to AOM in Lake Kivu's upper anoxic waters. The maximal aerobic and anaerobic CH_4 oxidation rates decreased when molybdate was introduced for half of the experiments, clearly indicating the presence of AOM connected to sulfate reduction, but increased for the other half.

Methane generation in lakes is predominantly caused by anoxic sediments, with various emission pathways rising to the surface and into the atmosphere (e.g., diffusion, ebullitive and storage fluxes, and emissions

from aquatic vegetation). Due to vertical and lateral transfer from bottom and littoral sediments, surface waters in small and shallow ponds can be frequently oversaturated with CH_4. As a result of recognized mechanisms of oxic methanogenesis mediated by light-, nutrient-, and salt-dependent microbial metabolisms, as well as the availability of pelagic micro-anoxic habitats, methane oversaturation has been recorded in lake waters with low sediment-to-water fluxes. Notably, methanogenic microorganisms were found in oxygenated epilimnion in conjunction with either Cyanobacteria or algae, and experimental cultures of chosen Cyanobacteria were likely to create methane in saturated oxic conditions [136]. The overlap of metalimnetic CH_4 maxima with oxygen oversaturation and chlorophyll maxima, as well as the positive relationship between surface CH_4 flux rates and chlorophyll-a levels, also supports a close relationship between algal biomass and CH_4 release [137].

Although methane emissions in surface layers bring the starting point of CH_4 pretty close to the water–air interaction, where it contributes significantly more to overall emissions [138], it is unclear whether, how, or to what extent methanogenic processes can counter-balance aerobic methanotrophy. The importance of tropical aquatic habitats in terms of methane emissions is being debated. Because in situ measurements are poorly recorded and frequent cloud cover decreases satellite data densities/estimates, the focus has shifted to Africa [139]. Significant salinity, consistent solar radiation, warm temperature, and a constant pH in African soda lakes promote high primary production with high amounts of autochthonous dissolved OM and diverse haloalkaliphilic-associated microorganisms [130]. They are being used as model environments for a better understanding of microbially-driven processes, including all conceivable methanogenic pathways, which were discovered to be present simultaneously up to near-salt saturation [140].

Methane has a global warming potential that is 28–36 times that of CO_2 over 100 years, making it the second most significant greenhouse gas. Although the current observational network cannot unambiguously link recent methane variations to specific sources, the sharp increase in atmospheric CH_4 levels observed since 2007 has been attributed to fossil fuel combustion, biomass burning, accelerated release from biogenic sources, and agricultural practices [141]. In addition, Pierangeli et al. [142] stated that freshwater reservoirs generate GHGs such as CH_4 and CO_2, which contribute to global warming, primarily when damaged by untreated sewage and other anthropogenic sources, according to the

study. Microbial OC breakdown can produce these gases, but little is known about the microbiota's role in GHG power systems in these conditions. Bottom sea hydrogeological variables, such as oxygen concentration, OM availability, temperature, and groundwater level, may influence methanogenesis and/or CH_4 destruction, altering gas fluxes in aquatic habitats [143]. However, little is known about the microbiota and environmental factors that promote gaseous flows in tropical urban reservoirs, and data on natural conditions and facilitating microbiota linked with gaseous flows both spatially and within/across these habitats are lacking [144]. Furthermore, given the ability of freshwater reservoirs to enhance CH_4 and CO_2 fluxes and microbial engagement in creating and consuming these gases, knowledge of microbial communities will provide a better understanding of gaseous dynamics in these environments [142]. *Methanosarcina* spp. and relatives in the *Methanosarcinales* order are common in such freshwater sediments. Such can indeed be highlighted by the fact that, in addition to the existence of methanogenic bacteria, the activity of other microbial community members or substrate availability might influence methanogenesis potential in freshwater sediments [145].

7.5.2.5 Photoferrotrophy

Iron is the most available metal on the Earth's crust. Also, it is among the most abundant elements on Earth [146]. Under neutral pH conditions, its ionic form Fe^{2+} is rapidly oxidized by O_2 to insoluble Fe^{3+}oxides. As a result, iron can be a limiting nutrient for producers in vast zones of well-oxygenated ecosystems. Under hypoxic conditions, Fe^{2+} is the predominant iron shape and more soluble than $Fe^{3+}$and can reach high concentrations in pore waters of freshwater sediments and the water columns containing iron. However, iron reacts with dissolved sulfide to form insoluble iron sulfide minerals in sulfur-rich environments [147,148].

The biological importance of iron is based on its redox behavior, with Fe^{2+} and Fe^{3+} as the main oxidation states, resulting in a suitable acceptor or electron donor, respectively, for different dissimilatory processes that greatly influence the iron cycle on Earth. Before demonstrating its occurrence, photoferrotrophy was hypothesized as a possible autotrophic metabolism for different types of phototrophic prokaryotes. On the other side, anoxygenic photosynthesis using Fe^{2+} as an electron donor was unequivocally explained initially in purple bacteria, some of which were able to grow either photoheterotrophically or photoautotrophically [149].

At the same time, photoferrotrophic bacteria have been detected in different phylogenetic groups of bacteria either from marine origin or freshwater. This includes green sulfur bacteria, purple sulfur bacteria, and purple nonsulfur bacteria. Certain strains have been demonstrated to perform Fe^{2+}- dependent anoxygenic photosynthesis [149]. These include strains phylogenetically related to purple sulfur bacteria, such as *Thiodictyon* sp. [150], freshwater purple nonsulfur bacteria such as *Rhodobacter ferrooxidans* sp. strain SW2 [150], *Rhodopseudomonas palustris* [151], and *Rhodomicrobium vannielii* [152], as well as a green sulfur bacteria, *Chlorobium ferrooxidans* [153]. The purple nonsulfur bacteria are the best-studied photoferrotrophs. When comparing purple nonsulfur bacteria with purple sulfur bacteria, the percentage of Fe^{2+} photooxidation is affected by the response to light of each species of photoferrotrophic [154]. However, several steps of iron utilization are simply illustrated in Fig. 7.7.

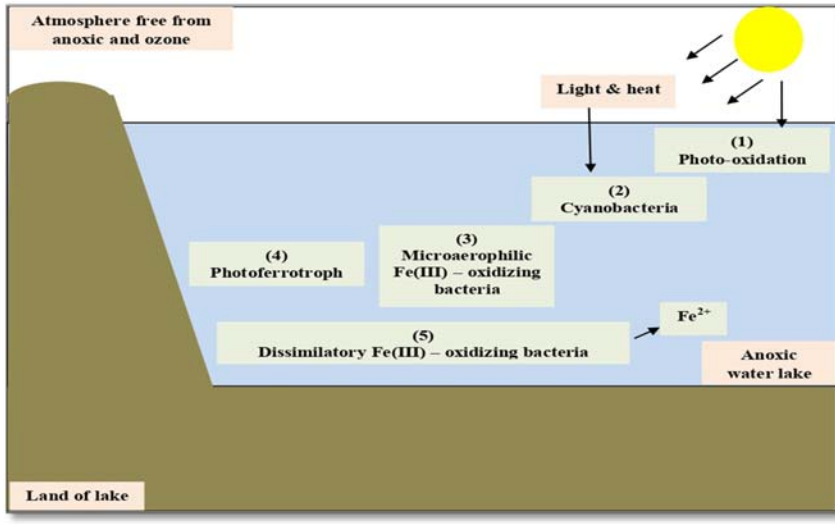

Figure 7.7 Schematic diagram showing the photooxidation of Fe^{2+} by UV light leading to the abiotic formation of Fe^{3+} (step 1). O_2 produced by Cyanobacteria leads to the oxidation of the coating with dissolved Fe^{2+} to form metals Fe^{3+} (step 2). Microaerophilic Fe^{2+}-oxidizing bacteria reducing oxygen produced by Cyanobacteria for direct oxidation of $Fe^{2+}_{(aq)}$ to Fe^{3+} minerals (step 3). Direct oxidation of dissolved Fe^{2+} by Fe^{2+} (photosynthetic) bacteria (step 4). partial reduction of deposited Fe^{3+} minerals to the mixed valence state Fe^{2+}/Fe^{3+} minerals by dissimilatory of Fe^{3+}-reducing bacteria (step 5) [155].

Most meromictic lakes and other permanently layered water bodies are euxinic, that is, anoxic and sulfidic, below the chemocline [156]. The sulfidic basins of these lakes might resemble the sulfidic ocean of the Paleoproterozoic and Mesoproterozoic. Contrastingly, the stratified lakes are the most recent environments similar to the iron-rich Archean oceans, where the low-oxygen sulfide layers are iron-rich. However, photoferrotrophy could have played a critical role in the biochemical control and energy provision to drive the growth and evolution of microorganisms [157].

According to current knowledge, the most suitable analogs of Archean oceans are natural meromictic lakes rich in iron. Meromictic lakes have a persistent stratification in which the bottom water (monimolimnion), which has greater dissolved salt concentrations, does not mix with the overlying waters due to the water density gradient and other variables related to climate, lake morphometry, and water movement [157]. Other dissolved chemicals, such as calcium bicarbonate, are often responsible for the largest density gradient in these lakes. In iron-rich stratified lakes, the interface between oxidized and nonoxidized water bodies, oxycycline, is accompanied by a sharp gradient of iron shapes, the so-called "ferrocline" [158].

7.6 Biotechnological applications of geomicrobes of African lakes

Biological bleaching, or the employment of bacteria to remove minerals from trash, is one of geomicrobiology's uses. Microbial remediation is utilized to remove pollutants and toxins from soils. Microbes play a significant part in many biogeochemical cycles and can affect a range of soil characteristics, including metal and mineral speciation biotransformation, mobility, toxicity, mineral precipitation, and mineral dissolution. Microorganisms are also important in the detoxification and immobilization of a wide range of components in the soil, including minerals, radionuclides, sulfur, and phosphorus. Thirteen metals are classified as priority pollutants (Zn, Sb, As, Cd, Cr, Pb, Cu, Ni, Se, Ag, Tl, Hg, and Be). Sediments and soils act as sinks for minerals that come from both natural and human sources, including agriculture, industry, mining, and waste disposal [67].

Sulfate-reducing bacteria, for example, create H_2S, which precipitates minerals as a metal sulfide, making biological bleaching one of the most

effective applications of geomicrobiology. Heavy metals were removed from mine waste, which was a serious environmental issue related to acid mine drainage (together with low pH) [159].

Surface water and contaminated groundwater, which are frequently connected with acidic mine drainage, are also treated with bioremediation procedures. Studies have shown that the generation of bicarbonate by microbes such as sulfate-reducing bacteria adds alkalinity to mine effluent, neutralizing the acidity. During the synthesis of bicarbonate, hydrogen ions are consumed, resulting in a rise in pH (low acidity). Bioremediation processes are also used to treat surface water and contaminated groundwater, which are typically associated with acidic mine drainage. The production of bicarbonate by microbes such as sulfate-reducing bacteria adds alkalinity to mine effluent, neutralizing the acidity, according to studies. Hydrogen ions are consumed during bicarbonate production, resulting in a pH increase (low acidity) [160].

Microbial communities isolated from soda lakes can be used to remove nitrate via denitrification, decolorize dyes, such as in textile wastes, dehair and hydrolyze keratin in tannery wastes, generate CH_4 in a biogas plant, and generate H_2 and acid for various purposes [18]. Metabolic mechanisms in microorganisms can impact the quality of oil and gas deposits. Microbes can influence hydrocarbon production by being present during source sediment deposition or dispersing through the rock column to populate the reservoir or rock source following hydrocarbon generation [161].

Another aspect of geomicrobiology is the study of microbes that flourish in conditions that are normally considered unfriendly to life. Excessively hot habitats (hot springs or a black smoker in the middle of the ocean), extremely salty environments (Martian comets or soil), and even space environs (Martian comets or soil) are examples of these environments [162].

At the moment, scientists are looking for microorganisms that can produce new enzymes with good activity at low temperatures for biotechnology. Due to their exceptional biodegradability and stability, extremophilic bacteria are a promising source for extremozymes with vital commercial applications. The usage of cellulases, amylases, xylanases, pectinases, proteases, lipases, pullulanases, isomerases, chitinases, esterases, dehydrogenases, etc. in biotechnological, chemical, biomedical, and agricultural processes has enormous potential. Extremozyme research and its primary uses have grown in popularity in recent years [163].

The agriculture, food and beverage, pharmaceutical, detergent, textile, leather, pulp and paper, and biomining industries all have potential economic uses for the extremozymes. Extremophile research is very interested in the development of new industrial processes based on extremozymes and the rising need for novel biocatalysts in the biotech sectors. In some examples, these zymes have been identified in metagenomes as overcoming bottlenecks related to the noncultivable extremophiles [164]. Extremophilic microorganisms are renewable resources that might be more effectively used in a variety of biotechnological fields to advance a bio-based economy. Extremophile enzymes have a significant impact on biotechnology and commerce thus far [163].

Furthermore, many enzymes such as proteinases, cellulases, lipases, and xylanases are expected to be involved in the fermentation of various substrates and other metabolic activities taking place in soda lakes, which can be linked to various mechanical, pharmaceutical, and waste treatment applications. The ability of these enzymes to catalyze reactions at high pH has been the foundation for many applications, and several of these enzymes have been used commercially. Alkaliphilic extremozymes, for example, are important in texture manufacturing; certain cellulases from gram-positive Soda Lake isolates are used in the apparel and material sectors; and alkaliphilic. Alkaline proteases, notably those from *Bacillus* sp., are widely used in the preparation of detergent formulations. Such enzymes are essential for controlling a diverse range of sources. Similarly, phospholipase, a bakery enzyme derived from lake lipolytic bacteria, is utilized in bread production, the egg yolk industry, and the purification of vegetable oils. Another important enzyme is amylase, which is produced by bacteria and is used to hydrolyze starch molecules. It is used in many industrial processes and accounts for 25% of the global enzyme market [162]. In addition, many soda lakes are important sources of harvestable and cultivable cyanobacterial biomass, such as blue-green algae; *Arthrospira*, which is used to treat diseases, malnutrition, and protein deficiency, grows inexhaustibly in some alkaline lakes in East Africa (e.g., Lake Arenguade and Lake Chitu), forming a nearly monoalgal phytoplankton community [8].

7.7 Remarked conclusion

The majority of Africa's Great Lakes are located along a continental fault line called the East African Rift Valley, which is also home to a system of

deep lakes known as the Great Lakes of Africa. The special geochemistry of the lakes, especially lakes and soda lakes, encourages the creation of a variety of microorganisms with valuable ecological and commercial importance. However, these lakes include, because of their high productivity, pH, and salinity gradients, a wide range of microorganisms such as methanotrophs, methanogens, photosynthetics, denitrifiers, desulfurizers, and others. For instance, soda lakes make these habitats harbor complex microbial food webs between different biological cycles (carbon, nitrogen, and sulfur cycles) via redox coupling and affect the production and consumption of GHGs. On the other hand, the chemistry of those ecological ecosystems and the changes caused mainly by human activities. On the other hand, the uniqueness and the connectivity potential of these habitats have significantly much more benefits, particularly in biotechnological and industrial applications such as production and usage of their enzymes and biomolecules in such manner. Therefore, for the protection and well management of the African lakes from human pressures, a new concept is sharply needed.

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CHAPTER 8

Microbial ecology of desert Lakes Baringo and Turkana, Kenya, East Africa

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8.1 Introduction

8.1.1 Lake Turkana and Lake Baringo, Kenya

Microbes that are found at the base of the food web may play a significant role in determining nutrient cycling and productivity in the microbial food web in the desert freshwater Lakes Turkana and Baringo ecosystems. Due to climate change induced by human activities and the resulting negative impacts on these aquatic ecosystems, paleolimnologists, geochemists, fisheries experts, limnologists, and microbiologists have examined the productivity of these lakes [1]. Pieces of evidence show that anthropogenic factors have threatened Lakes Turkana and Baringo, including global warming [2], fisheries overexploitation [3–5], watershed erosion, and waste discharge [6–10], affecting both littoral and pelagic ecosystems. Furthermore, Lake Baringo has been influenced by additional pressures, such as changes driven by the introduction of alien species, with negative consequences on ecosystem functions, geochemistry, biodiversity, fisheries, and socioeconomics [1,11]. Lakes Turkana and Baringo share common features such as both lakes lie on the floor of the Eastern Rift Valley; they are both desert lakes with inlets but no outlet; they both receive less than 600 mm of rainfall annually; their ecosystem function is dominated by pelagic processes; Hence, bacteria, phytoplankton and protozoans are important components of the aquatic community, which respond to various factors driven by physical forcing, whose structure and production determine consumer production and fisheries yield.

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The East African Lakes in the Eastern Rift Valley are diverse and range from the large alkaline Lake Turkana in northwest Kenya to the small lakes in the central rift valley such as freshwater Lakes Baringo and Naivasha, and saline Lakes Bogoria, Nakuru, Elementaita, and Lake Magadi in the southern part of the rift valley. These lakes are situated in the arid and semiarid lands of Kenya. In comparison to other important African lakes, the microbial ecology of Lake Turkana has not received much attention from earlier workers. The basin is remote and inhospitable, which probably contributes to this situation. The 1930–31 Cambridge University Expedition to the East African Lakes carried out most of the pioneer algology on Lake Turkana in areas such as Ferguson's Gulf and Central Island [12,13]. These studies described filamentous blue-green alga such as *Hormidium subtile* as the dominant species in the open water plankton whereas La Mission Scientifique de 1'Omo [14] described algal material from the shallow northern inshore regions. They reported few species encountered in the lake [13]. *Coscinodiscus rudolfii*, the centric diatom, the end of the has been described as typical of the phytoplankton of the lake and identified algae material of the Omo expedition that was littoral, including the genus *Rhopalodia* that frequently dominated the associations [15]. The two most important lakes, which are located in the eastern rift valley deserts are Lake Turkana and Lake Baringo (Fig. 8.1A and B).

Lake Turkana is situated in the northwest of Kenya, in what was formerly the Northern Frontier District, but currently the Turkana County, within the coordinates 35°50′ to 36° 40′ East and 2°27′ to 4°40′ North. The northern tip of the lake lies on the Ethiopia-Kenya border, close to the point where the Kenyan, Ethiopian, and Sudanese frontiers meet. The region is one of the most desolate and arid in East Africa and is served by a few tracks and roads. The county headquarters at Lodwar is some 300 km from the nearest railhead at Kitale. The environment surrounding the lake is semiarid desert with sparse vegetation of grass tussocks, thinly scattered bushes, and stunted trees, the latter chiefly confined to the areas of dry watercourses including Turkwel River, Kerio River, and the seasonal Kawalasi and Napasinyang Rivers. The vegetation is usually dominated by the grass *Chrysopogon aucheri* [18]. The dominant trees of the open areas are *Acacia tortilis, Acacia nubica*, *Balanites aegyptiaca*, and Commiphora spp. and, more locally, *Boswellia hildebrandtii*. The trees in the environment of the larger watercourses include *Hyphaene* spp., *Pseudomussaenda flava*, and *Salvadora persica* which form dense stands. Lake Turkana lies in an area of land classified as 'very arid', with very low

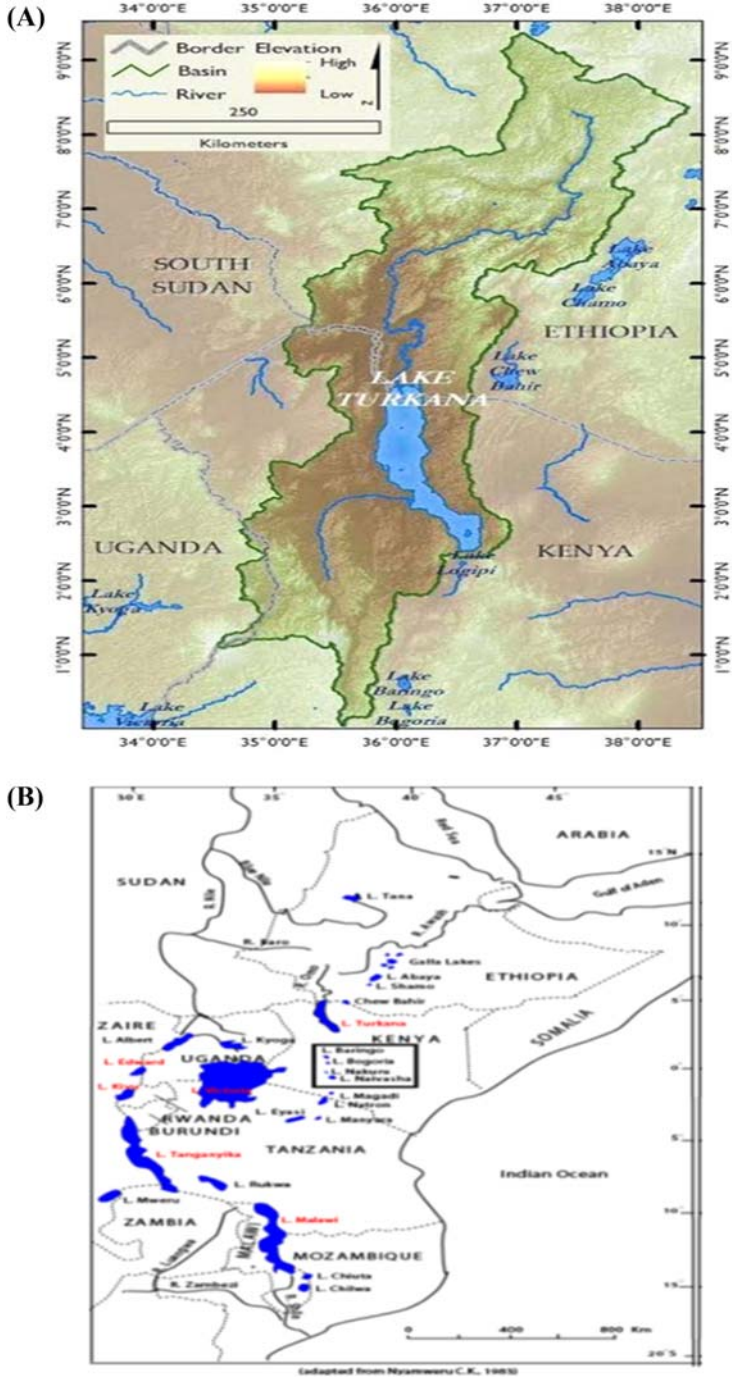

Figure 8.1 (A) Important drainage rivers and catchment system of Lake Turkana, Kenya. (B) The rift valley lakes, including Lake Turkana and Lake Baringo [16,17]. *For (A) Kenya Marine and Fisheries Research Institute. Courtesy: D. Olago, A. Opere, Holocene palaeohydrology, groundwater and climate change in the lake basins of the Central Kenya Rift, Hydrol. Sci. J. 54 (4) (2009) 765–780. Available from: https://doi.org/10.1623/hysj.54.4.765.*

microbial potential with soil moisture indices ranging from −51 to −57 [19–23]. In Lake Turkana, the structural and functional microbial variables such as abundance, biodiversity, and metabolism may support several ecosystem services such as biodiversity, food webs, eutrophication, contaminants, and contaminants in fish from the lake with beneficial effects. These microbial variables may help detect the effects of human pressures on the lake environment and to assess changes in the environmental health status of the lake.

Fig. 8.2 shows Lake Turkana and Lake Baringo drainage basins in northwest Kenya, which is an arid and semi-arid land (ASAL), while Fig. 8.3 shows the formation of the rift valley lakes, including Lakes Turkana and Baringo.

Figs. 8.4 and 8.5 show the morphometric characteristics of the rift valley lakes, including water level changes of Lake Turkana (Table 8.1).

Lake Baringo is a freshwater lake in the eastern arm of the Great Rift Valley in Kenya (Fig. 8.6). It is located between latitude 0°30′ N and 0°45′ N and longitude 36° 00′ E and 36° 10′ E and lies approximately 60 km north of the equator at an altitude of 975 m above sea level [29]. The lake has a surface area of approximately 150 km^2 and a catchment of 6820 km^2. It has a mean depth of 8 m with the deepest point being about 14 m at high water levels. Lake Baringo waters remain fresh despite the lack of surface outlet, shallow depth, and high net evaporation that characterizes the rift floor. Recent hydrogeological evidence confirms the original assumption [12] that some lake water is lost by underground seepage through the fractured lake floor [30]. This flow was estimated that its outflow could exceed 108 m^3/year [31]. Lake Baringo has five islands, the biggest being the volcanic Kokwa. The island is a remnant of a small volcano that belongs petrogenetically to the Korosi volcano. This erupted during the Middle Pleistocene, approximately 2.6 million years ago [32]. This area is characterized by dry and wet seasonality with unpredictable timing. The dry season usually starts from September to April, while the wet season occurs between May and August. Annual rainfall ranges from about 600 mm on the east and south of the lake to 1500 mm on the western escarpment of the rift valley. Lake Baringo experiences very high annual evaporation rates of 1650–2300 mm, and its survival depends on the inflows from rivers originating from the hilly basin, where rainfall varies from 1100 to 2700 mm [33]. The rivers that feed into Lake Baringo include the seasonal ones such as Ol Arabel, Makutan, Endao, and Cameron, and perennial ones such as Molo and Perkerra.

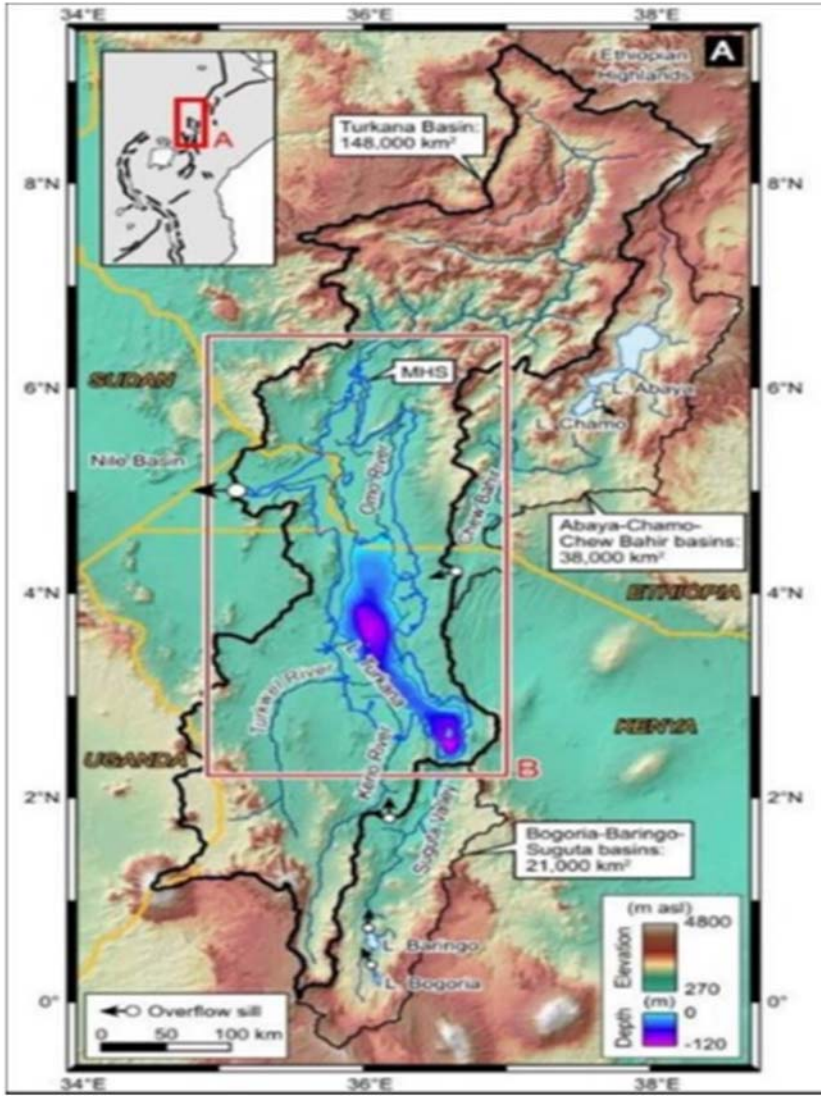

Figure 8.2 Lake Turkana and Lake Baringo drainage basins [16,24]. *Courtesy: D. Olago, A. Opere, Holocene palaeohydrology, groundwater and climate change in the lake basins of the Central Kenya Rift, Hydrol. Sci. J. 54 (4) (2009) 765–780. Available from: https://doi.org/10.1623/hysj.54.4.765.*

The burgeoning human population around Lake Baringo needs good quality of water to support this growth. The type and nature of algae in the lake determine the eutrophic nature of the water and the quality. High phytoplankton biomass, especially Cyanobacteria, may impair the

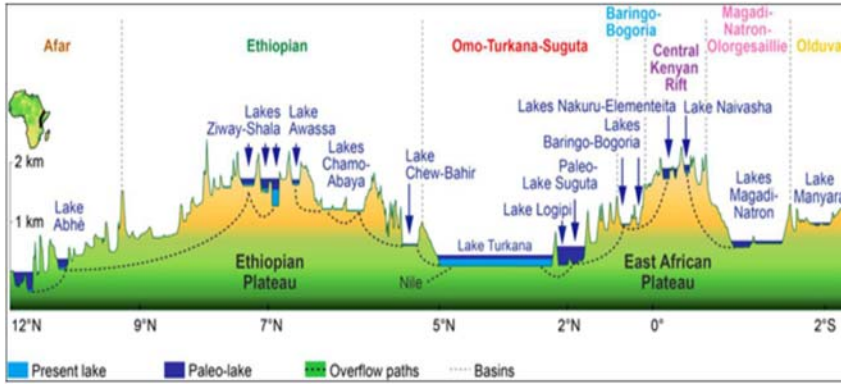

Figure 8.3 Formation of the rift valley lakes, including Lakes Turkana and Baringo [16]. *Courtesy: D. Olago, A. Opere, Holocene palaeohydrology, groundwater and climate change in the lake basins of the Central Kenya Rift, Hydrol. Sci. J. 54 (4) (2009) 765–780. Available from: https://doi.org/10.1623/hysj.54.4.765.*

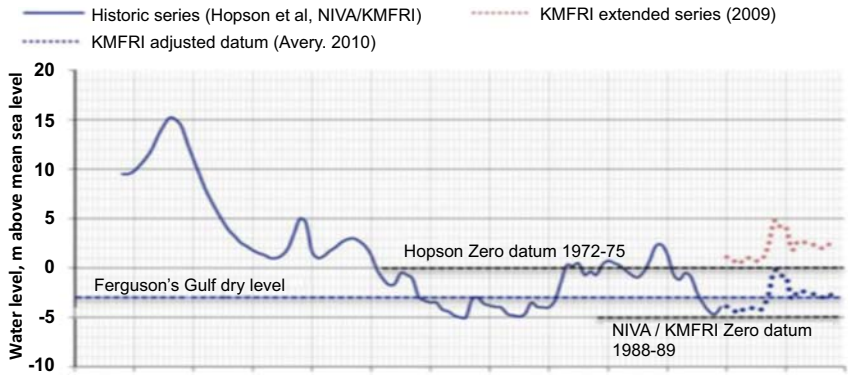

Figure 8.4 The changes in the water levels of Lake Turkana from 1910 to 2020. *Courtesy: A.J. Hopson, G. Britain, Lake Turkana: a report on the findings of the Lake Turkana project, 1972–1975, Vol., Inst. of Aquaculture, University of Stirling. UK, 1982.*

quality of drinking water supply, recreational activities, and fisheries. Water quality management is, therefore, important, including monitoring the toxic algae to control and prevent fish kills [34]. Nutrients in the lake enhance phytoplankton biomass in the lake. These allochthonous nutrients form building blocks of protein molecules and intercellular metabolic regulation [34]. Soluble reactive phosphorous, nitrate nitrogen ($N0_3$ -N), and dissolved silica (SiO_2), are the key nutrients that regulate algal growth in the lake [34,35]. The bulk of diatom cell walls forms silicate mass in the lake. Some of the most important environmental factors that enhance

Figure 8.5 The changes in the water levels of Lake Turkana from 1910 to 2010 [25–28]. *Courtesy: A.J. Hopson, G. Britain, Lake Turkana: a report on the findings of the Lake Turkana project, 1972–1975, Vol., Inst. of Aquaculture, University of Stirling. UK, 1982.*

Table 8.1 Physical and chemical factors of Lake Turkana and Baringo, Keny [26].

Factor	Unit	Lake Turkana	Lake Baringo
Volume	km^3	204	150
(i) Length	km	257	15
(ii) Width	km	mean = 31.12, min. = 13 max. = 44	
(iii) Depth	m	mean = 31.4 max. = 114	
(iv) Catchments' area	km^2	= 7560	160
(v) Volume =	km^3	237.36	
(vi) Altitude	a. m.s. 1.	365.4 ± 5	
Residence time	Year	12.5 ± 1	1.5 1
Surface temperature	°C	27.2–29.4 2	19.5–27. 6
Secchi depth	m	0.8–1.2 3	10.7–0.9 5
PH	pH	9.4–10.6	6.5–10.5
Number of fish species	No	47	8
Conductivity	µS/cm	2500–3600	800–1200
Alkalinity	mg/L CaCO4	10 3 3.2 5	450–600
Surface dissolved oxygen	mg/L	6.8–8.42	6.0–8.6 3
Chlorophyll	Top 1 m, mg/L	126–146	29–58
Fish species	No	60	8

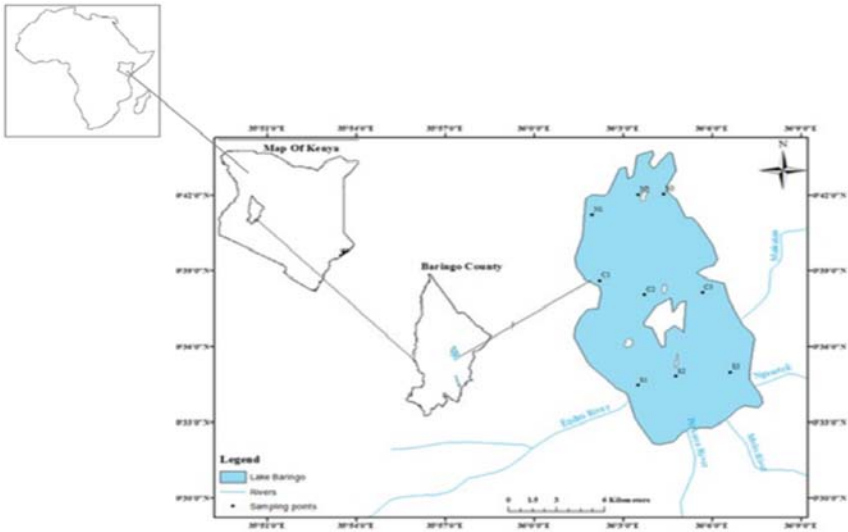

Figure 8.6 Important drainage rivers and microbial sites of Lake Baringo, Kenya. *Kenya Marine and Fisheries Research Institute. Courtesy: Kenya Marine and Fisheries Research Institute. KMFRI Annual Report 2012. Lake Turkana Station 48 pp., 2012.*

the development of phytoplankton in the lake include water temperature and turbidity. The phytoplankton of the lake is dominated by blue-green algae *Microcystis aeruginosa* Kutz, and to a less extent by *Anabaena circinalis* Rabh. ex Born [12,29,34]. Some of the notified ecological disruptions in the lake include decreased fish yields, siltation, deteriorating water quality, frequent algal blooms, and increasing levels of poverty in the adjacent lake communities [36,37].

8.1.2 Archaea, bacteria, and biofilms in Lake Turkana and Lake Baringo

In the water samples, some of the most important microbial taxa included Cyanobacteria, Chlorophyta, and Bacillariophyta [20,25,34,38]. In the sediment of Lakes Turkana and Baringo, the most frequently occurring taxa included Bacillariophyta. Macrophytes are associated with the following taxa: Cyanobacteria and Chlorophyta (Fig. 8.7).

The most predominant microbial taxa in Lake Turkana and Lake Baringo were Cyanobacteria (82.7%), Chlorophyta (29.8%), Bacillariophyta (9.2%), and others 6.3% [20,25,34,38]. The dominant microbial genera in the lake sediments included *Thiomonas*; *Gallionella*; *Acidithiobacillus*, *Acidimicrobium*; *Leptospirillum*; *Acidiphilium*; *Acidobacterium*.

Figure 8.7 Microbial habitat showing Water Hyacinth weed and Cyperus spp. in the northern zone of Lake Turkana, Kenya. *Kenya Marine and Fisheries Research Institute. Mr. Nicanor Omire and Mr. Casianes Olilo. Courtesy: Kenya Marine and Fisheries Research Institute. KMFRI Annual Report 2012. Lake Turkana Station 48 pp., 2012.*

The epiphytic community in the lakes included the taxa *Gallionella*, uncharacterized Actinomycetales, Xanthomonadaceae, *Leptospirillum*, and unknown Betaproteobacteria [25]. In most of the samples, isolated from the lake, Acidobacteria, Acidimicrobiales, and Saccharibacteria have been recorded in proportions above 6%, while Cyanobacteria dominated in surface water. Rivers Omo, Turkwel, and Kerio mouth waters were characterized by the presence of Betaproteobacteria, unclassified Ca. Saccharibacteria, and *Leptospirillum*. Archaeal phylum Euryarchaeota has been recorded as predominant in all samples of Lake Turkana and Lake Baringo [20,25,34,38]. Crenarchaeota were detected only in rocks, sediment, and in subaerial biofilm. Archaea Ca. Parvarchaeota members have been detected in both lakes' waters [20,25,34,38]. Class Thermoplasmata has been observed in the wetlands of Lake Turkana and Lake Baringo. The acidic water displayed a higher proportion of Ca. Micrarchaea. Thaumarchaeota (13.25%), unclassified Crenarchaeota (0.3%), and Ca. Parvarchaeota (0.1%) have been detected in the epiphytic on macrophytes [20,25,34,38]. Genera *Ferroplasma* and *Thermogymnomonas* have been recorded as predominant archaea in the Lake Turkana samples [20,25].

The diversity of eukaryotes across different microhabitats of Lake Turkana primarily belongs to the class Stramenopiles, Alveolata, Rhizaria, and Opisthokonta [20,25]. The Stramenopiles, mainly diatoms, included families, Bacillariophyceae and Chrisophyseae [20,25]. Alveolata included Ciliophora of the class Spirotrichea [20,25]. The phylum Cercozoa is the

main representative of the Rhizaria group in Lake Turkana [20,25]. Opisthokonta has been recorded in all samples and was mainly represented by the fungal phyla, Ascomycota, Chytridiomycota, Basidiomycota, and Holomycota [20,25]. The taxa with abundances less than one percent included representatives of the super groups Amoebozoa and Excavata [20,25]. The microbial community inhabiting acidic water, sediment, biofilms, and epiphytes on macrophytes corresponded to lineages previously affiliated to the phyla Proteobacteria, Nitrospirae, Actinobacteria, Firmicutes, and Acidobacteria [20,25].

8.1.3 The structure of microbial community in Lake Turkana and Lake Baringo

Methanogen diversity and richness have been studied based on Methyl coenzyme M reductase gene (*mcrA*) transcripts and 16S ribosomal RNA (rRNA) gene for other lakes in the world having similar structures to Lake Turkana sites across the northern zone, central zone, and southern zone of the lake [20,25,34,35]. Lake Turkana and Lake Baringo's microbial diversity and richness show critical differences that exist between these freshwater lakes' environments in the eastern arm of the rift valley. These freshwater ecosystems also show significant differences in terms of community structure and species diversity [34,35]. This implies that in these freshwater ecosystems, the differences may reflect the extensive diversity of metabolic strategies needed to be exploited or to contribute to the various geochemical gradients encountered in the lakes. Although no incubation experiments to quantify methane production and consumption or determine the methanogenic pathways involved in these lakes, existing knowledge indicates the environmental variables (Table 8.1) [29]. Accordingly, the number of active microbes in lake sediments may be inferred by the presence of Glutamine synthetase (*glnA*) and Methyl coenzyme M reductase gene (*mcrA*) transcript abundance [35]. The environmental factors, including carbon, nitrogen, and phosphorus, decline sharply from maximum levels on the surface to minimum levels at the bottom sediment of Lake Turkana [20,25]. However, in the top layer of lake sediment, the labile algal-derived carbon increases several folds in concentration [29]. This implies that the increase in labile carbon at the surface of lake sediments corroborates well with Lake Turkana and Lake Baringo recently experiencing an increased lake water level leading to increased primary productivity [35,38]. This implies that the greater

content of labile carbon in recently deposited sediments in both lakes is consistent with RT-qPCR results, which suggests a greater microbial activity at the surface [25,34,38]. However, the wetlands of these lakes may be expected to contain much more organic carbon than open water. Two lines of evidence support this expectation. First, a survey of wetlands in the same area revealed that carbon content range between 7% and 70% [38], as compared to 75% in Lake Baringo surface sediment [25]. Second, organic matter in Lake Turkana sediment originates predominately from algal sources [25]. This implies that active methanogenesis in wetland surface sediment has not been detectable [25]. Oxygen may penetrate, at least seasonally, into surficial sediments in Lake Turkana, due to acid volatile sulfide profiles in sediments used to infer S redox cycling [25]. This implies that sediments collected during the short rains (December–March) in Lakes Turkana and Baringo would exhibit a large oxygen demand because of enhanced algal production in the water column [25,34,38]. This suggests anoxic conditions and active methane cycling at the sediment surface of both lakes, which is consistent with the detection of *mcrA* transcripts at the surface. Furthermore, this implies that methanogenic precursors vary considerably, both temporally and spatially with the resulting sediments that are spatially chemically heterogeneous, thus, indicating the presence of micro-oxic niches in the otherwise anoxic sediments. This is due to the activity of burrowing macrofauna in the lakes' ecosystems. Consequently, there is active methane cycling and discrepancy between Methyl coenzyme M reductase gene (*mcrA*) and 16S microbial community structure [35]. This observation was supported by the consistency existing between the diversity of methanogenic communities and rates of methane production [35]. Greater genetic diversity in the wetlands, therefore, may have a higher potential for methane cycling than in desert Lakes Turkana and Baringo because of a higher abundance of *mcrA* transcripts, which potentially support methane production and oxidation pathways [35]. Lake Turkana and Lake Baringo and their associated wetlands have the potential to be sites for active methane cycling, [34,35], and additional work is required to estimate net methane emissions from these tropical desert aquatic ecosystems. Furthermore, molecular diversity of microbes in current tropical freshwater desert lakes and surrounded wetland sediments uncovered uncultured microbes involving in diverse methane cycling strategies.

Moreover, in these already fragile lakes and surrounding wetland environments, some of the methanogenic archaea have the potential for

mercury methylation, thus, showing that there is an interaction between methane and mercury cycles [34,35]. It is opined that molecular screening of microbial organisms in the wetlands set surrounding tropical deserts may be sites conducive to methane cycling, despite uncertainty in the fate of methane produced in these ecosystems. Finally, targeted functional gene transcript analyses with environmental genomics may help to gain a functional viewpoint on the composition of microbial communities in the desert lakes and associated wetlands [34,35].

8.1.4 The taxonomy, morphology, and biology of microbial communities in Lake Turkana and Lake Baringo

Taxonomy is a branch of science that concerns evolutionary relationships, grouping, naming, and arranging organisms according to their level of genetic similarity. Thus, taxonomy relates to the nomenclature, classification, and phylogeny of organisms. The microbial community in Lakes Turkana and Baringo like all other microorganisms falls into phylum, class, higher orders, families, genera, species subspecies, and species variety. In Lakes Turkana and Baringo, the predominant microorganism is *Micrcystis aeruginosa* belonging to the Cyanophyceae algae [20,25,34,38].

8.1.5 Water scarcity and climate change in relation to environmental degradation, aquatic microbial ecology for management and adaptation in Lakes Turkana and Baringo

Water scarcity in Kenya poses major challenges and impacts to the local human population particularly in the recent past. Water management, which is a major challenge, needs to be addressed because poor sanitation and poor hygiene, both collectively pose great health risks to low-income people living around Lakes Turkana and Baringo. These populations use raw lake water before it is treated posing great health and disease risks. The rural populations residing along these desert lakes lack portable water despite living near these large water bodies. The ASAL of the lake faces these challenges. These challenges impact heavily on women and children, who spend 6 h collecting water for domestic use. Water shortage increases the vulnerability of children by affecting their learning and education process when they miss school in search of water for livestock and domestic use. Children who reside in informal settlements in these lake regions suffer from morbidity and mortality due to diarrhea and consumption of unsafe lake waters in these areas. On the other hand, changes in the hydrologic cycle including balancing the temperature and rainfall cycles

in these lakes may influence these desert lake ecosystem dynamics. These changes may include circulation and hydrological cycle that may lead to stratification, for example, in Lake Turkana. These stratifications in the lake may influence the distribution of fish in the lake by as much as 20% of the lake area [29]. Since stratification of the water temperature may restrict vertical mixing of the water and enhance temperature gradients between the surface and bottom waters, this may lower oxygen exchange and impede nutrient exchange within the water column. These changes in the lake water level may expose/submerge littoral algae and macrophyte plant communities. Thus, the changes in the volume of water may result in changes in water physicochemical properties that may lead to changes in inhabiting species. Thus, reducing precipitation and higher temperatures may result in increased concentrations of pollution in the desert lakes due to reducing lake level and volume, thus, impacting the lake microbes' ecology and function [39,40].

8.1.6 Phytoplankton distribution in Lake Turkana and Lake Baringo

The initial description of the phytoplankton population composition and distribution in Lake Turkana was made by Rich [13] and Cambridge-Expedition to the East African Lakes' team. Rich [13] further made the following descriptions of phytoplankton species composition in the open water of Lake Turkana, namely *Microcystis flos-aquae, Botryococcus braunii*, and *H. subtile*; the algae taxa identified at Ferguson's waters included *Botryococcus braunii, Phormidium mole, Cyclotella meneghiniana*, and *H. subtile*. Rich [13] described epiphytic algae on the macrophytes in the lake that included *Rhopalodia gracilis, Lyngbya lutea, Calothrix* sp., and *Nostoc* sp. Rich [13] described the following algae in the enclosed pools of the lake including *Arthrospira fusiformis, Arthrospira platensis forma minor, Kirchneriella lunaris, Crucigenia quadricauda*, and *Anabaenopsis arnoldii*. Rich [13] and Cambridge-Expedition to the East African Lakes' team described the following algae around the Central Island National Park and Crater Lake: *Rivularia biasolettiana, Surirella biseriata var. lanceolata, Calothrix* sp, *Rhopalodia gibberula, H. subtile*, and *L. lutea*. Rich [13] and Cambridge-Expedition to the East African Lakes' team described that the following macrophytes in the Crater Lake had epiphytic algae including *Athrospira fusiformis, Rhopalodia hirudini formis, Cymbella grossestriata var. obtusiscula, Navicula pupula, Rhapis gracilis, Rhapis ventricose, Rhapis gibberula var. rupestris formacrassa, Cymbella helvetica, Gomphocymbella bruni, Gomphonema*

intricatum, Cymbella meneghiniana, Navicula hungarica, Navicula sphaerophora, and *Navicula cryptocephala*. Rich [13] and Cambridge-Expedition to the East African Lakes' team described the algae, *Gymbphonema bruni, R. gracilis, Phormidium autumnale* and *Gomphonema* sp, in the stomach of *Clarias gariepinus* inhabiting the studied lakes.

Bachmann described the following algae in Lake Turkana [14]: *Cymbella lanceolata, Nitzschia palea, S. biseriata var, H. subtile, C. meneghiniana, Rhopalodia vermicularis, R. gracilis C. rudolfii, Navicula placentula var. lanceolata, R. vermicularis perlonga, Cymbella maculata, G. intricatum*, and *Anomoneis sphaerophora*.

Of note, 110 different algae species from the littoral habitats have been described in Lake Turkana [25]. The algae data have been obtained along 10–30 km of the coastline of Lake Turkana. Hopson and Britain [25] have described the following algae species in the open water and littoral areas of Lake Turkana, namely *Achnanthes exigua, Asterionella formosa, Nitzschia punctata, Nitzschia spiculum, Amphora ovalis, Nitzschia sub communis, A. sphaerophora, Rhopalodia gibb, Rhopalodia gibberula, Caloneis aequatorialis, Rhopalodia gracilis, Cocconeis placentula, Rhopalodia hirudini formis, Cocconeis rudolfii, Rhopalodia ventricose, Cyclotella comta, Rhopalodia vermicularis, Cyclotella meneghinlana, Stephanodiscus astraea, Cymatopleura solea, Surirella birostrata, C. lanceolata, Surirella biseriata, Cumbella mulleri, Surirella constrict, Diploneis ovalis, Surirella engleri, Fragilaria construens, Surirella fontinicola, Fragilaria crotonensis, Surirella fulleborni, Fragilaria intermedia, Surirella ovalis, Fragilaria virescens, Surirella ovulum, Gomphocymbella beccari, Hantzschia amphyoxis, Gomphonema aequatorialis, Chlorophyta: Melosira granulata, Melosira distans, Melosira italica, Botryococus brauna, Meridion circulars, Cosmarium* sp., *Navicula cryptocephala, Oedogonium* sp., *Navicula decussus, Planctonema lauterbornii, Navicula exiguiformis, Scenedesmus quadricauda, Tetrastrum heteracanthum, Navicula insociabilis, Navicula menis cuius, Schroederia setigera, Navicula perventralis, Spirogyra* sp., *Navicula pupula, Staurastrum* sp., *Navicula severascens, Navicula radios, Stigeoclonium* sp., *Cyanophyta: Navicula subcostulata, Navicula submollesta, Anabaena circinalis, Navicula tuscula, Anabaena constricta, Nitzschia adapta, Anabaena sphaerica, Navicula aequalis, Navicula apiculata, Anabaena variabilis, Anabaena vaginicola, Navicula asterionelloides, Anabaena arnoldii, Navicula elliptica, Calothrix brevissima, Nitzschia bacata, Chroococcus minutus, Nitzschia epiphyticoides, Navicula fontinicola, Calothrix turgidus, Navicula frustulum, Cylindrospermum mucicola, Nitzschia granulate, Dacty lococcopsis, Nitzschia hungarica, Nitzschia palea, Lyngbya lucidum, Nitzschia perspicula, Microcystis aeruginosa, Microcystis*

flos-aquae, Merismopedia punctata, Nodularia spumigena, Microchaete aeruginea, Microchaete tenera, Microchaete epiphytica, Phormidium angus tissimum, Oscillatoria curviceps, Monoraphidium contortum, Oscillatoria schultzii, Phormidium lutea, Phormidium autumnale, Phormidium mucicola, Phormidium molie, Raphidiospsis curvata, Phormidium tenue, Spirulina platensis, Spirulina laxissima, Synechocystis aquatilis, Synchocystis subsala, Pyrrophyta, and *Cymnodinium aeruginosum, Cymbella maculata, Navicula hungarica, Surirella constrica, Melosira granulata, Navicula menisculus, Navicula subcostulata, Nitzschia elliptica, Calothrix javanica, Nitzschia frustulum, Nitzschia fontinicola, Chroococcus turgidus*.

In Lake Turkana, diatom (phylum Bacilliarophyta) species have been recorded as dominant algae in the shoreline areas, where they formed the largest littoral algal group both in the numbers of taxa and of individuals. Sheltered habitats such as the Longech area had a higher number of diatom species than the shorelines that had unstable substrates. This indicated that different substrate types had different algae species. Inshore algae communities that dominated the area comprised *C. aequatorialis, N. granulate, N. palea*, and *C. rudolfii*, *R. gibba*, *R. vermicularis*, *R. gracilis Gomphocymbella beccari*, *G. beccari*, *Surirella* spp., *Surirella astraea*, and *C. meneghiniana*. The algae densities ranged from 100−2500-cells/mL. Other diatom species described around macrophyte areas in the lake included *N. epiphyticoides, N. palea, C. mulleri*, and *A. sphaerophora*. In the eastern shores' rocky areas of the lake, the following algae species have been described and included *N. palea*, *R. gibberula, R. gracilis*. *A. sphaerophora, C. mulleri*, *Surirella f ulleborni*, *N. pupula*, and *N. punctata*. The species *N. cryptocephala*, *N. bacata, A. exigua*, *Cymbella muller, R. gracilis*, *C. placentula*, *A. sphaerophora*, and *Rhopalodia* spp have been recorded in the western shores of the lake.

Blue-green algae (phylum Cyanophyceae) have been observed in Lake Turkana, where *A. fusiformis* dominates in the Central Island National Park area of the lake. A larger number of species have been found around Ferguson's area of the lake which is also a sheltered gulf. The key blue-green algae species described at Ferguson's area of the lake are *Spirulina laxissima, Anabaena circinalis, Anabaena fusiformis Anabaena arnoldii*, *Calothrix* spp, and *Microcystis auruginosa*.

Hopson and Britain have described green algae (phylum Chlorophyta) in Lake Turkana [25], and included species *B. braunii, P. lauterbornii, T. heteracanthum, S. setigera, S. quadricauda, Cosmarium* sp., *Staurastrum* sp., *Oedogonium* spp., *Stigeoclonium* spp., and *Spirogyra* spp. These green algae,

just like *Microcystis* spp., have also been transported by north-easterly winds and currents to open waters from the littoral zones of the lake. Species *Gymnodinium aeruginosum* have been recorded in the sheltered bays of Lake Turkana as described by Hopson and Britain [25].

The gross primary production of Lake Turkana was described by Hopson and Britain [25]. In the lake, the gross primary production was measured as daily carbon production (mg/Cm^2/day). The area of the northern sector is about 2290 km^2, and the daily gross primary production has been recorded as 1318–6222 mg/Cm^2/day and 3009–14,230 tons. The central sector has an area of 2929 km^2, and the daily gross primary production of 190–3935 and 569–11512 tons. The Turkwel Sector has an area of 1027 km^2, and a daily gross primary production of 1387 mg/Cm^2/day and 1426 tons. The southern sector has an area of 1321 km^2 and daily gross primary production of 259–295 mg/Cm^2/day and 340–387 tons. The Ferguson's Gulf has an area of 30 km^2, and daily gross primary production value of 4148 mg/Cm^2/day and 125 tons. In the littoral region, the Periphyton values are 26–78 mg/Cm^2/day, 220–380 mg/Cm^2/day for the plankton and for both the Periphyton and plankton, the values are 299–448 (mg/Cm^2/day). Regarding macrophytes: El Molo Bay has a value of 930 mg/Cm^2/day and Allia Bay a value of 4616 mg/Cm^2/day. Lake Turkana open water has a low density of *Microcystis* spp., while Ferguson's sheltered bay has a high number of cells per mL of water (4500 cells/mL) [25]. The open water is dominated by phytoplankton biomass that includes *P. lauterbornii* and *B. braunii*. The northern sector of the lake had the highest primary production and concentration of phytoplankton. The main lake shows low biomass, however, when the Omo River floods, concentrations increase. This implies that the Omo River contributes some nutrients such as nitrogen, which could be supporting phytoplankton growth, but limiting in other sectors of the lake. The Ferguson's sheltered area is a shallow and sheltered bay that may provide a dense, inshore phytoplankton population. The blue-green algae, heterocystous *Anabaena circinalis* and *Microcystis aeruginosa*, for example, are the dominant algae at the bay and support the cichlid Nile Tilapia (*Oreochromis niloticus* Trewavas) fishery in the area. The autochthonous nature of this environment provides the high organic production rates of such inshore regions, thus providing important sources of material for open water areas. Epibenthic diatoms also enhance productivity in littoral zones, including the southern sector. *Potamogeton pectinatus* dense stands are supported by sheltered bays and enhance oxygen production in association with epiphytic

algae. Thus, the macrophytes together with phytoplankton biomass provide important organic nutrient inputs that fertilize the entire lake ecosystem.

In Lake Baringo, microbial population taxa include blue-green algae (Cyanophyta), which include *A. circinalis* and *Microcystis aeruginosa*. *Microcystis aeruginosa* contains cells that form vacuoles containing air that assists it to regulate its buoyancy on the water surface [29,34]. This contrasts with most other algae including diatoms and green algae that sink in the trophogenic zones during calm weather in the lake [41]. *M. aeruginosa* move to the water surface due to their buoyancy to get light energy for photosynthesis [42]. *M. aeruginosa* uses this characteristic to enable it to float and form green scums on the surface of Lake Baringo. The algae that associate with *Microcystis aeruginosa* on the water surface in the lake include *Closterium* spp. and *Ankistrodesmus falcatus* [34]. The most dominant algae in the lake are *A. circinalis* Rabh. ex Born, *Microcystis aeruginosa* Kutz, and *Merismopedia* sp. Phytoplankton populations are recruited from May to August, which is the rainy season. *Anabaena circinalis* concentrations improve between June and September [43]. In Lake Baringo, *Anabaena circinalis* and *Microcystis aeruginosa* algae have been identified in the stomach of Nile Tilapia. Furthermore, green algae (Chlorophyta) include *Cosmarium moniliforme* Turp, *Oocystis* sp., *Pediastrum* sp., Ralfs var. falcatus, *Closterium* sp., *Ankistrodesmus falcatus* Corda. Ralfs, *Chlorella* sp., and *Scenedesmus* sp. [29,43]. Most of the green algae identified in the lake *Cosmarium moniliforme*, *Pediastrum* sp., *Ankistrodesmus falcatus*, *Closterium* sp., *Oocystis* sp., *Scenedesmus* sp., and *Chlorella* sp. *Coelastrum* sp., *A. falcatus*, and *C. moniliforme* showed concentrations of 9×104 cells/mL. The rains improved concentrations probably due to improved nutrients of phosphates and nitrates. The diatoms (Bacillariophyta) such as *Rhizoselenia* sp, *Cyclotella* sp., and *Aulacoseira agassizii* (Ostenf.) Sim have been identified in the lake. Diatoms that are pinnate in nature have been shown to exist among the algae of Lake Baringo. The diversity of diatoms in the waters of Lake Baringo is low throughout the year [29,43,44]. In the lake, the concentration of *A. agassizii* was < 300 cells/mL, while that of *Cyclotella* sp. was < 10 cells/mL.

8.1.7 Challenges in studying microbial ecology in Lake Turkana and Lake Baringo

Major challenges in understanding the structure and functions of microbial diversity in the East African Great Lakes have been pointed out in freshwater reviews [45]. These challenges also exist in the remote desert Lakes

Turkana and Baringo [20,25,34,38]. These challenges include the need for advanced technology, and the application of technologies such as molecular techniques, epifluoresence microscopy, and flow cytometry. Although the diversity of the microbial community in Lake Turkana and Lake Baringo is low compared to the other large East African Lakes [37,46,47], these challenges hinder the understanding of the link between microbial food web, ecosystem production, and nutrient recycling in these desert ecosystems. These lakes are dominated by Cyanophyceae (e.g., Microcystis spp.), Chlorophyta (e.g., Botryococcus), and Bacillariophyceae (e.g., *Nitzschia* spp.) [20], which contribute significantly to the microbial food web and fishery production in these desert lakes [25].

Although the scientific community relies increasingly on molecular biology to explore and evaluate microbial communities and to distinguish one organism from the other as described by McCartney [45], these techniques are hardly used to probe microbial diversity in Lakes Turkana and Baringo. These new technologies, which include gene sequencing, genetic fingerprinting, oligonucleotide probes, and specific primer selection as described by McCartney among others [41], are completely missing in the microbial analysis of Lakes Turkana and Baringo. This implies that molecular biology is an important modern field of science in interpreting microbial communities in the desert lakes but lacks in Lakes Turkana and Lake Baringo. Applications of molecular technical approaches, such as next generation sequencing, Denaturing Gradient Gel Electrophoresis or Temperature Gradient Gel Electrophoresis, fluorescent in situ hybridization, and others are very limited and have hardly been used for these desert lakes, but are essential to access uncultured complex microbiota. Current molecular methods are used to study culturable microorganisms that may help understand the genetic content information of these microbes. The four approaches which are important in studying microbial ecology using molecular biology techniques are lacking in Lakes Turkana and Baringo. These techniques include classification of microbial diversity within the lake water samples; providing enumeration of phylogenetically associated groups of microbials of the water samples; both quantitative and qualitative tracking and monitoring of specific microorganisms or populations in water samples; and finally, the specific identification and description of isolates, especially the microbial techniques. The important aspects may be important research issues that would attempt to examine the microbial food web with molecular methods to detect forms of life, or look for possible endemism, which have gone undetected by other methods.

The third challenge is the microbial sample preservation technique for producing good science in Lakes Turkana and Baringo. Fourth, basic information including auto- and heterotrophic picoplankton diversity, biomass, and its significance in the pelagic food webs is lacking in these remote desert lakes. Fifth, heterotrophic and mixotrophic protists, which are significant components of the food web are unknown, but there are indications that they are an important link between producers and consumers and may be a significant component in nutrient recycling. Sixth, complete and updated microbial ecological studies in Lake Turkana and Baringo are still missing but are significant for the local population. Seventh, these remote desert lakes also show a higher level of adverse response to organic loading and eutrophication [20,27,34,38]. Increasing human population and settlements along Lakes Turkana and Baringo shores, environmental degradation, global warming, and alien species introductions increase problems for these remote desert lakes. Eighth, the international scientific community and bilateral organizations give low attention to the remote desert Lakes Turkana and Baringo. Ninth, few communities of scientists and technicians have received adequate training, coupled with a lack of financial and technical means for undertaking and sustaining the effort in the key biodiversity areas of the desert lakes. However, a new generation of Kenyan students is emerging, which has benefited from the support of well-funded projects, and who have become involved in microbial studies of these remote desert aquatic ecosystems in the country. Nevertheless, more scientific and technical cooperation initiatives are still needed. There is an increasing awareness of the environmental problems threatening these desert freshwater lakes.

In conclusion, four principal phenomena come to play in the phytoplankton distribution in Lakes Turkana and Lake Baringo. First, seasonality affects the algal community succession with temperature stratification and mixing regimes that are influenced by south-easterly winds. These temperature and wind variations affect algae growth and succession. Second, the Omo River, Turkwel River, and Kerio River flood waters into Lake Turkana due to rains in the months of May to October and influence algae populations and succession. The Perkerra River and Molo River for Lake Baringo flood waters influencing algae populations and succession. Third, *M. aeruginosa* is the dominant algae species in these two lakes, particularly during periods when the influence of the Omo River floods and *Perkerra River water is high. The algae species diversity and succession of the* open water are quite low. Near rocky areas of the lake, epibenthic

diatoms diversity is recruited into phytoplankton. Fourth, Lake Turkana and Lake Baringo experience low algae biomass including mean annual standing crops of planktonic algae.

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CHAPTER 9

Diversity of extremophiles in African brine lakes

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9.1 Hypersaline environments: origin and distribution

Saline lakes are water bodies located within endorheic basins around the globe [1–5]. A distinguishing characteristic of these water bodies is elevated levels of dissolved salts (usually above 35 gm of dissolved salts per liter of water). Saline lakes that originate from marine environments are termed thalassohaline [6], while those formed when surface water dissolves the preexisting salt deposits or saline soils are referred to as athalassohaline [7]. In most cases, the lakes are found in geographical locations that are arid or semiarid, and therefore, experience intense irradiation, high surface temperatures, high rates of evaporation, and low precipitation. Therefore, water losses through evaporation exceed the rates of replenishment either by precipitation, inflows from seasonal rivers and streams, or groundwater discharge. This creates a negative hydrological water balance [8]. Changes in the climatic conditions within these geographical regions impacts water levels, surface area, and overall water chemistry [9].

9.2 Distribution

Several hypersaline lakes have been reported across the African continent. They include salt flats, human-made brine evaporation ponds, salt marshes, salterns, and deep-sea brine pools [10]. In Egypt, seven hypersaline alkaline lakes having depths between 0.5 and 2 m are located within the Wadi An Natrun depression [11]. High evaporation rates are experienced in this region due to the arid climatic conditions and this leads to elevated salinity levels beyond 30% (w/v). Their total dissolved solids range between 91.0 and 393.9 g/L, while the pH values range from 8.5 to 11 [12]. The athalassohaline Lakes Aghormy, Zeiton, and Maraqi within the Siwa oasis (29° 05′ N and 29° 25′ N and longitudes 25° 05′ E

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and 265° 06′ E) in Egypt have high salt concentrations and unique water chemistry [13]. The total dissolved salts (TDS) levels in these lakes have been recorded as 220.03, 239.29, and 280.45 g/L, respectively [14]. Low rainfall and high evaporation are the key factors of the observed salinity levels. The hypersaline lakes in Tunisia are referred to as Sebkhat or chott. Lake El Jerid covers about 5000 Km^2 in the south of the country and has a salt concentration that varies between 250 and 330 g/L [15,16]. The main ions in the brines are sodium chloride followed by sulfate [15,17]. However, flooding due to occasional rains followed by evaporation in a dry desert leaves salt mineral deposits. Several multipond solar saltern of Sfax (Tunisia) are artificial evaporation ponds for salt production via seawater evaporation. This process progressively concentrates the salinity from 37 g/L in the seawater to 400 g/L. Some moderately halophilic strains have been isolated and investigated for their phenotypic characteristics, phylogenetic affiliation, and enzymatic activities in these ecosystems [18]. In Algeria, salinity levels in the hypersaline waters of lakes Sidi Ameur and Himalatt have been recorded as 20% (w/v) and 11.7% (w/v), respectively [19] with the major ions being sodium (Na^+) and chloride (Cl^-) levels ranging from 67 to 170 g/L. The authors reported that magnesium and sulfate ions were less abundant at 1.1 to 3 g per liter while biological oxygen demand (BOD) values were 39 and 73 mg/L, respectively. These BOD values could be attributed to their close proximity to human activity and is consistent to what has been observed in similar ecosystems e.g., Lake El Golea [20]. However, Lake Sidi Ameur and Himalatt have relatively neutral with pH values ranging from 7.15 to 7.4 as compared to the more alkaline lakes such as Lake Wadi Natrun (pH 11) and El Golea (pH 9) [19].

Gaet'ale Pond in Ethiopia's Afar region is small hypersaline crater lake located in the Danakil Depression. Pérez and Chebude [21] reported a TDS value of 433 g/kg in water from the Gaet'ale Pond. This is equivalent to a salinity level of 43.3 ± 0.9%, making it the most saline water on Earth. LakeAfrera is another saline lake that is located between the ErtaAle and the Alaita-TatAli ridges in Ethiopia at around 90 m below sea level and has a salinity of approximately 159 g/L [22]. The soda lakes in the Kenyan part of the rift valley have varying levels of salinity characterized by roughly equal amounts of sodium carbonate (Na_2CO_3) and sodium chloride (NaCl) and pH values between 11 and 12. However, brines of Lake Magadi which is located in the more arid zone have a total salinity exceeding 30% (w/v) [23]. Lake volume shrinkage during dry

months concentrates the water to brines with elevated electrolyte concentration. However, due to climate change, some of these lakes flood during the rainy season leading to significant dilution. Philip and Mosha, [24] observed that in January 2011, 60% of Lake Natron in Tanzania dried up and TDS in the brine rose to 24,900 ppm. The Katwe-Kikorongo volcanic area in Uganda has eight saline crater lakes and Lake Katwe which is the largest has a pH above 9, while salinity varies between 128 and 149 ppm [25]. The brine water is comprised of mainly Na^{+}, Cl^{-}, $SO_4{}^{2-}$ $CO_3{}^{2-}$, HCO^{3-} ions. There are numerous salt lakes reported in Namibia, Botswana, and South Africa [26,27]. However, lakes in southern Africa are shallow, ephemeral and have salinities below 50 g/L [27].

9.3 Role of hypersaline lakes in biogeochemical cycling

Saline lakes play an important role in the global carbon (C), nitrogen (N) and sulfur (S) cycles [28–30]. High primary productivity in these lakes is due to limitless amounts of CO_2, high intensities of solar radiation and warm temperatures throughout the year [31]. Oxygenic phototrophs such as halophilic Cyanobacteria and algae such as *Dunaliella salina* are some of the key primary producers [32]. Diverse groups of halotolerant bacteria, Cyanobacteria, green algae, diatoms, fungi, and protozoans have all been reported to thrive at salinities between 25% and 33% [33,34]. Their decomposition may eventually add significant quantities of organic matter that supports heterotrophs and syntrophs. In addition, organic matter from activities around the lake adds significant amounts of organic matter into the hypersaline system. Being closed basins, nutrients are recycled more efficiently as compared to freshwater systems [35].

9.4 Water chemistry

Hypersaline lakes are characterized by very high concentrations of salts [19] with Na^{+} and $C1^{-}$ being the major ions in hypersaline habitats such as Lake Magadi and Lake Assal [36]. Several cation/anion incompatibilities have been shown to exist in concentrated brines. Soda lakes which are stable high-pH environments with pH values above 9 are characterized by high concentrations of bicarbonate (HCO^{3+}) and carbonate ($CO_3{}^{2+}$) but very low amounts of dissolved calcium (Ca^{2+}) and magnesium (Mg^{2+}) [37]. Therefore, saline waters have been distinguished into various types and subtypes using a salinity baseline of 25% (w/v). Hypersaline soda

brine can be categorized as rich in various combinations of ions such as sodium-carbonate ($Na\text{-}CO_3$), Sodium-bicarbonate-carbonate ($Na\text{-}HCO_3\text{-}CO_3$), sodium-carbonate-chlorine-sulfate ($Na\text{-}CO_3\text{-}Cl\text{-}SO_4$), or sodium-bicarbonate-carbonate-chlorine ($Na\text{-}HCO_3\text{-}CO_3\text{-}Cl$). Brackish and saline-alkaline lakes rich in Na^+ and HCO^{3-} and CO_3^{2-} are also known as "soda lakes" [36]. Owing to their shallow depths, continuous evaporation leads to drying out and eventual crystallization of salts especially at lower temperatures [38].

9.5 Microbial diversity in hypersaline environments

Halophilic organisms are capable of growth at salinities above 150 g/L [39]. Whereas some require a minimum of 9% (w/v) of NaCl for growth, majority will grow optimally at 20 to 26% (w/v) of NaCl and some can grow very well above 30% (w/v) of NaCl [40]. Advances in culture-independent methods have greatly contributed to the understanding of the diversity and ecology of these groups [41]. Archaeal groups in the family *Halobacteriaceae* can grow a wide range of substrates [42] and this may explain their abundance in extreme environments that are rich in organic matter. Alkaliphilic Haloarchaea coexist with anaerobic anoxygenic bacteria like *Halorhodospira* spp [43]. Previous investigations on the bacterial populations of the Solar saltern in Tunisia have shown the presence of various phylotypes affiliate to Proteobacteria, Firmicutes, Bacteroidetes, and Cyanobacteria [17,44]. Anaerobic halophilic fermentative bacteria described from hypersaline environments are mainly affiliated to the order *Halanaerobiales* [45]. *Salinibacter ruber* is one of the extremely halophilic species in the phylum Bacteroidetes that is widely distributed in hypersaline environments [46,47]. Anoxic zones and varying degrees of sulfidic environment are common in these highly productive ecosystems [48]. More than 80 isolates of sulfur-oxidizing bacteria have been identified and described from soda lakes around the globe and they include both heterotrophic and obligatory autotrophic species [49].

Photosynthetic primary productivity, in general, is thought to be a consequence of Cyanobacteria blooms. However, in certain lakes and depending on seasonal circumstances, other Cyanobacteria such as *Spirulina* spp. (now *Arthrospira*) and unicellular forms such as *Synechococcus* or *Chroococcus* spp. may predominate [50]. Salt levels between 22% and 62% are ideal for *A. fusiformis*. However, the current molecular methods are not able to adequately discriminate between the two genera [51].

A study by Edwin et al. [52] recovered 11 isolates affiliated to the orders Chroococcales, Oscillatoriales, Pleurocapsales and Nostocales. Isolates affiliated to genus *Chroococcidiopsis* and had similarity values below 90% to currently characterized taxa, indicating that these could be completely new phylotypes. This taxon has not been isolated before from the soda lake indicating the power of molecular techniques in identifying novel cyanobacterial taxa. Only two of the recovered isolates had 99% similarity to known organisms.

Halophilic or halotolerant fungi and yeasts have been described from hypersaline habitats worldwide. The black yeast *Hortaea werneckii* tolerates a wide range of salinities from 0 to 30% NaCl and broad optimum between 1 and 2.5 M NaCl [53]. The true-halophile *Wallemia ichthyophaga* is part of the *Wallemia sebi* species complex [54] and has a lower growth limit at around 1.5 M NaCl [55] while the optimum is between 2.6 and 3.4 M NaCl [56]. Although fungi are to be moderately or poorly alkali-resistant in salty settings, Orwa et al., [57] reported 18 different fungal genera from culture dependent studies in Lake Magadi, Kenya. The isolates include different species as *Aspergillus, Penicillium, Acremonium, Phoma, Cladosporium, Septoriella, Talaromyces, Zasmidium, Chaetomium, Aniptodera, Pyrenochaeta, Septoria, Juncaceicola, Paradendryphiella, Sarocladium, Phaeosphaeria, Juncaceicola*, and *Biatriospora*. Hyper-saline-alkaline water is home to a wide variety of crustaceans, including the brine shrimp *Artemia salina* and several copepod species [58].

Viruses are everywhere from the deepest seas to the harshest deserts [59,60] and it has been shown that their influence extends beyond affecting microbial communities to having an indirect but substantial part in the Earth's biogeochemical cycles [61]. Though important, little is known about the ecology in salt lakes, salt flats, and salt deposits across the globe. In certain hypersaline habitats, viruses infecting haloarchaea outweigh cells by 10–100 times. Recently, Akhwale et al., [62] isolated and characterized 17 phages from Lake Elmenteita. There are reports of phages from Soda Lakes Magadi [63–65] and Nakuru [66].

9.6 Microbial adaptation to the extreme environments

Nutrient uptake, protein biosynthesis and several enzymatic activities are all affected by shifts in osmotic potential [33]. Organisms residing in highly saline habitats must therefore regulate their osmotic balance for survival. Halophiles prevent water loss by either producing organic solutes/osmoprotectants that

stabilize cellular macromolecules [67] or accumulate large amounts of intracellular salt concentrations (high-salt-in strategy) to match that in the surrounding environment [68]. Extreme halophiles of the archaeal family Halobacteriaceae as well as bacteria such as *S. ruber* maintain their osmotic balance by accumulating potassium ions inside the cells [43,69]. Survival in environments that experience fluctuations salinity due to flooding alternating with dry seasons requires a more flexible mechanism of maintain osmotic balance. The preferred strategy would be de novo synthesis or importation of osmolytes to cope osmotic shocks [70]. Examples of osmolytes that help cope with increasing salt concentrations include Glycine betaine, ß-glutamine, N-acetyl-ß-lysine and α-glucosyl glycerate [71]. Several species of Cyanobacteria accumulate sucrose, trehalose glycerol while archaeal osmolytes include glycerol, glycosyl glycerol, betaines, proline, glutamate, glutamine, and ectones [72].

9.7 Molecular analysis of the uncultured diversity

Techniques in molecular biology have made it possible to explore non-cultivable organisms without having to worry about separating various species based on their ability to grow in vitro. These techniques overcome the "great plate count anomaly" leading to discovery of novel lineages of microorganisms. The ribosomal RNA gene (rRNA) is one indispensable markers for taxonomic and phylogenetic research. These markers when coupled to amplicon sequencing, provides a wealth of data on the microbial diversity and abundance in complex ecosystems without the need for culture. Even though these approaches are quite effective, a large number of taxa are still unidentified [6]. Different molecular methods have been used to study the microbial diversity in hypersaline lakes. Abdallah et al. [73] used Quantitative real-time PCR (qPCR) and Denaturing Gradient Gel Electrophoresis (DGGE) and reported significant bacteria and archaea diversity in Chott El Jerid, Tunisia. A more detailed study by Ben Abdallah et al. [16] using Illumina Miseq sequencing, DGGE and qPCR showed that Proteobacteria were the most dominant followed by Firmicutes, Bacteroidetes, Cyanobacteria, Actinobacteria and Verrucomicrobia. Relative abundance of archaea was dominated Halobacteria (especially *Halorubrum* spp) and anaerobic members of Methanomicrobia. Baati et al. [74] investigated the solar salterns of Sfax (Tunisia) using 16S rRNA clone library analysis. They reported that *S. ruber* within the phylum Bacteroidetes was the dominant

group followed by Proteobacteria. All the archaeal sequences clustered in the order Halobacteriales.

Kambura et al. [75] did an analysis of the bacterial and archaea diversity in the hypersaline Lake Magadi and reported that bacteria are more abundant (85.55%) as compared to archaea (11.27%). The groups with highest relative abundances at phylum level belonged to members of Proteobacteria (16%–31.4%), Firmicutes (2.8%–28.9%), Bacteroidetes (3.4%–23.8%), Actinobacteria (1.0%–14.4%), Cyanobacteria (1.1%–8.3%, Chloroflexi (0.3%–7.2%), and Deinococcus-Thermus (0.3%–5.3%). The most abundant archaeal families were Halobacteriaceae (21.31%), deep-sea Hydrothermal Vent Gp 6 (DHVEG-6) (8.59%), and Marine Benthic Group D and DHVEG-1 (2.29%). Members of the phylum Crenarchaeota belonged to the families Desulfurococcaceae (1.11%) in wet sediment samples at 81°C and Sulfolobaceae (0.28%) in wet water samples at 45.1°C, while Thaumarchaeota were mainly assigned to uncultured archaeon with up to 1.15% relative abundance in wet sediment samples at 45.1°C. Fungal diversity studies in the hypersaline lakes have been carried out using either general or group specific primers based on the large subunit of the rRNA gene. However, taxonomic resolution at lower taxonomic levels as well as coverage is always an issue particularly in less investigated areas. Primers for the Internal Transcribed Sequences (ITS) first gained widespread popularity in fungal investigations and were later updated by numerous researchers [76]. Illumina sequencing of ITS generated amplicons was done by Kambura et al. [77] from Lake Magadi and Little Magadi. The reads recovered in this study were assigned to phylum Ascomycota (83.3%), Basidiomycota (15.8%), Glomeromycota (0.02%), and unclassified fungi (0.9%). However, there are reports of poor resolution at lower levels or inability to distinguish between taxonomic groups with extremely hypervariable ITS regions using these primers.

9.8 Comparative analysis of the microbial diversity in Kenya soda lakes using amplicon sequencing

The Kenyan soda lakes are all situated on the floor of the Kenyan portion of the East African rift valley and therefore have no outlet. The surrounding ecosystem is characterized by high surface temperature, high evaporation rates, and low annual rainfall. The hypersaline Lake Magadi (2°00′S and 36°13′E) covers an area of 90 km^2 and evaporation is intense during the dry season when surface temperatures reach 40°C. Lake Elmenteita

(0°27′ S, 36°15′ E) is a moderately saline lake located 1776 m above sea level and has no direct outlet. The lake size is approximately 20 km^2, but the total surface area changes with seasons as often flooding during heavy rains occurs. Lake Bogoria (0°20′N and 36°15′E) is situated at an altitude of 975 m, with several geysers around the lake and an annual average rainfall is 708 mm. The crater Lake Sonachi is in a closed basin on the Eastern Rift valley (0°49′S, 36°16′E). The salinities of these lakes range from approximately 5% (Lakes Bogoria, Nakuru, Elmenteita, and Sonachi), to saturation (30% or greater) in the southern lakes (Magadi, Little Magadi, and Natron). Several studies have explored the microbial diversity in these lakes isolation efforts [57,75,77,78,79,80]. In a more detailed study, we collected from each lake: mud (referred to as wet sediment), water, microbial mats and dry sediments (from the dry part of the lake) as well as grassland soil from outside the lake area. Each sample was collected in triplicate and homogenized to form a composite sample that was packed in sterile 50 mL falcon tubes and frozen immediately on dry ice. Water samples were collected (5 L), filtered through a filter sandwich consisting of 0.45 μm (pore size) and 0.22 μm (pore size) polycarbonate filters (Whatman GE Healthcare, United States), which were immediately preserved on dry ice. All samples were stored at −80°C until further use. Total dissolved solids, dissolved oxygen, conductivity temperature and pH were recorded on site from the water samples.

Total community DNA was extracted from 0.1 gm of the soil or sediment samples. In the case of the water samples, the filter was cut into small pieces with a sterile scalpel and transferred to a sterile tube. In the initial step,100 μL sterile resuspension buffer (50 mM Tris pH 8.5, 50 mM EDTA pH 8.0 and 25% sucrose solution) amended with 20 mg/mL of lysozyme were added to the sample and then incubated at 37°C in a water bath for 30 min. After this step, 400 μL of lysis buffer (10 mM Tris pH 8.5, 5 mM EDTA pH 8.0 and 1% SDS), 10 μL of Proteinase K (20 mg/L) were added, gently mixed and the mixture incubation at 65°C for 120 min. Phase separation was achieved by addition of an equal volume of phenol: chloroform: isoamyl alcohol (25:24:1, pH 7.7−8.3) and centrifugation at 13,200 rpm for 10 min at 4°C. The supernatant was carefully transferred to a new tube. The phenol:chloroform: isoamyl alcohol extraction step was repeated a second time. An equal volume of chloroform:isoamyl alcohol (24:1) was added, shaken to mix, and centrifuged for 10 min. DNA was recovered using the standard sodium acetate/isopropanol/ethanol method. An aliquot (3 μL) of the recovered DNA was

run on 1% agarose to confirm the quality while the quantity was checked on a Qubit 3.0 Fluorometer using the Qubit dsDNA BR assay kits (Thermo-Fisher Scientific).

Amplicon-based sequencing of the V3−V5 16S rRNA gene hypervariable regions was done using DNA extracted from samples collected from Lakes Magadi, Bogoria, Elmenteita, and Sonachi. We also designed a new primer set for enriched amplification of Cyanobacteria and designated them as Cya-f (GGAATTTTCCGCAATGGG) and Cya-R (GACTA CWGGGGTATCTAATCC). For fungi, we used a new primer set designated as Fung_576f (5′-GCTCGTAGTTGAACCTTTGG-3′) and Fung_975r (5′-TCTGGACCTGGTGAGTTTC-3′). The primers were modified for pyrosequencing by attaching an adapter sequence, a key and a unique 12 Nucleotide MID for multiplexing purposes. Each PCR reaction (50 μL) contained forward and reverse primers (10 μM, each), dNTP's (10 mM each), Phusion GC buffer (Finzymes), Phusion high fidelity polymerase (0.5 U/μL-1) and 25 ng of template DNA. Cycling conditions were: initial denaturation at 98°C for 3 min, followed by 25 cycles of denaturation at 94°C for 45 s, annealing for 45 s at 59°C, and extension at 72°C for 60 s, and a final extension step of 72°C for 5 min. Amplification was confirmed by separating 2 μL of the PCR product on a 1% TAE agarose gel (40 mM Tris base, 20 mM glacial acetic acid, 1 mM EDTA, 1.5% (w/v) agarose) run for 1 h at 100 V. Later, three independent PCR products per sample were pooled in equal amounts, separated on a gel and extracted using the peqGOLD gel extraction kit (PeqLab Biotechnologie GmbH, Erlangen, Germany). Quantification of the PCR products was performed by using the Nanodrop (PEQLAB Biotechnologie GmbH, Erlangen, Germany) method and a Qubit fluorometer (Invitrogen GmbH, Karlsruhe, Germany) as recommended by the manufacturer. Sequencing of the PCR derived amplicons was performed on a Roche GS-FLX 454 pyrosequencer (Roche, Mannheim, Germany).

9.9 Results

Physicochemical characteristics measured in situ are typical of the soda lake ecosystems (Table 9.1). Changes in temperature and pH are observed at different points within the lakes and this is driven by hotsprings flowing into the lakes. For example, site 1 in Lake Bogoria is a hotspring that feeds into the lake. However, on mixing with the open lake water, the pH

Table 9.1 Metadata at the sampling points within the different lakes.

Lake		Co-ordinates	pH	Temp. (°C)	D.O (mg/L)	Conductivity (mS/cm)	TDS (mg/L)
Bogoria	Site 1	0.25S, 36.08E	7.63	88	5.8	4.81	1
	Site 2	0.27S, 36.08E	10.09	29.2	9.2	0.29	11
Magadi	Site 1	−1.90S, 36.30E	9.4	45.0	12.4	56.5	1
	Site 2	−1.75S, 36.27E	9.42	85	0.03	48.3	1
	Site 3	−1.88S, 36.29E	10.3	37.4	7.3	178	114
Elmenteita	Site 1	−0.47S, 36.25E	9.7	22.7	17.6	11.34	18.74
Sonachi		−0.78S, 36.26E	9.9	26.9	15.8	22.0	15.7

values go up while the temperature goes down. The lakes are shallow hence there is continuous mixing because of wind currents. Therefore, temperatures recorded ranged from 22.7°C to 88°C within the hotsprings.

The bacterial dataset comprised 130,743 high quality sequences. The sequences were clustered into 4709 operational taxonomic units (OTUs) at 3% genetic distance and the numbers of OTU per sample ranged from 88 (water sample BW2) to 945 (Dry sediments sample BS-9). The classified bacterial sequences were affiliated to 43 phyla and 8 candidate divisions. Bacterial community composition showed that members of the phyla Actinobacteria (8.4%), Bacteroidetes (12%), Cyanobacteria (20.6%), Firmicutes (12.4%), Gemmatimonadetes (4.8%), Proteobacteria (30.0%) and Spirochetes (0.8%) were present in all samples regardless of the water chemistry. The Proteobacteria were the most significant in terms of abundance and number of genera. The role of these groups in soda lake functioning is very significant because their metabolic diversity includes anoxygenic phototrophs, nonphotosynthetic bacteria, aerobic chemolithotrophs, heterotrophs, and symbiotic as well as parasitic bacteria (Fig. 9.1).

A total of 72,973 16S rRNA gene sequences could be assigned to the domain archaea. These were clustered into 1397 OTUs at 3% genetic

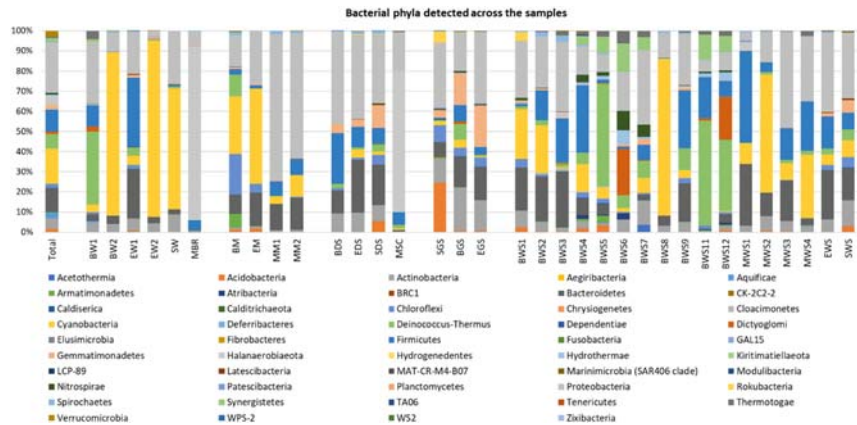

Figure 9.1 Bacterial diversity across the different samples at the phylum level. Key: The samples are designated as *BDS*, Bogoria dry sediments; *BGS*, Bogoria grassland soil; *BMM*, Bogoria microbial mats; *BW*, Bogoria Water; *BWS*, Bogoria wet sediments; *ED*, Elmenteita Dry sediments; *EG*, Elmenteita grassland soil; *EM*, Elmenteita microbial mats; *EW*, Elmenteita water; *MBR*, Magadi Brine; *MM*, Magadi microbial mats; *MSC*, Magadi salt crust; *MWS*, Magadi wet sediments.

distance. Ten different archaeal phyla were represented in the dataset as shown in Fig. 9.2. The phylum Crenarchaeota and Euryarchaeota were detected in all the samples and in fact 84% of the reads in the brine collected from Lake Magadi were affiliated to Euryarchaeota (Fig. 9.2). Sequences belonging to the order Halobacteriales were the most abundant order followed by Thermococcales at 61.3%. Members of the order Halobacteriales form the dominant microbial population when hypersaline waters approach saturation, frequently imparting pink coloration. In this study, 19 genera from this order were represented.

Strictly anaerobic archaea detected in this study, such as *Methanobacterium*, *Methanosarcina*, *Methanosaeta* and *Methanoculleus*, and *Methanothermobacter*, can produce methane via the reduction of carbon dioxide (CO_2) using electrons (most often) from hydrogen gas (H_2) chemolithoautotrophically. Separately, we amplified for only Cyanobacteria and found out that the genera *Cyanobium* PCC-6307, *Leptolyngbya* RV74, *Thermosynechococcus* BP-1, *Arthrospira* PCC-7345 and *Oxynema* BDU 92071 were the most abundant across the samples. The genus *Cyanobium* PCC-6307 was the most dominant with > 60% relative abundance across the lake samples, especially in wet sediment samples from Lake Magadi and Sonachi as well as the water samples from Elmenteita and Sonachi (Fig. 9.3).

The genus *Leptolyngbya* RV74 was detected in high relative abundances (> 30%) in most of the L. Bogoria samples. Notably, the genus

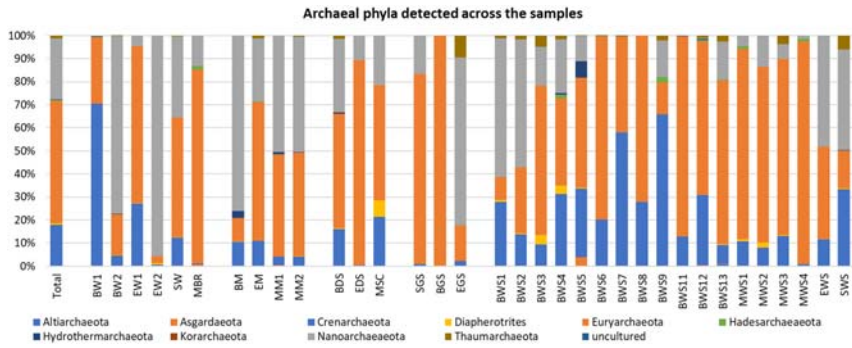

Figure 9.2 Archaeal diversity across the different samples at the phylum level. Key: The samples are designated as *BDS*, Bogoria dry sediments; *BGS*, Bogoria grassland soil; *BMM*, Bogoria microbial mats; *BW*, Bogoria Water; *BWS*, Bogoria wet sediments; *ED*, Elmenteita Dry sediments; *EG*, Elmenteita grassland soil; *EM*, Elmenteita microbial mats; *EW*, Elmenteita water; *MBR*, Magadi Brine; *MM*, Magadi microbial mats; *MSC*, Magadi salt crust; *MWS*, Magadi wet sediments.

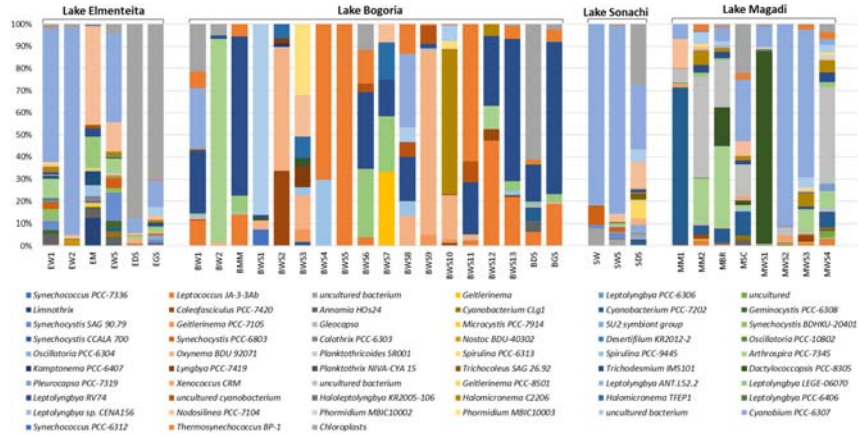

Figure 9.3 Cyanobacteria diversity across the different samples at the genus level. Key: The samples are designated as *BDS*, Bogoria dry sediments; *BGS*, Bogoria grassland soil; *BMM*, Bogoria microbial mats; *BW*, Bogoria Water; *BWS*, Bogoria wet sediments; *ED*, Elmenteita Dry sediments; *EG*, Elmenteita grassland soil; *EM*, Elmenteita microbial mats; *EW*, Elmenteita water; *MBR*, Magadi Brine; *MM*, Magadi microbial mats; *MSC*, Magadi salt crust; *MWS*, Magadi wet sediments.

Thermosynechococcus BP-1 accounted for 100%, 70% and 62% relative abundance in some wet sediment samples (BWS5, BWS4 and BWS11, respectively) of L. Bogoria. The genera *Arthrospira* PCC-7345 and *Oxynema* BDU 92071 were most dominant in samples BW2 (91%) and BWS9 (83%), respectively. Cyanobacteria are not only capable of performing photosynthesis but some groups e.g., members of the genus *Nostoc* (not identified in this study) are able to fix nitrogen in the presence of light and oxygen. The findings from this study show that larger survey sizes can broaden our view of the microbial diversity.

The 432 fungal OTUs were distributed across 107 fungal genera affiliated to the phylum Ascomycota, Basidiomycota, Glomeromycotina and Incertae Sedis. 3% of the sequences were clustered as unclassified fungal groups. The phylum Ascomycota was the most dominant phylotype with the orders *Capnodiales*, *Pleosporales*, *Hypocreales*, *Myrmecridiales*, *Sordariales* and *Xylariales* being the most abundant. The order *Pleosporales* was the most diverse with 13 genera followed by the orders Capnodiales (9), Hypocreales (11) and Xylariales (11) that had 9 genera. Whereas the Ascomycota were the most abundant across the samples, we noted that in Elmenteita wet sediments the phylum Bacillariophytina accounted for 45% of the OTUs (Fig. 9.4). The Pezizomycotina were the most

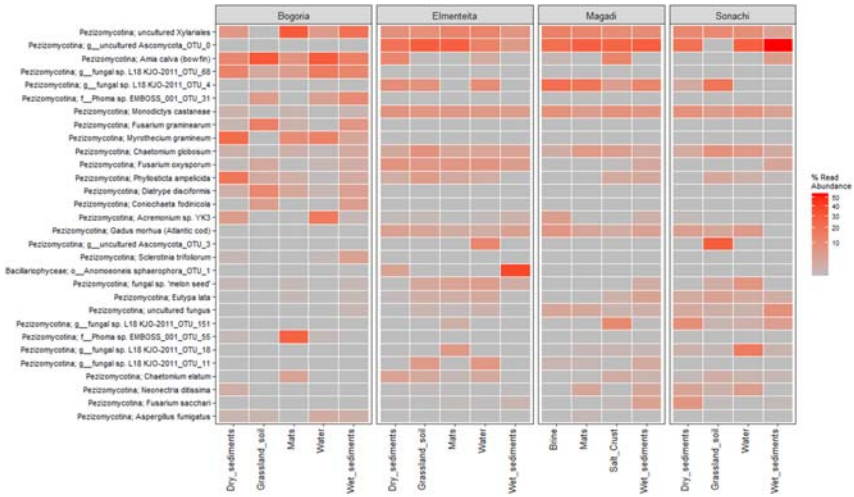

Figure 9.4 Heatmap showing the % abundance of the top 30 phylotypes.

abundant across the samples. The read abundance across the samples and lakes is shown in Fig. 9.4.

9.10 Future perspectives

The studies highlighted above illustrate the power of next generation sequencing in elucidating the microbial diversity of less explored extreme ecosystems in Africa. Culture-independent investigations on hypersaline lakes have come a long way from the era of clone libraries to the current state where a few studies have reported use on next generation sequencing technologies. The big data generated by High Throughput Sequencing technologies provides a better coverage and provides better insights on the microbial diversity in a habitat. However, methods such as Whole metagenome shotgun sequencing-based, (metagenomics), RNA (metatranscriptomics) and single cell genomics have not been widely used in these ecosystems whereas they are best suited to unravel the functional potentials of the microbiome. RNA sequencing could be particularly useful understanding the viromes of extreme environments. Furthermore, complete analysis of functional genes could help unravel what biogeochemical cycles are present as well the adaptive mechanisms of extremophiles. As sequencing costs become affordable, we project that they will be adopted as methods of choice even in resource limited settings in developing economies for scientific explorations. Exploring the microbial

communities for novel enzymes would also catalyze development of the African bioeconomy.

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CHAPTER 10

The Wadi An Natrun lakes, Egypt: diversity, physiology, and biotechnological potential

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10.1 Introduction

The Wadi An Natrun is located in a geographical depression approximately 100 km northwest of Cairo and 40 km from the Rosetta branch of the Nile [1,2]. The valley is 50 km long and 5–10 km wide and runs in a southeast to northwest direction between latitudes 30°15′ and 30°38′N and longitudes 30° 02′ and 30°30′ (Fig. 10.1). The altitude of the depression ranges from 24 m below sea level to 80–90 m above sea level at the southwest side, and eventually leads to two mountains 20–30 km away, Gebel Hadid (185 m above sea

Figure 10.1 Satellite image of the Wadi An Natrun. Red asterisks denote the largest of the lakes. Satellite image from Google Earth.

Lakes of Africa
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level) and Gebel Qantara (198 m above sea level). The area is arid to semiarid and receives 33.67 mm of rain/year [3,4].

Within the valley are 13–20 shallow, disconnected lakes and brine pools, many of them not deeper than 50 cm. The number of the lakes present varies according to the time of year, as many of the shallow pools completely dry out by evaporation during the summer months. The lakes are situated 38 km below the Rosetta branch of the Nile and are fed by underground seepage from the Nile. The water level of the lakes is directly correlated with the water level of the Nile [5]. Several lakes are also fed by underwater springs present inside them [6].

The lakes of the Wadi An Natrun differ greatly in mineral content, salinity, pH, and appearance. Evaporitic deposits are made up of carbonates, sulfates, and chlorides of sodium. The main ions in the lakes' water are sodium, chloride, carbonate, bicarbonate, and sulfate [7]. The pH of the water ranges between 9 and 11, and water temperatures between 30° C and 60°C have been recorded in the lake waters [4,5,8].

Natron (a mixture of sodium carbonate, bicarbonate, chloride and sulfate), soda ($Na_2CO_3.10H_2O$), and trona ($Na_2CO_3 \cdot NaHCO_3 \cdot 2H_2O$) have been collected from the Wadi An Natrun for hundreds of years. Natron mined from the Wadi An Natrun was used by the pharaohs of ancient Egypt in mummification, where it was used for desiccation of the cadaver before treatment with resins to prevent putrefaction and microbial degradation [9,10]. Many ancient Egyptian texts described natron deposits in the Wadi An Natrun [11]. The geographers Strabo (Geography XVII, I, 22, 23) and Pliny (Natural History XXXI, 46) mentioned natron deposits of Egypt [4]. Strabo described "two pits" which provide large quantities of natron; the two pits most likely being the two lakes in the Wadi An Natrun [12]. Pliny mentioned that sometimes there was a red color associated with the natron mined from the region [5]. Different shades of red are indeed present in the soda lakes of the Wadi An Natrun, mainly due to dense communities of halophilic archaea of the *Halobacteriaceae* (Fig. 10.2). Natron and soda are also mined from the Wadi An Natrun and used in glass manufacturing [13].

10.2 Microbial diversity of the Wadi An Natrun

10.2.1 Culture-dependent studies of the Wadi An Natrun

Several bacterial and archaeal species have been isolated from the water and sediment of the Wadi An Natrun lakes (Table 10.1). The isolates are halophilic, alkaliphilic, and of diverse phylogeny and metabolism.

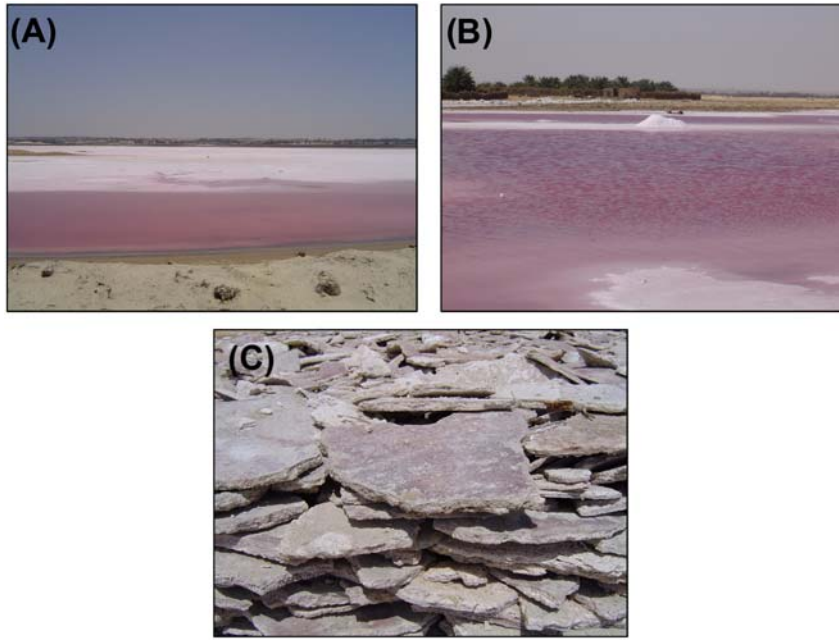

Figure 10.2 Photographs from the Wadi An Natrun taken in May of 2015, with red coloration due to microbial communities. (A) Lake UmRisha (B) Lake Abo Dawood. (C) Natron and halite deposits gathered on the shore of Lake Fazda. *Photographs: by the author.*

10.2.1.1 Sulfur metabolizers

The first detailed report on microbiological phenomena of the Wadi An Natrun lakes was published more than 120 years ago by Schweinfurth and Lewin, who described bacterial sulfate reduction in the largest of the lakes [5,37]. Jannasch later described the red color in the lakes and attributed it to anoxygenic phototrophic bacteria. In his report, micrographs of microorganisms identified as *Rhabdochromatium, Chromatium, Thiocystis, Thiospirillum* and *Desulfovibrio*, based on morphology, were published [38]. Abd-el-Malek and Rizk reported on bacterial sulfate reduction in the lakes and linked it to the alkalinity of the area and the deposition of natron. However, they could not detect sulfate-reducing bacteria in bottom lake sediments [39]. Research on six lakes of the Wadi An Natrun by Imhoff and colleagues showed mass development of photosynthetic sulfur bacteria (*Ectothiorhodospira* and *Halorhodospira*) and chemoautotrophic sulfur-oxidizing bacteria, and enrichment cultures with aerobic sulfide oxidizers and autotrophic ammonia oxidizers were reported [7]. Imhoff and colleagues were successful in the isolation of five extremely

Table 10.1 Halophilic alkaliphiles isolated from the Wadi An Natrun.

Name	pH range	pH optimum	NaCl range (M)	NaCl optimum (M)	Reference
Sulfur oxidizers					
Thialkalivibrio nitratireducens	8.0–10.5	9.5–10	0.2–1.5	0.4–0.5	[14]
Thioalkalispira microaerophila	8,0–10.4	10.0	0.3–1.5	0.5	[15]
Thioalkalivibrio paradoxus	8.5–10.5	9.5–10.2	0.3–2.5	0.5	[16]
Thiohalospira alkaliphila	7.0–10.2	8.5	0.5–4.0	2.0	[17]
Sulfate reducers					
Desulfonatronospira delicata	8.0–10.6	10.0	0.8–3.5	1.0	[18]
Sulfur reducers					
Desulfurivibrio alkaliphilus	8.5–10.3	9.5	0.2–2.5	0.5–1.0	[19]
Anoxygenic phototrophic bacteria					
Ectothiorhodospira haloalkaliphila	8.0–11.0	8.5–10.0	0.4–2.3	0.8	[20]
Ectothiorhodospira variabilis	7.5–10.0	9.0–9.5	0.3–3.0	0.8–1.2	[21]
Halorhodospira abdelmalekii	7.5–10.0	8.0–9.2	1.0–4.0	1.5–2.7	[22]
Halorhodospira halochloris	7.5–10.0	8.1–9.1	2.1–4.0	3.0	[23]
Halorhodospira halophila	7.5–10.0	8.5–9.0	1–4.0	1.5–4.8	[24]
Heliorestis acidamininvorans	8–10.5	8.0–9.0	0–0.7	0.1–0.6	[25]
Heliorestis convoluta	7.5–10.0	8.5–9.0	0–0.5	0–0.2	[26]
Anaerobic organotrophs					
Natranaerobius thermophilus	8.3–10.6	9.5	1.5–3.3	1.7–2.3	[27]
Natranaerobius trueperi	8.0–10.8	9.5	1.6–3.9	2.2	[28]

Natronovirga wadinatrunensis	8.5–11.5	9.9	1.6–3.7	2.3	[28]
Chitinispirillum alkaliphilum	8.5–10.0	9.5–10.0	0.4–1.8	0.5–1.0	[29]
Endospore-formers					
Alkalibacillus haloalkaliphilus	7.5–11.0	9.7	0.5–3.8	1.5	[30]
Natronobacillus azotifigens	7.5–10.6	9.5–10.0	0.2–4	1.0–1.5	[31]
Archaea					
Natronomonas pharaonis	7.7–9.3	8.5	2.0–5.0	3.5	[32]
Natrarchaeobaculum aegyptiacum	7.5– 10.1	9.2–9.5	2.5–5.0	3.2–4.6	[33]
Methanobacterium alcaliphilum	7.5–9.9	8.1–9.1	n.r.	n.r.	[34]
Methanosalsum zhilinaeae	8.0–10.0	9.2	0.2–2.1	0.7	[35]
Methanonatronarchaeum thermophilum	8.2–10.2	9.1–9.7	3–4.8	4.0	[36]

n.r., Not reported.

halophilic, phototrophic bacteria from Lake Abu Gabara. The strains were identified as *Ectothiorhodospira halophila*, later renamed *Halorhodospira halophila* [7,24]. Two additional photosynthetic bacteria were isolated from the lakes. *Halorhodospira halochloris* is extremely halophilic (optimal salt concentration 14%–27%), alkaliphilic (optimal pH 8.5), and moderately thermophilic (optimal temperature 47°C–50°C) [20,23]. *Halorhodospira abdelmalekii* is extremely haloalkaliphilic and contains bacteriochlorophyll b [22].

Halotolerant *Ectothiorhodospira* spp. with optimal growth at NaCl concentrations between 5% and 7%, were isolated from the Wadi An Natrun lakes and identified as *Ectothiorhodospira haloalkaliphila* [20]. *Ectothiorhodospira variabilis*, growing optimally at 5%–8% NaCl and pH 9–9.5, was isolated from Lake UmRisha [21]. A heliobacterium, *Heliorestis convoluta* was isolated from the soil and water of Lake Hamra. It grew optimally at pH 8.5–9 and 33°C, and had no requirement for sodium [26]. *Heliorestis acidaminivorans* was isolated from the shoreline soil of Lake Hamra. It was an anaerobic phototroph, with bacteriochlorophyll g and OH-diaponeurosporene glucosyl esters and photosynthetic pigments [25]. *H. acidaminivorans* has diverse photoheterotrophic growth and utilizes several amino acids and carbon compounds such as acetate, pyruvate, and propionate. *H. acidaminivorans* is alkaliphilic, growing optimally at pH 8–9 and moderately halophilic, with optimal growth at 0.5%–4% NaCl [25].

The Wadi An Natrun lakes are also populated by haloalkaliphilic, chemolithoautotrophic sulfur-oxidizing bacteria, the majority of which belong to the Gammaproteobacteria. These include *Thioalkalispira microaerophila* [15], *Thialkalivibrio nitratireducens* [14], *Thioalkalivibrio paradoxus* [16], and *Thiohalospira alkaliphila* [17]. These microorganisms oxidize elemental sulfur, thiosulfate, sulfide, and polysulfide. They are aerobic. *T. nitratireducens* can grow anaerobically with nitrate, nitrite, or nitrous oxide as an electron acceptor. *T. microaerophila* grows under micro-oxic conditions only (1%–2% oxygen in gas phase). All the chemolithoautotrophic sulfur-oxidizing bacteria isolated from the Wadi An Natrun are extremely alkaliphilic, growing between pH 8 and 11, and halophilic, growing between 0.5 and 5 M of Na^+.

Desulfurivibrio alkalphilus is strictly anaerobic and sulfidogenic and was isolated from a mixed sediment sample from eight lakes of the Wadi An Natrun [19]. It is gram-negative, belonging to the family *Desulfobaceae* of the *Deltaproteobacteria*. *D. alkaliphilus* uses elemental sulfur, polysulfide, and thiosulfate as electron acceptors with sulfide as the final reduced product. It can also utilize nitrate as an electron acceptor with ammonia as the final

product. *D. alkaliphilus* is also facultatively autotrophic with hydrogen as an electron donor. It is obligately alkaliphilic growing optimally at pH 9.5 and no growth below pH 8.5, and moderately salt-tolerant with optimal growth at 0.5−1 M Na^+, and growing over the Na^+ range 0.2−2.5 M [19]. An analysis of the complete genome sequence of *D. alkaliphilus* showed the *dsr* cluster of genes which catalyzes the reduction of sulfite to sulfide [40,41]. The *D. alkaliphilus* genome also has a sulfate adenylyltransferase gene *sat* and two adenylylsulfate reductase subunits, *aprAB*, indicating that it can participate in the oxidative branch of sulfite disproportionation. Genes for the reduction of thiosulfate and elemental sulfur were also annotated [40].

Desulfonatronospira delicata is another deltaproteobacterium isolated from mixed sediment samples from the Wadi An Natrun. *D. delicata* is obligately anaerobic with fermentative or respiratory metabolism. It utilizes sulfate, sulfite, and thiosulfate as electron acceptors during autotrophic growth with hydrogen or formate as electron donors, or with 2−3-carbon organic compounds as pyruvate, lactate, and ethanol. *D. delicata* can grow fermentatively by the inorganic chemolithoautotrophic mode by dismutation of sulfite/thiosulfate to sulfide and sulfate. It is alkaliphilic, growing over the pH range 8−10.6 (optimal growth at pH 10) and halophilic, growing over the Na^+ range 0.8−3.5 M (optimal growth at 1 M Na^+) [18].

10.2.1.2 Anaerobic organotrophs

Most of the fermentative anaerobes of the Wadi An Natrun belong to Firmicutes, and include members of the genera *Natranaerobius* and *Natronovirga* [42]. They are all halophilic alkalithermophiles, with optimal growth above 3 M Na^+, pH 9.5, and 51°C. They are obligate anaerobes and were isolated from the sediments of lakes of the Wadi An Natrun. They are obligate chemoorganotrophs and produce energy by substrate-level phosphorylation through mixed acid fermentation pathways with formate, acetate, hydrogen, and CO_2 as fermentation products. *Natranaerobius thermophilus*, type species of the genus *Natranaerobius*, utilizes fructose, ribose, xylose, cellobiose, trehalose, and amino acids as carbon and energy sources. It has an obligate requirement for yeast extract and tryptone in the culture medium, and its growth is enhanced in the presence of pyruvate (0.2% w/v) [27]. *N. trueperi* also has an obligate requirement for yeast extract and tryptone in the culture medium [28]. Similarly, *Natronovirga wadinatrunensis* catabolizes fructose, mannose, glucose, trehalose, and amino acids [28]. *Natranaerobius* and *Natronovirga* spp. grow very poorly using anaerobic respiration [42].

Analysis of the genome sequence of *N. thermophilus* showed homologs for enzymes catalyzing a nonoxidative pentose phosphate pathway and a complete glycolytic pathway. The *N. thermophilus* genome encoded for enzymes involved in the biosynthesis of thiamine and riboflavin, but not folate. This may explain the obligate requirement of *N. thermophilus* for yeast extract and tryptone in the growth medium [43].

Belonging to the novel class Chitnispirilla, phylum Fibrobacteres, *Chitinispirillum alkaliphilum* was isolated from a combined sediment sample collected from seven lakes of the Wadi An Natrun. *C. alkaliphilum* is obligately anaerobic with fermentative metabolism. Its only growth substrate was chitin, and it produced acetate, formate, glycerol, ethanol, and H_2 as fermentation products. It is mesophilic, obligately alkaliphilic growing over the pH range 8.5–10 (optimum 9.5–10), and halotolerant, growing over the Na^+ range 0.4 to 1.75 M (optimum 0.5–1 M Na^+) [29].

The analysis of the genome sequence of *C. alkaliphilum* showed a homolog to a glycoside hydrolase family 19 endochitinase with an N-terminal secretion signal, a chitin-binding domain, and a Por sorting domain, indicating that the endochitinase is secreted out of the cell and is responsible for extracellular hydrolysis of chitin. Numerous other polysaccharide deacetylases, in addition to endo-1,4-b-glucanases, xylanases, and α-amylases, were also present in the genome [29].

10.2.1.3 Endospore-forming bacteria

A haloalkaliphilic *Bacillus* strain, named WN13^T, was isolated by Weisser and Trüper from the brine and mud of Wadi An Natrun lakes [44]. It was later described as *Bacillus haloalkaliphilus* [30], and then renamed *Alkalibacillus haloalkalphilus* [45]. *A. haloalkalphilus* has terminally located spores with swollen sporangia. It is chemoorganotrophic and mesophilic, with no growth above 45°C. It is obligately alkaliphilic, growing optimally at pH 9.7, and no growth at pH 7. It is also extremely halophilic, growing at NaCl concentrations up to 25% w/v [30].

Natronobacillus azotifigens was isolated from mixed water–sediment samples from the Wadi An Natrun lakes as well as from the alkaline soil from the Kulunda Steppe, Russia [31]. It forms terminal endospores and is obligately alkaliphilic and halophilic (optimal growth at pH 9.5–10 and 1–1.5 M Na^+). It is also diazotrophic and obligately fermentative, producing acetate, formate, and ethanol as fermentation products from glucose [31].

10.2.1.4 Archaea

Imhoff and colleagues were the first to report massive developments of haloarchaea in the Wadi An Natrun lakes [7]. *Natronomonas pharaonis* (formerly *Halobacterium pharaonis*) was the first archaeon isolated from the Wadi An Natrun. *N. pharaonis* grows optimally at pH 8.5 and 3.5 M NaCl and remains viable at pH 11 [32]. *N. pharaonis* is chemoorganotrophic, with an obligate requirement for leucine as a carbon source [46]. *N. pharaonis* possesses an unusual electron transfer chain, including a halocyanin, cytochrome *bc*, cytochrome ba_3, succinate dehydrogenase, cytosolic cytochrome *c*, and cytosolic ferredoxin [47]. *N. pharaonis* is a popular model organism for the study of the light-driven chloride pump halorhodopsin [48] and nitric oxide synthase [49].

Other halobacteria isolated from the Wadi An Natrun include *Natrarchaeobaculum aegyptiacum* (Basonym: *Natronolimnobius aegyptiacus*). *N. aegyptiacum* is obligately aerobic and chemoorganotrophic utilizing sugars and organic acids as carbon and energy sources. *N. aegyptiacum* is extremely halophilic, growing over 2.5–5 M Na^+ (optimal growth at 3.2–4.6 M Na^+), obligately alkaliphilic, growing over the pH range 7.5–10.1 (optimal growth at 9.2–9.5), and thermophilic, growing over 38°C–56°C (optimal growth at 52°C) [33,50].

Several methanogens have been isolated from the Wadi An Natrun. *Methanobacterium alcaliphilum* was isolated from the sediment of four lakes of the Wadi An Natrun. The sole substrate for growth is H_2-CO_2. It grows optimally at pH 8.1–9.1, 37°C and has an obligate requirement for either trypticase peptone or yeast extract, indicating a need for a growth factor(s) within the medium [34]. *Methanosalsum zhilinaeae* was isolated from the sediments of Lake Bosa [35]. It is thermotolerant, with optimal growth at 45°C (range 20°C–50°C), alkaliphilic, with optimal growth at pH 9.2 (pH range 8–10), and halotolerant, with optimal growth at 0.7 M NaCl (NaCl range 0.2–2.1 M). It utilizes methanol, methylamine, and dimethylsulfide as substrates [35,51]. The *Methanonatronarchaeum thermophilum* strain AMET2 was isolated from a mixed water/sediment sample from eight lakes of the Wadi An Natrun. It is extremely alkaliphilic, thermophilic, and halophilic, growing optimally at pH 9.1–9.7, 60°C, and 4 M Na^+ [36].

A pure culture of a sulfur-reducing natronarchaeon was isolated from a mixed sediment–brine sample from the Wadi An Natrun. The strain, designated AArc-Wn, represents a novel species within the genus *Natronolimnobius*. Strain AArc-Wn grew anaerobically as a lithoheterotroph with formate or H_2 as an electron donor and yeast extract or acetate

as carbon sources. The terminal electron acceptor was elemental sulfur/polysulfide or dimethyl sulfoxide [52].

10.2.1.5 Culturable diversity of Lake Hamra

The culturable diversity of the water and sediment samples from Lake Hamra was examined by inoculation of the samples into modified Horikoshi I broth [53,54]. All of the isolates obtained belonged to *Firmicutes*, 46% were *Alkalibacillus* spp., 18% were *Gracilibacillus* spp., 18% were *Salinococcus* spp., 9% were *Staphylococcus* spp. and 9% were *Halobacillus* spp. [53]. The abundance of the halotolerant species reflects the more dilute nature of Lake Hamra.

10.2.2 Culture-independent studies of the Wadi An Natrun

Analysis of 16S rRNA gene clone libraries constructed from water and sediment from three of the largest lakes of the Wadi An Natrun, Lakes Fazda, UmRisha, and Hamra, revealed diverse bacterial communities. Nearly 40% of the detected sequences had less than 90% similarity with previously cultured microorganisms [55]. The populations differed between sediment and water samples; Firmicutes, Bacteroidetes, and Alphaproteobacteria dominated the sediment of all three lakes [55]. There was no single dominant group in the water samples; the Firmicutes and Alphaproteobacteria dominated the water of Lake Fazda, Bacteroidetes dominated the water of Lake UmRisha, and *Alpha-proteobacteria* dominated the water of Lake Hamra [55]. The archaea of the Halobacteriales were abundant in the water of Lakes Fazda and UmRisha, but were not present in the water of Lake Hamra, most likely reflecting the more dilute and oxygenated nature of this lake.

Clones related to the Firmicutes were mostly abundant in sediments of the sampled lakes and included members of the Clostridiales and Halanaerobiales. The majority of the Clostridiales clones were related to members of the genus *Alkaliphilus*, which are an abundant species in the sediment of alkaline and haloalkaline environments [56]. The *Halanaerobiales* clones were detected mostly in the sediments of Lakes Fazda and UmRisha. *Halanaerobiales* are an obligately anaerobic, fermentative, halophilic group abundant in the bottoms of soda lakes, hypersaline lakes, and solar salterns [57]. None of the clones were closely related to the *Natranaerobiales*, indicating that they are not prevalent in the environment.

Anoxygenic phototrophic bacteria of the Alpha- and Gamma-proteobacteria were detected in all three lakes, consistent with previous culture-dependent analyses. The majority of the Alphaproteobacterial

clones were related to the Rhodobacterales, and clustered with *Rhodobaca bogoriensis* and *Roseinatronobacter thiooxidans*, which were isolated from soda lakes in Kenya and Russia [58,59]. Consistent with the previous studies performed by Imhoff [20,24], most of the gamma-proteobacterial clones belonged to the Chromatiales, and clustered with the genera *Ectothiorhodospira* and *Halorhodospira*. Several clones clustered with *Thialkalivibrio* [55].

Sulfate-reducing bacteria were detected in the sediment of the lakes and were related to the Desulfovibrionales and Desulfobacterales. They were not detected in the water samples from Lakes Hamra and UmRisha. *Bacteroidetes* were abundant in the water and sediment of all lakes. Many of them were closely related to *Salinibacter ruber*, an extremely halophilic, red-pigmented bacterium isolated from a saltern crystallizer pond in Alicante, Spain [60]. Many clones formed a separate lineage within the *Bacteroidetes*, and were distantly related to a clone retrieved from hypersaline MonoLake, CA, USA [61]. The more oxygenated and dilute nature of Lake Hamra was reflected in a broader bacterial diversity, where clones related to the Spirocheates, Verrucomicrobiales, Chloroflexaceae, Cyanobacteria, and Actinobacteria were detected [55].

The diversity of the archaeal clones retrieved from Lakes Fazda and UmRisha was low compared to the bacterial diversity. Most of the clones clustered with the *Halobacteria*, and a small proportion clustered with the Methanosarcinales. A small number of clones were closely related (92%–96% identity) to *N. pharaonis*, indicating that *N. pharaonis* is not abundant in the environment. Most of the archaeal clones were not closely related to previously cultured species. There was some similarity to archaeal clones from a salt-crystallizing pond in Lake Magadi, Kenya [62]. All archaeal clones belonged to the Euryarchaeota. No clones affiliated with the Crenarchaeota, Korarchaeota, or Nanoarchaeota were detected [55].

10.3 Physiology of the halophilic alkaliphiles of the Wadi An Natrun

Microorganisms inhabiting the Wadi An Natrun lakes must cope with salt concentrations near saturation, alkaline pH values, high temperature, intense UV radiation as well as low water activity and anoxygenic conditions. All these extreme conditions pose physiological and bioenergetic problems and necessitate special adaptations.

10.3.1 Osmoadaptation

To maintain turgor pressure and to prevent cell shrinkage, halophiles must keep their cytoplasm hyperosmotic or at least isosmotic with their surroundings to prevent loss of water. Halophiles evolved two separate strategies for osmoadaptation. The salt-in strategy is where the overall ion concentration of the cytoplasm equals that of the environment. This is achieved by accumulating large concentrations of inorganic ions, mainly potassium and chloride in the cytoplasm. The salt-out strategy is where the microorganism accumulates osmoprotectants or compatible organic solutes in the cytoplasm [42,63].

The salt-in strategy necessitates that all the cell structural components and proteome and enzymes be adapted to molar concentrations of inorganic ions. Evolutionary modifications to make proteins salt-stable include the incorporation of acidic amino acids (aspartate and glutamate) into the surface of proteins, low content of surface hydrophobic amino acids, and a smaller protein core. The carboxylic groups of acidic amino acids sequester a tight network of hydrated K^+ and water molecules at the protein surface, thus maintaining protein structure and solubility [64]. Weaker hydrophobic interactions increase protein flexibility in an ionic environment because a weak hydrophobic core will not become rigid [65].

The salt-in strategy is commonly used by the halophilic archaea of the *Halobacteriales* and the fermentative anaerobes of the *Halanaerobiales* [66]. Consistent with this, analysis of the proteome of the archaeon *N. pharaonis* showed acidic cytoplasmic proteins with an average isoelectric point (pI) of 4.6. The proteome was also moderately hydrophobic. The genome of *N. pharaonis* contains several homologs for the Trk-type K^+-transport systems [46]. The light-driven chloride pump halorhodopsin transports chloride into the cell against the membrane potential [67]. The genomic sequence also had a homolog for a compatible solute transporter (tp58), but no homologs for genes for de novo synthesis of compatible solutes such as trehalose and glycine betaine were detected. There were also no homologs for osmolyte-binding proteins [46]. *N. pharaonis* was reported to produce the compatible solute 2-sulfotrehalose. The intracellular concentration of 2-sulfotrehalose increased with increasing concentrations of external NaCl, indicating that it functions as an osmoprotectant [68]. These data imply that *N. pharaonis* uses a combined salt-in and salt-out strategy for osmoadaptation.

The compatible solute glycine betaine was first discovered in *H. halochloris* [69]. The intracellular concentration of glycine betaine in *H.*

halochloris increased with increasing NaCl in the growth medium and reached approximately 10% of the cell dry weight at 24% NaCl [70].

The synthesis of glycine betaine occurs by methylation of glycine in three consecutive steps and produces sarcosine (monomethylglycine) and dimethylglycine as intermediates. This process is catalyzed by two enzymes with overlapping activities [71,72]. *H. halochloris* has two enzymes, glycine and sarcosine methyltransferase (GMT) which catalyzes the formation of mono- and dimethylglycine, and dimethylglycine methyltransferase (DMT) catalyzes the formation of dimethylglycine and glycine betaine (Table 10.2). The genome sequence of *H. halochloris* has a complete gene cluster for glycine betaine synthesis from glycine which includes, in addition to GMT and DMT, adenosylmethionine synthetase (MAT), adenosylhomocysteinase (SAHase), and a 5,10-methylene tetrahydrofolate reductase (MTHFR) (the GMT-DMT-MAT-SAHase-MTHFR cluster) [69].

H. halochloris can take up glycine betaine from the medium via a saturable active transport system driven by a light-powered electrochemical proton gradient [73]. The genome sequence of *H. halochloris* has several homologs for transport systems for compatible solutes. There are two copies of BetT, a high-affinity secondary transporter specific for choline and glycine betaine and OpuD, a secondary transporter for glycine betaine (Table 10.2) [69]. Having multiple osmolyte transporters is advantageous as it allows cells to reabsorb osmolytes that may have leaked out of the cells.

The compatible solute ectoine (1,4,5,6-tetrahydro-2-methyl-4-pyrimidinecarboxylic acid) was also first discovered in *H. halochloris* [74]. Ectoine was only accumulated in the cytoplasm under conditions of osmotic stress, and its intracellular concentration increased with increased extracellular NaCl. *H. halochloris* synthesizes ectoine from aspartate semialdehyde, an intermediate in amino acid metabolism. Aspartate semialdehyde is converted to L-2,4-diaminobutyric acid, then acetylated to Nγ-acetyldiaminobutyric acid, which is cyclized to form ectoine [75,76]. Ectoine synthesis requires three genes, *ectABC*. All three are present in the genome of *H. halochloris* (Table 10.2) [69]. The *ectA* gene encodes for diaminobutyric acid acetyltransferase, the *ectB* gene encodes for diaminobutyric acid aminotransferase, and *ectC* encodes for ectoine synthase [76].

The third compatible solute present in *H. halochloris* is trehalose. Trehalose is not a major compatible solute in *H. halochloris*, and is synthesized in cells in larger amounts only when they are grown under nitrogen-limiting conditions and ectoine synthesis is decreased [77].

Table 10.2 Genes of compatible solute synthesis and transport systems in genomes of halophiles isolated from the Wadi An Natrun.

Species	Ectoine biosynthesis	Glycine Betaine synthesis		Compatible solute transport			
		From glycine GMT-DMT	From choline *betAB*	*betT*	OpuA OpuD	proW1	Glycine betaine/ L-proline ABC transporters
Halorhodospira halochloris	*ectABC*	GMT-DMT-MAT-SAHase-MTHFR	–	betT (x2)	OpuD	–	–
Halorhodospira abdelmalekii	*ectABC*	GMT-DMT-MAT-SAHase-MTHFR	–	*betT*	OpuD (x2)	ProVWX	–
Halorhodospira halophila	*ectABC*	GMT-DMT-MAT-SAHase-MTHFR/ GMT-B	–	*betT* (x5)	OpuD	–	–
Ectiothiorhodospira haloalkaliphila	–	GMT-DMT-MAT/GMT-B	*betAB/proX*	*betT* (x2)	OpuA	–	–
Natranaerobius thermophilus	–	GMT-DMT	–	–	–	–	+ (x19)
Natranaerobius truerperi	–	–	–	–	–	–	+ (x14)

Trehalose-6-phosphate synthase was partially purified from *H. halochloris* and catalyzed the reaction between UDP-glucose and glucose-6-phosphate to form trehalose-6-phosphate. Trehalose-6-phosphate synthase lost activity at NaCl concentrations greater than 300 mM. Glycine betaine had a protective effect against NaCl-inhibition of the synthase [77]. Under low salinity, intracellular trehalose is degraded by trehalase. Trehalase is activated by betaine, indicating that trehalose is not a major compatible solute in *H. halochloris*, and that betaine is the preferred osmolyte [78].

The genome of *H. abdelmalekii* has the GMT-DMT-MAT-SAHase-MTHFR gene cluster for synthesis of glycine betaine from glycine, as well as the *ectABC* gene cluster for ectoine synthesis (Table 10.2) [69]. It also has several copies of the secondary betaine transporters OpuD, BetT and ProVWX.

H. halophila can also synthesize glycine betaine from glycine. Its genome has the GMT-DMT-MAT-SAHase-MTHFR/GMT-B cluster. The sequence for GMT in *H. halophila*, GMT-B, differs phylogenetically from that of *H. halochloris* and *H. abdelmalekii*. Its exact role is unknown. *H. halophila* also has five copies of the BetT transporter, one copy of the OpuD transporter, and the *ectABC* cluster for ectoine synthesis (Table 10.2) [69].

Among the *Ectothiorhodospira* spp., only *E. haloalkaliphila* has a sequenced genome. *E. haloalkaliphila* has homologs for the GMT-DMT-MAT cluster for glycine betaine synthesis. *E. haloalkaliphila* can also synthesize glycine betaine from choline. It has homologs for the *betAB/proX* cluster in its genome [69]. The gene *betA* encodes for choline dehydrogenase, *betB* encodes for betaine-aldehyde dehydrogenase, and *proX* encodes for a secondary betaine transporter [76]. The *E. haloalkaliphila* genome also has several copies of genes for the BetT and OpuA transport systems. Like other members of the *Ectothiorhodospira, E. haloalkaliphila* lacks the genetic ability to synthesize ectoine (Table 10.2) [69].

A. haloalkaliphilus took glycine betaine up from the culture medium when grown at high NaCl concentrations. It synthesized ectoine when grown in a mineral medium with 10% NaCl [30]. Key intracellular enzymes such as malate dehydrogenase and isocitrate dehydrogenase were inhibited by NaCl concentrations between 0.5 and 1 M, proving that *A. haloalkaliphilus* utilizes the salt-out strategy for osmoadaptation and does not accumulate large concentrations of inorganic ions [44].

It was previously assumed that anaerobic, fermentative halophiles do not synthesize compatible solutes, and utilize the salt-in strategy for

osmotic adaptation [57,64]. Genomic and physiological data from the chemoorganotroph *N. thermophilus* disagree with this presumption. When grown in 3.3 M of Na^+, *N. thermophilus* accumulated 293 mM of K^+ and 1.2 M Cl^- in its cytoplasm, not sufficient to osmotically balance extracellular Na^+. Physiological assays showed that *N. thermophilus* accumulated 400 mM of glycine betaine when grown in 3.3 M Na^+, pH 9.5 and 52°C, and this increased to 1 M glycine betaine when *N. thermophilus* was grown in 4.5 M Na^+ [42]. Intracellular glycine betaine content was affected only by changes in external Na^+ concentration. It was not altered by changes in external pH or temperature. The intracellular concentration of glutamate also increased with increased external Na^+ concentration, rising from 19 mM in the presence of 3.3 M Na^+ to 200 mM at 4.5 M Na^+. Genomic data confirmed physiological analyses. *N. thermophilus* has the genetic ability to synthesize glycine betaine. The homologs for GMT and DMT are present in the genome, as well as three genes encoding betaine/choline/carnitine transporters, four genes encoding glycine betaine/L-proline ABC transporters, and 15 genes encoding glycine betaine active transporters (Table 10.2) [43].

The genome sequence for *Natranaerobius trueperi* has similar features to that of *N. thermophilus*. *N. trueperi* has 14 homologs for genes for glycine betaine ABC transporters, three genes for sodium-proline symporters, one gene for a sodium-glutamate symporter, and six genes for sodium-alanine symporters. It also has two genes for sodium-solute symporters [79]. This means that *N. trueperi* accumulates compatible solutes and amino acids for osmoadaptation. The *N. trueperi* genome also has five genes for K^+ uptake systems. Taken together, these data indicate that *N. thermophilus* and *N. trueperi* utilize a combination of the salt-in and salt-out strategies for osmoadaptation [8].

10.3.2 Alkaline adaptation

Microorganisms inhabiting the Wadi An Natrun lakes must survive in alkaline pH values reaching pH 11. The major problem faced by alkaliphiles is the maintenance of a near-neutral cytoplasmic pH. Alkaliphilic microorganisms have developed several adaptive strategies to alkaline pH.

10.3.2.1 Alkaline adaptation in the cell wall and plasma membrane

The cell wall of alkaliphiles is essential for survival under alkaline stress. The protoplasts of alkaliphilic *Bacilli* are unstable in alkaline conditions [80]. Peptidoglycan hydrolysate from *N. thermophilus* and *N. trueperi* contained amino acids and no isomers of diaminopimelic acid. Peptidoglycan

hydrolysate of *N. wadinatrunensis* also did not contain isomers of diaminopimelic acid. It was of the α-4-β type [27,28]. A very small amount of peptidoglycan could be isolated from all three species, indicating the absence of peptidoglycan from their cell walls.

N. pharaonis does not have a typical S-layer like other archaea but forms a complex cell envelope consisting of varying glycosylated cell surface proteins which are glycosylated at threonine-rich tetrapeptide repeats [46].

Plasma membranes of alkaliphiles typically have a higher membrane lipid: membrane protein ratio and higher cardiolipin content. The fatty acid composition allows for a fluid membrane, with diverse branched-chain fatty acids, and saturated and unsaturated fatty acids [81].

The haloalkaliphilic *Thioalkalivibrio* spp., when grown at pH 10.5, have a large amount of anionic cardiolipin as well as polar lipids with unsaturated (C16:1, C18:1) and cyclopropane fatty acids (cyc-C19) in their plasma membrane [82]. Respiratory complexes in the plasma membrane require cardiolipin for activity and stabilization [83]. Cardiolipin also functions as a proton trap. Its anionic head group restricts the movement of protons, thus supplying them to the ATP synthase and facilitating oxidative phosphorylation [84].

The phospholipid fatty acid (PLFA) profile for the anaerobic *N. thermophilus, N. trueperi*, and *N. wadinatrunensis* was similar, and was dominated by polar fatty acids, neutral fatty acids, and iso-branched fatty acids. There was a small amount of anteiso-branched fatty acids. There were minor amounts of straight and branched monoenoic fatty acids. Cardiolipin was not reported. The PLFA of *N. thermophilus* did change in response to changing pH, indicating that it does not play a major role in alkaline adaptation [27,28,42]. The PLFA profile of *N. thermophilus* did show a unique pattern of branched dimethyl acetals. The role of dimethyl acetals in pH adaptation is unclear.

10.3.2.2 Membrane transport systems

Membrane transport systems of the haloalkaliphiles of the Wadi An Natrun are taxed with the job of maintaining optimal intracellular [Na^+] and [H^+] and water activity in salt- and alkaline-stressed cells. This is achieved by a repertoire of ion channels, primary and secondary transporters. Intracellular pH homeostasis in alkaliphiles is usually linked to Na^+ cycling, where cells expel excess intracellular Na^+ by secondary Na^+-expelling systems and Na^+/H^+ antiporters powered by either a proton or sodium motive force [81].

Energized cell suspensions of *N. thermophilus* showed that it acidified its cytoplasm, and maintained a ΔpH of 1 unit ($acid_{in}$) over the entire pH range for growth [85]. The genome of *N. thermophilus* contained 17 homologs for monovalent cation-proton antiporters (CPA). Cloning and heterologous expression of 12 of these homologs showed that eight of them were capable of $Na^+/H+$ antiport, and four were capable of K^+ uptake [85]. The functional antiporters belonged to different families, including CPA-1, CPA-2, and NhaC. All expressed Na^+/H^+ antiporters displayed electrogenic antiport, i.e., they exchanged a larger number of H^+ for every Na^+ molecule extruded, and thus, are capable of cytoplasmic acidification [85]. Seven of the expressed Na^+/H^+ antiporters also transported K^+. This is beneficial to *N. thermophilus*, which relies on Na^+-coupled transporters for solute uptake. *N. thermophilus* also has a Na^+-coupled F_1F_o-type ATPase that is geared in the hydrolysis direction. It expels Na^+ from the cell at the expense of ATP [86]. Being able to transport K^+ as well as Na^+ will avoid any possible competition for Na^+ between the ATPase and antiporters and will ensure continued cytoplasm acidification by the antiporters even in conditions of a decrease in cytoplasmic Na^+.

The Na^+/H^+ antiporters of *N. thermophilus* were active over a range of salinities and pH values. They were also constitutively expressed when *N. thermophilus* was exposed to both acid and alkaline stress. This indicates that the Na^+/H^+ antiporters of *N. thermophilus* all work together to extrude excess Na^+ from the cell and acidify the cytoplasm [85].

Similar to *N. thermophilus*, the genome of *N. trueperi* contained seven genes for NhaC type Na^+/H^+ antiporter, four genes for NhaP type $Na^+(K^+)/H^+$ antiporter, two genes for the Na^+/H^+ dicarboxylate symporter, and one gene for a CPA-2 Na^+/H^+ antiporter [79].

The genome sequence of the phototrophic *H. convoluta* has a homolog for an electrogenic NhaA type Na^+/H^+ antiporter. *H. convoluta* appears to utilize Na^+-coupled bioenergetics. It possesses several genes for Na^+-coupled symporters [87].

The genome of *N. pharaonis* has nine genes for Na^+/H^+ antiporters. The genome sequence also has genes for Na^+-coupled symporters and an H^+-coupled ATPase [46].

10.4 Biotechnological potential

Haloalkaliphiles produce numerous economically, biotechnologically, and medically relevant products, including extremozymes, compatible solutes,

and rhodopsin. Haloalkaliphiles can also be used in the bioremediation of saline waters.

10.4.1 Extremozymes

The Wadi An Natrun has been the source of several halophilic, alkaliphilic, and thermotolerant proteases, amylases, cellulases, lipases, and other enzymes with potential biotechnological applications.

10.4.1.1 Protease

Proteases are hydrolytic enzymes that cleave peptide bonds and degrade proteins into oligopeptides and amino acids. Proteases are among the most commercially relevant group of enzymes and have been extensively used in diverse industries including laundry detergents, leather tanning and dehairing, pharmaceuticals, food processing, and molecular biology [88].

Several protease-producing strains were isolated from mixed water–sediment samples of Lakes Fazda, UmRisha, and Hamra. Among these *Alkalibacillus* sp. NM-Fa4, isolated from Lake Fazda, produced an extracellular protease with maximal activity at pH 9.5, 1 M NaCl and 50°C–52°C. The protease, AbCP, was a cysteine protease. It was very robust and resisted the effects of reducing agents, oxidizing agents, anionic and nonionic surfactants, and the chemical denaturant urea. Consistent with being a halophilic enzyme, AbCP retained greater than 50% of its maximal activity in the presence of ethanol and methanol. It had a broad substrate utilization pattern and hydrolyzed both natural and synthetic substrates [89].

Another species, *Alkalibacillus* sp. NM-Da2, was isolated from a mixed water–sediment sample from Lake UmRisha. *Alkalibacillus* sp. NM-Da2 produced an extracellular protease. The protease was extreme in several aspects. It had maximal activity at 56°C, pH 9 and 2.7 M NaCl. It retained greater than 80% of its maximal activity after incubation at 55°C for 2 h, and after incubation at pH 10.5 for 30 min. The protease hydrolyzed complex proteinaceous substrates including tryptone, yeast extract, gelatin, casein, and peptone. As with most halophilic enzymes, it was stable in the presence of organic solvents and retained greater than 70% of maximal activity in the presence of isopropanol, benzene, and ethanol. Its activity was stimulated with isopropanol. The protease was resistant to the nonionic surfactant Tween 80 but was inactivated in the presence of other surfactants such as Tween 20 and sodium dodecyl sulfate. In a simulated wastewater treatment system, the protease degraded dissolved proteins, degrading 50% of total proteins after incubation for 5 h at 55°C [90].

A *B. haloalkaliphilus* strain NA7 was isolated from a root sample of a plant abundant in the Wadi An Natrun, *Helianthemum nummularium*. *B. haloalkaliphilus* strain NA7 produced an extracellular alkaline protease in shake culture. The protease was active at pH 9.5, 37°C and 1.5 M NaCl. The production of the protease by *B. haloalkaliphilus* strain NA7 was increased when the pH of the medium was 10 and NaCl concentration was 3 M [91].

The *Salipaludibacillus agaradhaerens* strain AK-R was isolated from the Wadi An Natrun lakes [92]. It produced an alkaline serine protease with maximal activity at pH 10, 0.4 M NaCl, and 60°C. The thermostability of the enzyme was improved in the presence of $CaCl_2$. The protease was robust, and resistant to reducing agents, organic solvents, and detergents [93]. The protease was immobilized onto mesoporous core-shell silica nanospheres. The immobilized protease had improved pH and thermal properties, with maximal activity at pH 10.5 and 65°C, and retaining stability for longer incubation times at 50 and 60°C. The immobilized enzyme also had greater salt stability, retaining greater than 80% of maximal activity at 3 M NaCl. The immobilized enzyme had great operational stability, retaining greater than 50% of initial activity after 15 hydrolytic cycles [94].

A haloalkaliphilic archaeon *Natrialba hulunberensis* strain WNHS14 was isolated from mixed water–soil samples from Lake Hamra. *N. hulunberensis* produced an extracellular serine protease with maximal activity at pH 10, 2 M NaCl, and 75°C. It was resistant to anionic and nonionic surfactants and inorganic ions [95].

10.4.1.2 Cellulase

Cellulase refers to three enzymatic activities, exoglucanase (1,4-β-d-glucan cellobiohydrolase), endoglucanase (1,4-β-d-glucan glucohydrolase), and β-glucosidase (β-d-glucoside glucohydrolase). Together, these enzymes catalyze the depolymerization of cellulose to glucose [96]. There are numerous applications for cellulases. They are used in the food, textile, and detergent industries. Cellulases are also essential for the degradation of lignocellulosic biomass for the production of biofuels.

Anaerobic cellulase enrichment cultures containing microcrystalline cellulose were made from lake sediments of the eight lakes of the Wadi An Natrun and soda soils surrounding the lakes [97]. Endocellulase activity was observed in only one soda soil sample, collected near Lake Khadra, and in all lake sediment samples. Endocellulase activity in all

samples was enhanced by the addition of sulfate. Genomic DNA libraries were constructed from these enrichment cultures, and clones were screened for cellulolytic activity. Among the over 70,000 clones screened, four clones from the lake sediment samples and 12 clones from the soda soil samples were positive for cellulolytic activity. Sequence analysis of the clones from the lake sediment samples showed a high identity to a glucanase from a gammaproteobacterium *Xanthomonas campestris* [97]. Clones from the soda soil samples were similar to an endoglucanase from a fibrobacterium, *Fibrobacter succinogenes*. The clones were not studied further.

A putative endoglucanase was cloned from the genome of *Akalilimnicola* sp. NM-DCM-1, a haloalkaliphile isolated from Lake Abo Dawood. The endoglucanase, En5H, was expressed and purified to homogeneity. En5H was halophilic, alkaliphilic, and thermophilic, with maximal activity at 2.5 M NaCl, pH 8.8, and 52°C–55°C [98]. Salt was essential for the activity of En5H. The enzyme had only 20% of maximal activity in the absence of NaCl. En5H is a β-1,4 linkage-specific cellulase, and it had β-glucosidase, endo- and exo- β-1,4-glucanase activities. En5H was resistant to reducing agents and chemical denaturants. Its activity was inhibited by ethylene diamine tetraacetic acid (EDTA), indicating that divalent cations are necessary for activity or enzyme structure. Consistent with being a halophilic enzyme, En5H was active in organic solvents and ionic liquids. En5H was capable of saccharification of ionic liquid-pretreated rice straw in an in situ system, reaching 40% saccharification after 24 h [98]. These data indicate that En5H can be part of an enzyme cocktail for the production of biofuels from lignocellulosic biomass.

A recombinant cellulase *cellSNSY* was identified and cloned from a metagenomic library constructed from soil samples collected from the Wadi An Natrun [99]. The enzyme was thermotolerant and alkaliphilic, with optimal activity at 45°C and pH 8.5. The enzyme was stable after freezing at −20°C for 8 weeks. It was stable in the presence of organic solvents, chelators, and inorganic ions [99].

10.4.1.3 Amylase and pullulanase

Amylases and pullulanases are carbohydrate-degrading enzymes. α-Amylase hydrolyzes internal α-1,4-glycosidic bonds in polysaccharides, producing maltose, glucose, and dextrins [100]. Pullulanase is a debranching enzyme, and hydrolyzes α-1,6-glycosidic bonds in pullulan, starch, amylopectin, glycogen, and other polysaccharides. Some types of pullulanases can also hydrolyze α-1,4-glycosidic bonds [101].

An extracellular halophilic, alkali- and thermostable amylopullulanase from *Amphibacillus* sp. NM-Ra2 was purified. *Amphibacillus* sp. NM-Ra2 was isolated from a mixed water–sediment sample from Lake UmRisha [102]. The amylopullulanase had maximal activity at pH 8, 1.9 M NaCl, and 54°C. It was resistant to enzyme inhibitors and detergents but was inactivated by EDTA indicating that divalent cations are important for activity and/or structure stability. The amylopullulanase had a broad substrate utilization spectrum and hydrolyzed linear and branched substrates [102].

Alkalilimnicola sp. NM-DCM-1 is also the source of a haloalkaliphilic amylase AmyD8 and haloalkalithermophilic amylopullulanase PulD7 [103,104]. AmyD8 was cloned, expressed, and purified. AmyD8 was extreme in several aspects, it had maximal activity at 2.4 M NaCl, pH 10.5, and 55°C [103]. AmyD8 hydrolyzed both linear and branched substrates and was stable in anionic and nonionic surfactants and organic solvents. AmyD8 was physically entrapped in an agar-agar matrix. The entrapment did not affect AmyD8's extreme properties and enhanced its thermostability. The entrapped AmyD8 had excellent recyclability. It retained greater than 50% of its maximal activity after 16 hydrolysis cycles [103].

Recombinant amylopullulanase PulD7 had maximal activity at 2 M NaCl, pH 9.5, and 55°C. PulD7 had excellent thermal stability, with a half-life of 693 min at 50°C. It hydrolyzed both α-1,4- and α-1,6-glycosidic bonds, and was resistant to organic solvents, surfactants, reducing agents, and chelators. PulD7 was capable of binding to raw starch granules, giving it potential for application in starch saccharification [104].

10.4.1.4 Lipase

Lipases hydrolyze ester bonds in glycerides producing glycerol, fatty acids, and partial glycerides. Lipases prefer long-chain acyl glycerides. There are many applications for lipases. They are used by the detergent, pharmaceutical, fragrance, fuel, and food industries [105].

A haloalkaliphilic lipase LipR2 was cloned from the genome of *Alkalispirillum* sp. NM-ROO2, which was isolated from a water–sediment sample from Lake UmRisha [106]. LipR2 had maximal activity at 1.9 M NaCl, pH 9.3, and 52°C, and was resistant to organic solvents and surfactants. Consistent with being a lipase, LipR2 preferred esters with long-chain fatty acids as substrates. LipR2 was covalently immobilized on Florisil nanoparticles. The immobilization enhanced LipR2's thermostability. The immobilized

LipR2 was an effective biocatalyst for the esterification of levulinic acid with fatty acids [106]. Levulinic acid esters are applicable in the areas of fragrances, flavorings, and pharmaceutical synthesis. This gives LipR2 the potential for application in chemical synthesis.

An alkalithermophilic lipase LipWN1 was produced by *Streptomyces* sp. strain SBLWN_MH2, which was isolated from the shore soil of Wadi An Natrun lakes [107]. The lipase was extremely alkaliphilic and thermophilic, with maximal activity at pH 10.7 and 60°C, and retaining over 90% of maximal activity at pH 11.5 and 70°C. The activity of LipWN1 was enhanced in the presence of NaCl, $MgCl_2$, and $CaCl_2$, and was inhibited in the presence of EDTA. LipWN1 was resistant to organic solvents [107].

10.4.2 Compatible solutes

Compatible solutes from halophiles have diverse biotechnological applications. They can be used in therapeutics, cosmeceuticals, cryoprotectants, and as stabilizers in molecular biology applications.

10.4.2.1 Compatible solutes in therapeutics and cosmeceuticals

Ectoine is a zwitterionic molecule and protects against dehydration by interacting with water instead of directly binding with macromolecules. This is termed the "preferential exclusion model." Ectoine is excluded from the external hydration shells of proteins and stabilizes proteins and membranes by altering hydrogen bond strength between ectoine and surrounding water molecules; it forms a water shell around macromolecules [108]. When applied externally, ectoine stabilizes membranes and hydrates the surface of the tissue treated. Ectoine has the potential to reduce inflammation and has been tested for the treatment of numerous inflammatory conditions such as atopic dermatitis, allergic rhinitis, acute pharyngitis, and chronic obstructive pulmonary disease. Ectoine is used in externally applied products such as nasal spray, eye drops, and skin creams [109–114]. The topical application of ectoine in an oil/water emulsion is as an effective and long-term moisturizer, preventing transepidermal water loss, and protecting the cell membrane from the damage caused by surfactants [108]. An ectoine mouthwash is effective in the treatment of oral mucositis developed as a result of chemotherapy, and patients reported the ectoine mouthwash to be more tolerable than a calcium phosphate mouthwash [115]. The addition of ectoine to a skin cleanser decreased surfactant-related cytotoxicity and skin irritation. These results were

attributed to the ability of ectoine to accumulate in cells without interfering with any cellular processes, the osmoprotective role of ectoine, and its antioxidant effect [116].

Topically applied ectoine had an immunoprotective role in sun-exposed skin of healthy individuals; pretreatment with ectoine before sun exposure minimized ultraviolet (UV)-induced reduction in epidermal dendritic Langerhans cells [117]. Ectoine has superoxide anion-quenching properties and can prevent UV-induced oxidative damage to the skin [108]. Ectoine was also reported to protect DNA from ionizing radiation. It does this by free radical scavenging and displacement of water molecules surrounding DNA [118].

Betaine is an ingredient in moisturizing and antiaging creams. It is nontoxic, nonirritant, and hypoallergenic and is present in several commercially available creams [119,120]. Betaine has been reported to have beneficial effects on metabolic syndrome, lung cancer, and Alzheimer's disease. Betaine inhibited the growth of prostate cancer cells by enhancing oxidative stress-induced apoptosis [121].

10.4.2.2 Compatible solutes as cryoprotectants

Betaine was superior to serum albumin and trehalose/dextran as a cryoprotectant during the lyophilization of bacteria and was better than other treatments for the preservation of long-term viability. Betaine matched glycerol's efficacy in liquid nitrogen freezing of halophilic archaea [76]. Betaine was also effective in cryopreservation of three cancer cell types using an ultrarapid freezing protocol; the cells had excellent postthaw survival efficiency and betaine had very little cytotoxicity even after long-term exposure [122]. Betaine combined with disaccharides and/or amino acids was effective in the cryopreservation of red blood cells and could be used directly on whole blood without separation. The osmotic regulation ability of betaine allowed a quick, single-step cryoprotectant removal process, and holds potential for improved long-term storage of red blood cells [123].

10.4.2.3 Compatible solutes in molecular biology

Betaine and ectoine outperform other enhancers in polymerase chain reaction (PCR) amplification of GC-rich DNA templates with high melting temperatures. Ectoine in particular is very effective and works by reducing the DNA melting temperature [124].

Hereditary diseases are diagnosed by multiplex PCR, where several alleles in a given locus are amplified simultaneously. When included in multiplex PCR reactions, betaine decreased the amplification of nonspecific products. Being a denaturant, it decreased the stability of mismatches at the 3'—end of allele-specific primers, thus reducing the chance of misextension by the polymerase. Betaine reduced primer hair loop formation and mishybridization. It prevented the preferred amplification of low-GC regions in the DNA. This leads to balanced amplification, which is critical for the success of any multiplex PCR [125,126].

10.4.3 Halorhodopsin

Optogenetics uses genetically encoded proteins, particularly opsin, to control the activity of target cells with light. It is a noninvasive technique used to study brain circuits on multiple scales through manipulation of neuronal activity [127]. Optogenetics has applications in drug targeting and therapeutics. Opsins are proteins which are light-sensitive because they are covalently bound to a chromophore, namely retinal. The retinal—opsin complex is called rhodopsin. Rhodopsin consists of seven transmembrane proteins and is present in bacteria, archaea, and eukaryotes. In prokaryotes, fungi, and algae, rhodopsin participates in phototaxis and energy development. In higher eukaryotes, rhodopsin is responsible for vision [128].

Halorhodopsin from *N. pharaonis* is an electrogenic ion pump that transports Cl^-, as well as I^-, Br^-, NO_3^- and SCN^- into the cell against the membrane potential. Ion transport is powered by light [129]. Halorhodopsin was the first archaeal protein to be applied in neuroscience research. Heterologously expressed halorhodopsin from *N. pharaonis* (*Np*HR) functioned in metazoan neurons in vivo and blocked hypercellular activity and action potential by polarizing neurons with inward Cl^- currents. In response to yellow light, inactivation allowed steady, steplight currents for several minutes [130]. Parkinson's disease occurs due to inhibitory/excitatory imbalances in the basal ganglia circuits. Oncogenetic therapies can target neuronal populations at the basal ganglia level. *Np*HR loaded onto an adenovirus led to optical inhibition in the subthalamic nucleus in hemiparkinsonian rats, which caused improvement in forelimb akinesia. This means that *Np*HR-mediated inactivation in the subthalamic nucleus can reduce the firing pattern of output nuclei in the basal ganglia causing an improvement in motor functions in Parkinson's disease [127,131].

Retinitis pigmentosa is a genetic disease characterized by degeneration of photoreceptor cells in the retina. Rods degenerate first, followed by the cone outer segments, then the cones, resulting in insensitivity to light and vision loss. The expression of enhanced *Nt*pHR in cones restored light sensitivity in mouse models of retinitis pigmentosa [132]. A lentivirus construct expressing enhanced *Nt*pHR under control of the human arrestin promoter reactivated degenerated cones in postmortem human retinas that had lost their outer segments and light sensitivity [133]. These studies indicate that halorhodopsin can potentially be used for the treatment of retinitis pigmentosa in humans.

10.4.4 Bioremediation

Hexavalent chromate is common in effluents from several industries including leather tanning, textiles, and electroplating, among others [134]. *Bacillus* sp. KSUCr5 isolated from water–soil samples from the Wadi An Natrun detoxified hexavalent chromate under saline and alkaline conditions and reached 100% chromate reduction within 72 h [135]. The reduction could occur over NaCl concentrations 0–3 M, and maximal reduction occurred under alkaline conditions, pH 10. Chromate reduction by *Bacillus* sp. KSUCr5 was not affected by the presence of other heavy metals including nickel, molybdenum, copper, and manganese [135]. Similar chromate reduction abilities were reported for *Bacillus* sp. KSUCr9a which was also isolated from the Wadi An Natrun. It was also able to reduce chromate completely over NaCl concentrations 0–3 M and at pH 9 [136]. *Amphibacillus* sp. KSUCr3 was also able to reduce hexavalent chromate, but under milder conditions, 0.3 M NaCl and pH 9.5 [137].

Alcanivorax sp. HA03, isolated from soil samples from the Wadi An Natrun, degraded benzene, chlorobenzene, and toluene under saline conditions. It degraded 20 μmol of either benzene, toluene, or chlorobenzene at 0.5 M NaCl, and was able to degrade benzene at 2.3 M NaCl [138], giving it the potential to be a component of an enzyme cocktail for bioremediation of hydrocarbon-contaminated saline water.

10.5 Preservation of the ecosystem of the Wadi An Natrun

Since ancient times, the soda lakes of the Wadi An Natrun have been exploited for trona, which was used by ancient Egyptians as embalming and desiccating agents for mummification [9]. Ancient texts also

documented the use of natron as a cleaning agent, which is consistent with the ability of sodium carbonate to break down grease and fats [4]. A letter dating back to the time of Ramesses II, approximately 1250 BCE, features a washerman in the village of Deir El Medina describing his need for natron for his work in the cleaning of textiles [139]. Ancient reports also describe the use of natron as a desiccant in the preservation of meat and the cooking of radishes [4,140]. Natron was also used in the manufacture of glass, and there is evidence of the presence of glass-making factories before the first century AD near several lakes of the Wadi An Natrun [141,142]. In the modern day, exploitation of the Wadi An Natrun lakes has decreased significantly, but they are still used for the extraction of sodium carbonate, calcium, and magnesium salts [6].

Anthropogenic activities such as agriculture and extraction of minerals can cause physical and chemical changes in hypersaline systems [143]. Continuous degradation and loss of hypersaline environments will undoubtedly lead to a loss in taxonomic and functional diversity. Thus, hypersaline environments need conservation.

Data on the alteration of the ecosystem of the Wadi An Natrun lakes are scarce. It has been reported that extensive agricultural activity in the lands surrounding the soda lakes of the Wadi An Natrun has led to increased extraction of groundwater from the Pleistocene aquifer, the major source of drainage water to the Wadi [144]. Extraction of groundwater occurred more than aquifer recharge, which led to a fall in the water table and salinization [145]. It is also projected that evapotranspiration, which is a combination of evaporation of water from the land and transpiration of water from the stomata of plants, will increase by more than 9% by 2025 due to climate change, which will further impact the groundwater supply to the Wadi An Natrun [146]. This will cause salinization of the source water to the Wadi An Natrun lakes, which may affect biogeochemical cycling and taxonomic diversity. Thus, green economic models are needed to address the effects of groundwater depletion and preserve the ecosystem of the Wadi.

Several policies and conservation measures have been suggested to address groundwater depletion in the Wadi An Natrun. These include piping water from the River Nile, recycling wastewater, recharging the Pleistocene aquifer artificially, more efficient irrigation methods, and desalination [147]. However, the efficacy of these measures has not been evaluated. Several green economic strategies were proposed to reduce groundwater degradation. The most effective of these strategies was

optimized irrigation and crop rotation [147]. However, climate change is a constant uncertainty, and it is unknown how the ecosystem will cope with this change.

10.6 Conclusions

The alkaline, hypersaline lakes of the Wadi An Natrun have been studied sporadically by scientists for over two centuries, and have been the source of major discoveries. *N. pharaonis* has been a model organism for the study of the retinal pigment halorhodopsin for over 20 years. The compatible solutes ectoine and glycine betaine were first discovered in *H. halochloris*. The polyextremophiles of the *Natranaerobiales* represent the first examples of microorganisms combining more than two extreme properties, and present models for studying the bioenergetic, metabolic, and physiological mechanisms for concomitant adaptation to multiple extreme conditions.

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CHAPTER 11

Phytoplankton ecosystem dynamics and seasonal changes in African Lakes: the case of Lake Victoria

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11.1 Introduction

Africa is the Mother Continent because it is the oldest inhabited continent on Earth and is the second largest one after Asia, bounded by the blue built of the Mediterranean Sea, the Red Sea, the Indian Ocean, and the Atlantic Ocean. It is divided in half almost equally via the Equator. According to the World Lake database (https://wldb.ilec.or.jp/), Africa has 677 lakes, of which 88 are listed as principal lakes. Some are natural and the others are artificial lakes. These lakes are distributed in various African countries, where most of them are in eastern Africa. Lake Victoria or Victoria Nyanza is in a shallow depression between two ridges bordered by the western and eastern rifts. Lake Victoria has a mean depth of 40 m with a surface area of 68,800 km^2 [1].

11.2 The importance of the African Great Lakes

The African lakes and their basins are important sources of fish which have been the main sources of food. Some of these lakes have species of fish faunas of great interest to science. Uganda ranks as one of the world's largest producers of freshwater fish. Small lakes and basins are more productive for commercial fisheries than large lakes. So, the lakes have an extensive array of fishes of economic and ecological importance. The lakes supply water for exploitation opportunities in aquaculture, hydropower generation, transportation, urban and industrial development, recreation,

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mining, oil exploitation, an irrigation source for agriculture, and domestic use. The favorable conditions along the lake shores have been one of the positive factors that attract large numbers of visitors in which tourism is a leading contributor to national economies and strengthens the economy of these countries. The lakes also positively influence the water quality of downstream watercourses and groundwater and preserve biodiversity and habitat [2].

11.3 Climate changes and African Lake water

The most important effects of climate change on African lakes are changes in the hydrological cycle, such as increasing temperature and decreasing rainfall [3]. Increasing temperatures, reducing precipitation, and less windy conditions can decrease lake levels, alter the nutrient balance and, in turn, increase pollution concentrations in Lake Tanganyika [4]. Climate warming has lost 90% of the lake water via evaporation [5] and may cause a change in the physicochemical properties of the water, consequently leading to reduced phytoplankton biomass and production.

11.4 Phytoplankton production in African lakes

Phytoplankton production is an essential parameter for perceiving aquatic ecosystems' shape and tropic degree [6]. The African lakes showed significant attain in phytoplankton production, suggesting their trophic state. Lake Kainji is an ordinary model of an African oligotrophic lake with biomass production of 0.3 g Carbon/m^2/h (g/Cm^2/h) [7]. Lake Nasser exhibited high phytoplankton production (eutrophic), with an average of 4.48 g/Cm^2/h [8]. Lake Chivero is a clear example of outburst primary production levels, which increased by over 10 times in magnitude from 1.64 to 6.03 g/Cm^2/h in 1979 to 18.5 g/Cm^2/h to a g/Cm^2/h in 2003 [9]. In deeper lakes, nutrient inflow exerts significant effects on primary production. In Lake Malawi, the levels of primary production have increased from the values of 0.24 and 1.14 g/Cm^2/h to reach the values of 14.04 g/Cm^2/h 26.20 g/Cm^2/h [10]. Also, the primary production in Lake Victoria has increased from 3.30 to 13.50 g/Cm^2/h to reach a value of 234 g/Cm^2/h [11]. Meanwhile, the primary production in Lake Kivu has increased from the levels of 0.85 and 2.2 g/Cm^2/h [1] to reach the levels of 9.332 and 18.14 g/Cm^2/h [12].

Light is the most important factor for phytoplankton growth and surface light is moderately steady and most of the lakes are straightforward, but low mean light conditions would possibly appear through the most excessive flow because of the great depth of the mixed layer [1]. Stratification negatively affects primary production by limiting nutrient supplements to deeper waters behind the euphotic zone [13]. It usually occurs during high summer temperatures because of thermal fluctuations between the warm upper layer (epilimnion) and the lower cold layer (hypolimnion).

The seasonal pattern of thermal stratification in the African lakes incorporates a brief time of limited vertical blending, which is joined by a peak of algal production to which diatoms make a significant commitment, and a subsequent peak dominated by Cyanobacteria often develops after re-stratification [14]. A comparable example is found in other African lakes, such as Lake Victoria, where Cyanobacteria dominate during summer stratification and diatoms tend to typically dominate in winter at turnover when stratification breaks down [1]. Chemical factors such as nitrogen (N) and phosphorous (P) have been classified as the most important nutrients affecting the phytoplankton's primary productivity in tropical African lakes [15].

11.4.1 Phytoplankton abundances in the African Lakes

Phytoplankton abundances and community structure have well-established seasonal variations in most African lakes and are governed mainly by climate and nutrient status. The Chlorophyceae dominated between 21°C and 23°C [16], and the increase in water temperatures (>25°C) due to global warming led to shifting in phytoplankton succession from diatoms to Chlorophyceae to the predominance of Cyanobacteria [17], which affect the zooplankton production and consequently fish stocks.

In the oligotrophic, Lakes Edward, Kivu, Malawi, and Tanganyika, fundamental algal groups have low phytoplankton biomass and species range [1]. During the rainy season, the blue-green algae (*Cylindrospermopsis*, *Anabaena*, *Pseudoanabaena*) dominate the phytoplankton, and biomass reaches its peak (up to 1.52 mg chlorophyll-*a* [Chl-*a*/L]), but the community dominates during the dry season with diatoms [17]. Lake Kivu, which place it in an intermediate position between the oligotrophic lakes Tanganyika and Malawi and the more eutrophic Lake Victoria, with

predominant *Fragilaria danica*, *Nitzschia bacata*, and *Urosolenia* sp. [18]. Many African lakes (e.g., Chivero and Victoria**)** are subjected to a huge amount of nutrients coming from increasing anthropogenic practices and have caused eutrophication, where N concentrations reached over 50 mg^{-1}. In many lakes, nitrogen-fixing genus such as *Anabaena* and *Cylindrospermum* is overwhelming because nitrogen is a limiting nutrient for different phytoplankton species [14,19,20].

11.4.2 Lake Victoria: the largest African Lake

Lake Victoria is a part of the Nile River Basin and lies between the western and eastern branches of the rift valley system [21] at an altitude of 1134 m above sea level [22], and lies between latitudes 0°20′N and 3° 00′S and longitudes 31°40′E and 34°55′E (Fig. 11.1).

Lake Victoria is considered the source of the Nile River in northern Sudan and Egypt and is divided into three countries: Kenya (6%), Uganda (43%), and Tanzania (51%). In terms of the surface area (68,800 km^2), it is the second largest freshwater lake in the world, after Lake Superior in North America [23]. The mean depth of Lake Victoria is 40 m with a maximum depth between 80 and 84 m, a shoreline of 3450 k, and a catchment area (drainage basin) that covers 183,000 km^2 and stretches out

Figure 11.1 Lake Victoria, bordering countries, and the entire catchment area, including major towns found within the catchment area including major towns found within the catchment area [22].

into Rwanda, Burundi, Uganda, Kenya, and Tanzania. The lake is fed by 23 rivers, of which Kagera and Katongaare the largest, and drained completely through the Nile River close to Jinja, Uganda (the lake's northern shore). The water degree in Lake Victoria rose to 13.42 m (May 2020), outperforming the 13.41-meter level recorded in 1964 (source: https://storymaps.arcgis.com/stories/bd820937c06845faa86f7f8944d56f47).

Lake Victoria is characterized by two main environments: an inshore area with shallow semienclosed bays and gulfs with no stratification and an offshore area with open lake waters with stratification [24]. Thus, the lake showed a marked difference in the biotic and abiotic characteristics between the two types of environments [25,26].

11.4.3 Environmental characteristics in Lake Victoria

The environment of the Lake Victoria basin is described using two wonderful seasons: a dry season from July to September and two wet seasons, which include mild rain from October to December and heavy rains from March to May with moderate stratification [27]. The changes in the environmental factors have been shown to directly affect phytoplankton species composition, numerical abundance, spatial distribution, and total biomass [28]. These factors are illumination per cell, temperature, nutrient availability, alkalinity, and mixing depth. Also, the different nutrients are likely to be limited to phytoplankton structure and growth rates among species [29], and consequently, exceptional species can continue to exist on nutrient concentrations, and others compete for the same nutrients [30].

In the mid-1980s, Lake Victoria experienced extreme eutrophication [30], resulting from excessive nutrient loading from agricultural and industrial development besides urban expansion. These are considered major factors causing phytoplankton blooming, with a fourfold and eightfold increase in the Chl-*a* values in inshore and offshore lake waters [28]. Recent changes in the hydrological system of the lake are becoming a great concern for many scientists because the lake has already been experiencing abnormal fluctuations in its unique system. Several studies about the impact of physical and chemical properties of Lake Victoria, inshore and offshore areas, are presented in several tables found in the text.

Water temperatures in Lake Victoria changed in a narrow range throughout the years [31]. From 1973 to 1974, surface and deep-water temperatures increased from 22°C during the cool, dry season to 26°C in

the hot, rainy season [32]. Meanwhile, the mean temperature during 2005–08 was 24.89°C ± 1.02°C in inshore waters and 24.20° C ± 0.37°C in offshore waters, and the value increased to 26.26° C ± 0.82°C in 2009 [33]. The Secchi depth values were inversely related to turbidity and significantly lower inshore than offshore waters. They ranged between 0.95 and 1.9 m in inshore and 1.1 and 3.4 m in offshore waters [34]. Generally, the water conductivity was higher in littoral waters (109.69–123.29 μS/cm) than in pelagic waters (91.53–97.72 μS/cm) [31]. The higher conductivity in littoral waters can be credited to the impact of land inflow through streams and surface run-off (Table 11.1).

In the inshore waters, the dissolved oxygen (DO) was 6.34 ± 2.31 mg/L in 2005s and increased to 7.92 ± 4.20 mg/L in 2007s and was 7.69 ± 0.74 mg/L in 2014s [33]. The same trend was observed in waters > 40 m. It was 4.36 ± 0.71 mg/L (2005s) and increased to 4.95 ± 1.48 mg/L (2014s). During 2000–2001, the DO was 3.2 times higher in the surface layer than the deep one, but this had diminished to only 1.2 times higher in 2005–2008. This means that the differences between DO in the surface layer and deep water diminished and the DO in deep waters increased dramatically from 2.55 mg/L (2000–2001) to 6.15 mg/L (2005–2009) [30]. Between 2000 and 2005, the DO was 6.52 mg/L in the littoral waters, increased to 6.77 mg/L, and decreased to 4.2–5.7 mg/L in depth <20 m [31]. Between 2002 and 2004s, the DO fluctuated between 8.02 ± 0.73 mg/L(surface waters) and 3.2 ± 4.36 mg/L (bottom waters), while in the littoral waters, it raised from 8.4 ± 1.2 to 10.0 ± 0.9 mg/L [33]. Noticeable differences were observed during 2005–2008 between inshore and offshore waters, where the DO values varied between 6.97 ± 0.57 mg/L and 5.80 ± 0.72 mg/L, respectively,

Table 11.1 Physicochemical characteristics of water in selected bays and gulfs in Lake Victoria, Tanzania, during 2002 [23].

Parameter	Range
Secchi depth m	0.7–2.4
Temp. (°C)	24.6–25.8
Dissolved oxygen mg/L	4.4–8.9
Silicates mg/L	1.0–10.8
Nitrites μg/L	0.7–35.9
Conductivity EC μS/cm	94.2–110.5
Ammonium NH4 μg/L	89.5–260.4

and decreased to 0.28 mg/L in the bottom of the offshore water [35]. Hypoxia which occurred only in deep waters in the 1980s, is now more frequent and is spreading into shallow [36].

11.4.4 Nutrient salts

Concentrations of nutrient salts in Lake Victoria have changed significantly over the past years. The levels of soluble reactive silica (SRSi) decreased from a mean of 1.961 mg/L in 1960–61s [37] to a mean of 0.71 ± 0.24 mg/L (range of 0.2 ± 0.0 to 1.1 ± 0.1 mg/L) for inshore waters and 0.86 ± 0.44 mg/L (range of 0.2 ± 0.1 to 1.7 ± 0.2 mg/L) for offshore waters during 2005–08 [35] and ranged between 0.79 ± 0.29 mg/L in the surface waters and 1.17 ± 0.68 mg/L in the bottom waters during the same period. As SRSi decreased 5–20-fold compared to the 1960s and 1970s, nitrate-nitrogen (NO_3-N) and soluble reactive phosphorus (SRP) increased during the same period [33]. SRP and nitrate ranged between 36 and 127 μg/L and between35 and 726 μg/L during 2002s [34]. Also, it was relatively low in the inshore waters (60.1 ± 4.6–200.6 ± 29.9 μg/L) compared to the offshore waters (100.4 ± 13.9–201.5 ± 46.3 μg/L) [35]. In contrast to SRP and NO_3-N, the ammonium concentrations were significantly higher in the pelagic waters (12.6–54.5 μg/L) than inshore (0.4–11.6 μg/L) [34].

The concentrations of total phosphorus (TP) were about twice as high as in 1960; [35] registered 43.9 ± 7.7 to 224.3 ± 29.3 μg/L in the inshore waters and 65.6 ± 15.9 to 184.0 ± 38.9 μg/L in the offshore waters during 2005–08 (Table 11.2). Correspondingly, the concentration of total nitrogen (TN) was higher in the inshore waters (range: 563 ± 60 to 1655 ± 229 μg/L) than in the offshore waters (range: 274 ± 44 to 932 ± 123 μg/L) during 2005–08 [35]. The littoral zone has high TN, TP, and SRP concentrations, chlorophyll, and organic matter than the pelagic zone. The process of N fixation occurs in the shallow littoral zone allowing Cyanobacteria to grow and phytoplankton biomasses and chlorophyll increase greatly [38].

11.4.5 Case studies on environmental changes in Lake Victoria

Kishe [23] studied the physicochemical characteristics of water in selected bays and gulfs (Tanzania part) in Lake Victoria in 2002. The results showed that temperature and conductivity were homogeneous among the

Table 11.2 Ranges and means of physical and chemical conditions in Lake Victoria in the littoral, pelagic, and pelagic deep zones between 2000 and 2005 [31].

Parameters	Littoral zone		Pelagic zone (<20 m)		Pelagic deep zone (>20 m)
	Range	Mean	Range	Mean	
Temp. °C	24.16–26.37	25.36	24.63–25.39	24.6	24.4–24.8
Dissolved oxygen mg/L	6.01–7.08	6.52	6.64–7.00	6.77	4.2–5.7
Electrical conductivity EC μS/cm	109.69–123.29	116.72	91.53–97.72	92.7	90.8–94.5
pH	8.08–8.53	8.33	7.26–8.43	7.55	7.3–7.8
Secchi depth m	1.15–1.49	1.26	2.69–3.39	-	-
Total Nitrogen mg/L	0.90–1.72	1.23	0.53–1.39	0.899	033–1.39
Nitrate NO_3 μg/L	33–85	66	10–52	63	9–102
Total Phosphorus μg/L	103–194	156	108–214	168	108–214
PO_4-P μg/L	57–89	71	58–72	63	66–93
Dissolved Si mg/L	2.12–3.07	2.62	0.67–1.27	1.337	1.00–1.69
Alkalinity mg/L	48.12–52.33	50.54	45.97–48.71	47.284	45.96–48.71
Chlorophyll-*a* μg/L	20–40	30	7–90	6	4–9

studied bays and gulfs. Concentrations of dissolved oxygen ranged from 4 to 9 mg/L with significant differences between locations. Secchi depth was < 2 m. Ammonium, TP, and SRSi concentrations were high at bottom waters, and the reverse was true for nitrate and nitrite. The differences in nutrients and physical parameters among bays and gulfs were noticed, where temperature and nutrient levels were higher in the studied areas than 15 years ago, and the trend reversed for DO and transparency.

Ssanyu and Schagerl [39] studied the physicochemical characteristics of two wetlands (Gaba and Walukuba) situated within the Lake Victoria basin, Uganda. The water temperature fluctuated from 23.47°C to 27.17°C, pH value (7.95–9.14), and dissolved oxygen (3.63 to 6.95 mg/L) for both sites. Water turbidity levels were lower in the Walukuba ponds than in the Gaba ponds. The nutrient salts ranged between the Gaba and Walukuba ponds as follows: NO_3-N ranging between 0 and 500 μg/L and nitrite–nitrogen (NO_2–N) (0 and 330 μg/L), and SRSi concentration (12.9–54.1 mg/L) and SRP ranged from 15 to 318 μg/L (Walukuba ponds) and 12 to 143 μg (Gaba ponds). Water temperature exceeded 23°C with a mean of 26.2 (± 1.0)°C in the inner bay and 25.7 (± 1.1)°C in the outer bay. The water in the bay was well-oxygenated. Water transparency was, on average, 0.8 m. The mean TP was 91 ± 27.8 μg/L (inner bay) and 65 ± 22.5 μg/L (outer bay). The mean of SRP was 33.5 ± 19.8 μg/L and 19.6 ± 12.6 μg/L and the mean concentration of silicon (Si) was 0.9 ± 0.6 and 0.370 mg/L. However, there were low concentrations of NO_3-N in the Murchison Bay (<10 μg/L) with an average of 39 ± 75 μg/L and 8.6 ± 9.0 μg/L, the TN was high with a mean of 1127 ± 253 μg/L (inner bay) and 806 ± 194 μg/L (outer bay).

In the Napoleon Gulf, PO_4 was 3–7 μg/L [40] and 18.2 μg/L [26]. A slight increase in the TP was observed from 44 to 76 μg/L [40], but according to Olokotum et al. [26], it was 39.8, max TP = 164 μg/L.

The Nyanza Gulf is a semienclosed gulf (1400 km^2, mean depth 7–30 m) situated within the Lake Victoria basin, Kenya. The water quality in the gulf has extensively decreased over the years because of the high yearly inflow of nutrients from the land and the atmosphere, and noticeable differences were recorded between offshore and inshore waters. Unlike nitrogen and phosphorus, which have been increased, Si has decreased [41,42].

A recent study was performed by Mwirigi et al. [31] on Lake Victoria's physical and chemical conditions between 2000 and 2005 and was undertaken in Kenyan, Ugandan, and Tanzanian waters and extended

over 6 years from 2000 to 2005. The study area was classified into three zones: littoral zone (0–20 m deep and <5 km from the shoreline), pelagic zone (<20 m deep and is 5 km beyond the shoreline), and deep pelagic zone (>20 m deep). The physicochemical water characteristics indicated strong differences between the littoral and pelagic zones and between the surface pelagic and deep pelagic zones. The littoral zone showed higher values of each temperature, pH, turbidities, and electrical conductivity, but a drastic reduction in water transparency occurred. Ngupula et al. [35] made sure of the same note during the period 2005–2008 about the reducing trend in the direction of the offshore sites for almost all the parameters, except for Secchi transparency and NO_3, which elevated toward the offshore water. Low Secchi depths, high pH, and high turbidities may be governed by the higher phytoplankton abundances in the little oral zone compared to the pelagic one.

11.4.6 Chl-*a* content and primary productivity of phytoplankton in Lake Victoria

Chl-*a* concentrations in Lake Victoria have increased since the 1960s, which means that they are highly affected by eutrophication, especially in the area near the lakeshore (e.g., Nyanza Gulf, Murchison Bay, Napoleon Gulf, Mwanza). The data reported by Mugidde [11] indicated that Chl-*a* concentration in 1960–61s was low (maximum of 5.5 μg/L) in offshore and inshore waters and rose to reach mean values of 60 and 40 μg/L in 1990–92s, and the offshore mean total biomass rose 7x between the 1960s and 1990s. In the Nyanza Gulf, the concentration of Chl-*a* was lower in the offshore waters (mean = 7.5 and 5.8 μg/L) than in the inshore waters (mean = 11.9 and 15.3 μg/L) in 2000–01 and 2005–08 [30]. In littoral waters, it was 60.6 μg/L [43] and reached a mean of 210 μg/L [44]. Also, the Chl-*a* concentrations were affected by season where they ranged from 2.0 to 71.5 μg/L in the dry season and 2.0 to 17.2 μg/L in the rainy season [28]. The value of Chl-*a* in the Kenyan section of the lake in the 2000s was 650 μg/L (Nyanza Gulf) [41]. However, the lake's primary productivity has increased by a factor of 2, and the Chl-*a* concentration has increased by 8–10 times [11]. In the Tanzanian waters of Lake Victoria, Chl-*a* ranged from 7.57 ± 0.01 to 69.14 ± 0.87 μg/L (average = 22.14 ± 5.14 μg/L), indicating eutrophic condition [45]. During the heavy rainy season, Chl-*a* exhibited comparatively higher concentrations (30.22 ± 3.37 μg/L) than in the light rainy season (25.34 ± 2.64 μg/L) and dry season (18.91 ± 0.53 μg/L). During

the period 2005–08, Chl-a varied between 8.09 ± 4.38 μg/L and 17.36 ± 6.13 μg/L in the offshore and inshore waters, respectively [35].

11.4.7 Phytoplankton assemblage in Lake Victoria

Lake Victoria was stable between 1820 and 1940 and was considered mesotrophic and mainly dominated by diatoms [46]. During the first study in 1892 [47], a total of 601 phytoplankton species belonging to 117 genera were recognized. On the other hand, Wakwabi et al. [48] recorded 344 species in 140 genera and 8 phyla in Lake Victoria satellite water bodies (SWBs) and small SWBs. The eight phyla are Bacillariophyta, Chlorophyta, Cyanophyta, Euglenophyta, Dinophyta, Pyrrophyta, cryptophyta and Chrysophyta. The Kenyan side sustained the most diversity with 169 species followed by the Tanzanian side (72 species), and the Ugandan side (67 species) (Table 11.3). There is considerable evidence that the eutrophication began early in the Kenyan waters (in the 1950s) than in Uganda and Tanzania, with the phytoplankton altering from a dominant diatom flora to one dominated by Cyanobacteria. This dominance of Cyanobacteria is now often located in the three countries bordering the lake (Tanzania, Kenya, and Uganda), in the numerous bays and gulfs.

The Cyanobacteria species: *Anabaena circinalis, Microcystis aeruginosa*, and *Microcystis flosaquae* are the most frequent in the inshore waters of Lake Victoria (especially in Nyanza, Mwanza, and Napoleon Gulfs, and in the bays). The filamentous cyanophytes (*Cylindrospermopsis* which was the most common cyanobacterium throughout the year) are often abundant on rocky shores and in the littoral zone. Also, the *Anabaena, Anabaenopsis*,

Table 11.3 Numbers of algal species in different phyla of the various sectors of Lake Victoria [48].

Group/water body	Victoria-Uganda	Victoria-Kenya	Victoria-Tanzania
Cyanobacteria	29	31	20
Chlorophyta	25	21	26
Bacillariophyta	9	111	15
Dinophyta	0	1	7
Euglenophyta	2	5	2
Pyrrophyt	1	0	0
Chrysophyta	0	0	2
Cryptophyta	1	0	0
Total number of taxa	67	169	72

Planktolyngbya, and *Pseudoanabaena* species are often common. The non-mucilaginous green algae, for example, *Ankistrodesmus, Scenedesmus, Coelastrum*, and *Cosmarium* species, are the most common green algae in shallow nutrient-rich waters. The diatom, *Nitzschia acicularis*, was found to dominate the phytoplankton in the open waters of Lake Victoria, even though it is frequently overtaken through Cyanobacteria all through the nonmixing periods. The dominance of *Aulacoseira* spp and *Cyclostephanos* spp. has been changed through *Nitzschia* spp. since the 1990s [49]. Individuals of Euglenophyta, for example, *Euglena, Phacus*, and *Trichelomonas*, are often distributed in many shallower SWBs.

In the beginning of the 20th century, the presence of Cyanobacteria blooms in the lake was evident as recorded by Ostenfeld [50], and then, the mass populations of Cyanobacteria close to the shores turned into a frequent phenomenon [28]. Some species like *Anabaena* spp, *Aphanocapsa* spp, *Lyngybya* spp., *Merismopedia* spp, *Microcystis* spp, and *Nitzschia* spp were recorded by Komarek and Kling [51]. Kendall [52] found that the green algae were dominated by *Coelastrum* spp, the diatoms by *Aulocisira* spp, *Nitzschia s*pp, and *Stephanodiscus astraea*.

After years of anthropogenic pressures, the phytoplankton composition in Lake Victoria has shown some remarkable changes and is undergoing accelerating eutrophication [26]. In any case, anthropogenic pressures are not equally distributed, thus, bays and gulfs are more impacted through eutrophication than the open lake [26]. Many of the embayments are shallow and vulnerable to pollution and, thus, modification in phytoplankton diversity and multiplying biomass led to harmful algal blooms. While many studies have autonomously explored the phytoplankton assemblages from various bays and gulfs, understanding the drivers of phytoplankton composition changes under different eutrophication pressures in Lake Victoria is required.

Besides the shifting from dominance by diatoms to that of Cyanobacteria in the open waters of Lake Victoria, the phytoplankton abundance has increased dramatically [53]. Cyanobacterial blooms were recorded in the lake at the beginning of the twentieth century [50], and many other records focus on the massive Cyanobacteria blooms, especially in nearshore areas [28,34,54]. The primary production rates have accelerated near the lake surface, and the algal community was composed of more than 90%. *Microcystis* have been found to produce cyanobacterial toxins, and the increased algal biomass has caused some problems, for example, the fish kills and deoxygenation of the deep lake waters [55]. As

a result, deterioration in drinking water quality consumed by human populations has been observed [27,56].

11.4.8 Phytoplankton succession in Lake Victoria

Lake Victoria is viewed as exceptionally eutrophic and cyanobacterial blooms with the ability to produce hazardous cyanotoxins that have become common [56]. The eutrophic bays and gulfs like the Nyanza Gulf Murchison Bay in Uganda [57] and Kenya [25] have Cyanobacteria as the predominant taxonomic group. For this, the lake has attracted researchers since the late 19th century.

11.4.9 Case studies on bays and shore waters of Lake Victoria

The heavy rainy season exhibited higher biomass (30.22 ± 3.37 μg/L) than the light rainy (25.34 ± 2.64 μg/L) and dry seasons (18.91 ± 0.53 μg/L). Cyanophyta was the dominant phytoplankton group (54.1% of the total count) during 2006–07 in the Sango Bay, located west of Lake Victoria at the boundary between Uganda and Tanzania [58]. Diatoms are second in importance (24.4%) followed by green algae (14.7%). Euglenophytes and dinoflagellates both constitute <10% of the algal density.

In the period from September 2005 to October 2007, phytoplankton samples were collected by Ngupula et al. [27] from three areas, shallow nearshore waters (<10 m), intermediate (20–30 m), and deep offshore waters (40–50 m). The shallow nearshore waters (mean 2.12×10^8 cells/L) were more productive than the intermediate (1.96×108 cells^{-1}). The diatoms were the most abundant group, Cyanobacteria, which decreased with distance offshore, and Chlorophyta, which increased with distance offshore. Chlorophyta (37 species) was the most diverse group, of which Staurastrum sp. and Siphonctosiphonpolymorphus were the most abundant species, followed by Bacillariophyta (25 species) and Cyanobacteria (21). *N. acicularis* (Bacillariophyta), *Lyngbya circumcreta*, and *M. flosaquae* (Cyanobacteria) were the dominant species. Other recorded groups were Euglenophyta (4 species), Dinophyta (3 species), and Chrysophyta (2 species). The shallow nearshore zone (< 10 m) was the most diverse (Shannon's $H' = 3.08$) and species-rich (richness index = 3.84), but with low equitability (evenness) (0.72). The composition and average abundance of diatoms species in the different ecological zones by Ngupula et al. [59] are shown in Table 11.4.

Table 11.4 Species composition and corresponding average abundances ($\times 10^4$ cells/L) of diatoms in different depths in the Tanzanian waters of Lake Victoria in 2005–07 [59].

Bacillariophyta	Depths (m)					
	<10 m	10.1–20	20.1–30	30.1–40	40.1–50	>50
Aulacoseira nyassensis	196	68	47	44	7	7
Cyclotella sp.	345	708	613	633	315	179
Cymbella sp.	34	0	0	0	0	0
Diatoma sp.	7	0	0	0	0	0
Fragilaria sp.	20	0	0	0	0	7
Navicula sp.	274	396	132	190	88	47
Nitzschia sp.	41	68	41	68	14	0
Nitzschia acicularis var. *major*	27	14	264	27	0	0
Nitzschia asterionelloides	42	106	85	186	59	17
N. acicularis	2346	3884	3172	3043	1314	826
N. nyassensis	91	244	105	41	81	0
Nitzschia lacustris	305	423	498	484	112	78
Urosolenia victoriae	34	88	47	47	34	0
Rhapolodia sp.	7	7	0	0	0	0
Cyclostephanos sp.	27	7	14	20	40	27
Surirella africani-orientalis	7	0	0	0	7	0
Surirella linearis var. *elliptica*	14	0	7	0	0	0
Surirella engleri var. *constricta*	34	41	0	0	0	0
Surirella nyassae	0	0	0	7	0	0
Surirella sp.	71	0	7	14	0	0
Synedra cunningtonii	230	267	169	190	135	0
Synedra acus	7	0	0	0	20	0
Ulnaria ulna	7	34	14	14	0	14

In November–December 2009, Mbonde et al. [60] surveyed two sites of Tanzanian waters; (1) closed bays—with a narrow opening and large surface area, and (2) open bays—where the water exchanged with the main lake. A total of 88 species were observed (77 and 67 species, respectively, in closed and open bays). The Shannon Diversity Index (H'), indicated higher diversity in open bays compared to the closed bays. The total phytoplankton density and biovolume were $3.4 \times 108 \pm 6.1 \times 10^7$ cells/L and $45 \pm 11\ mm^3$/L in closed bays versus $4.1 \times 107 \pm 0.3 \times 106$ cells/L and $5.4 \pm 1.5\ mm^3$/L in open bays. On average, phytoplankton biovolume was eight higher times in closed bays compared to open bays. Cyanobacteria were the dominant group in both bays, however, the proportion of cyanobacterial biovolume in closed bays was 82 ± 9% of the total biovolume compared to 44 ± 5% in open bays. Conversely, the percent abundance of diatoms in closed bays (6 ± 1.4%) was lower than in open bays (36 ± 6%), ($P < .001$). The most frequent Cyanobacteria species distributed by the two bays are as follows: *Anabaena* spp (closed: 31 ± 11%; open: 7.2 ± 4%), *Planktolyngbya* spp. (closed: 19 ± 9%, open: 6 ± 2%) and *Microcystis* spp. (closed: 29 ± 11%; open: 22 ± 7%). Meanwhile, within the diatoms, the most frequent species were *Nitzschia* spp. (closed: 2 ± 0.5%; open: 21 ± 4%) and *Cyclotella* sp. (closed: 2.6 ± 0.7; open: 8.1 ± 2.6%).

11.4.10 Case studies on the Mwanza Gulf (Tanzania)

The Mwanza Gulf is one of the biggest gulfs at the southern end of Lake Victoria (Tanzania). It lies at an altitude of 1134 m and extends 60 km southward, with a width of 5 km, and a surface area of 500 km^{-2}. It has a mean depth of 6 m and a maximum depth of 25 m. From May to August 2002, phytoplankton samples were collected from two zones of the gulf, inshore (3 m depth) and offshore (18 m depth). Generally, there were no significant variations in phytoplankton composition between the offshore and inshore areas. *N. acicularis* dominated in both zones (5%–90% of total phytoplankton) followed by *Planktolyngbya undulata* and *Planktolyngbya circumcreta* (3%–37%) [61]. *Aphanocapsa* sp. made up 1%–39%, meanwhile, *Microcystis* and *Anabaena* contributed 0%–5% and 0%–2.5%, respectively.

From August 2009 to March 2011, the study of Cornelissen et al. [62] on Mwanza Gulfreveal that the total Chl-*a* was decreased with depth. Cyanobacteria and Bacillariophyta fluctuated annually, with the highest abundances during the short rains, whereas chlorophytes occurred only at

very low contributions in all areas. The contribution of N-fixing species to the density of phytoplankton in September 2010 and April 2011 was very low. The nitrogen-fixing algal were species found in September 2010. The N:P ratio was highest in shallow water (36.4−71.1) and lowest in deep water (24.5−19.1). A study performed by Mchau et al. [20] in December 2018 on the Mwanza Gulf showed that the gulf faced severe eutrophication caused by the blooming of *Microcystis, Anabaena*, and *Merismopedia*. The predominance of these genera has been linked with excessive nutrients (e.g., nitrogen and phosphorus).

11.4.11 Phytoplankton succession in the Kenyan part of Lake Victoria

The Kenyan section of Lake Victoria lies just south of the Equator and comprises the northeastern part of the lake and is at 1134 m above sea level and is located between 0°04′S−0°32′S 34° and l3′E−34°52′E. The Kenyan section has been divided into four ecological zones, namely the Nyanza Gulf, Rusinga Channel, open waters inshore, and open waters. Signs of degradation of its water resource had been first visible in the early 1980s [63]. In general, the excessive stage of eutrophication is one of the most serious potential dangers to the lake waters. The increased Cyanobacteria mainly in inshore areas will negatively impact the water quality [49,64].

11.4.12 Case studies in the Kenyan part of Lake Victoria

1. Phytoplankton samples were collected in the dry season (September 1994) and the rainy season (March 1995) by Lung'ayia et al. [28]. A total of 103 species (45 genera) were recorded from the main lake and the Nyanza Gulf, and out of these, 84 were recorded in the rainy season and 93 species were recorded in the dry season. Cyanophyceae, Bacillariophyceae, and Chlorophyceae were the most diverse groups with 35, 34, and 33 species, respectively. During the dry season, the Nyanza Gulf was emphatically dominated by Cyanobacteria, while diatoms dominated in the open lake. During the rainy season, Cyanobacteria stayed dominant in the Nyanza Gulf even though the number of species decreased during the dry season; in the open lake, Cyanobacteria replaced diatoms as the dominant group and there was a higher species number than in the dry season. During the dry season, phytoplankton density showed no variations among the Nyanza Gulf

and open lake, however, the Cyanobacteria species *Anabaena flosaquae, A. circinalis, Anabaenopsis circularis, M. aeruginosa, M. flosaquae*, and *Chroococcus* spp. were prominent in the Nyanza Gulf, while the diatom *N. acicularis* was the most important species in the open lake. The most frequent diatoms in the Nyanza Gulf were *Aulacoseira anyassensis, Aulacoseira agassizii*, *Navicula* spp., *Synedra* spp., *Cocconeis placentula*, and *Cyclotella* spp. Furthermore, Cyanobacteria such as *Anabaena* spp., *Anabaenopsis tanganyikae*, *Planktolyngbya* spp., *Leptolyngbya lagerheimii*, and *Spirulina laxissima* were also abundant in the main lake. In the open lake, diatoms were most abundant with *N. acicularis* and the green alga *Staurastrum anatinum* was observed. During the rainy season, phytoplankton abundance was dominated by Cyanobacteria both in the open lake and in the Nyanza Gulf, but diatoms and green algae were more abundant in the open lake than in the Nyanza Gulf. The dinoflagellate was not found in the rainy season. The relative importance of Cyanobacteria in the deep water increased to equal that of diatoms. *N. acicularis*, *M. aeruginosa*, *P. subtilis*, *A. tanganyikae*, and *S. laxissima* were the most important species.

2. A study that occurred during 2000–05 by Mwirigi et al. [44] identified 63 species (38 genera) from both the littoral and pelagic parts of the lake. The phytoplankton community included diatoms, Cyanobacteria, and green algae. Cyanobacteria dominated followed by diatoms, while green algae were very few. *M. aeruginosa* dominated other cyanobacterial species and *Nitzschia* species dominated other diatoms. Other common species were *A. circinalis*, *A. circularis, Nitzschia*, and *Synedra* species. This compares well with the work done by Lung'ayia et al. [28]. The studies by Wakwabi et al. [48] indicated that there were 169 species of phytoplankton existing on the Kenyan side of the lake in which diatoms are the most diverse group, with 111 species, and Cyanobacteria, especially Microcystis, were well represented in the small water bodies.
3. Peter et al. [65] classified the Kenyan waters of Lake Victoria into three zones: The pelagic zone (deep >20 m), offshore zone (>5 km from the shoreline), and littoral zone or the Nyanza Gulf (<20 m deep and <5 km from the shoreline). The phytoplankton samples collected between 2000 and 2004 indicated that phytoplankton biomass (chlorophyll) and abundance were lower in the main lake than in the Nyanza Gulf. The phytoplankton biomass (chlorophyll-*a*) showed a reduction from the gulf to the main lake, with the highest average

of 21.1 μg/L in the gulf and the lowest average of 6.9 μg/L in the main lake. Cyanobacteria (45%–65%) and diatoms (20%–40%) were the most abundant groups in both zones. *Cyndrospermopsis africana*, N-fixing, and highly toxic species were present in both zones. *Anabaena sporoides* was more common in the main lake and *M. aeruginosa* was more common in the gulf. Among diatoms, *N. acicularis* was dominant in the main lake, whereas *Aulacoseiranya assensis* was dominant in the gulf.

4. The phytoplankton community composition was investigated by Sitoki et al. [41] from the Kisumu Bay (a part of the Nyanza Gulf) between July 2008 and September 2009. *Microcystis* constituted >50%–90% of the cyanobacterial biovolume. Cyanobacteria were the most dominant, contributing 50% to the total phytoplankton biovolume. The *Microcystis* spp. constituted the major part (78% ± 16%) of the total Cyanobacteria. Within the *Microcystis* spp. four species were observed according to morphological characteristics: *Microcystis wesenbergii*, *Microcystis botrys*, and the tropical species *Microcystis protocystis* and *Microcystis panniformis*. Bacillariophyceae were abundant during 2008 and 2009 (the dry seasons) and peaked in September. *Nitzschia* spp. occurred most frequently in June–July (early in the dry season), whereas *Aulacoseira* sp. was the most abundant in September (the late dry season). The species diversity was significantly lower in the wet season ($H = 0.88$) in 2009 than in the dry season ($H = 1.79$). In total, 101 phytoplankton species were identified. Cyanobacteria were the dominant group and *Anabaena* spp. was the most abundant. The diatoms primarily comprised *Synedra cunningtonii*, *Aulacoseira* spp., *Nitzschia* spp., and *Urosolenia victoriae*.
5. Samples were collected from SWBs within the Lake Victoria basin, Kenya, during 2010–11 [66] and registered a total of 1392 phytoplankton species (20 genera) belonging to four families in Kessesdam, while in the Kerita Dam, a total of 376 phytoplankton species (ten genera) belonging to four families were identified. They were Bacillariophyceae (seven genera), Chlorophyceae (nine genera), Cyanophyceae (one genus), and Desmidiaceae (three genera). In the Kerita Dam, the same four families were recorded, but Bacillariophyceae was the richest with six genera, Euglenophyceae and Cyanophyceae had only one genus each (*Phacus* sp., and *Phormidium* sp., respectively), and Chlorophyceae had two genera (*Scenedesmus* and *Botryoccoccus*). Yengadam had three families of phytoplankton: Chlorophyceae (with three genera), Euglenophyceae (two genera),

and Cyanophyceae (one genera). In the Mauna Dam, four families were present: Chlorophyceae (three genera), Bacillariophyceae, Desmidiaceae (four genera), and Cyanophyceae. *Botryococcus* and *Cosmarium* have appeared clearly.

6. The phytoplankton community composition was studied by Misiko et al. [42] in the Kisumu Bay from April 2009 to April 2010. Chlorophyceae were the most diverse with 23 genera recorded, Cyanophyceae with 12 genera, Bacillariophyceae with 8 genera, Euglenophyceae with 6 genera, and the Dinophyceae with only 2 species. The most abundant phytoplankton group was Cyanophyceae (57%), followed by Chlorophyceae (39%), Bacillariophyceae (4%), and Euglenophyceae (1%). From Cyanophyceae, the most abundant genera were *Microcystis*, *Anabaena*, and *Cylindrospermopsis*. The other genera recorded in considerable numbers were *Nitzschia*, *Chroococcus, Tetraedron, Euglena, Cosmarium, Planktolyngbya, Stephanodiscus*, *Phacus, Aulacoseira, Coelastrum, Navicula, Aphanocapsa*, and *Kirchneriella*.
7. Adhiambo [67] recorded 36 phytoplankton genera belonging to Cyanophyta (13 genera), Bacillariophyceae (12 genera), Chlorophyta (9 genera), and Pyrrophyta (2 genera) in the Kisumu Bay (Nyanza Gulf). *Chroococcus* sp. was the dominant species forming 72% of the total count. Diatoms have also become abundant with high densities of *Nitzschia*, which may be an indication of high silicate levels in the gulf. High phytoplankton abundance was observed due to continuous high nutrient inputs and shallowness of the gulf. The Chl-*a* concentrations do not exactly follow that of phytoplankton densities. This could be due to the presence of picoplankton which could also be present but could not be identified or counted. In the Nyanza Gulf, the study of the phytoplankton community showed changes in the blue-green algae Chroococcus species, which can be attributed to both anthropogenic and climate change factors.
8. Phytoplankton samples were collected by Aura et al. [68] from four rivers discharged into the Kenyan part of Lake Victoria. The four rivers being the Nzoia, Yala, Sondu-Miriu, and Kuja. The samples were collected in March (wet season) and July (dry season) from 2016 to 2018. These rivers constitute over 45% of the total influx to Lake Victoria [69]. The authors recorded 70 species of phytoplankton during March 2016, 2017, and 2018 (the wet season) and 65 species during July 2016, 2017, and 2018 (the dry season). Diatoms dominated in both the wet (60%) and dry seasons (55%) in which *S. cunningtonii* and

Aulacoseira spp. were predominant. Cyanobacteria were common in the dry season, especially Anabaena sp. and *Microcystis* sp. Species of chlorophyceans frequently appeared as *Ankistrodesmus falcatus*, *Bottrycoccuss* sp., *Coelomolon* spp., and *Scenedesmus* spp., and from Euglenophyceae *Euglena* spp., *Phacus* spp., *Strombomonous* spp., and *Trachelemonous*. These species were like the results of Talling [70], who noted the dominance of such phytoplankton species in the Lake Victoria basin.

11.4.13 Phytoplankton succession in the Ugandan waters of Lake Victoria

Historical data indicated that the phytoplankton density in the Ugandan waters of Lake Victoria was relatively low in the 1960s in both nearshore and offshore waters and was dominated by *A. flosaquae*, *L. circumcreta*, *P. circumcreta* (from Cyanobacteria); *Staurastrum, Scenedesmus, Pediastrum, Coelastrum*, and chlorococcoid greens (from chlorophytes); *Aulacoseira* and *Cyclostephanos* (from diatoms); and *Ceratium brachyceras* and *Glenodinium pulvisculis* (from dinoflagellates). The phytoplankton community had changed completely between 1960 and 1990. *Aulacoseira* and *Nitzschia* were still present from 1987 to 1988 in the Pilkington Bay and Napoleon Gulf [70] and the last observation of *Aulacoseira* in the offshore northern part of the lake occurred in 1989. Other filamentous (nonnitrogen fixing) blue-green Planktolyngbya tallingii were also significant components during the 1990s. *Anabaena flosaquae f aptekariana, A. tanganyika*, and the low abundance of *Aphanizomenon* sp. during 1990–92s. *Anabaena* sometimes formed blooms in the inshore areas of Napoleon Gulf and Pilkington Bay. Diatoms, *N. acicularis* and *Nitzschia* cf. *paleacea*, became less frequent. *M. aeruginosa* or *M. wesenbergii* were not obvious in the Pilkington Bay in 1990. However, the two species in the previous years have been found in bloom in the Kenyan regions of the lake [63].

Regardless of the diatom's reduced numbers, the mean biomass of the diatoms in 1990–95s was 4–5 × their means in 1960–61s. However, the mean of the *N. acicularis* biomass in 1990–92s was 3x the mean in 1960–61s [70]. In 1994–95s, the mean diatom biomass was slightly lower than that of the 1990–92s. The mean biomass of the Cyanobacteria species *Cylindrospermopsis* in 1990–91s was 30x greater than that of *Anabaena* in 1960–61s, while in 1994–95s, the mean biomass of *Anabaena* was 24x greater than in the 1960–61s. The chlorophytes also increased in total biomass, and a significant change occurred in the composition, from the large-celled and colonial species of the genera *Staurastrum, Cosmarium,*

Botryococcus, Pediastrum, and *Coelastrum* to the small-celled species of the genera *Chlorella, Choricystis, Eutetramorus*, as well as *Dictyosphaerium, Monoraphidium*, and *Oocystis*.

11.4.14 Case studies in the Ugandan waters of Lake Victoria

1. The Napoleon Gulf and Murchison Bay are most important in the northern section of the lake. The Murchison Bay is strongly affected by pollution from the Ugandan capital Kampala than the Napoleon Gulf. Furthermore, the Murchison Bay is more enclosed and has a substantially greater popular watershed than the Napoleon Gulf and is divided into two parts: the inner bay (average depth is 3.2 m) and the outer bay. The phytoplankton biomass was generally lower in the Napoleon Gulf than in the Murchison Bay, however, Cyanobacteria were dominant in both sites, contributing >70% of the total biomass. Early reports about the phytoplankton community before anthropogenic eutrophication (the 1960s) report the dominance of diatoms, Cyanobacteria, and chlorophytes [71]. Then, the community was dominated by Cyanobacteria and the diatom *Nitzschia* [49].
2. During the period 2003–04s, the phytoplankton community in the Murchison Bay was dominated by Cyanobacteria and Bacillariophyta. Cyanobacteria were prevailing in the whole bay, whereas diatoms were more plentiful in the outer part. Additionally, the outer part of the bay was dominated by *Anabaena* sp., while *Microcystis* sp. was most frequent in the inner part. Haande et al. [72] recorded 80 phytoplankton taxa belonging to 56 genera during 2003–04s. These taxa are within nine classes and six phyla: Bacillariophyceae, Heterokontophyta, Cyanobacteria, Chlorophyceae, Zygnemophyceae, Trebouxiophyceae, Cryptophyta, Euglenophyta, and Dinophyta. Bacillariophyceae and Cyanobacteria were the most abundant groups in the inner and outer zones. In the inner zone, the percentage of Bacillariophyceae and Cyanobacteria was 23% and 64%, respectively, and the proportion of Cyanobacteria in the outer zone was equivalent to the inner part of the bay (62%), though the diatoms were more bountiful (31%). The Chlorophyta included the most different phylum; however, they just represented around 2% of the total biovolume in both zones. The most plentiful species in the inner zone were *Aulacoseira granulata* (15.4%), *Anabaena* sp. (12.4%), *M. wesenbergii* (11.6%), *Gomphosphaeria aponina* (8.6%), and *M. aeruginosa* (8.5%). In the outer zone, the most frequent

species were *Anabaena* sp. (25.3%), *P. circumcreta* (6.7%), *M. wesenbergii* (5.8%), and *G. aponina* (5.5%).

3. A total of 135 species (49 genera), comprising 62 taxa (21 genera) Chlorophyta/Euglenophyta, 44 taxa (13 genera) Cyanophyceae, 27 taxa (11 genera) Bacillariophyceae, 2 taxa (2 genera) Dinophyta, 2 taxa (one genus) Cryptophyta and one taxon (one genus) Chrysophyta were recorded from the Napoleon Gulf and Murchison Bay during 2017–18 [26]. Out of these, 29 and 35 species were specific to the Napoleon Gulf and Murchison Bay, respectively. From these 135 taxa, 53% were found in both sites, with a total richness of 100 in the Napoleon Gulf and 106 in the Murchison Bay. The Shannon Diversity Index and evenness (equitability index) were 2.12 ± 0.26 and 0.672 ± 0.09 in the Napoleon Gulf and were 2.01 ± 0.28 and 0.685 ± 0.07 in the Murchison Bay, respectively. However, the dominant phytoplankton taxa differed between the two sites, where the two cyanobacterial taxa *Dolichospermum circinale* and *P. circumcreta* dominated the phytoplankton community in the Napoleon Gulf and *D. circinale*, *P. circumcreta*, *Microcystisf los-aquae*, and *M. aeruginosa* dominated in the Murchison Bay.
4. The other two wetlands are situated within the Ugandan waters of the Lake Victoria basin, namely Gaba and Walukuba. Ssanyu and Schagerl [39] recorded 37 and 31 phytoplankton species in the Gaba and Walukuba ponds distributed among six taxonomic groups as follows: Cyanobacteria (17%), Bacillariophyceae (18%), Euglenophyta (16%), and chlorophytes (52%) in Gaba ponds, while Cyanobacteria (13%), Bacillariophyceae (19%), Euglenophyta (19%), Chrysophyceae (6%) and chlorophytes (39%) were reported in Walukuba ponds. The dominant Cyanobacteria genera were *Anaphanocapis, Microcystis*, and *Planktonlyngbya*, and among the Bacillariophyceae, *Nitzschia* and *Navicula*. Green algae were predominant by *A. falcatus*, *Scenedesmus* spp., and *Monoraphidium* spp. while among the other groups' *Euglena* spp. and *Tracheomona*s spp. were also very common.

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CHAPTER 12

Prokaryotic communities in African lakes and water quality of cyanobacteria in some African lakes: their occurrence, ecology, associated toxicity, consequences, and safety plans ☆

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12.1 Introduction

12.1.1 Mass-developing cyanobacteria

Mass-developing Cyanobacteria is a worldwide phenomenon that is causing problems by creating water blooms. The photosynthetic nature of Cyanobacteria species allows them to rise to water surfaces with the aid of gas vesicles to capture sunlight, forming part of the plankton community in the aquatic environments (Fig. 12.1). These blooms give an esthetic impression, bad smell and taste, discolor the water, and pose a health risk for humans and animals by producing a large number of toxins. However, not all blooms are associated with toxin-producing species [1]. Toxic cyanobacterial blooms have been reported for more than one half-century. In 1878, the first acute cyanotoxin poisoning of domestic animals was reported by Australian assayer and chemist George Francis [2].

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Figure 12.1 A sampling of Cyanobacteria in the Weija Reservoir, Ghana. July 2008. *Photo: Heléne Annadotter.*

Cyanobacterial toxins are a diverse group of natural toxins, both chemically and toxicologically. Based on their chemical structure, the cyanobacterial toxins are mainly classified into alkaloids, cyclic peptides, lipopolysaccharide endotoxins, and nonprotein amino acids [3]. These toxins are causing acute and chronic health problems in humans and fatal poisoning of animals [4,5]. Most cyanotoxins are compounds that are not utilized by the organism's primary metabolism [4]. The mechanisms of toxicity include neurotoxic, hepatotoxic, cytotoxic, dermatotoxic, and pyrogenic effects on the general inhibition of protein synthesis [6].

In northern Europe, North America, Africa, Asia, and Australia, cyanobacterial blooms began to appear in some, but far from all lakes, at the end of the 20th century [7].

Even if more than 2600 cyanobacterial species have been described, a large number of unknown species likely remain to be discovered [8].

Toxin-producing Cyanobacteria are globally distributed in fresh, brackish, and saltwater as well as in Artic and desert regions. In Africa, toxin-producing Cyanobacteria have so far been reported from 16 countries: Algeria, Botswana, Egypt, Ethiopia, Ghana, Kenya, Lesotho, Morocco, Mozambique, Namibia, Nigeria, South Africa, Tanzania,

Tunisia, Uganda, and Zimbabwe [1,9,10]. However, available data about cyanotoxin contamination are still very scarce for most African countries and are nearly absent for regions such as West and Central Africa [11].

The factors behind the increased frequency of blooms are not yet proven and there are probably several factors involved that play different roles for different lakes. Some researchers have suggested increased access to nutrients in combination with elevated temperatures and an extended growing season [7]. More research is, however, needed to be able to understand the factors that cause cyanobacterial blooms. If we do not know which factors cause these blooms, it is difficult to eliminate Cyanobacteria from lakes.

12.1.2 Cyanobacterial neurotoxins

Several cyanobacterial genera, for example, *Aphanizomenon, Anabaena, Dolichospermum, Lyngbya, Planktothrix, Oscillatoria, Raphidiopsis, Cylindrospermum, Cylindrospermopsis*, and *Trichodesmium* are producers of neurotoxins [4,5,12,13]. The major neurotoxins are anatoxin-a (ATX), homoanatoxin-a, anatoxin-a(s), and saxitoxins (STXs) [14].

12.1.2.1 Anatoxin-a

ATX is an amine that is a structural analog of cocaine and the neurotransmitter acetylcholine [14]. The primary target organ in mammals is the nerve synapse. There is no antidote to ATX [5]. Signs of poisoning are convulsions, staggering, muscle fasciculations, and gasping. Depending on species and dose, death by respiratory failure occurs within minutes to a few hours [4,5,15].

12.1.2.2 Homoanatoxin-a

Homoanatoxin-a, an amine alkaloid, methylene-anatoxin-a [16] is a potent neuromuscular blocking agent [14]. Lethal doses of homoanatoxin-a result in convulsions, severe body paralysis, and death by respiratory failure.

12.1.2.3 Anatoxin-a(s)

Anatoxin-a (s) is a naturally occurring phosphate ester of cyclic N-hydroxyguanine and functions as an acetylcholinesterase inhibitor similarly to the organophosphate insecticides malathion and parathion [4,5]. The *s* in anatoxin-a (s) denotes salivation in vertebrates. The symptoms resemble those of ATX with the addition of ataxia, diarrhea, hypersalivation, and

tremors. Anatoxin-a (s) differs chemically from ATX. Even though anatoxin-a(s) differs structurally from the synthetic organophosphate, the killing power, just like that of the pesticides, stems from its ability to inhibit acetylcholinesterase.

12.1.2.4 Saxitoxins

The STXs are alkaloid neurotoxins that interfere with neurotransmission by blocking the neuron sodium channels across the axon membrane [13]. The STXs cause symptoms such as loss of coordination, irregular breathing, twitching, and death due to respiratory failure [4,5,15].

12.1.2.5 Hepatotoxins

The cyclic peptide hepatotoxins (liver toxins) are the major cyanotoxins causing death and illness in animals [4,5]. Microcystins (MCs) have been identified in the genera of *Anabaena, Anabaenopsis, Dolichospermum, Geitlerinema, Leptolyngbya, Microcystis, Planktothrix, Oscillatoria, Nostoc, Phormidium*, and *Synechocystis* [1,4,5,17,18].

Nodularin, a monocyclic pentapeptide, is structurally and toxicologically similar to microcystin. The toxin has been isolated from the brackish water cyanobacterium *Nodularia spumigena* [15,17]. The cyclic nature of MCs suggests that they are highly stable in water across a wide pH and temperature range [19].

Cylindrospermopsin (CYN) is an alkaloid hepatotoxin [20] that has been isolated from *Cylindrospermopsis raciborskii*, *Umezakia natans*, and *Aphanizomenon ovalisporum* [21,22]. The liver is the primary target of CYN, which also is a cytotoxin. CYN can, according to recent findings, also cause damage to the nervous system [20]. Acute hepatotoxicosis is the main type of poisoning caused by Cyanobacteria [4,5,17]. The symptoms of poisoning in laboratory mice include diarrhea, pallor of the mucous membranes, vomiting, weakness, anorexia, and death [4,5,15]. Death occurs within 1–2 h due to intrahepatic hemorrhage/liver necrosis and the disintegration of the architecture of the liver, i.e., hepatic parenchyma and hypovolaemic shock [4,5,15]. As a consequence of internal hemorrhaging, the weight of the liver of the mouse may increase up to 100% [4,5].

MCs enter the body from the intestine, probably via the bile acid transporter system [23]. From the blood, MCs then bind quite specifically to the liver tissue where they form adducts with serine protein phosphatases 1 and 2A resulting in the inhibition of these important enzymes.

These enzymes are vital to various cellular processes such as cell growth and tumor suppression, and therefore, these toxins are possible potent cancer promoters [4,5]. Microcystin-LR is an extremely potent tumor promoter in laboratory animals [24] and is the most potent liver carcinogen yet characterized.

12.1.2.6 Nonprotein amino acids

Nonprotein amino acids contain carboxyl and amino groups. They do not constitute proteins and are naturally occurring compounds. The nonprotein amino acids are mainly found in plants and microorganisms and are important bioactive substances [25].

β-N-methylamino-L-alanine, BMAA, is a nonprotein amino acid that is formed by several different phytoplankton groups such as Cyanobacteria, diatoms, and dinoflagellates [26].

BMAA can act as a poison on the nervous system and is suspected by some researchers to be involved in several severe nerve diseases, such as Alzheimer's, ALS, and Parkinson's [27]. The suspicion arose on the Pacific island of Guam. On this island, food with high levels of BMAA was consumed while Guam had an extremely high incidence of certain nerve diseases. Exposure to BMAA can occur through drinking water, inhalation of aerosols from lakes, or by eating fish and shellfish that have lived in the water with Cyanobacteria [28].

12.1.2.7 Lipopolysaccharide endotoxins

Lipopolysaccharides (LPS), also known as endotoxins and lipoglycans, are molecules of a polysaccharide and a lipid. Gram-negative bacteria and Cyanobacteria form LPS as a part of their outer cell membrane and cover 75% of their surface area [29]. Both groups are prokaryotes with similar chemical composition and morphological organization. Endotoxins have been isolated from many common, mass-developing Cyanobacteria [30]. In the bloodstream, endotoxins cause various pathophysiological reactions such as fever, leukopenia, tachycardia, tachypnea, hypotension, disseminated intravascular coagulation, and multiorgan failure [31].

12.2 Monitoring of cyanobacteria

The detection of cyanotoxins involves a range of indirect methods, including Enzyme-linked immunosorbent assay (ELISA), antibody-based techniques, and molecular approaches [32]. However, these indirect

methods lack sensitivity and specificity, while direct detection with chromatographic techniques and mass spectrometry has high selectivity and sensitivity, but is expensive and requires a skilled operation, making detection and monitoring all the more difficult, especially for developing countries [32].

12.3 Poisoning incidents of animals

Animal deaths, in particular cattle, sheep, and dogs, have been reported in many parts of the world [1,4]. In contrast to pathogenic bacteria, the cyanobacterial cells do not proliferate within the mammal body after uptake, only in the aquatic environment before uptake. The cyanobacterial toxins are normally contained within the cells and released in substantial amounts only on cell lysis.

Most poisoning incidents are connected with the bloom-forming genera of Cyanobacteria, such as *Microcystis, Anabaena/Dolichospermum*, and *Aphanizomenon*. Winds and currents can concentrate the floating Cyanobacteria to form scum on the shores [5].

Benthic Cyanobacteria have also caused the poisoning of animals [17,33]. They may grow on bottom sediments in waters that are sufficiently clear to allow light penetration to these surfaces.

12.4 Effects on human beings

Even if numerous cases of cyanobacterial poisonings among animals exist, data on exposure of humans to cyanotoxins are limited worldwide. This is probably because cases of illness are not sufficiently rapidly associated with cyanobacterial toxins as a potential cause, and thus, no investigation is undertaken as to whether they are present or not, nor at what levels.

The key concern for human health is exposure to toxic Cyanobacteria via drinking water. Cyanobacteria may mass-develop in water resources over extended periods. Water-borne outbreaks, associated with the occurrence of Cyanobacteria in a drinking water reservoir, have been reported in Africa, North America, South America, Europe, and Australia [1].

In 1996, in Brazil, 131 renal dialysis patients fell ill after having been provided with contaminated dialysate at a hemodialysis center; 100 patients developed acute liver failure and 76 of these patients died [34].

12.4.1 The role of cyanobacteria in cholera epidemiology

In the middle of the 19th century, a relationship between cholera outbreaks and contaminated water supplies was discovered by English physician John Snow. Some decades later, the causative agent of cholera, *Vibrio cholerae*, was discovered by Koch [35].

At the end of the 20th century, cholera epidemics became a worldwide health problem [36]. Cholera is an acute intestinal illness, caused by the toxin-producing bacterium *V. cholerae* [37]. Processes in the mucosal epithelium of the gastrointestinal tract cause vomiting and acute watery diarrhea which, in turn, result in water loss and severe dehydration. If left untreated, the mortality from cholera may be as high as 50%. Cholera has become endemic in many areas and is a recurring problem in others. The biology of cholera is among the best understood infectious diseases. Much remains still, however, to be highlighted [37]. Cholera is more complex and durable than earlier thought. *V. cholerae* may exist permanently within the environment rather than living only for a few days outside the human intestine, as previously thought. The reservoir of cholera remained a mystery until Colwell et al. [38] hypothesized that *V. cholerae* are autochthonous flora of estuaries and brackish water. Colwell and Huq [39] showed that toxigenic *V. cholera* can survive in aquatic environments for months to years.

Islam et al. [40] have demonstrated that some cyanobacterial genera, *Anabaena, Hapalosiphon*, and *Nostoc*, can act as long-term reservoirs of *V. cholerae*. The bacterium lived symbiotically in the mucilaginous sheath of the cyanobacterium. Islam et al. [40] suggested that the cyanobacterium benefited from the carbon dioxide produced by *V. cholerae* and the bacterium used oxygen and nutrients produced by the cyanobacterium.

When humans consume surface water containing Cyanobacteria they potentially consume the associated *V. cholerae*. An improved understanding of environmental factors controlling the development of cyanobacterial blooms is important for further development of management to prevent their proliferation, and hence, the control and eventually prevent outbreaks of cholera.

12.5 Cyanobacteria in the Lakes of Ghana

12.5.1 Cyanobacteria in the drinking water reservoirs of Weija, Kpong, Owabi, and Barekese

Safe drinking water is one of the most crucial factors to human health. In Ghana, the increase in the pollution of surface water bodies and reservoirs

utilized in the production of drinking water has created a shift in the phytoplankton composition of Cyanobacteria [41]. Pioneering work by Addico [42] and Addico et al. [19,43] indicates that the Weija reservoir, located in the southern part of Ghana, has the maximum diversity of cyanobacterial species, *Aphanocapsa nubilum, Merismopedia tenuissima, Planktolyngbya minor*, and *Pseudanabaena recta* are the dominating species. *Cyanogranis ferruginea*, formerly unknown to Ghana and tropical Africa, dominated the Kpong reservoir while the Owabi and Barekese reservoirs, both with substantial rainfall and human activity, were dominated by *Geitlerinema unigranulatum*.

12.5.2 Cyanobacteria in raw and treated water

C. ferruginea accounted for 95%–97% of the total cyanobacterial cell counts in the Owabi drinking water treatment plant. Apart from *C. ferruginea*, the cyanobacterial species *Aphanocapsa holsatica*, *P. recta*, and *Leptolyngbya* sp. were found in the treated water from Owabi most frequently with total cyanobacterial counts ranging from 95 to 1099 cells/mL [41]. The most prevalent cyanobacterium in the Kpong Reservoir was *G. unigranulatum*, which accounted for 65%–78% of the total cyanobacterial cell counts in raw water samples. However, *Planktothrix agardhii* was the most abundant species in the treated water (Fig. 12.2) from the Kpong reservoir on average, followed by *G. unigranulatum* and *C. raciborskii*.

Figure 12.2 Gloria Addico (*left*) at the water works in Kpong, July 2008. *Photo: Heléne Annadotter.*

12.5.3 Detection and monitoring of cyanobacteria in Ghana

In Ghana, in the Council for Scientific and Industrial Research, Water Research Institute (WRI) is the foremost government institution mandated to carry out research into the surface and groundwater resources in the country. Thus, by extension, the monitoring of Cyanobacteria lies in WRI, Ghana. Other institutions such as the Environmental Protection Agency, the Ghana Water Company, and the Water Resources Commission are all government agencies with the mandate to regulate and manage the water resources in Ghana.

The World Health Organization (WHO) has standardized a guideline value of 1 μg/L but this is hardly ensured in routine drinking water analysis [43,44]. Unfortunately, microcystin monitoring is not a quality criterion in most developing countries including Ghana.

Little effort has been made in the stride to eliminate or reduce the occurrence of cyanotoxins in Ghana's water, especially in potable water. Due to population dynamics and the highly varied distribution of Cyanobacteria populations in water bodies, monitoring Cyanobacteria in freshwater ecosystems is a time-consuming and expensive task. The financial cost of long-term monitoring initiatives in developing nations, particularly in Africa, is a significant impediment to their adoption.

12.6 Cyanobacteria in Zimbabwean reservoirs

The trophic status of a water body is the major determinant of the occurrence and dominance of Cyanobacteria in Zimbabwean freshwater bodies. Lake Chivero (Fig. 12.3) is the only reservoir that is characterized by the predominance of Cyanobacteria in Zimbabwe. Detailed studies on cyanobacterial dynamics are thus only available for Lake Chivero. *Microcystis aeruginosa* and *Anabaena* sp. became the dominant cyanobacterial species in Lake Chivero immediately after impoundment [46], where the former species occurred in large populations of approximately 1–3 million colonies/L, and formed noxious surface scums [47]. The reservoir became eutrophic immediately after impoundment. *M. aeruginosa* was the dominant species and contributed most to the phytoplankton biomass and exhibited seasonal changes with a noticeable decline in winter, populations building up in the epilimnion from August, and large populations were present by November 1969 [46,48]. Populations of *M. aeruginosa*

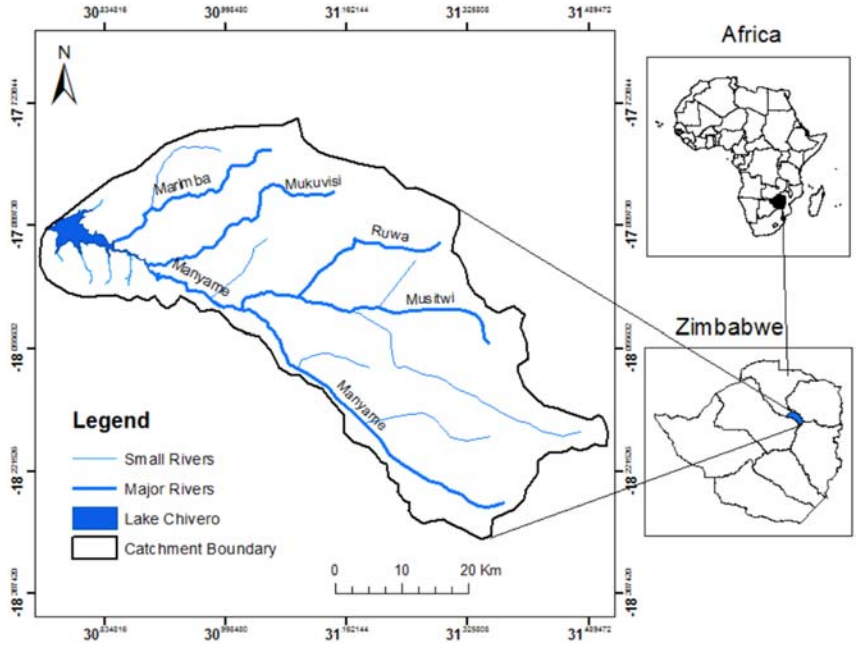

Figure 12.3 Map of Lake Chivero [45]. *Reprinted from, and with permission from P. Sibanda, Sediment Characteristics, Nutrient fluxes and Aspects of the Ecology of Benthic Invertebrates of Lake Chivero, Zimbabwe, University of Zimbabwe, 2020.*

showed a strong relationship to the seasonal development of thermal stratification and the populations did not occur below 10 m depth.

A winter peak of *Anabaena* when oxygen tensions were lowest in the epilimnion was also observed [46]. *Anabaena* sp. followed the thermal stratification cycle and never occurred in high numbers below a depth of 8−10 m during thermal stratification. It was distributed throughout the water column at overturning. *Anabaenopsis tanganyike* occurred in the epilimnion from February to April 1969 and for the rest of the time, it was uncommon or absent. Its filaments (4×10^5 L^{-1}) occurred exclusively in the upper layers of the epilimnion.

In 1975 and 1976, Robarts et al. [49] carried out a study in Lake Chivero and established that *M. aeruginosa* dominated for most of the year, particularly during summer, while *Anabaena* sp. and/or *A. tanganyike* were prevalent particularly during early spring. Although *M. aeruginosa* was perpetually dominant, a "seasonal paradigm" of phytoplankton succession was exhibited [49]. The vertical distribution of *M. aeruginosa* and *Anabaena* sp. was influenced by the annual cycle of temperature stratification [48].

The phytoplankton population remained in the euphotic zone for most of the year, and concentrations were never appreciable below 10 m in response to the permanent summer thermal stratification. Phytoplankton populations followed the pattern of thermal stratification and rarely exceeded 5×10^4 colonies/L below the thermocline. Surface maxima occurred in January, July, September, and December 1969, and surface scums of phytoplankton occurred on calm days when the algae would float up to the surface and form large concentrations by midday [48].

A later study by Ndebele [50] established that the highest Cyanobacteria concentrations were in the top 3 m with biomasses ranging from 0.8 to 7.6 mg/L. Data are too limited to determine the trends in cyanobacterial biomass changes in Lake Chivero. The mean monthly biomasses in summer were estimated to range between 5 and 6.8 mg/L [51] in October 1998. Annadotter et al. [52] estimated average biomass of 25.7 mg/L (range 10.9 to 46.9 mg/L) while Ndebele [50] reported average phytoplankton biomass of 4.9 mg/L (range 0.8–7.6 mg/L) between March and April 2003. Algal blooms were common and the main bloom species was *M. aeruginosa*.

Eutrophication is the major factor that has influenced the dominance of Cyanobacteria in Lake Chivero since its impoundment. The reservoir has been perpetually hypereutrophic. The persistence of seasonal blooms of *M. aeruginosa*, which first appeared in 1960 and later became established as a permanent bloom in 1963, has been a management challenge in Lake Chivero [53]. Magadza [54] has reported a short-lived clear-water state ("metastable mesotrophic condition") following the nutrient reduction in 1979 when the effluent was diverted through irrigated pastureland. The lake reverted, however, to a turbid state as nutrient levels increased again and the lake has never switched back to a clear-water state. Mhlanga and Mhlanga [55] established the existence of two distinct algal assemblages; one dominated by Cyanobacteria under relatively stable environmental conditions and another dominated by eukaryotic algae under unstable environmental conditions.

The dominance of Cyanobacteria in other reservoirs like Lake Kariba and Mazvikadei Dam only occurred during the postimpoundment eutrophic phases. Lake Kariba is, at the time of writing (in 2022), mesooligotrophic. In Lake Kariba, Cyanobacteria dominated during the filling phase (eutrophic phase) but subsequently declined when the reservoir assumed oligotrophic status. The dominant cyanobacterial genera in Lake Kariba are *Cylindrospermopsis*, *Anabaena* and *Pseudoanabaena* [56]. The

recently impounded Tugwi-Mukosi reservoir in southeastern Zimbabwe also showed that Cyanobacteria was the dominant group at all sites (50% − 70%) and *M. aeruginosa* abundances ranged from 3200 − 28 800 cells/L [57].

12.6.1 Cyanobacteria in small reservoirs

Few studies have been undertaken in small reservoirs. Dalu and Wasserman [58] recorded 15 cyanobacterial taxa in Malilangwe with *Microcystis* spp. and *Cylindrospermopsis* spp., known cyanotoxins producers, being the most prevalent bloom-forming taxa. Cyanobacteria-relative abundances were highest during the cool-dry season as nutrient concentrations increased following decreased river inflows and increased reservoir mixing. Thus, the cool-dry season would then be associated with a high risk of potential exposure to toxigenic Cyanobacteria in animals and humans from the genera *Anabaena*, *Microcystis*, and *Cylindrospermopsis* [58]. Information on in situ cyanotoxin production in Zimbabwean reservoirs is not available, thereby, limiting the understanding of the potential risk of exposure.

12.6.2 *Microcystis aeruginosa* bloom dynamics in Lake Chivero

A study on the development of phytoplankton assemblages in relation to environmental variables between 2003 and 2006 established that there had been a decline in the dominance of Cyanobacteria [59]. Two states were exhibited in the reservoir, namely a clear state with lesser dominance of *Microcystis* and proliferation of cryptophytes and chlorophytes and a turbid state where *M. aeruginosa* dominated and competitively excluded other species. The change in the relationship between nitrate and orthophosphate explained the decline in the *Microcystis* domination whereby *Microcystis* was favored during a short-lived "gap" of high nitrate concentration with relatively higher dissolved oxygen levels, which occurred during the turbid state. The built-up of *Microcystis* biomass within the 0−5 m zone resulted in a decline in light, thereby, becoming a limiting factor for other species which were then competitively excluded. The reservoir assumed a clear state after the collapse of the cyanobacterial bloom. The clear state lasted for 15 months during which the phytoplankton community showed a typical successional pattern with Cyanobacteria dominating in summer, diatoms in winter, and chlorophytes and

cryptomonads dominating during the hot dry period. Cryptomonads dominated despite high nutrient levels, high mean pH (7.0–9.7), high temperature (17.4°C–26.8°C), and mean N:P ratios of 10.5 which should favor Cyanobacteria according to the proposed theories of cyanobacterial dominance. This illustrates that the dynamics of Cyanobacteria in hypereutrophic reservoirs is complex and requires continuous monitoring. The major determinant of the development of the phytoplankton assemblage was the temporal changes in the availability of nitrogen and phosphorus. The clear state occurred when phosphorus was abundant and nitrogen limiting. The turbid state, dominated by Cyanobacteria, occurred at a critical nitrogen concentration of about 0.3 mg/L and was maintained within a range of 0.3 and 1.7 mg/L. The major determinant of the state of the lake concerning Cyanobacteria dominance was nitrogen although other factors like predator-grazer pressure could have affected the phytoplankton assemblage. The clear state was a metabolic relatively low-oxygen hypertrophic state favored mainly by osmo-mixotrophic cryptophytes. This observation was supported by experiments in enclosures whereby it was established that turbulence is favoring opportunist species in the lake [60]. Non-equilibrium dynamics during the clear phase favored chlorophytes which are ruderal plants and cryptomonads, which are neither true opportunists nor true ruderals [60]. In enclosures, chlorophytes and cryptomonads were replaced by the specialist *M. aeruginosa*. Nitrogen addition experiments in microcosms and field observations showed that smaller species with the highest ability to utilize N over *M. aeruginosa* were more competitively successful in Lake Chivero. The TN: TP ratio rather than the absolute concentration of N and P favored cryptophytes.

According to Mhlanga et al. [60], the decrease in cyanobacterial dominance, which was a widespread public concern, is central to the management of Lake Chivero. The shift between the two states and the period spent in each state showed that hypereutrophy in Lake Chivero with total phosphorus $>$ 1 mg/L and ammonium at levels of 3 mg/L, would normally not develop cyanobacterial dominance as expected.

12.6.3 Cyanotoxin production and the presence of algae in drinking water

The danger of the predominance of Cyanobacteria in Lake Chivero to humans was recognized in the 1960s when Zilberg [61] observed that children living in areas of the city supplied by Lake Chivero developed gastroenteritis each year at the time when natural blooms of *M. aeruginosa* were

decaying in the reservoir. Later, Marshall [62] established a correlation between incidences of gastroenteritis and toxic Cyanobacteria blooms in Lake Chivero. There is limited information on toxin production in Lake Chivero despite potential health concerns. After taking a bath or shower in Harare, Annadotter et al. [52] established that lipopolysaccharide endotoxin caused an acute febrile reaction in humans. Within 2–5 h after a shower or bath, a transient flu-like syndrome with fever, muscle pains, chest tightness, and respiratory-tract symptoms developed. These symptoms were associated with massive blooms of Cyanobacteria in Lake Chivero, and consequently, the formation of high concentrations of lipopolysaccharide endotoxin yielding high concentrations in tap water. The algal assemblage in the lake was dominated by *M. aeruginosa* and *Microcystis botrys*. The concentrations of endotoxins ranged from 1000 to 7750 EU/mL while endotoxins in the Harare tap water ranged from 60 to 205 EU/mL. Comparatively treated water in South Africa and Namibia had levels of 5–71 EU/mL [63].

In a study by Ndebele and Magadza [64], the average microcystin concentration detected in Lake Chivero was 19.9 μg/L, ranging from 18 to 22.5 μg/L [64]. A study by Mhlanga et al. [59] performed between 2003 and 2004, when the phytoplankton community in Lake Chivero comprised non-microcystin-producing species for the greater part, assessed the presence of cyanotoxins in treated drinking water and algae in the lake. *M. aeruginosa, Microcystis Novacekii*, and *Microcystis wesenbergii*, known producers of the toxin microcystin, dominated during summer. The highest cyanobacterial biomass coincided with the highest concentrations of MCs and lipopolysaccharide endotoxins. The lipopolysaccharide endotoxin concentrations in the lake and treated drinking water ranged between 8 and 3200 Endotoxin Units (EU)/mL and from 0.15 to 11 EU/mL, respectively. The microcystin concentrations in treated water were below the recommended safe limit for drinking water.

Other risks associated with the presence of Cyanobacteria in Lake Chivero include periodic fish kills due to the depletion of oxygen in the hypolimnion [65]. The massive fish kills in Lake Chivero have been linked to the collapse of cyanobacterial blooms [66].

MCs have been detected in fish [67], which poses potential risks to people who eat fish from Lake Chivero.

12.6.4 Cyanobacteria in raw and treated water from Lake Chivero—a serious health threat

Other challenges associated with the presence of Cyanobacteria in Lake Chivero are objectionable tastes and odors in drinking water [53]. This is

because the predominance of Cyanobacteria in raw water makes water purification difficult [68]. Dandadzi et al. [69] established that *M. aeruginosa*, *Anabaena* sp., and *Oscillatoria* sp. occurred in both raw water and the distribution system in Harare. Due to high algal density in raw water, the Morton Jaffray Water Treatment Works is failing to completely remove Cyanobacteria causing a carryover of algae into the distribution system [69]. This poses a potential threat to human health due to the likely occurrence of toxins in drinking water. The concentration of Cyanobacteria increased in the distribution systems which suggests regrowth. Detailed studies and monitoring are required to avert a potential health risk. This is especially so because, under climate change forecasts, potentially harmful algal species may proliferate in the Zimbabwean reservoirs [58].

Cyanobacteria should be the focus of lake management in Lake Chivero because it is the city of Harare's main water supply source for drinking water. More understanding is required of the development of Cyanobacteria in hypereutrophic systems as illustrated by the change from the expectations observed in Lake Chivero during the course of its evolution. The exhibition of "bistability" with distinct and turbid states in Lake Chivero provides a basis for beginning to understand the possible existence of two states within the algal assemblage under hypereutrophic conditions.

12.7 Cyanobacteria in Mozambican freshwaters

Cyanobacteria are common in the plankton composition of many lakes, reservoirs, lagoons, and wetlands in Mozambique, but species composition, density, and ability to produce cyanotoxins differ.

Although many studies have been conducted, particularly in America and Europe, addressing certain aspects such as (1) the occurrence of cyanobacterial mass populations, (2) cyanobacterial toxins, (3) adverse health effects of cyanotoxins and health, and (4) adverse impacts of cyanobacterial blooms on water supply, the use of water bodies and ecological status, surveys or studies in Mozambique are scarce. We have found a few published data regarding Cyanobacteria and cyanotoxins in Mozambique lakes. Apart from the below information from published papers, personal experiences and hitherto unpublished raw data about recent occurrences of Cyanobacteria in Mozambique are presented. Previous studies on Cyanobacteria and cyanotoxins in Mozambican environments were

performed by Mussagy et al. [70] who analyzed strains of the cyanobacterium *Arthrospira fusiformis* isolated from ponds in Mozambique as well as from Lake Nakuru, Kenya. Both strains tested negative for microcystin and ATX. The two strains were also tested for the presence of the *mcy*E gene, a part of the operon encoding for microcystin synthetase, and both strains were found negative. Bojcevska and Jergil [71] conducted a study on two water bodies in Mozambique, Pequenos Libombos Reservoir and Chitenguele lagoon, to investigate the removal efficiency of sand filtration coated with activated carbon. In this study, they used raw water from the two water bodies. The microcystin concentration in Pequenos Libombo varied between < 0.10 and 0.28 μg/L and in Chitenguele lagoon from 0.57 to 6.83 μg/L. Tamele et al. [10] summarized a few studies regarding Cyanobacteria and cyanotoxins from Mozambique based mainly on published studies. Pedro et al. [72–74] tested water collected from different places located in southern Mozambique, namely the Pequenos Libombos Reservoir, Lake Nhambavale, Chókwé irrigation channels, and Chidenguele lagoon.

Results from these studies indicated the presence of the Cyanobacteria *Microcystis* sp. (*M. novacekii, M. botrys*, and others) and *C. raciborskii*. The presence of the MC-LR, -YR, and -RR was detected. The concentrations of MCs in the Pequenos Libombos dam water was 0.02; in the Chókwé irrigation channels, it was 0.68; in Lake Nhambavale, it was between 0.86 and 7.82; and in Chidenguele, it was 0.57 to 6.83 μg/L.

12.7.1 Case studies

To document other observations of cyanobacterial developments in Mozambique, we will present a case study reporting heavy algal blooms that occurred in 2009 and 2011 at the Corumana Reservoir, southern Mozambique, where the lake surface was completely covered by masses of algae in a way never observed before (Fig. 12.4).

What is this bright green scum? Where does it come from? Is this bad? Can we drink the water and eat fish from the lake? Due to the lack of scientific knowledge regarding algal blooms, the first interpretation was that someone had dumped the green stuff in the water.

The Corumana Reservoir is a human-made lake located in the Maputo Province in Mozambique. The reservoir receives water from the Komati River, a river that runs from South Africa to Mozambique. The reservoir is mainly used to supply water to the local community for

Figure 12.4 View of an algal bloom at the Corumana Reservoir in 2011. *Photo: Aidate Mussagy.*

fishing, irrigation, and recreation. A team from the Department of Biological Science, Eduardo Mondlane University, was contacted by the water authorities and water samples were urgently collected at the Corumana Reservoir during the first bloom in 2009 and during the following bloom in 2011.

The collected water samples were observed under a light microscope for species identification. ELISA was used for the direct determination of total MCs in natural water. The ELISA analysis was done by using the EnviroGard-Microcystin Plate Kit. To understand the impact of these blooms on the local community, short interviews were conducted.

Microscopic examination of the water samples during the bloom period showed nearly a monospecific composition with the dominance of the genus *Microcystis*, particularly the species *Microcystis ichtyoblade* (Fig. 12.5). The microcystin contents, determined by the ELISA test, revealed the presence of microcystin. In the water bloom of 2009, the microcystin ranged from 460 to 550 μg/L, and in the water bloom in 2011, it ranged from 46 to 5500 μg/L.

According to the WHO guideline, the permitted limit of MC.

LR for drinking water is 1.0 μg/L, and the tolerable daily intake is 0.04 μg/kg. The microcystin concentration found in the Corumana Reservoir during the heavy bloom of Microcystis was much higher than the maximum limit (1 μg/L) recommended by WHO.

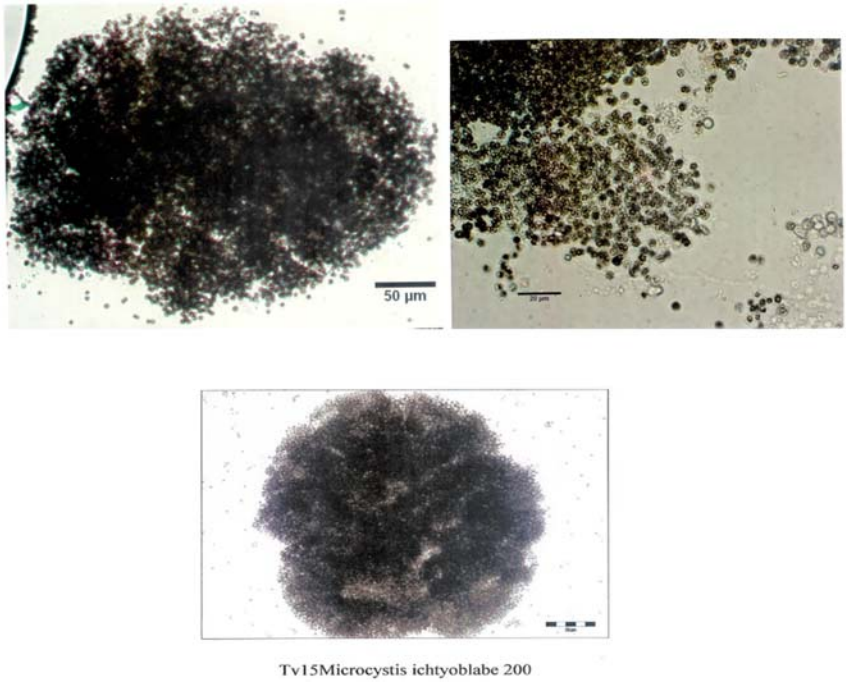

Figure 12.5 Microphotographs of *Microcystis ichtyoblade* found in the algal bloom at the Corumana Reservoir. *Photo: Aidate Mussagy.*

The fishermen interviewed during the period of the heavy bloom reported that they got skin problems after contact with the lake water, but did not report any other symptoms.

In 2021, two cases of cyanobacterial blooms occurred in two other reservoirs located in southern Mozambique, namely the Massingir Reservoir (Figs. 12.6 and 12.7) and Pequenos Libombos Reservoir (Fig. 12.8).

Microscopic observations of water samples taken during the bloom period in both reservoirs revealed that the algal community was dominated by a monospecific composition of *Microcystis* sp. Due to the lack of analytical facilities in Mozambique for testing cyanotoxins, it is unknown if the observed blooms of *Microcystis* sp. were toxic or not.

Mozambique is one of Africa's most vulnerable countries regarding climate change. Located on the southeastern coast of the continent, it is exposed to several extreme weather events including droughts, floods, and tropical cyclones. In addition, the biggest river in Mozambique runs from

Figure 12.6 An extremely heavy bloom of Cyanobacteria at Massingir Reservoir, 2021. *Photo: João Massicane.*

the neighboring countries of South Africa, Eswatini (former Swaziland), and Zimbabwe. Consequently, the water quality of rivers and lakes is influenced by activities and land use in the upstream drainage area.

In tropical waters, cyanobacterial blooms can be triggered as a consequence of environmental factors such as high temperatures, high light intensities, stagnation, the water residence time, and increased nutrient loading from drainage basins, particularly during heavy rain. All these factors may occur in tropical waters, thus, there is a potential that many waterbodies in Mozambique can experience severe cyanobacterial blooms in the future.

Toxicity screening of some water bodies where the Cyanobacteria occurred was found to be toxic, and in some of the sites, extremely toxic. The presence of cyanotoxins could be a threat since some of the water bodies are used for drinking water purposes for humans, and in many

Figure 12.7 Bloom at the Massingir Reservoir, 2021, was dominated by the *Microcystis* sp. *Photo: João Massicane.*

Figure 12.8 The dam and outlet of the Pequenos Libombos Reservoir. Some kilometers downstream, the people in a small village were using the river water for consumption without any treatment. September 2002. *Photo: Heléne Annadotter.*

cases, drinking water treatment is absent (Fig. 12.9). Therefore, the problem of cyanobacterial blooms formation and the subsequent risks to human health is an increasingly important and topical issue in Mozambique. This is a country with few people with ecological understanding regarding eutrophication and cyanobacterial blooms. Moreover, there is an urgent need for a water management strategy to reduce

Figure 12.9 People in the small village, downstream from the dam of Pequenos Libombos Reservoir, who are using the river water for consumption, laundry, and washing. September 2002. *Photo: Heléne Annadotter.*

nutrient inputs by changing agricultural practices. Fertilizers and manure are often spread without considering the effect on freshwater ecosystems. Moreover, in Mozambique, there is a reduced capacity to treat sewage water resulting in the loading of nutrients and organic matter that may pollute the water bodies and trigger cyanobacterial blooms.

12.8 Cyanobacteria in South African freshwaters

In a review by Harding and Paxton [75], relevant information is presented on cyanobacterial occurrences, associated toxicity, and poisonings in South Africa. Based on a chronology of cyanobacterial research in South Africa, Cyanobacteria were recorded from 1941 to 1943, the early phase of filling the Vaal Dam (Fig. 12.10). Since this period, a lot of cyanobacterial mass developments have been observed in many other lakes in South Africa.

Scott [76] reported the presence of toxic *Microcystis* in the Hartbeespoort Dam, a hypertrophic, warm, monomictic lake with high nitrogen and phosphorous loading from the surrounding area. Toxicity tests on *M. aeruginosa* forma *aeruginosa* using mouse bioassays confirmed that it was repeatedly toxic. Robarts [77] pointed out that the nutrients N and P, and wind, were the factors that, for a long period of the year, had caused the massive cyanobacterial blooms in the Hartbeespoort Dam. High N and P loading rates ensured that nutrients did not become limited

Figure 12.10 Water sampling in the Vaal Dam, October 2002. *Photo: Heléne Annadotter.*

and were therefore initially responsible for the high primary production. Wind patterns were responsible for the considerable spatial and temporal changes in the standing crop. The buoyancy mechanism of *M. aeruginosa* is a factor that made it easier for the population to remain within the euphotic zone.

Quibell et al. (1995), cited by Harding and Paxton [75], reported toxic forms of *M. aeruginosa* forma *aeruginosa* in several water bodies such as the Bon Accord Dam, Boskop Dam, Bospoort Dam, Buffelspoort Dam, Grootdraai Dam, and Klerkskraal Dam.

Quibell et al. (1995), cited by Harding and Paxton [75], reported livestock deaths associated with cyanobacterial toxicity from 1976 to 1986 in the Hartbeespoort Dam, Vaal Dam, Bon Accord Dam, Rietkuil Dam, Vanderkloof (PK Le Roux), Klipvoor Dam, and Allemanskraal Dam. By mouse bioassay tests, they detected cyanobacterial toxicity in several dams such as the Witbank Dam, Bronkhorstspruit Dam, Roodeplaat Dam, Rietvlei Dam, Bospoort Dam, Volksrus Dam, Erfinis Dam, Van Ryneveldspass Dam, Lake Arthur, and Stink Pan. Four different cyanobacterial genera were present in the samples taken from these waters but *Microcystis* spp. was the most common Cyanobacteria in the studied water bodies in South Africa.

Fosso-Kankeu et al. [78], analyzed water in containers used by households from rural villages in the district of the Limpopo Province, South Africa, and found the cyanobacterial genera *Microcystis, Anabaena,*

Oscillatoria, and *Pseudanabaena*. *Microcystis*, and *Anabaena* were the dominant genera. Additionally, *C. raciborskii* and *Oscillatoria* sp were recorded in containers from some of the villages.

The diversity of Cyanobacteria and cyanotoxins in the Hartbeespoort Dam was studied by Ballot et al. [79]. In this study, the presence of Cyanobacteria was assessed and isolated cyanobacterial strains were classified morphologically and phylogenetically and tested for MCs, CYN, STXs, and ATX and screened for toxin-encoding genes.

The study identified the following cyanobacterial species: *Sphaerospermopsis reniformis*, *Sphaerospermopsis aphanizomenoides*, *Cylindrospermopsis curvispora*, *Raphidiopsis curvata*, *Raphidiopsis mediterrranea*, and *M. aeruginosa*. They found that one of the *Microcystis* strains produced MCs and they detected 41 microcystin variants. All the strains found in the Harbeesport Dam tested negative for CYN, STXs, and ATX and their encoding genes, but in one of the microcystin-producing *Microcystis* strains, they found the *mcyE* gene of the microcystin gene cluster.

Mathews and Bernard [80] assessed 50 of the largest water bodies in South Africa by satellite remote sensing. They found that about 62% of the 50 waterbodies were hypertrophic with mass development of Cyanobacteria. From the few examples brought above, it is obvious that there is a strong likelihood that a large number of water bodies in South Africa undergo eutrophication with mass developments of Cyanobacteria. Toxicity screening of some water bodies where the Cyanobacteria occurred was found to be toxic. The presence of cyanotoxins is a real threat as some of the water bodies are used for drinking water purposes for humans. It is particularly alarming that some groups of people have to consume water with Cyanobacteria without having the facilities to purify the water.

12.9 Concluding remarks

In this review, we have shown that African waterbodies, just as in other parts of the world, have experienced developments of toxin-producing Cyanobacteria. Mass developments of Cyanobacteria have negative consequences for the freshwater ecosystem and may, for example, result in fish kill. The toxic Cyanobacteria blooms may also constitute a health risk for cattle, dogs, birds, and other wild animals who drink water from the lakes.

When water from lakes with mass occurrences of Cyanobacteria is used as a source of drinking water, cyanotoxins constitute a high-risk health threat for humans. The treatment in conventional water works may, as demonstrated in studies from Ghana and Zimbabwe, not efficiently remove cyanobacterial cells from the raw water, and consequently, toxin-producing Cyanobacteria can be present in the treated water that is distributed to consumers. The health risk is even more serious when humans, in impoverished communities, have to consume surface water with Cyanobacteria without any treatment.

Sustainable Development Goals, SDGs, particularly Goal 6, to ensure clean water and sanitation, require not only investments in infrastructure but also the protection and restoration of aquatic ecosystems. To counteract the development of toxin-producing Cyanobacteria in water bodies, it is important to implement monitoring and control measures in the catchments of vulnerable water bodies.

To reverse the development of Cyanobacteria in lakes and reservoirs, it is urgent to reduce the nutrient loads in runoff water, particularly phosphorus, nitrogen, and organic matter, from agricultural land. Moreover, the nutrients and organic matter in the effluents from sewage treatment works is another factor that may trigger cyanobacterial blooms. The discharge of untreated sewage water to lakes may occur during events of heavy rains. Other activities that may promote cyanobacterial blooms in the lakes are the discharge from industries, such as sugar factories, who may discharge organic material which result in oxygen deficit and promote Cyanobacteria.

It is also important to implement control measures to reduce erosion, since African countries, due to climate changes, are vulnerable to cyclones. These causes runoff from agricultural areas which will contribute to increasing the number of nutrients in lake ecosystems.

The scientific knowledge about Cyanobacteria and cyanotoxins may be inadequate among those that are responsible to protect and manage freshwater ecosystems. Hitherto, most studies on this matter are found in academic literature, which may not be available for every lake manager.

It is urgent that academic studies on Cyanobacteria and the management of eutrophic lakes are transformed into safety and action plans to increase awareness and define sharp measures to protect our water sources in case of the presence of Cyanobacteria blooms. WHO has already set guidelines regarding cyanotoxins in drinking water, but in most African

countries, cyanotoxins, due to lack of resources, are not monitored, and consequently, cannot be controlled.

Most people have a poor perception of exposure to Cyanobacteria and cyanotoxins, particularly the long-term effects of cyanotoxin exposure. Therefore, it is imperative to inform water authorities and the public about the risks of Cyanobacteria and cyanotoxins in lakes and drinking water.

Although some studies and publications have been conducted in some African countries, as exemplified in this chapter where we brought information from Ghana, Zimbabwe, Mozambique, and South Africa, more effort is needed to understand the relationship between nutrients, agriculture, industry, population growth, sanitation, and climate changes patterns and the Cyanobacteria bloom dynamics in African waterbodies.

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CHAPTER 13

Microbial ecosystem and climate changes in the African lakes, the Case of Lake Nasser

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13.1 Introduction

Lake Nasser was formed due to the construction of the High Dam at Aswan, Upper Egypt in 1964. It lies between latitudes 22°00′ and 23°58′ N and longitudes 30°35′ and 33°15′ E, and it is about 300 km long (Fig. 13.1).

The main channel of Lake Nasser is the deepest area of the lake, while several khors (side embayments) are also found. The khors occupy about 79% of the total lake's surface and represent 55% of the lake's volume [1]. The SO_4^- content of Lake Nasser is relatively high compared with other

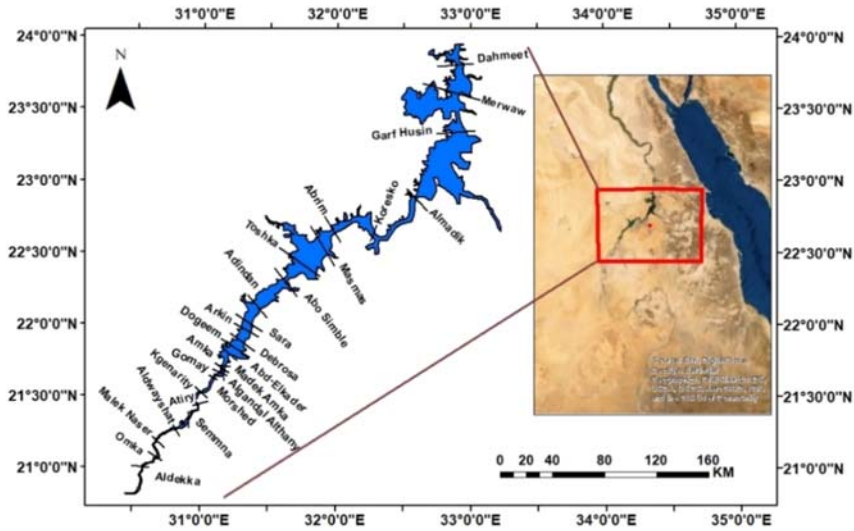

Figure 13.1 Image satellite of Lake Nasser.

Lakes of Africa
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human-made lakes. Lake Nasser has SO_4 content of about 30–50 times that of the Volta Lake (15–25 mg/L and 0.5 mg/L, respectively) [2]. The liberation of H_2S gas either as water or air pollutants during hot (spring and summer) and fairly hot (autumn) seasons might be due to the SO_4^- reduction by sulfate-reducing bacteria (SRB), under anaerobic conditions prevailing in bottom water and sediment, causing the change in taste and odor of the lake's water during these seasons [3]. In hydrothermal sediments of Lake Tanganyika, thermophilic SRB have been demonstrated at up to 80°C, with optimum temperatures for H_2S production of 63°C and 71°C. They were morphologically similar to the spore-forming *Desulfotomaculum* spp. [4] Lower bacterial counts ($3–5.1 \times 10^5$ cells/mL) were recorded in the middle part compared to the northern ($3.0–14 \times 10^5$ cells/mL) or the southern ($5.4–10 \times 10^5$ cells/mL) ones of Lake Tanganyika [5]. They demonstrated that the predominant bacteria of Lake Tanganyika were small bacilli (biovolume, 0.25 μm^3) with a width of 0.5 μm and a length of 1.3 μm, while bacterioplankton represented about 20% of the primary production [6]. During the dry season of 2002, Cyanobacteria, Actinobacteria, Nitrospirae, green nonsulfur bacteria, and Firmicutes divisions, and the Gamma and Delta proteobacteria subdivisions were identified in Lake Tanganyika. The vertical distribution of bacteria was related to oxygen and nutrient concentrations which were influenced by the thermal stratification of the water column. There is a positive diversity–productivity relationship in the epilimnion of the lake [7]. In Lake Victoria, the cyanobacterial blooms comprised over 90% Microcystis at concentrations of 34×10^3 colonies/mL (77.6 mg/L) [8]. The preponderance of Cyanobacteria in Lake Tanganyika at higher water temperatures (> 25°C) has led to concerns that increased water temperatures due to global warming could result in impairing phytoplankton dynamics, changing the phyto/zooplankton relationship, and reducing fish production [9]. Similar impacts of climate warming were recorded in tropical African lakes by Ndebele-Murisa et al. [10]. In Lake Nasser, *Microcystis comperei*, *Microcystis aeruginosa*, and *Lyngbya limnetica* were the dominant Cyanobacteria [11]. Studies by Conrad [12] and Bastviken et al. [13] revealed that 63% of CH_4 is emitted to the atmosphere due to human activities, while non-tropical freshwaters (14%), tropical freshwaters (9.5%), plants (6%), marine ecosystems (3%), termites (3%), and gaseous hydrates (2%). Although deep anoxic waters of Lake Kivu are characterized by high CH_4 (60 km^3 at 0°C and 1 atm), significant rates (up to 0.37 μmol/L/d) of pelagic CH_4 production were also measured in

oxic waters. However, the low release of CH_4 into the air might be due to high CH_4 oxidation. Aerobic and anaerobic CH_4 oxidation rates were 27 ± 2 and 16 ± 8 μmol/L/d, respectively [14]. Climatic change, water pollution, and overfishing are among the global and local environmental challenges that threaten the African Great Lakes. However, these challenges are not fully monitored [15]. In Lake Nasser, despite the relevance of microflora, their role in emissions of heat-trapping gases and the influences of climate change on microbial communities have not been addressed.

13.2 Microflora of Lake Nasser

13.2.1 Viruses

Viruses can readily contaminate surface waters. So, the study of viruses is extremely important to estimate the associated public health risks. However, little virological information is available on Lake Nasser water. Enteroviruses were detected in nine sites, especially in the Abu-Simbel region. Poliovirus type 2 was the most common virus detected and the virus count ranged from 6 to 42 Pfu/L [16].

13.2.2 Bacteria

13.2.2.1 The main channel

13.2.2.1.1 Total bacterial counts

Samples were collected along Lake Nasser from winter to autumn both during 1974 and 1984. The lowest total bacterial counts (TBCs) at 22°C and 37°C were detected in winter, while the highest was in summer due to a renewal of nutrients carried by the flood. Spatially, TBCs decreased from south to north except near the High Dam. Compared to 10 years earlier, TBCs at both incubation temperatures were increased (Fig. 13.2A and B). The ratios of TBCs at both incubation temperatures were over 1.0 [17].

The bacterial flora along 150 km at various depths and localities of Lake Nasser was studied by Elwan [18]. All the isolated thermophilic bacteria (9 strains) belonged to *Bacillus stearothermophilus*. Two strains were facultative, while seven were obligate thermophiles. During 1996, TBCs in Lake Nasser varied from 4×10^3 to 187×10^6 and 3×10^3 to 52×10^3 Cfu/mL at both incubation temperatures [19]. A more than 100-fold increase in TBCs was recorded at all sites in 1996 by Rabeh

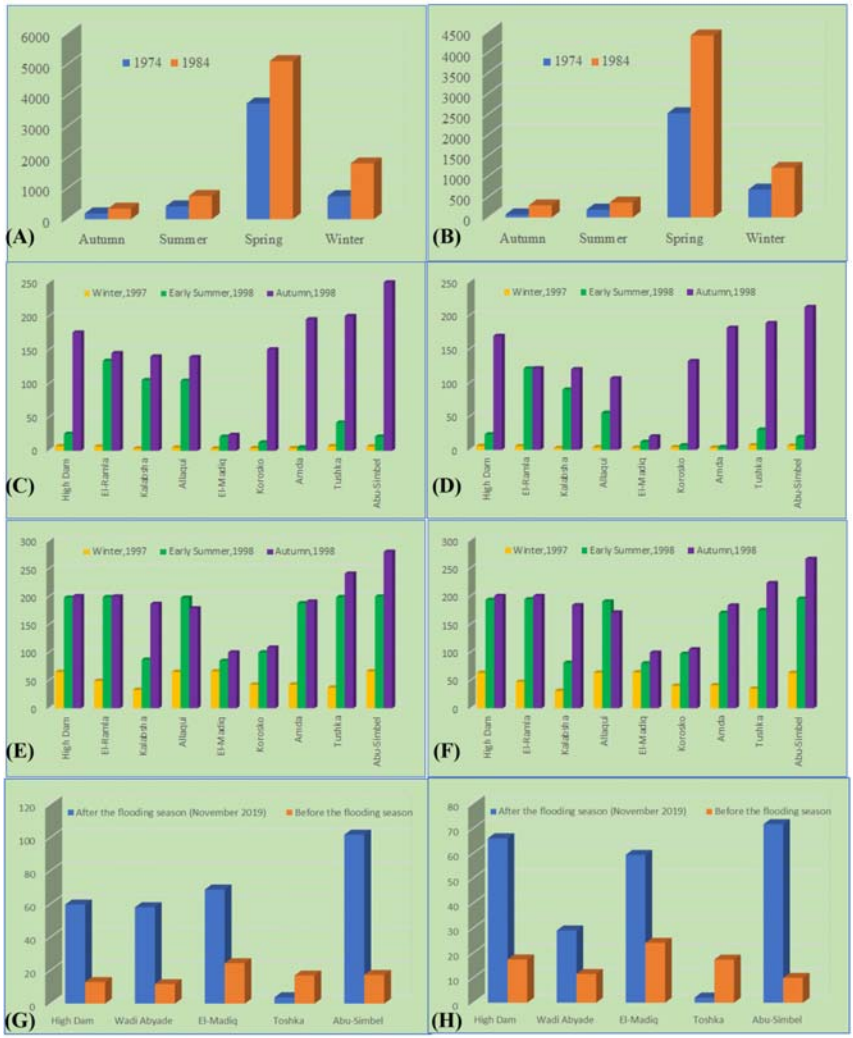


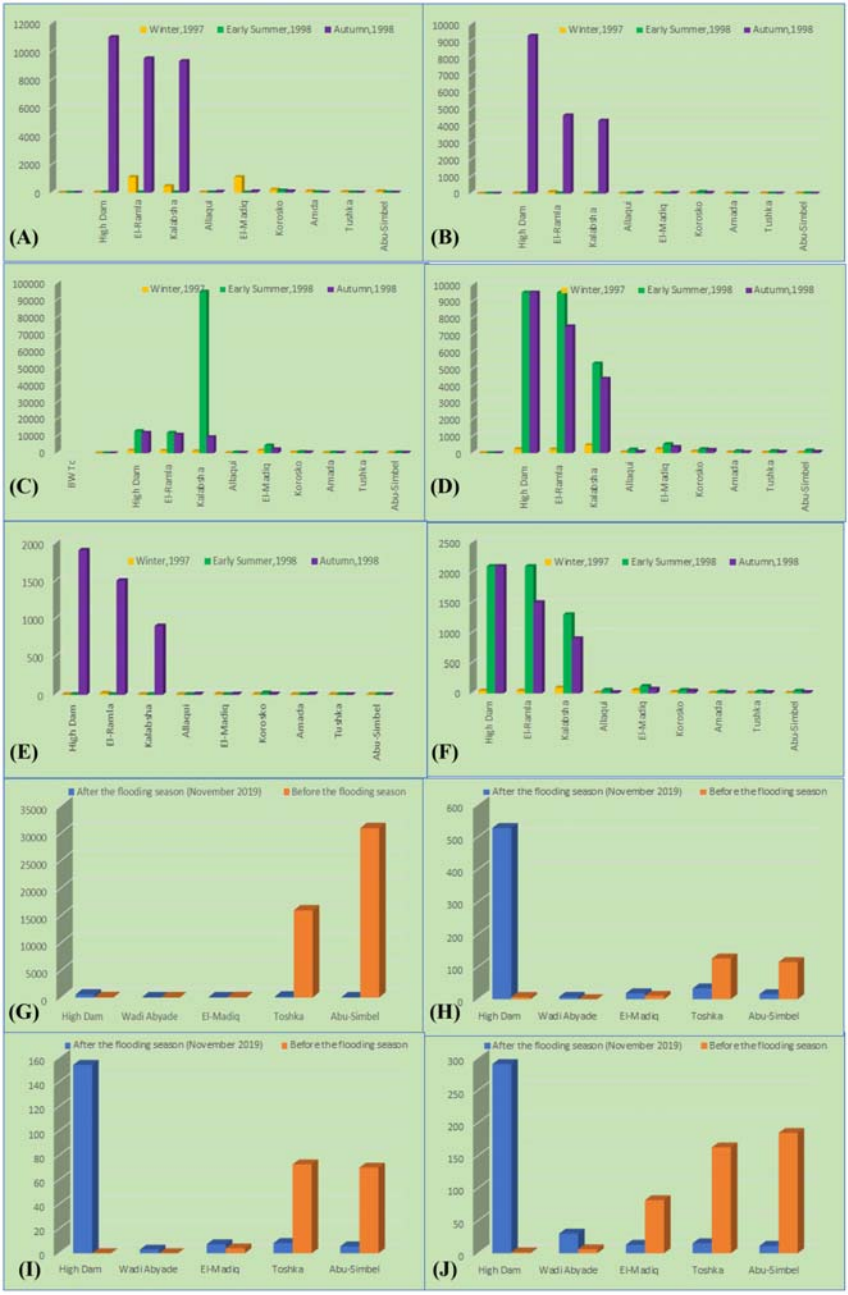
Figure 13.2 (A) Changes in total bacterial counts (TBCs/mL) at 22°C in Lake Nasser during 1974 and 1984. (B) Changes in total bacterial counts (TBCs/mL) at 37°C in Lake Nasser during 1974 and 1984. (C) Total Bacterial Counts (TBCs × 106 Cfu/mL) at 22°C in surface water of main channel of Lake Nasser during 1997 and 1998. (D) Total Bacterial Counts (TBCs × 10^6 Cfu/mL) at 37°C in surface water of main channel of Lake Nasser during 1997 and 1998. (E) Total Bacterial Counts (TBCs × 10^6 Cfu/mL) at 22°C in the bottom water of main channel of Lake Nasser during 1997 and 1998. (F) Total Bacterial Counts (TBCs × 10^6 Cfu/mL) at 37°C in the bottom water of main channel of Lake Nasser during 1997 and 1998. (G) Averages of Total Bacterial Counts (TBCs × 10^3 Cfu/mL) at 22°C in main channel of Lake Nasser after the flooding season, 2019, and before the flooding season, 2020. (H) Averages of Total Bacterial Counts (TBCs × 10^3 Cfu/mL) at 37°C in main channel of Lake Nasser after the flooding season, 2019, and before the flooding season, 2020.

et al. [19] compared with those obtained by Elewa and Azazy [17] in 1974–84.

Rabeh [20] studied the effect of a higher-than-average flood on the microbial water quality of Lake Nasser during 1997–98. During winter, the lowest TBCs at 22°C (3.32×10^6 Cfu/mL and 33.01×10^6 Cfu/mL for subsurface water (SW) and bottom water (BW), respectively) and 37°C (3.01×10^6 Cfu/mL and 31×10^6 Cfu/mL for SW and BW, respectively) were recorded. The highest TBCs at 22°C (250×10^6 Cfu/mL and 280×10^6 Cfu/mL for SW and BW, respectively) and 37°C (212×10^6 Cfu/mL and 266×10^6 Cfu/mL for SW and BW, respectively) were during autumn (flood), when new nutrients and allochthonous microflora arrived in the lake (Fig. 13.2C–F). In Lake Nasser, TBCs at both incubation temperatures were lower in subsurface water than at the bottom [21]. Changes in TBCs at both incubation temperatures were similar, and thus, ratios between them were slightly higher than 1. APHA [22] reported that the ratio of 22°C:37°C counts in non-polluted waters is usually 10 or more, while it is usually below 10 in polluted waters. Thus, the subsurface and bottom waters of the lake are polluted [20]. Low ratios were previously recorded for Lake Nasser by Elewa and Azazy [17] and Rabeh [23] and for other inland waters of Egypt [24,25]. The bacteria were monitored by Goher et al. [26] after (November 2019) and before (June 2020) flooding. After flooding, TBCs at both incubation temperatures ranged from 1.5×10^3 to 135×10^3 Cfu/mL and 1×10^3 to 110×10^3 Cfu/mL, respectively. Before the flooding, TBCs were lower than after flooding varying between 0.8×10^3 and 34×10^3 Cfu/mL and between 0.9×10^3 and 32×10^3 Cfu/mL at both incubation temperatures, respectively (Fig. 13.2G and H).

13.2.2.1.2 Bacterial indicators of sewage pollution

The numbers of total coliforms (TC) and fecal coliforms (FC) during 1996 varied from 0.0 to 54×10^4 for TC and from 0.0 to 33×10^4 org.100 mL^{-1} for FC. The highest counts of both indicators recorded during winter might be due to floating hotels along the lake. The Aswan fish factory might add to the pollution problem [19]. During 1997–1998, the TC ranged from 3 to 11×10^3 and from 150 to 95×10^3 org 100 mL^{-1} for SW and BW, respectively, while FC ranged from 0.0 to 93×10^2 and from 24 to 95×10^2 org 100 mL^{-1} for SW and BW, respectively. On the other hand, fecal streptococci (FS) ranged from 1 to 19×10^2 and from 6 to 21×10^2 org 100 mL^{-1} for SW and BW, respectively (Fig. 13.3A–F) [20].


Winter,1997
Early Summer,1998
Autumn,1998
High Dam
El-Ramla
Kalabsha
Allaqui
El-Madiq
Korosko
Amada
Tushka
Abu-Simbel
(A)
(B)
(C)
(D)
(E)
(F)
After the flooding season (November 2019)
Before the flooding season
Wadi Abyade
Toshka
(G)
(H)
(I)
(J)

The highest TC and FC were recorded at the High Dam, while the lowest TC and absence of FC were observed in the south of the lake during the flood due to dilution by the flood. During winter, high bacterial indicators might reflect the polluting effect of tourism activities along the lake. This is in harmony with the high concentration of ammonia nitrogen (3−171.36 and 24.05−345.74 μg/L) in both water layers during this season. The highest counts of both indicators in bottom waters might be due to either lower bactericidal effects of UV, higher concentrations of ammonia nitrogen, sedimentation of adsorbed bacteria, or resuspension from sediment [20]. The numbers of FC in sediments may amount to $1 \times 10^2 - 1 \times 10^3$ times those in water [27]. During low water levels (2005), the highest counts of FC (ranging from 400 to 800 Cfu/100 mL) were observed, while the lowest ones (ranging from 110 to 140 Cfu/100) were recorded during high water levels (2001) [28]. The TC/FC ratios ranged between 0.0 and 0.845 and between 0.025 and 0.791 in both water layers [20]. As regards FS, they ranged from $0.0 - 19 \times 10^2$ and from $6 - 21 \times 10^2$/100 mL in the surface and bottom waters, respectively [20]. Water samples were collected seasonally from three sites in Lake Nasser (Adendan, Abou Simbel, and Tushka) from 2010 to 2011. All bacterial indicators were recorded in low densities, following the order TC>FS>FC. The densities of these indicators were within international standard limits (5000, 2000, and 1000 Cfu/100 mL) for TC, FC, and FS, respectively. Consequently, the lake is safe from a bacteriological point of view [29].

Figure 13.3 (A) Most Probable Numbers (MPNs/100 mL) of Total Coliforms (TC) in surface water of main channel of Lake Nasser. (B) Most Probable Numbers (MPNs/100 mL) of Fecal Coliforms (FC) in surface water of main channel of Lake Nasser. (C) Most Probable Numbers (MPNs/100 mL) of Total Coliforms (TC) in the bottom water of main channel of Lake Nasser. (D) Most Probable Numbers (MPNs/100 mL) of Fecal Coliforms (FC) in the bottom water of main channel of Lake Nasser. (E) Most Probable Numbers (MPNs/100 mL) of Fecal Streptococci (FS) in the surface water of main channel of Lake Nasser. (F) Most Probable Numbers (MPNs/100 mL) of Fecal Streptococci (FS) in the bottom water of main channel of Lake Nasser. (G) Averages of Total Coliforms (TC MPN/100 mL) in main channel of Lake Nasser after the flooding season 2019 and before the flooding season, 2020. (H) Averages of Fecal Coliforms (FC MPN/100 mL) in main channel of Lake Nasser after the flooding season 2019 and before the flooding season, 2020, (I) Averages of *E. coli* (Cfu/100 mL) in main channel of Lake Nasser after the flooding season 2019 and before the flooding season, 2020. (J) Averages of Fecal Streptococci (FS MPN/100 mL) in main channel of Lake Nasser after the flooding season 2019 and before the flooding season, 2020.

After flooding (November 2019), the TC bacteria fluctuated between 0 and 1100 MPN 100 mL^{-1}, and between 4 and 46,000 MPN 100 mL^{-1} before flooding (June 2020), while the FC numbers were in the range of 0.0–1100 MPN 100 mL^{-1} and 0.0–240 MPN 100 mL^{-1} in the post- and pre-flood periods, respectively. The numbers of FS in both periods were similar and ranged within 0–460 MPN 100 mL^{-1}. The numbers of *E. coli* fluctuated between 0.0 and 250 Cfu 100 mL^{-1} after flooding and between 0 and 150 Cfu 100 mL^{-1} before flooding (Fig. 13.3G–J) [26]. More recently, the TC varied from 15 to 460 MPN/100 mL^{-1} after flooding (December 2020), while their numbers ranged from 0 to 1500 MPN/100 mL^{-1} before flooding (June 2021). On the other hand, the FC fluctuated from 0 to 36 MPN/100 mL^{-1} and from 0 to 1100 MPN/100 mL^{-1} after and before flooding, respectively. The numbers of FS ranged from 0 to 210 MPN/100 mL^{-1} and from 0–1200 MPN/100 mL^{-1} after and before flooding, respectively [30].

13.2.2.1.3 Bacteria involved in biogeochemical cycles

High counts of aerobic nitrogen fixer *Azotobacter* were in summer and autumn, while the counts of anaerobic clostridia were lower in water than the *Azotobacter*, especially in the oxygenated water during winter and spring. In comparison to 10 years earlier, nitrifying bacteria and nitrification activity increased in the lake after the period of drought (Fig. 13.4A–C) [17]. Aerobic cellulose-decomposing bacteria increased markedly in summer and autumn in parallel with organic carbon content (Fig. 13.4D) [17]. SRB were completely absent both from bottom water and sediment during winter, while in early summer, they varied from 0.21 to 0.64 MPNs/mL and 1.4 to 450 MPNs/g (Fig. 13.4E and F) for both bottom water and sediment, respectively [20].

13.2.2.2 The Khors

13.2.2.2.1 Total viable bacterial counts

During 1996, TBCs at 22°C in subsurface water varied between 0.12×10^5 Cfu/mL at Khor Korosko in autumn and 933×10^5 Cfu/mL in spring at Khor El-Allaqui. Those at 37°C ranged between 0.06×10^5 and 650×10^5 Cfu/mL at Khor El-Allaqui in autumn and spring [23]. In bottom waters, TBCs at 22°C varied between 0.06×10^5 Cfu/mL at Khor El-Ramla in autumn and 961×10^5 Cfu/mL at Khor El-Allaqui in spring. TBCs at 37°C ranged between 0.1×10^5 Cfu/mL in autumn at Khor El-Ramla and Kalabsha and 680×10^5 Cfu/mL at El-Allaqui in

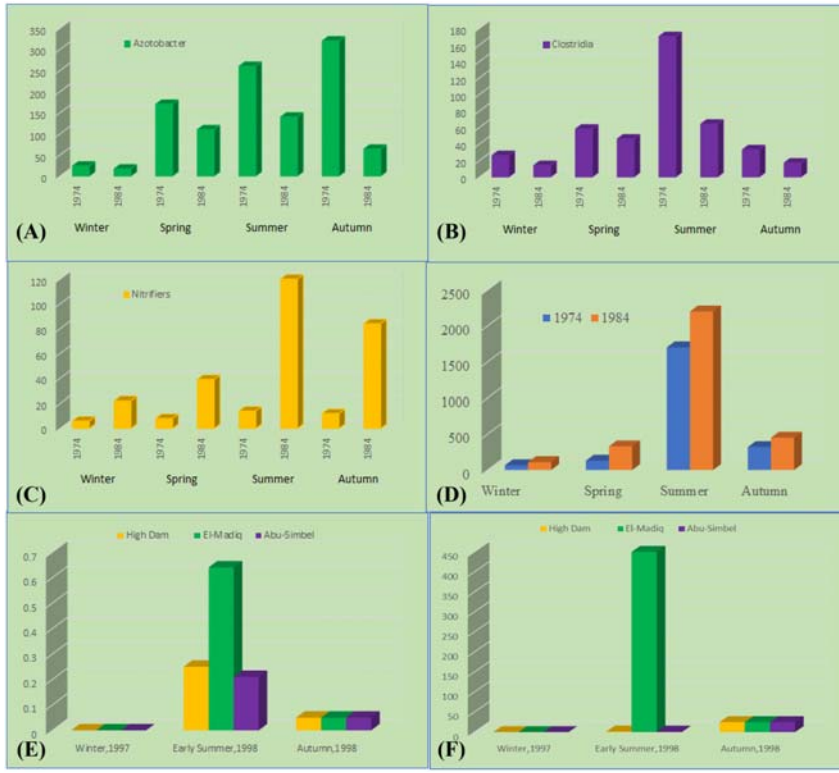


Figure 13.4 (A) Changes in nitrogen cycle bacteria (*Azotobacter*)/mL water in Lake Nasser during 1974/1984. (B) Changes in nitrogen cycle bacteria (Clostridia)/mL water in Lake Nasser during 1974/1984. (C) Changes in nitrogen cycle bacteria (Nitrifiers)/mL water in Lake Nasser during 1974/1984. (D) Changes in aerobic cellulose-decomposing bacteria/mL water in Lake Nasser during 1974/1984. (E) Most Probable Numbers (MPNs/mL) of sulfate-reducing bacteria (SRB) in the bottom water of main channel of Lake Nasser. (F) Most Probable Numbers (MPNs/g) of sulfate-reducing bacteria (SRB) in the sediment of main channel of Lake Nasser.

spring (Fig. 13.5A–D). Khor El-Ramla showed the lowest average TBCs at both incubation temperatures in both water layers [23]. Also, TBCs at both incubation temperatures were higher in the bottom than in subsurface water. The ratios at 22°C to that at 37°C were slightly more or less than one [23].

During 1997–98, the source point (intake) for Tushka Project as well as Khor El-Ramla and Kalabsha was selected for bacteriological examination. The lowest Total viable bacterial counts at 22°C (6×10^6 Cfu/mL and 35.29×10^6 Cfu/mL for SW and BW, respectively) and 37°C

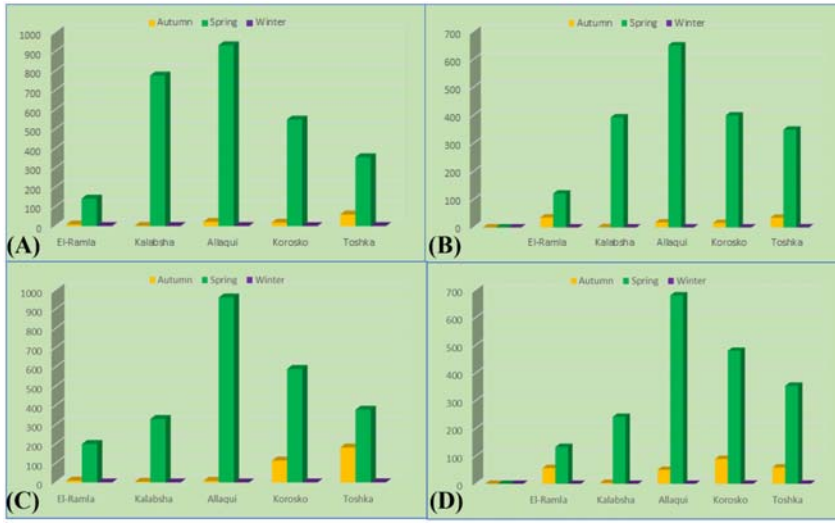


Figure 13.5 (A) Total bacterial counts (TBCs × 105 Cfu/mL) at 22°C in surface water of some important Khors of Lake Nasser during 1996. (B) Total bacterial counts (TBCs × 10^5 Cfu/mL) at 37°C in surface water of some important khors of Lake Nasser during 1996. (C) Total bacterial counts (TBCs × 10^5 Cfu/mL) at 22°C in the bottom water of some important khors of Lake Nasser during 1996. (D) Total bacterial counts (TBCs × 10^5 Cfu/mL) at 37°C in the bottom water of some important Khors of Lake Nasser during 1996.

(6.17×10^6 Cfu/mL and 34.94×10^6 Cfu/mL for SW and BW, respectively) were recorded during winter, with high counts in summer. The highest TBCs at 22°C (199.6×10^6 Cfu/mL and 242×10^6 Cfu/mL for SW and BW, respectively) and 37°C (165.5×10^6 Cfu/mL and 221.4×10^6 Cfu/mL for SW and BW, respectively) were during autumn's flood that carries allochthonous microflora and new nutrients to the lake. Also, the flood rises the lake level and the khor's shore is flooded where fresh organic matter is provided from drowned vegetation [20]. During spring, 2006, the total viable counts of bacteria developing at 22°C ranged from 4×10^3 to 1.4×10^6 Cfu/mL, while those developing at 37°C varied from 2×10^3 to 3×10^6 Cfu/mL. The lowest bacterial counts were recorded at Khor Korosko. This reflects the effect of grazing pressure of zooplankton on the bacteria since this khor recorded the flourishing of zooplankton (60000 org./m^3) [31]. These results agree with those reported by Rabeh [20&23] and Rabeh et al. [19&32]. During 2015, bacteriological analyses for surface and bottom waters of four khors (Wadi Abyad, Rahma, El-Ramla, and Kalabsha) were studied during the winter

and spring seasons by Ali et al. [32] who found that TBCs either growing at 22°C or 37°C ranged from 10^2 to 10^6 Cfu/mL, respectively. Mahmoud et al. [33] studied TBCs during the drought season (May 2015) and high flooding season (December 2015) in Dahmeit and Tushka Khors and found that TBCs growing at 22°C or 37°C ranged from 1.8 to 4.2 and 1.3 to 4.1 Log No/mL for the Dahmeit and Tushka Khors, respectively in the drought season; and from 1.3 to 3.1 and 3.1 to 4.5 Log No/mL in the high flooding season. Statistically, positive correlations between the bacterial counts at 22°C/37°C ($r = 0.758$) and between water temperature and TBCs ($r = 0.276$) were recorded, which agree with those reported by Sabae and Rabeh [34]. The ratio of TBCs at 22°C−37°C varied between 0.01 and 6.2 [32], while this ratio varied between 0.6 and 2.1 during the drought season and from 0.5 to 1.3 during the high flooding season [33]. A higher mean of thermophilic bacteria (250 Cfu/mL) was recorded during the spring season, while the lowest ones (1 Cfu/mL) were in the winter season. The Wadi Abyad Khor recorded the highest means of thermophilic bacteria (188 and 260 Cfu/mL) in both the surface and bottom water layers, respectively. The highest means (123 and 180 Cfu/mL) were recorded both in the water layers at beginning of the khor [32]. Compared to thermophilic bacteria, the numbers of spore-forming bacteria were minimal. The highest number of spore-forming bacterial was recorded in Wadi Abyad (means of 111 Cfu/mL) and Rahma (means of 76 Cfu/mL) compared to Kalabsha (means of 38 Cfu/mL) and El-Ramla (means of 30) [32]. In the sediment, TBCs varied between 5.1×10^7 and 3.7×10^9 Cfu/g, with the highest mean count (1.8×10^9 Cfu/g) in the Rahma Khor during winter as well as the Rahma (mean of 7.4) and El-Ramla (6.0×10^8 Cfu/g) khors during the spring season. The lowest numbers were found in the El-Ramla Khor (means of 6.1×10^7 Cfu/g) in winter and the Kalabsha Khor (means of 2.1×10^8 Cfu/g) during the spring [32]. On the other hand, the spore-forming bacteria fluctuated between <1 and 1.7×10^7 Cfu/g sediment. The Rahma Khor recorded higher counts of spore formers in winter (means of 9.7×10^6) and spring (means of 2.2×10^4 Cfu/g). The Spore formers constituted >40−85 of the total bacteria and >48%−101% of diazotrophs [32].

13.2.2.2.2 Bacterial indicators of sewage pollution

Rabeh [23] reported that during 1996, the TC ranged between 2 org 100 mL^{-1} in the subsurface water of Khors El-Ramla, Kalabsha, El-Allaqui,

and Korosko in autumn, and 5×10^4 org/mL at Khor El-Ramla during winter (Fig. 13.6A–D). The FC was absent in autumn at Khors El-Ramla, Kalabsha, and Korosko; the highest value was 32×10^2 org 100 mL^{-1}. The high coliforms during winter may be due to increasing fishing activities and/or high pH values (8.61) [23]. The TC was absent in bottom waters in autumn and then recorded 9×10^4 org 100 mL^{-1} at The Khor Kalabsha during winter. The FC was completely absent at Khors Kalabsha and Korosko in autumn and recorded 9×10^3 org 100 mL^{-1} at Khor Kalabsha in winter. As regards khor variations, Khor Tushka had the lowest average TC in both layers of water, while Khor El-Ramla and Khor Kalabsha had the highest in parallel with pH averages, where the lowest average (8.17) was in Khor Tushka and the highest (8.29 and 8.37) were in Khor El-Ramla and Kalabsha, respectively. Khor Korosko recorded the lowest average FC, while the highest was in Khor Kalabsha. The high TC and FC at Khors El-Ramla and Kalabsha is attributed to the fishing activities (1997 fishing boats and 6841 fishermen) in 1997 [35]. Against low numbers in Khor Tushka, the

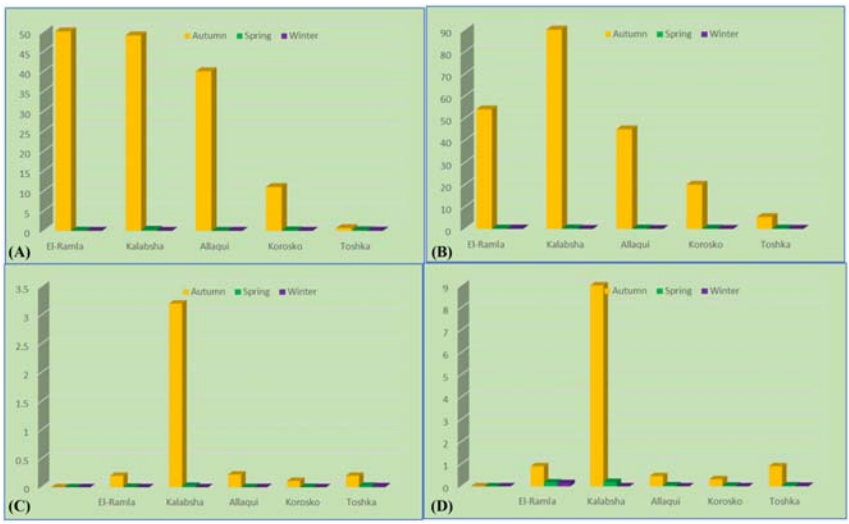


Figure 13.6 (A) Most probable numbers (MPNs × 103org/100 mL) of total coliforms (TC) in surface water of some important Khors of Lake Nasser during 1996. (B) Most probable numbers (MPNs × 10^3org/100 mL) of total coliforms (TC) in the bottom water of some important khors of Lake Nasser during 1996. (C) Most probable numbers (MPNs × 10^3org/100 mL) of fecal coliforms (FC) in surface water of some important khors of Lake Nasser during 1996. (D) Most probable numbers (MPNs × 10^3org/100 mL) of fecal coliforms (FC) in bottom water of some important khors of Lake Nasser during 1996.

high numbers of coliforms in Khor El-Ramla is in harmony with a high concentration of ammonia in the latter (26.94 μg/L). Hosny [36] and Rabeh [24] reported that ammonia was required for the proliferation of these bacteria. In concordance with Rabeh [21,37], coliforms were higher at the bottom than in subsurface waters.

During 1997–1998, The TC ranged from 3 to 93×10^2 and from 23 to 11×10^3 org/100 mL for SW and BW, respectively, while the FC ranged from 0.0 to 43×10^2 and from 9 to 75×10^2 org/100 mL for SW and BW, respectively. The FS ranged from 2 to 21×10^2 and from 3 to 39×10^2 org/100 mL for SW and BW, respectively [23]. The TC/FC ratios ranged from 0.25 to 0.77 and 0.25 to 0.68 in both water layers, respectively. At the beginning of the El-Sheikh Zayed canal, the TC and FC were 3–460 org. 100 mL^{-1}, 0.0–21 org. 100 mL^{-1}, and 23–9300 org. 100 mL^{-1}, and 9–900 org. 100 mL^{-1} in both water layers. The ratios varied from 0.0 to 0.18 and 0.016 to 0.39 in both water layers. In the khors, the FC/FS ratio varied from 1.4 to 2.25 and 1.8 to 3 for subsurface and bottom waters due to fishing activities and about 2×10^4 heads of grazing cattle around the lake [23]. The TC, FC, and FS were completely absent at both Khor Korosko and East Tushka. Also, the FC and FS were not detected in Khor Kalabsha and West Tushka. This might be attributed to (1) grazing pressure of zooplankton on these bacteria, (2) the lethal effect of solar radiation, which increases the death rate of the indicator bacteria, in addition to the absence of point source of pollution [31]. These findings agree with those of Rabeh et al. [38] as well as Sabae and Rabeh [34]. The highest counts of the indicator bacteria were recorded at Khor El-Ramla (93, 45, and 70/100 mL water for TC, FC, and FS, respectively) and Garf Hussein (90, 45, and 55/100 mL water). This reflects the high fecal pollution from the fishermen's activities and their frequentation at both khors [31]. The same observation was previously reported by Rabeh, et al. [19] and Rabeh [20,21,23]. Geldreich [39] reported that the FC/FS ratio points to the source of pollution whether it is human (>4) or animal (<0.7). The FC/FS ratios in the studied khors were in the ranges of (0–1), (0–0.32), (0.81–1.75), (0–0.44), and (0–4) for El-Ramla, Kalabsha, Garf Hussein, East Tushka, and West Tushka, respectively [31]. As per Rabeh [20,23] and Rabeh and Azab [40], this may indicate the mixed origin of fecal pollution. According to the guideline criteria for indicator organisms of the European Commission (EC) guide standard (1998), which accepts the guide values of up to 500/100 mL for TC and 100/100mL for both FC and FS, the survey of the

indicator bacteria in the studied khors showed that the bacteriological quality of the water is suitable for drinking and aquaculture purposes [31]. The highest counts of FC (ranged from 500 to 900 Cfu/100 mL) were observed during low water levels (2005), while the lowest ones (ranged from 110 to 140 Cfu/100) were recorded during high water levels (2001) in the khors of the lake [28]. The FS counts ranged in the surface water of the studied khors from 2 to 2100 org/100 mL while they ranged in the bottom the water from 3 to 3900 org/100 mL. On the other hand, they ranged at the source point from 0.0 to 4 and 2 210 org/100 mL in the surface and bottom waters, respectively [20]. The MPN of the bacterial indicators of pollution varied between >0−1800, >0−350, and >0−15 MPN/100 mL for TC and FC as well as FS, respectively. The ratio of FC to FS varied from 0 to 22 during winter and 0 to 55 during spring [32]. The MPN varied from 0 to 240, 0 to 23, and 0 to 29 MPN/100 mL for TC, FC, and FS, respectively in the high flooding season (December 2015), while they respectively varied between 0 and 240, 0 and 21, and 0 and 460 MPN/100 mL in the drought season (May 2015) [33]. During the drought season (May 2015) and high flooding season (December 2015), the FC:FS ratio varied from 0 to 0.8 in all samples except for site one for Tushka Khor which recorded 5.3 [33].

13.2.2.2.3 Bacteria involved in biogeochemical cycles

During winter, SRB was absent from near-bottom waters and sediments at almost all eight stations at five khors, except the sediment of Korosko where they recorded 13 org/g [21]. Khor Kalabsha showed higher counts (varied between 0.02 and 0.05 org/mL and 25 and 55 org/g in the bottom water and sediment) than Khor El-Ramla (varied between 0.04 and 0.05 org/mL and 25 and 45 org/g in the bottom water and sediment). The lowest counts were in Khor Tushka at the source point station (varied from 0.0 to 0.021 org/mL and from 1.2 to 25 org/g in the bottom water and sediment) (Fig. 13.7A and B) [20]. From autumn 2001 to the spring of 2002, 322 isolates comprise five genera of purple sulfur bacteria (Chromataceae) were isolated from Lake Nasser at successive sites (Khor El-Ramla to the west and Khor Manam to the east). The five genera were 161 (50%) *Allochromatium*, *Thiocystis* 50 (15.53%), *Thiocapsa* 40 (12.42%), *Thiodictyon* 38(11.8%), and *Lamprocystis* 33(10.25%). These genera included six species, namely *Allochromatium vinosum* and *Allochromatium warmingii*; *Thiocystis violacea*; *Thiocapsa roseopersicina*; *Thiodictyon elegans* and *Lamprocystis roseopersicina* [41]. On the other hand, nitrogen-fixing bacteria

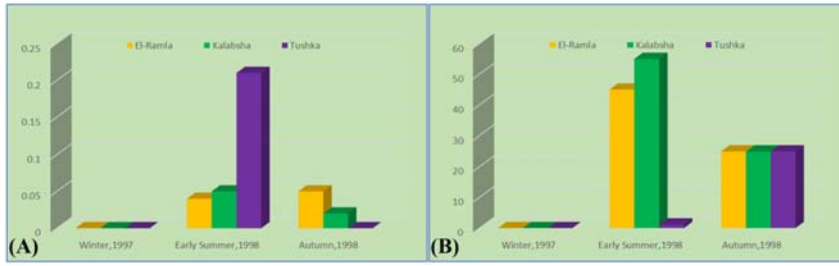


Figure 13.7 (A) Most Probable Numbers (MPNs org/mL) of sulfate-reducing bacteria (SRB) in the bottom water of some important khors of Lake Nasser, (B) Most Probable Numbers (MPNs org/g) of sulfate-reducing bacteria (SRB) in the sediment of some important khors of Lake Nasser.

(diazotrophs) were present in high population density in all samples during high flooding (December 2015) and drought seasons (May 2015) ranging from 3.0 to 5.7 Log No/mL. The Tushka Khor recorded higher nitrogen-fixing bacteria than the Dahmeit Khor (mean 4.5 and 4.1 Log No/mL, respectively). Also, the higher flooding season recorded higher populations of diazotrophic bacteria (mean 4.6 Log No/mL) than the drought season (mean 4.4 Log No/mL) for the Tushka Khor and Dahmeit Khor (mean 4.8 and 3.4 Log No/mL, respectively) [33]. Also, Ali et al. [32] found that the total diazotrophs count ranged from 6.2×10^6 to 1.9×10^9 Cfu/g sediment, while the spore-forming diazotrophs varied from $<1-2.7 \times 10^7$ Cfu/g sediment. The Kalabsha Khor recorded the highest diazotrophic bacteria (means of 2.2×10^8 Cfu/g) during winter and the El-Ramla Khor (1.0×10^9 Cfu/g) during spring.

13.2.2.2.4 Bacteria in various organs of Nile tilapia

Coliform and streptococcal groups on the skin surface and gills (32 samples each), intestinal tract, raw fish flesh, and raw flesh (4 samples each) of *Tilapia nilotica* Linn in Lake Nasser were studied. Streptococcus group was recorded in 13 samples taken from the fish surface and 12 samples out of 32 swabs from the gills. The streptococcal group was found in 100% of the intestine samples and raw fish flesh. Coliforms were recorded at about 43% of the skin or gill samples, all intestine and raw fish flesh samples [42]. The highest bacterial load of various fish organs was recorded in the Dahmeit Khor ($12-1715294$ Cfu $\times 10^3$/g) compared to the Tushka Khor ($53-1440000$ Cfu $\times 10^3$/g). In general, the drought season (May 2015) recorded a higher bacterial load ($2 \times 10^7-2 \times 10^9$ Cfu/g) than the higher

flooding season (December 2015) ($1 \times 10^4 - 5 \times 10^6$ Cfu/g) for both khors. The total spore-forming bacterial (TSF) count was higher in the Tushka Khor ($2-9 \times 10^4$ Cfu/g) compared to that in the Dahmeit Khor ($1-4 \times 10^4$ Cfu/g). The drought season (May 2015) recorded a higher TSF load than the higher flooding season (range $1 \times 10^3 - 9 \times 10^4$ Cfu/g and $1-3 \times 10^4$ Cfu/g, respectively) for both the khors. During the drought season (May 2015), Enterobacteriaceae recorded higher numbers (range $5 \times 10^6 - 8 \times 10^7$ Cfu/g) than in the higher flooding season (range $3 \times 10^3 - 8 \times 10^5$ Cfu/g, respectively). *Salmonella* sp. was detected in 50% of the tissue samples collected from the Dahmeit and Tushka Khors [33]. To understand the contribution of the microbiota to the health of the fish, the diversity of gut microbiome domains (bacteria, and archaea) of *Oreochromis niloticus* was studied. Bacterial phylotypes were in the branch of Cyanobacteria, and alpha proteobacteria, but most of them comprised unique phylogenetic lineages within the branch of uncultured bacteria. Archaeal phylotypes were in the branch of methanogenic uncultured Euryarchaeota [43]. The phylogenetic composition of the gut flora (bacteria and archaea) of the tilapia fish, *O. niloticus*, in four khors (Kalabsha, Wadi Abyad, Korosko, and Toshka) was studied by Elsaied et al. [44]. A total of 19005 and 9032 rRNA gene Operational Taxonomic Unit (OTUs) were detected for bacteria and archaea, respectively. The guts of fish from Khor Toshka recorded the highest diversity of bacterial and archaeal 16S rRNA gene sequences. Some 16S rRNA gene OTUs assigned to genus *Synechococcus*, phylum Cyanobacteria, were recorded in the guts from all the studied khors. The gut microbiome formed mainly from genus *Cetobacterium*, phylum Fusobacteria; genera, Methanobacterium and Methanosaeta, phylum Euryarchaeota [44].

13.2.2.2.5 Bacteria associated with macrophytes

The total bacterial count and diazotrophs ranged from 10^6 to 10^8 Cfu/g and 10^4 to 10^6 $g^{-1}$for the high flooding season and drought season, respectively. No significant differences can be attributed to the plant species. The TBCs and total diazotrophs in the endo-phyllosphere varied from 10^2 to 10^4 and 10^2 to 10^3 Cfu/mL. High TBCs and total diazotrophs detected in the endo-phyllosphere may indicate bacterial infection and significant contribution of diazotrophs closely associated and/or localized within the inner tissues of various macrophytes [33]. The TBCs and TSF bacteria as well as total and spore-forming diazotrophs of *Myriophyllum spicatum* collected from the northern khors during winter

and spring were recorded by Ali et al. [32]: TBCs of $3.0 \times 10^2 - 4.4 \times 10^7$ Cfu/g, spore formers of $1.3 \times 10^2 - 7.1 \times 10^4$ Cfu/g, total diazotrophs of $2.9 \times 10^5 - 7.7 \times 10^7$ Cfu/g, and spore-forming diazotrophs of $<1 - 6.1 \times 10^4$ Cfu/g. In the studied khors, spring showed higher bacterial and diazotrophs than winter except Kalabsha Khor. Higher total bacterial and diazotrophs (means of 4.3 and 4.5×10^7 Cfu/g, respectively) was maintained in Wadi Abyad Khor during spring. Also, Wadi Abyad Khor recorded lower spore formers both for total and diazotrophs (means of 3.4 and 5.8×10^2 Cfu/g, respectively) during winter. The Rahma Khor maintained lower total bacteria mean counts (1.1×10^6 Cfu/g) during winter.

13.2.2.2.6 Bacterial cell volume and biomass

During spring 2006, the bacterial cell volume varied from 0.29 μm^3 (70%) to 1.15 μm^3 (30%) [31]. They reported that bacterial cell volume in the studied khors was generally higher than those observed in tropical lagoon (Cabiunis, Brazil) (0.25 μm^3) and in the two temperate lakes (Stechlin and Dagow, Germany) (0.248 μm^3) [45]. The bacterial biomass in the studied khors during spring 2006 ranged from 1.15 to 403 μg/Cm. The lowest bacterial biomass was detected at Khor Korosko, while the highest was recorded at Khor El-Ramla [31]. Many authors reported that the bacterial cell volume and biomass are controlled by environmental variables, the nutrient supply, and predation by zooplankton [46–49].

13.2.2.3 Fungi

Along 18 months (July 1985–December 1986), 51 species and one variety belonging to 21 genera of mesophilic fungi were isolated from marginal water (44 species, 1 variety, and 18 genera) and submerged mud (78 species, 1 variety, and 30 genera) of Lake Nasser. The dominant fungi were *Aspergillus fumigatus*, *Aspergillus flavus*, *Aspergillus terreus*, *Aspergillus niger*, and *Penicillium funiculosum*. October and December 1985 as well as February 1986 maintained the highest fungal counts. Of the 12 thermophilic and thermotolerant fungal species, *A. fumigatus* and *Aspergillus nidulans* were dominant, while *Paecilomyces variotii*, *Rhizomucor pusillus*, *Thermomyces lanuginosus*, *Thermoascus thermophilus*, and *Sporotrichum thermophilum* were common in one locality or more [50]. The fungal population showed marked vertical variations where high counts of *A. fumigatus* and *A. terreus* were observed at the surface water. Till 30 m, the counts of fungi decreased and then gradually increased reaching its peak near the

bottom of the lake (at 70-meter depth) where high counts of *P. funiculosum* were recorded. During January to June 1992, El-Hissy, et al. [51] recovered 25 identified and 4 unidentified species belonging to 11 genera of aquatic phycomycetes from 100 surface water samples of Lake Nasser. At relatively low temperatures (15.9°C−20.3°C), phycomycetes were dominant, while rare at relatively high temperature (20.6°C−33.1°C). In the submerged mud samples, the most common genera were *Saprolegina* and *Pythium* whereas *Aphanomyces*, *Dictyuchus*, *Pythiopsis*, *Leptomitus*, *Allomyces*, and *Blastocladiopsis* were rare. Approximately 54% of the mud samples recorded only one species aquatic fungi per sample. Also here, the commonest genera of aquatic fungi recovered during this investigation were *Pythium* and *Saprolegnia*, whereas *Leptomitus* and *Nowakowskiella* were less frequent [52]. EI-Hissy et al. [53] studied the vertical and monthly fluctuations of aquatic fungi (zoosporic) during November 1992 to October 1993 at different depths (from surface to 20 m depth) in Khor Manam (10 km south of Aswan High Dam). Seventeen aquatic fungi were identified. The aquatic mycoflora showed marked vertical variations where surface water samples maintained the highest number genera (8 genera) and species, (13 species), while near the bottom water only recorded 3−4 genera or species. The decrease in the fungal taxa was correlated markedly with the decrease in the amount of dissolved O_2 and organic matter. The most common genera were *Achlya*, *Aqualinderella*, *Pythium*, and *Saprolegnia* (moderate occurrences), whereas *Allomyces*, *Aphanomyces*, *Dictyuchus*, and *Pythiopsis* were of rare occurrence and irregularly distributed in the vertical strata. The identified (36) and unidentified (4) species and one variety belonging to 11 genera of zoosporic fungi were recorded by El-Hissy et al. [54] from 76 surface water samples which were taken from four lakes: Nasser, Manzala, Borolous, and Qarun (19 samples from each). The most common species were *Phytophthora* (10 species+one variety) and *Achlya* (8 identified+unidentified species). *Saprolegnia*, *Pythium*, *Phytophthora*, and *Achlya* were the dominant genera. Compared to the other lakes, Lake Nasser was the poorest in zoosporic species.

13.3 Conclusions

- The available virological information on Lake Nasser water is little.
- The bacterial biomass is important as a trophic level in the food chain of Lake Nasser.

- From a bacteriological point of view, the water of Lake Nasser is suitable for drinking and aquaculture purposes.
- Bacterial indicators post-flooding were about threefold at the pre-flooding period and decreased northward of the lake.
- The effects of climate change on microbial communities and the role of microorganisms in releasing greenhouse gases have not been addressed.

13.4 Recommendations

- Periodic monitoring of microbiological water quality of Lake Nasser is a must.
- Environmental Impact Assessment (EIA) should be done before the establishment of any project around the lake.
- Renewable energy should be used in the Lake Nasser region.
- Several pieces of research were required to develop knowledge of the effect of climate change on microbial communities and vice versa.

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CHAPTER 14

Microbial pollution in African lakes

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14.1 Introduction

A lake is defined as a capacious area of water (the majority are freshwater) surrounded by land with no direct intrusion from the sea. The formation and the origin of lakes are diversified, where the great majority of them are formed by natural agents, while others are formed by tectonic movements. According to the African lakes inventory tables for the United Nations, the number of African lakes is 677 distributed along the African countries. For example, Uganda has approximately 10% of the total African lakes with a total number of 69 lakes, followed by Kenya with 64 lakes (9.5%), Cameroon with 59 lakes (8.7%), and the other lakes are dispersed throughout other African countries. It is expected that in the future some African countries could suffer from water scarcity or water stress because of climate change. Freshwater lakes are essential for African people as the water of the lakes is used for drinking and other human uses. Freshwater fisheries of the African lakes are the major sources of income as well as protein for millions of African people. Aquatic microorganism communities are defined as an assemblage of microorganisms that live, interact together, and are present in water environments as suitable and perfect habitats. Freshwater microorganisms and their ecological impacts are important for biodiversity, despite the fact that they are not easily visible as macroscopic fauna and flora as fish and higher taxa. These microorganisms are microscopic organisms that live in freshwater such as fungi, microalgae, bacteria, actinomycetes, and viruses. The different activities of microorganisms could appear through microlevels (e.g., enzymes secretion, nutrients adsorption) or community dynamics (e.g., the interactions within the planktonic and the benthic populations) or broad environmental effects (e.g., great inorganic nutrient concentrations changes inside an aquatic ecosystem, anaerobic hypolimnia formation, and

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mudflats stabilization) [1]. The African continent has abundant lakes that are supporting important fisheries, supplying a livelihood to many people, and share vigorously the food supply chain. For example, fisheries of just the 11 countries at the eastern African lakes are employing about 500,000 persons which are expected to exceed in number and numerous are engaged in secondary activities and related services. Thus, the fisheries and related services sectors are introducing the main support for approximately 4% of the region's entire population. This can lead to water conflicts between different countries despite the regional and national initiatives on integrated management of water resources.

The lakes' resource utilization differs greatly from one lake to another, depending on fishery types: demersal or pelagic (onshore or offshore). Onshore resources are being more heavily used nowadays. The Great Lakes of the African continent are receiving great attention from the country's government and several international authorities with the implementation of some funded research programs or projects for the Great Lakes of Africa but the governmental support for other lakes remains very low in several African countries with a limited budget allocated for lake conservation or development. In African countries, approximately 25% and 67% of the urban and rural populations, respectively, are without safe and clean drinking water, and/or even a higher percentage of lack of proper sanitation [2].

African lakes are still among the most significant of the continent's natural resources and they are suffering from a deficiency of wise and rational management and are being abused although they are limited as well as sensitive resources that need proper care and management.

The food chain supplies as well as the irrigation systems are suffering from water shortages in some African countries which still need to make use of the potential water supplies from their lakes. The negative human impacts have devastating consequences for the lakes including rapid siltation caused by accelerated soil erosion; water irreversible uptake and/or salinization due to irrigation; eutrophication; and acidification and contamination with the mine tailings and toxic chemicals [3]. Influential and wise integrated lake management requires not just rigorous soil conservation measures but also, great changes in the manner that water moves through the agroecosystem. Water supplies from African lakes and other resources are considered one of the great important resources for Africa's social, economic, and environmental welfare. Various pollution forms in African lakes lead to heavy economic losses and human health illnesses;

microbial pollution is a clear form of pollution in African lakes. The main pollution problems facing African lakes are the direct and continuous wastewater disposal into lakes that cause increasing harmful impacts on the lakes' ecosystem balance involving microbial status. Unfortunately, the global climate change impacts will probably produce a worse and more undesirable situation for African lakes. The major impacts affect poor countries and people who have limited access to safe and clean water resources [4]. African lakes are considered extremely exploited among all the continent's freshwater resources, if some countries in Africa have the annual needing for available water per capita. A lot of countries in Africa are already facing water scarcity or water stress. Fisheries at freshwater lakes are the main source of people's income as well as a source of protein for millions of people in Africa. The total estimated annual fish catch from freshwater lakes in African lakes is approximately 1.4 million tons of fish [1].

African lakes already suffer from different threats to water quality including different types of pollution, like chemical and biological pollution. For example, the eutrophication processes lead to the existence of toxins such as cyanotoxins. Moreover, the high reproduction of invasive species of aquatic plants (macrophytes), such as the water hyacinth, leads to pollution. In most African countries, industrial, agricultural, municipal and domestic wastes, including sewage with huge amounts, are still discharged directly into a majority of African lakes without any previous treatment and that is causing serious and continuous human health problems and environmental pollution. Discontinuous drought along African lakes is also considered a major threat and a cause of water scarcity in some communities. African lakes are a source of freshwater supply for many countries that are threatened by natural phenomena and human factors. These threats are considered big challenges in managing the African continent's lakes and other water resources as well as in meeting the demands for basic water supplies. In addition, the natural and human threats to African lakes are numerous such as the climate change phenomenon which is a great future hazard influencing the world and has direct harmful impacts on African lakes such as extreme and temporal variability of climate and rainfall [1]. Climate change and the global warming phenomena may cause various scenarios, such as exceeding water scarcity in African countries causing drought. The best example of this threat is Chad Lake, which once was one of the African continent's largest freshwater basins, which has dramatically decreased in size due to climate

change (due to global warming phenomena). The lake is now 1/20 of the size it was 35 years ago as mentioned by the National Aeronautics and Space Administration, NASA [5]. In other scenarios, climate change may cause flooding; the flooding poses extreme threats to human populations living close to them. An example is the flooding at Lake Kyoga in Uganda causing hardship for local communities which has led to displacing many people.

In other scenarios, climate change may cause broad desertification in African countries. Several challenges are to be met by the African lakes because of the weak investment in water resources, development, assessment, and protection. There is unsustainable financing of investments in water supply and sanitation. Also, great challenges are the depletion of water resources through pollution, environmental degradation, and deforestation [6]. The African lakes are undergoing quick environmental changes because of human activities on an enormous scale. In fact, the different anthropogenic threats affecting the African lake's ecosystem can be categorized as follows:

- Discharging great amounts of the different pollutants, agricultural, industrial, and sewage, into African lakes.
- Faulty and inappropriate fishing activities in African lakes as overfishing or illegal fishing or destructive fishing which means using explosives as cyanide is used to stun fish making them easier to catch and these practices are still used in some countries as well as deficiency or failure of effective government management practices.
- The destruction of the watershed's environment is leading to an excess of eutrophication and causing sedimentation problems.
- The translocation process for some species through human activities means the entrance of an exotic species into the African lakes' ecosystems which causes the extinction of the native species or drastically altered community structures.
- The regional and global climate change phenomena have direct effects on the African lakes [1].

14.2 Microbial pollution of African Lakes

The microbiological pollution sources of African lakes often are untreated human sewage or runoff from animal husbandry facilities into the lake's stream. In general terms, the greatest microbial hazards are associated with water ingestion. Feces has been considered a source of pathogenic

bacteria, viruses, protozoa, and helminths to humans. Fecally derived pathogens have been documented as the principal concern in setting health-based targets for microbial safety [7]. Pathogenic bacteria, viruses, and cysts of protozoan parasites detection or diagnosis are requiring costly and time-consuming procedures as well as well-trained staff. Thus, indicators of fecal pollution are much needed. Nowadays, the total and fecal coliform (FC) bacteria, and fecal streptococci bacteria are used as microbial indicators for predicting the pollution of water. The fecal contamination of nearshore waters in many African lakes is a great challenge for local communities as well as for the national public health organizations, as people in the nearshore communities mostly use the water of the lake for drinking, cooking, and washing. Globally, the microbial pollution in freshwater resources is notably increasing and the number of diseases caused by pathogenic microorganisms that spread in the water environment has also increased around the world in recent years. The microbial pollution in African lakes renders water undrinkable and harms local wildlife. The total coliform (TC) bacteria are found universally in a huge number in soil and vegetation and in the feces of warm-blooded animals, including humans [7,8].

The coliforms groups (total and FC bacteria) and *Escherichia coli* are of great importance among the microbial pollution indicators, especially the bacterial indicators used in the water quality determination for health risk assessment. The existence of pathogens or microorganisms is usually accompanied by the presence of classic indicators of contamination, such as *E. coli*, Enterococci, and other aerobic bacteria. Coliform bacteria have long been referred to as the indication of fecal contamination of water, and thus, a health hazard. The fecal streptococci bacteria are also considered to be alternative indicators of fecal contamination and health risks. Furthermore, the classic indicators can be considered efficient detectors of pathogens in most cases of microbial contamination of water. The bacterial indicators in freshwater resources such as total and FCs groups and fecal streptococci groups are used globally for the assessment of microbial pollution of water [9]. Pathogenic bacteria like *Vibrio* species that cause cholera disease, also *Shigella dysenteriae* that causes bacillary dysentery or shigellosis disease, *Salmonella* sp. that causes typhoid fever and another serious salmonellosis disease, and *E. coli* that causes acute diarrheas and gastroenteritis disease, all these bacterial species and others can be transmitted to humans through water causing a major public health problem [10].

Molds and yeasts are found in freshwater resources (rivers, lakes, and wetlands), and ichthyologists still fearing from fungi as parasites of fishes and their spawn. The ecological roles of the fungi in lake ecosystems are structured by responses to abiotic environment and interactions with other biota, which can lead to constant and effective associations like with lichens. Obligate biotic interactions already occur in the basal fungal phylum of the flagellated Chytridiomycota, whose members often depend on the aquatic and living or dead host materials. They act as decomposers of plant tissues and introduce allochthonous leaf litter compounds into the food web of streams. The current awareness of the fungal ecology in lake ecosystems is primal, with the exception of a few studies that examined allochthonous leaf litter in lake ecosystems. The carbon produced from allochthonous leaf offal degradation by fungi and others can participate in small lakes equivalent to 10% of the phytoplankton production that might be dependent on the lake size as well as on the surrounding vegetation. Aquatic fungi are playing crucial and important roles in nutrients and carbon cycling and interact with other organisms influencing the food web dynamics. The huge developments and the application of molecular methods have greatly increased the potential for resolving the biodiversity and ecological roles of the fungi inside lake ecosystems. Recent studies in the field of aquatic fungi have released and explained the high diversity of this mycoflora in the lake ecosystems and their habitats and also introduced different and essential processes that influence aquatic ecosystems [11]. Mycotoxins are defined as toxic secondary metabolites produced by fungi. Mycotoxins, when found in food or water can cause serious diseases that lead to the death of humans and animals. Modern studies evince fish-eating may become a direct pathway to reach mycotoxins to enter people's food chains and the investigators recorded the bioaccumulation of these toxic compounds inside the common freshwater fish species. Fish also may deliver mycotoxin residue along the food chain, thus, compromising human health. Moreover, different impacts of mycotoxin changes are depending on the fish type which consumed mycotoxins. This was widely investigated as a source of food contamination as well as a source of aquaculture feed. During the last years, several studies confirmed that the fish infected by mycotoxin is increasing, including different types of fish in different habitats such as zebrafish, Nile tilapia, rainbow trout, common carp, gibel carp, beluga, and channel catfish [12]. So, the fish that lives in freshwater habitats, such as African lakes, can be exposed to mycotoxin contaminations that can be transmitted to humans.

Fish contaminated by fumonisin mycotoxins and ochratoxin A affect the histology of organs such as the liver, make a depression in the immune system, reduce weight, and may cause cancer leading to death. The infections in humans by mycotoxins are dangerous and carcinogenic and related to esophageal and hepatic cancer [13,14]. Also, numerous aquatic fungus species related to Oomycetes have special harmful importance because of their effect on fish health and the following economic losses [15].

Cyanobacteria or blue-green algae are defined as microscopic organisms found naturally in all types of water, and these single-celled microorganisms live in fresh, brackish, and marine water, Cyanobacteria are considered among the original organisms on planet Earth. The freshwater algae live aggressively with abundance in different African lakes. Cyanobacteria are photosynthetic prokaryotes and use sunlight to make their foods. Cyanobacteria are the main sources of many secondary organic products in nature and are the pioneer organisms to have released oxygen into nature. Some species of Cyanobacteria can survive under extreme conditions from salinity, temperature, and low light intensity [16,17]. In the case of favorable conditions from high pH, high temperature, high light intensity, and excess concentration of nutrients, especially phosphorus (P) and nitrogen (N) in the environments, Cyanobacteria can grow rapidly in the surface waters and form blooms that spread across the water's surface. The blooms might become visible. The Cyanobacteria blooms form as a result of excessive growth followed by the production of toxic secondary metabolites in many lakes, ponds, and rivers throughout the world. Therefore, this phenomenon of cyanobloom formation is considered a global problem that affects the quality of water [18,19]. Cyanoblooms have harmful effects on people, animals, and the aquatic environment by blocking the sunlight that other organisms need to live. Cyanoblooms steal the oxygen and nutrients other organisms need to live and produce harmful toxins called cyanotoxins. Cyanotoxins are among the most powerful natural poisons known, which can infect people, their pets, and other animals. This harmful effect on animals and humans occurs either by direct ingestion of Cyanobacteria cells or the consumption of drinking water contaminated with cyanotoxins [19].

The risk of cyanotoxins on humans and animals depends on their concentration in the aquatic environment; it can cause poisoning and diseases like cancer or even death. Thus, cyanotoxins are very harmful chemical compounds produced by Cyanobacteria that affect the environment.

They have great effects on all types of aquatic organisms such as bacteria, algae, plants, and invertebrates, mainly zooplankton. In the United Kingdom, histopathological studies on the death of fish during cyanoblooms showed that this death is due to damage to the gills in addition in some cases causing damage to kidney, heart, skin, and liver due to cyanotoxins [20]. However, during the 1960s and 1970s, many scientists linked the formation and the growth of the algal blooms to nutrient enrichments resulting from anthropogenic activities such as agriculture, industry, and sewage disposal [21].

Eutrophication occurs along the majority of freshwater lakes at heavily polluted sites by untreated wastes. The direct reasons for the lakes' eutrophication are the introduction of external nutrients such as nitrogen and phosphorus into the lakes [22]. Eutrophication leads to the formation of high quantities of phytoplankton biomass and causes water turbidity. It also causes biological changes like loss of biodiversity, fish stock disappearance, and decreasing the topdown control by zooplankton on phytoplankton [23].

Viruses are microorganisms that exist everywhere. The aquatic ecosystems can be considered a frequent vehicle for virus transmission. These viruses may be a danger to aquatic animals and plants. All types of water, freshwater such as lakes and rivers; marine water, and groundwater are concerned by viruses' contamination. The African lakes can form a suitable environment for virus growth and transportation. This contamination may be occurring in many ways, such as human activities [24]. The common types of viruses that can transfer diseases to humans through water are noroviruses [25]. They are the most common cause of gastroenteritis, usually spreading through the fecal-oral routes via contaminated water or food. These viruses are enteric viruses and are considered the main ones responsible for diarrhea in children worldwide causing mortality in children less than 5 years of age in both the developed and developing countries. Therefore, the African lakes may be considered a suitable medium for virus occurrence and transmission. Different environmental factors affect viral spread in the water body and the extremely substantial one is the temperature which has a major influence. Scientists noted that viral inactivation is shown at a degree of high temperatures, while at low-temperature degrees, viruses can survive a long time and maybe reach several years. Another factor that causes viral inactivation is solar light through the action of ultraviolet radiation, while viruses survive better in the darkness. Also, the presence of an organic matter in the

water body enhances viral activation, and the effects of water salinity on viruses is not effective [25,26].

14.3 Case studies of microbial pollution at the African Lakes

14.3.1 Lake Victoria

Lake Victoria is the largest tropical and second largest freshwater lake in the world. The lake has a surface area estimated at 68,000 km^2. It is shared by several countries where Kenya represents 6%, Uganda represents 43%, and Tanzania represents 51%. Twenty-three rivers are feeding Lake Victoria and some of these rivers expand hundreds of kilometers when it rains in Burundi. These rivers discharge the freshwater directly into Lake Victoria from upstream countries and have more than doubled their inflows due to the heavy rains. The White Nile is only a unique outlet of this lake, where the freshwater flows directly through South Sudan, Sudan, and finally Egypt [27]. Several cumulative pressures are affecting the lake which threatens all of its ecosystems and fisheries. Recently, the entire ecosystem of Lake Victoria has been highly affected by climate change; increasing pollution of Lake Victoria has impoverished the system by the biodiversity decline. One of the problems facing the lake is the proliferation of aquatic weeds such as water hyacinth and algal bloom decreasing fish stock in the lake. Increasing pollution levels and eutrophication inside the lake are due to anthropogenic activities such as increased waste discharges, sediment transported by rivers, fertilizer runoff from agricultural-based farms, and wetland reclamations. The impacts of intensive pollution that come from the municipal and the industrial discharges are obviously visible in some rivers draining to Lake Victoria along Lake Shoreline, and in areas such as the shallow Winam Gulf near Kisumu in Kenya. The microbial pollution of Lake Victoria, Kenya, was estimated by many investigators [28–30].

The average of contamination with the TCs bacterial count into the ecological zones (Cluster C1) was 1937.78 ± 94 CFU/100 mL and the highest records were at the sites of the Ndere Island (7800 CFU/100 mL) and beside the Kisumu Pier (6166 CFU/100 mL) [31]. The ecological cluster zones (Cluster C2) recorded the high mean count of the TCs bacteria (1818.8 ± 102 CFU/100 mL), while the ecological zones (Cluster C3) exhibited the lowest counts throughout the sampling period [31]. FCs bacterial counts were highest at Cluster C2 (390 ± 21 CFU/

100 mL) during 2012, with the highest contribution being recorded at the Gingra Rock (5100 CFU/100 mL) [31]. Cluster zone C3 recorded lower counts of FCs during 2013 throughout the sampling period [31]. The Kisumu Pier and Homa Bay sampling sites in the Winam Gulf are exhibiting high counts of FC bacteria when compared to the other sites, and these sites are located in areas affected by urban sewage and industrial effluents [29].

The number of bacterial counts is exceeding the World Health Organization limits for irrigation use (1000 CFU/100 mL) or domestic use (0.0 CFU/100 mL). Higher FC numbers were recorded at the Kisumu Pier sampling site from 2010 to 2013 due to the discharge of raw sewage without previous treatment from the located wastewater treatment plant called the Kisat Sewage Treatment Plant. This plant was not functioning at its full capacity during this period due to the poor state of repairs [31]. The total count numbers decreased from 7800 CFU/100 mL in 2010 to 2100 CFU/100 mL in 2015 due to subsequent repairing of the Kisat Sewage Treatment Plant within the Lake Victoria Environmental Management Project during 2014 and subsequently reduced inputs of sewage into the lake. Fish abundance declined at Lake Victoria due to either the overexploitation or the deterioration of the water quality resulting from increased pollution levels and eutrophication processes [29].

Other investigators estimated the variation of the microbial pollution parameters and isolated several types of pathogenic bacteria from water samples collected from Luanda Rombo, Dunga, Marengo, Osieko, and Usoma in the Lake Victoria Basin of Kenya [32]. The results of the bacteriological measurements referred to that. Out of the 180 water samples, 163 water samples were 90.6% positive for TCs bacteria and had the most probable numbers (MPN) values above the World Health Organization recommended limits of 10 colony-forming unit/100 mL, and for the investigation of FCs bacteria, 163 water samples tested positive for TCs bacteria and 98 water samples with 60.1% were positive for FC bacteria [33].

Reasons for the high recoding of the total and FCs bacterial count at the lake are the organic deposits predominantly from human and animal sewerage and the high suspension of solid matter. The percentage of isolated pathogenic bacteria from the collected samples has been recorded as *Vibrio cholerae* (5.4%), *Shigella* spp. (6.5%), *Salmonella* spp. (18.5%), and *E. coli* (69.6%) [32]. Furthermore, *E. coli* has been recorded as the most predominant species during dry and wet seasons at all sites collected from

the lake, whereas, *V. cholerae* has been recorded as the least isolated of enterobacteria species with none being isolated in the Osieko site in the dry and wet seasons, and none being isolated in the Luanda Rombo and Usoma sites only in the wet season, while in Dunga site, it was in the dry season. Generally, the results confirmed great variations in the enumerations of pathogenic microbes in dry and wet seasons related to various sites [33].

A study was performed to understand the association between harmful algal blooms and health risks at Ukerewe Island [34]. That study was conducted on 432 water samples for Cyanobacteria species' identification at Lake Victoria shores. The concentrations and cell numbers of the Cyanobacteria species are beyond the acceptable limits of the World Health Organization; the species of *Microcystis aeruginosa* in the collected samples during the study period ranged from 90,361.63 to 3,032,031.65 cells/mL, in addition, *Anabaena* spp. ranged from 13,310.00 to 4,814,702 cells/mL [34]. The authors have decided that the percentage of people water usage was distributed as follows: approximately 31% of people were using the water directly from Lake Victoria, while 53% of people were using wells water and the rest with a percentage equal to 16% were using the treated supplied piped water. Throat irritation and vomiting were highly recorded by lake water users as compared to wells and piped water users ($P < .001$). Gastrointestinal illness had been significantly recorded among lake water users as compared to pipe water and well water users ($P < .001$). The visible blooms at Lake Victoria water were associated with some diseases such as gastrointestinal, skin irritation, and vomiting symptoms as compared to water without visible blooms ($P < .001$). Thus, cyanobacterial blooms concentrations have greater hazards when the water is used without previous treatment [34].

14.3.2 Lake Tanganyika

Lake Tanganyika is one of the largest freshwater lakes on Earth and the second-biggest lake considering the area after Lake Victoria. It is providing the fundamental sources of fish to millions of people in the surrounding regions. The lake is a large and deep (the mean lake width is 50 km; the mean lake length is 650 km; the mean lake depth is 570 m, and the maximum depth of the lake is 1470 m) north-south trending rift valley lake that is a significant source of people's nutrition and income for four countries of Burundi, Tanzania, Zambia, and the Democratic Republic of

Congo. Water pollution has been considered a major threat to Lake Tanganyika's sustainability. The pollution of the lake water is occurring because of the throwing of different wastes directly into the water bodies without prior treatment as well as other anthropogenic activities. The industrial, agricultural, domestic, municipal, and sewage is not currently treated before discharging into the lake and the riparian country governments do not have the legislation or laws that inhibit Tanganyika Lake contamination. Waste pollutants, such as household dirt and excrement, industrial wastes like tanneries, sugar refineries, slaughterhouses, oil mills, etc. in addition to other pollutants, such as chemical fertilizers, pesticides, oil from boats, and heavy metals pollutants have accumulated in the lake. The growth of huge quantities of cyanoblooms and invasive plant species in the Tanganyika lake environment has been observed due to the eutrophication process. The most obvious threat to the lake is growing with large quantities of invasive macrophyte species, such as the water hyacinth, scientifically named *Eichhornia crassipes*, which grows quickly along the shores of the lakes as well as in the shallow bays and backwaters of the northern extremity of Lake Tanganyika [35].

Under the different national and international programs, conventional water quality monitoring programs of Lake Tanganyika had been performed for several years. The investigators have studied and examined the use of citizen science for monitoring the dynamics of coliform bacteria concentrations inside the lake. Five coastal regions, Kibirizi, Ilagala, Karago, Ujiji, and Gombe, have monitored the total and FCs bacteria monthly for 1 year. The researchers reported that the coliforms bacterial counts recorded in Lake Tanganyika were similar to those measured in Lake Malawi, with the coliform enumeration of 35−400 CFU/100 mL in nearshore surface waters, and the highest coliforms count at the Ilagala, Kibirizi, and Ujiji [36].

14.3.3 Lake Nasser, Egypt

Lake Nasser is one of the largest human-made lakes in the world. The lake was established as a freshwater reservoir after Aswan High Dam's construction from 1959 to 1970. The lake extends for about (496 km), including 292 km in the Egyptian territory and 204 km, named Lake Nubia, in the Sudanese boundary. Lake Nasser is distinguished by various dendritic inlets or side extensions called khors. There are about 85 major

khors along the lake and the significant khors are Kalabsha, Ramla, El-Allaqi, and Tuoshka [37–39].

Little information is available on the microbial assessment of Lake Nasser during the last centuries. Lake Nasser represents the bank of water for Egypt, thus, the determination of bacteriological safety of this water supply is of vital importance to the life and well-being of the whole population. The microbial quality has to be regularly examined in public water supplies. This necessitates the periodic assessment of the safety of the water as regards the likely transmission of waterborne infectious diseases. A recent study estimated the microbial pollution on Lake Nasser before operating the Renaissance Dam [37].

The bacterial assessments at the lake were based on the total viable bacterial count at two different incubation temperature degrees, 22°C and 37°C, after flooding had been recorded to be 1.5×10^3–135×10^3 CFU/mL, and 1×10^3–110×10^3 CFU/mL, respectively, (Table 14.1). The total viable bacterial count before flooding was lower than that of after flooding and varied in a narrower range, that is, between 0.8×10^3 and 34×10^3 CFU/mL and between 0.9×10^3 and 32×10^3 CFU/mL, respectively (Table 14.2). The TCs bacteria have been recorded more abundant after flooding, and fluctuated between 0 and 1100 MPN/100 mL, while before flooding (drought season) fluctuated between 4 and 46,000 MPN/100 mL. The FCs numbers in the post and preflood periods were in the range of 0–1100 MPN/100 mL and 0–240 MPN/100 mL, respectively. The authors also recorded the numbers of the fecal Streptococci in the post and preflood periods and recorded similar numbers at two periods ranging from 0 to 460 MPN/100 mL. The numbers of *E. coli* were ranged after and before flooding from 0 to 250 CFU/100 mL and from 0 to 150 CFU/100 mL, respectively [37].

Finally, the microbial status characteristics of Lake Nasser water are better than River Nile water, based on the last updated investigations that detected the microbial status of the River Nile water at the main channel and the two branches inside Egypt which revealed high pollution levels of the bacterial indicators resulting from the drainage of various wastes such as agricultural, and industrial wastes along River Nile [31,40] (Fig. 14.1).

14.4 Lake Qarun, Egypt

Lake Qarun is located between the longitudes of (30° 24′ and 30°49′ E) and the latitudes of (29°24′ and 29°33′ N) in the western desert of Egypt. Lake Qarun is the third largest lake in Egypt. The lake is saline and

Table 14.1 The microbial assessment after flooding at Lake Nasser [37].

Sites	Total viable bacterial count at 37°C × 10^3 (CFU/mL)	Total viable bacterial count at 22°C × 10^3 (CFU/mL)	Total coliforms (MPN/ 100 mL)	Fecal coliforms (MPN/ 100 mL)	Fecal streptococci (MPN/100 mL)	*Escherichia coli* (CFU/ 100 mL)
1	68	60	35	21	120	12
2	85	80	460	460	290	250
3	45	39	1100	1100	460	200
4	29	50	Not detected	Not detected	43	Not detected
5	25	66	16	16	23	9
6	33	58	29	6	24	Not detected
7	110	102	29	15	5	9
8	22	29	53	24	14	8
9	46	75	16	16	20	5
10	1.2	2	460	93	43	25
11	4	8	11	7	Not detected	Not detected
12	1	1.5	Not detected	Not detected	3	Not detected
13	99	135	16	16	23	7
14	50	95	15	7	7	Not detected
15	66	75	23	23	4	10
Mean	45.6	58.4	150.9	120.3	71.9	35.7
Standard deviation	34.4	38.2	304.6	294.7	130.5	77.7
Coefficient of variation	75.5	65.5	201.9	245.0	181.5	217.9

The Corresponding Authors (Usama M. Tahoun) was shared in writing the results of this research paper.

Table 14.2 The microbial assessment before flooding at Nasser Lake [37].

Sites	Total viable bacterial count at 37°C × 10^3 (CFU/mL)	Total viable bacterial count at 22°C × 10^3 (CFU/mL)	Total coliforms (MPN/100 mL)	Fecal coliforms (MPN/100 mL)	Fecal streptococci (MPN/100 mL)	*Escherichia coli* (CFU/100 mL)
1	16	11	93	7	4	Not detected
2	12	10	9	4	Not detected	Not detected
3	24	18	43	9	Not detected	Not detected
4	12	10	9	n.d.	Not detected	Not detected
5	1.6	1.3	4	n.d.	9	Not detected
6	21	24	21	n.d.	9	Not detected
7	18	16	15	4	240	Not detected
8	29	23	4	4	4	Not detected
9	25	34	150	23	Not detected	12
10	32	28	46,000	240	23	150
11	0.9	0.8	460	93	460	46
12	19	22	1100	43	4	22
13	12	10	46,000	150	93	90
14	1.9	21	460	43	Not detected	25
15	16	21	46,000	150	460	95
Mean	16.0	16.7	9357.9	51.3	87.1	29.3
Standard deviation	9.6	9.4	18,966.4	73.7	164.0	46.4
Coefficient of variation	59.9	56.5	202.7	143.7	188.3	158.0

The Corresponding Authors (Usama M. Tahoun) was shared in writing the results of this research paper.
Sampling sites from 1 to 15 concern five sectors and their eastern, middle and western parts.

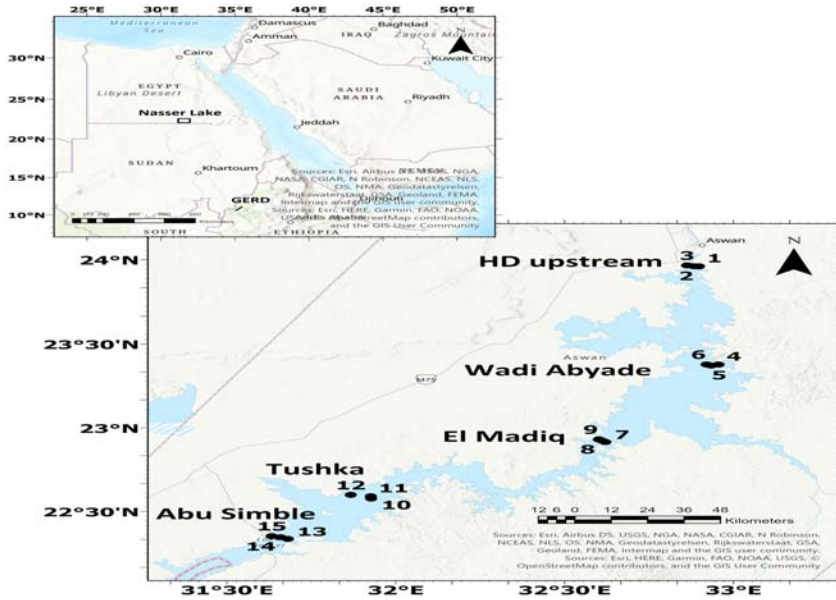

Figure 14.1 Lake map [37]. *GERD*, Grand Ethiopian Renaissance Dam. *The Corresponding Authors (Usama. M. Tahoun) was shared in writing the results of this research paper.*

located 44 m below sea level. Lake Qarun covers, as a whole, an area of about 226 km^2. The lake has become a reservoir for the daily discharge of different sources of pollution, such as agricultural wastewater, industrial waste, and sewage. The drainage water reaches the lake through two main drains, the El-Batts drain and El-Wadi drain. There are several factors affecting the Lake Qarun ecosystem as the amount of discharged wastewater reaches the lake in direct or indirect ways, through seepage from the surrounding cultivated land, and the climatic and geological aspects [9,32]. The microbial status of Lake Qarun has been estimated by Afify et al. [9]. The high pollution levels of water stimulate an abundance of different bacterial pollutant indicators, including total and FCs, fecal streptococci as well as *E. coli* (Table 14.1). In addition, the microbial assessment for two drains, El-Batts drain and El-Wadi drain, was recorded in Table 14.2. The annual average values of the Water Quality Index (WQI) were very poor for the aquatic life guidelines and poor for the irrigation guidelines [9] (Table 14.3).

Table 14.3 Microbiological status of Qarun Lake [9].

Parameters	Mean	Standard deviation	Minimum	Maximum
Total viable bacterial count at 37°C (CFU/mL)	68.9×10^5	85.7×10^5	0.4×10^5	330×10^5
Total coliforms (MPN/100 mL)	11×10^4	13.9×10^4	0.3×10^4	46×10^4
Fecal coliforms (MPN/100 mL)	53.8×10^3	100.6×10^3	3×10^3	460×10^3
Fecal streptococci (MPN/100 mL)	128.8×10^3	243.9×10^3	3×10^3	1100×10^3
Escherichia coli (CFU/100 mL)	15.5×10^2	18.9×10^2	0.1×10^2	69×10^2

The corresponding authors (Usama M. Tahoun) was shared in writing the results of this research paper.

14.5 Lake Tana, Ethiopia

Lake Tana is the second-largest subbasin of the Blue Nile. It is the largest freshwater resource in Ethiopia, representing approximately 50% of freshwater resources in Ethiopia. The lake covers a wide depression in the Ethiopian plateau; it occupies an area of 15,114 km^2 with a surface area of 3111 km^2. It is the source of the Blue Nile (Abay) River. The lake is a freshwater shallow with weak seasonal stratification. The lake is considered a wealthy ecosystem in the biodiversity of several plant species as well as the cattle breeds which contain large areas of wetlands and represent the shelter to several endemic animals and birds as well as archeological and cultural sites. The main rivers that feed Lake Tana are Gilgel Abay, Ribb, Gumera, and Megech. These rivers are participating in more than 90% of the inflow. Lake Tana is suffering from land, soil, and water degradation in different forms and the major problems of Lake Tana according to Goshu and Aynalem [41] are sedimentation, clearing of wetland, canalization of the tributaries, and the microbial pollution which is significantly recorded through the increasing spread in the waterborne diseases, toxigenic Cyanobacteria, and increasing eutrophication, especially in the communities which largely depend on the raw water for domestic uses. Furthermore, different challenges are facing the lake ecosystem sustainability, where the lake suffers from quick growth of invasive plant

species like water hyacinth which is called *E. crassipes*, inappropriate dam construction, waste management failure, continuous construction of buildings in the lakeshore areas that are natural breeding and feeding grounds for some fish and bird species, and stakeholders' conflict [42] (Table 14.4).

Climate changes impacts are also facing the lake ecosystem sustainability because it has the potential to reduce water resources availability in Nile Basin countries in the next years, and the major effects of climate change are likely to be alterations in hydrologic cycles and changes in water availability. The possibility of water resources reduction is a major threat to Lake Tana Basin. Climate change may cause agricultural drought unless there is water available for land irrigation, and a reduction in rainfall may cause reduced groundwater recharge, which could significantly reduce its contribution to the stream flow [42] (Fig. 14.2).

The investigators collected four sites from Lake Tana, Shum Abo Recreational area, Maremiabiet, Kibran area, and Felege Hiwot Referral Hospital. The results of TC enumerations were more than 180/100 mL in all collected sites, and *E. coli* existed in all these sites except the Kibran area, moreover, the detection of water quality by the Canadian WQI categorized the Tana Lake as poor for recreation, drinking, and aquatic life [43] (Fig. 14.3).

From Lake Tana, different bacterial species belonging to the family of Enterobacteriaceae, Aeromonadaceae, and Vibrionaceae were isolated and identified from a total of 510 swab samples taken from the kidney and

Table 14.4 Microbiological status of El-Batts and El-Wadi drainage water drains [9].

Parameters	Mean	Standard deviation	Minimum	Maximum
Total viable bacterial count at 37°C (CFU/mL)	236×10^5	105.02×10^5	145×10^5	460×10^5
Total coliforms (MPN/100 mL)	46×10^4	31.56×10^4	11×10^4	93×10^4
Fecal coliforms (MPN/100 mL)	40×10^3	27.34×10^3	11×10^3	93×10^3
Fecal streptococci (MPN/100 mL)	201.6×10^3	169.9×10^3	53×10^3	460×10^3
Escherichia coli (CFU/100 mL)	74.5×10^2	19.20×10^2	48×10^2	98×10^2

The Corresponding Authors (Usama M. Tahoun) was shared in writing the results of this research paper.

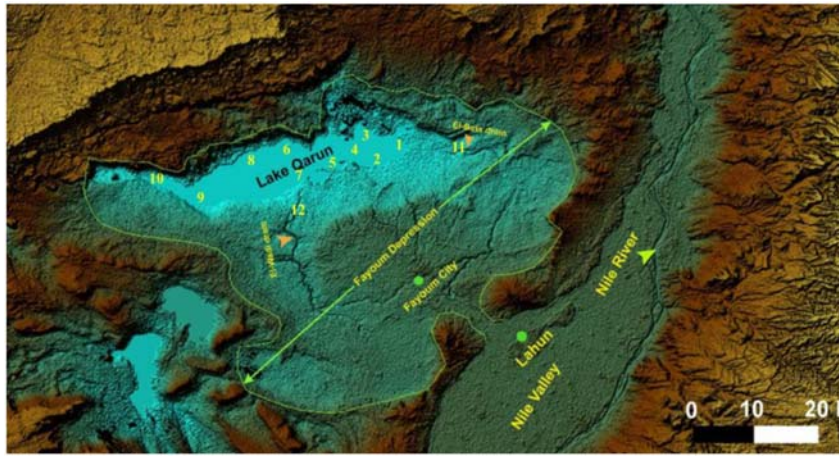

Figure 14.2 Lake Qarun locations Map [9]. *The Corresponding Authors (Usama M. Tahoun) was shared in writing the results of this research paper.*

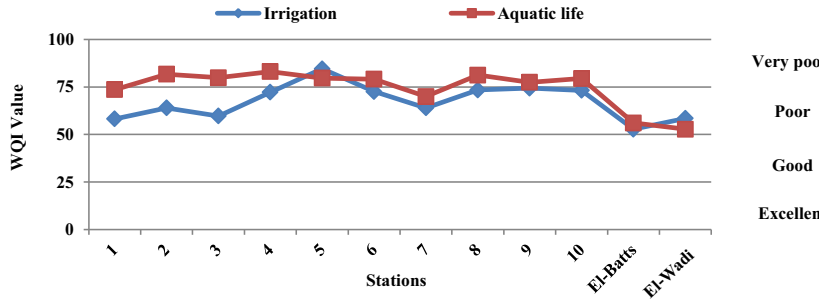

Figure 14.3 Water Quality Index of Lake Qarun [9]. *The Corresponding Authors (Usama M. Tahoun) was shared in writing the results of this research paper.*

intestine of 255 apparently healthy fish, and out of 62 water samples, 47 were positive for Enterobacteriaceae, and Aeromonadeceae [44]. So, increasing of microbial pollution at Lake Tana is mentioned by many authors and the pathogenic microorganism found aggressively and causing human illness. Briefly, the microbial pollution of Lake Tana is due to the human activities at the lake.

14.6 Lake Kivu

Lake Kivu is a mountain lake and considered one of the African Great Lakes. The lake is located on the border between Congo and Rwanda. It

empties into the Ruzizi River, which flows southward into Lake Tanganyika. The lake has been developed as a result of volcanic activity in the region. The surface area of the lake is 2.370 km^2, approximately 58% for Congo and 42% for Rwanda. The maximum depth of the lake is 489 m and the average lake water temperature is 23°C. The relative humidity has fluctuated between 59% to 83% and the average of rainfall is 1300 mm yearly. The investigation of the anthropogenic pollution impacts on the microbial contamination of the lake in Rwanda was estimated by Olapade [45]. The study was carried out in Gisenyi, Kibuye, and Cyangugu during a period of 24 months. The averages of total heterotrophic bacteria (THB) count are 168930, 82060, and 75710 CFU/100 mL at Gisenyi, Kibuye, and Cyangugu respectively. The means of TC bacteria were recorded as 76950, 60115, and 66780 CFU/100 mL at Gisenyi, Kibuye, and Cyangugu respectively, while the means of FC bacteria were 12360, 24893, and 12798 CFU/100 mL at Gisenyi, Kibuye, and Cyangugu, respectively. On the other hand, fecal streptococci bacteria were 532.3, 6.30, and 122.2 CFU/100 mL at Gisenyi, Kibuye, and Cyangugu, respectively. These bacterial densities are a great reflection of the anthropogenic activities that occurred at the lake. The densities of THB, total and FCs bacterial groups as well as fecal streptococci, were widespread in the selected locations of the lake with abnormally high values that indicated poor water quality. Bacterial indicators, as the author mentioned, were not significantly different ($P > .05$) with months, seasons, and locations. The poor microbial quality of Lake Kivu's water is due to the huge contamination caused by the different human activities and livestock [45].

Communities living along Lake Kivu discharge their domestic, agricultural wastes, and human excreta directly into the lake and people use the lake for bathing, washing clothes, and recreational purposes such as swimming, thus, contaminating the lake. Different types of pathogenic bacterial isolates from the water lake samples were of a wide range of groups, and their occurrence and distribution varied from location to location. The dominant bacterial species recorded in the Kivu lake water were *E. coli, Bacillus* sp., *Klebsiella pneumoniae*, *Citrobacter freundii*, and *Proteus* sp. [45]. The water microbial quality is considered very poor; the heavy contamination of the lake water may be coming from animals, human domestic wastes, and other human activities, such as laundry, swimming, transportation, farming, etc. Lake Kivu's water is unfit for human domestic uses without treatments [45].

14.7 Lake El-Manzala, Egypt

Lake El-Manzala has represented an extremely significant sector of Egyptian fisheries due to a significant total catch and a large number of economically important species. It is the largest lake in the northern region of Egypt. It expands slowly to cover a total area of 572.41 km^2 because there was a little rebound between 2016 and 2020 [46]. Lake El-Manzala has been recorded as a significant natural resource in Egypt for fish catching, wildlife, hydrological, and biological systems as well as food salt production [47]. It is bordered by Suez Canal from the east, the Nile-Damietta branch from the west, and the Mediterranean Sea from the north. It receives approximately 7500 million m^3/year of untreated drainage water, discharged directly to the lake without previous treatment through the number of drains as Bahr El-Baqer, Ramsis, Hadous, El-Serw, and Faraskour. Tahoun [48] has evaluated the microbial contamination of El-Manzala lake and the results referring to the total viable counts of bacteria at 37°C showed that the highest value recorded was 3000×10^4 CFU/m at the Old Bahr El-Bakar discharging site and the lowest value was 0.01×10^4 CFU/m at the Legan site. On the other hand, the total viable bacterial counts at 22°C had been recorded with the highest value of 850×10^4 CFU/mL at the New Bahr El-Bakar discharging site, while the lowest value of 0.01×10^4 CFU/mL had been recorded at the Old El-Gamil Boghaze site. The MPN of the maximum counts of TC at the El-Manzala lake were 110×10^3 MPN/100 mL, affected by discharge water, while the minimum counts of TC were 0.04×10^3 MPN/100 mL. The highest value of FC bacteria at the El-Manzala lake has been recorded at the New Bahr El-Bakar discharging point 110×10^4 MPN/100 mL, and the lowest value was 0.003×10^3 MPN/100 mL. The fecal streptococci bacterial group (FS) ranged between 9 and 110×10^3 MPN/100 mL. The author attributed high pollution levels of the microbial indicators to the direct harmful effects of surrounding drains which discharge agricultural, industrial, wastewater, and other human activities.

14.8 Lake Nyos

Lake Nyos has existed in the northwest region of Cameroon. Lake Nyos is a volcanic crater lake, located with the coordinates of 10°18′02.3″E and 06°26′23.0″N, and with a maximum depth of 230 m and surface area of

approximately 1.58 km^2. The bacterial abundance at Lake Nyos was higher than the viral abundance as mentioned by [49]. In the hypolimnion, the bacterial count ranged between (1.35×10^5) and (5.20×10^5) CFU/mL, while the viral count ranged between (6.60×10^4) and (3.50×10^5) viral particles/mL. The mean ratio of viruses to bacteria at Lake Nyos was 0.42 (with ratio 0.2: 1.2) [49].

Finally, there are many factors that can help in decreasing the microbial pollution in African lakes such as

1. Encouragement of successful investment in the freshwater resources; development, assessment, and protection.
2. Sustainable financing of investments in water supply and sanitation in African countries.
3. Decreasing the depletion of the water resources through preventing pollution resulting from anthropogenic activities such as preventing discharging the different pollutants, agricultural, domestic, industrial, and sewage, into the African lakes, and preventing deforestation.
4. Collaborative governance management of transboundary water lakes.

14.9 Conclusion

It is expected that in the incoming years, there will be an increase in the microbial pollution levels in the African lakes because of increasing disposal of untreated sewage and industrial effluents in the lakes and other anthropogenic activities. Therefore, water-related diseases associated with freshwater in the African lakes are among the most popular causes of illness and death, especially in poor communities in developing countries. These types of diseases are killing people and animals in developing countries each year exactly like war victims, thus, the people in developing countries bear the water pollution costs via infection with hazardous sickness that may lead to death. The pollution victims are not only humans but also animals and plants. Water-related diseases are divided into four categories according to the World Health Organization: waterborne, water-based, water-related, and water-scarce diseases. These diseases, like dysentery, cholera, typhoid, and hepatitis, exist among people living near the African lakes, and they are common waterborne diseases in African countries. These infectious diseases can transport between people and cause several health problems, where the causative agents are bacterial pathogens or viral infections that have endemic and epidemic periods. So the health protection programs in African countries require estimating the levels of the contamination in freshwater by these microbial pathogens (fungal, bacterial, or viral).

There are huge numbers of African people who lack access to clean and safe drinking water which raises the ratio of people being vulnerable to waterborne diseases. So, many authors and biology scientists suggested that it is extremely important to carry out the continuous monitoring of microbial pollution in the African lakes by each country's government. Also, each African country must be committed to combating the pollution in the lakes by drawing and implementing suitable programs to succeed in fighting the different types of pollution in the African lakes. Finally, the conservation of the lake's wealth from pollution is serving successive generations in African countries and contributing to sustainable development.

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CHAPTER 15

Microbial community and fish diseases in African lakes, the case northern Delta lakes, Egypt

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15.1 Introduction

Keeping fish healthy depends on the relationship between fish, the environment, and pathogens. Fish diseases are due to a variety of infectious organisms, including microbes (viruses, bacteria, fungi, protozoa) and parasites. Bacteria are responsible for the majority of the infectious diseases diagnosed in wild or cultured fish, with many acting as secondary opportunistic invaders that exploit diseased fish by overcoming their host's natural defensive response. Opportunistic bacteria are widespread in the aquatic environment and pose a threat every time a fish is exposed to a stressful event [1], which lead to economic losses in fish production. Fish health in natural resources is strongly influenced by the surrounding microbial communities in water.

Aquatic microbial community can be defined as a grouping of synchronous, potentially interacting microbes present in a specific habitat in space and time [2]. Radical changes in the structure of the microbial community may directly cause diseases in fish. Because of the enormous influence of ecological microbial community, the water quality is commonly manipulated based on bacterial community change [3,4]. The immune system of fish can also decline due to stress and environmental factors such as poor water quality and malnutrition, which make them susceptible to prevalent fish diseases. Fish obtains a large number of bacteria in their intestines from sediment, water, and food [5]. Thus, by determining the bacterial contents of surrounding water and sediment samples, the level of bacteria in fish can be predicted. Coliforms are not the normal flora of bacteria in fish. Due to the deposition of human excreta in the aquatic environment, the water becomes polluted, and when this water is ingested

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by fish, the fish also becomes contaminated. Bacteria most often occur in several parts of fish, such as scales, gills, and alimentary tract which indicate the extent to which the aquatic ecosystems are polluted [6].

Lakes are very important sources of inland fisheries [7]. The decline of the water quality, the shrinking of the lake area due to drought, and the decline of fish production and biodiversity lead to the deterioration of the livelihood of fishermen's society [8]. Efforts have been made to investigate the microbial communities in the northern Egyptian lakes. However, the pathogenesis of some microbial species caused by the disruption of the microbial community still needs further studies.

15.2 Northern Delta lakes of Egypt

Manzala, Burullus, Idku, and Mariout are the most important lakes along the coast of the Egyptian Mediterranean Sea (Fig. 15.1) [9]. These northern coastal lakes are directly connected to the Mediterranean Sea through protected inlets except for Lake Mariout which had no main connection to the sea [8,10]. These inlets are vital to several migratory fish species, which spend a part of their life cycles in the lakes. Northern Delta lakes contribute less than 0.3% of the total area of Egypt [11] and are inhabited by many aquatic organisms including fish. The Delta lakes are brackish and shallow (<2 m), with an average depth of about 1.0 m, and are receiving most of their freshwater sources from irrigation drains [8]. FAO

Figure 15.1 Map of the Egyptian northern lakes [9].

reported that Egypt has 2400 km of coastline in the Mediterranean and the Red seas, and lakes constitute about 15% of the total commercial fishing areas in Egypt [12].

The environmental problems of the Egyptian northern lakes are mainly due to anthropogenic activities [13].

15.2.1 Manzala Lake

Manzala Lake is the largest and most economically important coastal lake in Egypt, providing an abundance of fish, and a favorable wintering area for migratory waterfowl [7]. It is an important and valuable natural resource area for fishing, wildlife, hydrological and biological system, and table salt production. It produces about 50% of the total annual production of the fish caught from the Egyptian lakes [14–16]. Manzala is the largest northern lake in Egypt, with an area of 300,000 acres [8]. Manzala Lake receives about 7500 million cubic meters (m^3) of untreated industrial, urban, and agricultural wastewater, which was reduced to about 4000 million m^3 after the establishment of El-Salam Canal [17]. The agricultural discharge has become a risky source of pesticides, fertilizers, and organic materials, which have a definite effect on the aquatic environment and reflected on human and public health [12].

Manzala Lake is connected to the Mediterranean Sea by outlets, namely, El-Baghdadi, New Damietta, Al-Gamil, and the new Gamil Bougesses. However, these outlets enhance the water quality status of the lake [16]. The lake is a famous mariculture area in Egypt as it produces most of the Egyptian commercial marine fishes, such as mullets, seabream, and seabass. However, lake fishes have suffered from mass mortalities over the past few years, due to mainly microbial infectious diseases [18–20]. Various infectious diseases, such as photobacteriosis, vibriosis, and streptococcosis, have been recorded in several outbreaks among lake fishes [18,19,21,22].

15.2.2 Burullus Lake

Burullus Lake is the second largest lake among the Egyptian northern lakes, with an area of about 410 km^2. The lake is separated from the Mediterranean Sea by a sandy strip while it is connected to the sea through a single outlet [8]. The lake water is brackish, with salinity up to 3.51 ppt, due to discharging of agricultural drainage [23]. Burullus Lake has been considered as a valuable source of fish yield in Egypt [24].

15.2.3 Edku Lake

Edku Lake is the third largest wetland area among the northern Delta lakes. It is located in the western part of the Delta, about 40 km east of Alexandria city and 18 km west of the Rosetta branch of the Nile River. The lake is connected to Abu Qir Bay through Boughaz Al-Maadi. It is the mouth of the El-Khairy and Barsik sewage drains [25].

15.2.4 Mariout Lake

Mariout Lake is a coastal lake located in the Alexandria governorate. Fishing is one of the main activities at the lake, and the annual catch of fish is about 4000 tons, but it is constantly decreasing due to the poor water quality and the drying up of large areas for land holding [26].

15.3 Fish and fisheries in northern lakes

Fish provides a large proportion of animal protein consumed by the world population, where 60% of people in tropical and subtropical countries depend on fish for 40% or more of their protein [27,28]. Also, fishes are one of the most important biomarkers in the aquatic system for estimating levels of water pollutants [28]. In 2009, the marine and inland captured fisheries in Egypt totaled about 127,821 and 259,577 tons, respectively, which together were less than aquaculture production of 705,490 tons [29].

The average Egyptian fish production capacity during the period 2005–18 amounted to about 1.35 million tons, including126,100 tons from only northern Delta lakes. The tilapia species has dominated during the past 70 years in the northern Delta lakes; Nile tilapia (*Oreochromis niloticus*) is one of the most widely farmed fishes in the world [30], ranks first as the most important wild and cultured fish in Egypt [31], and is considered one of the best-growing fishes with desirable characteristics.

Mandal [32] indicated that fishes are highly susceptible to contamination with various bacteria because they have a perishable protein content in their body, and the quality of the fish indicates the degree of contamination with coliform bacteria [33–35].

15.4 Methods of diagnosis of fish pathogenic microbes

The diagnoses of microbial pathogens are carried out using various tools, including standard microbiological methods (culturing, isolation, and

biochemical testes) [36], AIP20E, and molecular methods, which is more accurate technique either by using the specific primers or universal primers, such as those targeting rRNA gene operon [37].

15.5 Microbial community and fish diseases in the Delta lakes

Monitoring of microbial community in a fish's environment is important to detect the presence of microorganisms that may pose a threat to the health of fish. Bacterial indicators of fecal contamination are used as a marker of water quality, as feces may contain pathogens that have the potential to adversely affect human health. Fecal pollution from terrestrial animals including humans poses public health risks due to potential exposure to a wide array of pathogens [38,39]. Fecal indicator bacteria such as coliforms, *Escherichia coli* and *Enterococci*, have long been used to detect the water biological pollution [7].

15.5.1 Bacterial fish diseases

During the past few years, Egyptian lake fisheries have suffered from mass mortality of freshwater and marine fish species, due to bacterial infections [39,40]. Numerous infectious diseases due to the pathogenic bacteria including Aeromonas septicemia, photobacteriosis, vibriosis, and streptococcosis have been isolated in many outbreaks in wild and cultured fish [22,41,42].

Generally, the majority of bacterial fish diseases are caused by gram-negative bacteria such as *Aeromonas, Citrobacter, Edwardsiella, Flavobacterium (Flexibacter), Mycobacterium, Pseudomonas*, and *Vibrio*, while, *Streptococcus*, a gram-positive genus has been shown to cause disease in a variety of fish species [43–45] and can represent the primary or the secondary infection.

The existence of diverse enteric bacteria, such as *Citrobacter braakii, Citrobacter freundii, Enterobacter sakazakii, Enterobacter cloacae, Vibrio cholerae, Proteus mirabilis, Proteus vulgaris, Klebsiella pneumoniae*, and *Aeromonas hydrophila*, besides mycotoxin-producing fungi, such as *Aspergillus* spp., *Fusarium* spp., and *Penicillium* spp., in fish indicated the degree of habitat and handlers pollution [46,47].

15.5.2 Fungal fish diseases

Fungal fish diseases are caused by the interaction of the fungus, fish, and the environment. Fishes are negatively affected by poor water quality and

poor management, which are stress factors that must be avoided to sustain fish [48]. Changes in temperature and water quality allow overgrowth of the fungal zoospores [49]. Fungi may be responsible for many fish diseases [50]. The risk of fungal diseases in fish is not stopped only to induce mortality, but also causes a decrease in the growth performance besides the production of mycotoxins [51]. Many fungi, such as *Aspergillus* spp., *Fusarium* spp., and *Penicillium* spp., that infect fish are opportunistic, attacking fish when they are stressed or immunocompromised due to bad environmental conditions, or when fish loses the mucosal layer responsible for protecting the skin from the secondary infection [52,53]. Mycotic infections are widespread in freshwater fishes, particularly Saprolegniaceae infection [54].

15.5.3 Viral fish diseases

Viruses cause clinical problems with negative effects on the economy of fish production. Unfortunately, there is no information about viruses infecting fish in Egyptian lakes. Only four records indicated the presence of infectious pancreatic necrosis virus (IPN) and spring viremia virus (SVV) among freshwater fishes [55–57], in addition to the Tilapia Lake Virus (TiLV) in some farmed fish Delta [58].

15.6 The recorded pathogenic microbial community in lake waters

The fecal indicator bacteria such as total bacterial count (TBC), coliform (CF), fecal coliform (*E. coli*), *Vibrio cholera*, *E. coli*, and enterococci have long been used to detect fecal pollution and the presence of potentially pathogenic microorganisms. The bacteriological examination of the water surrounding the fish is very necessary to detect the bacterial species being transferred into the fish [7].

15.6.1 Manzala Lake

The bacterial counting, from several studies, in the water samples at different sites of Manzala Lake is shown in Table 15.2. Beheary et al. [10] counted bacteria seasonally, 2017–18, from water samples at nine different sites in the eastern and southern parts of Lake Manzala to study the biological water quality, and the results showed high levels of fecal coliform in summer, autumn, and winter than spring, where the highest mean value was 46.6 ± 7.9 CFU $\times 10^3$/mL in the summer and the lowest

mean value was 2.2 ± 0.8 CFU $\times 10^3$/mL in the spring season. Also, the highest mean value of total bacteria count (TB) was 37.3 ± 4.2 CFU $\times 10^3$/mL in the summer season, while the minimum mean value was 3.6 ± 0.5 CFU $\times 10^3$/mL in the spring. In contrast, El-Fadaly et al. [13] observed that the highest value of TB was recorded in spring (4400 CFU/mL $\times 10^3$), while the lowest value was recorded in autumn (CFU/mL $\times 10^3$). On the other hand, the highest value of total fungal count (TF) was observed in summer (22,500 CFU/mL $\times 10^3$), while the lowest value was observed in the winter (0.06 CFU/mL $\times 10^3$). Moreover, data showed no bacterial growth in Salmonella Shigella agar medium.

Zaky et al. [59] isolated bacteria from water samples collected from four sites of Manzala Lake (Table 15.1) and showed high counts of total bacteria (TB) and fecal coliform, *E. coli*, (FC), which indicated high pollution in the different sampling sites, especially El Mataryia and El Kapoty areas. In the autumn season, 2016, the highest value of total bacterial count (TBC) was $6.70 \pm 0.88 \times 10^4$ CFU/mL in water of El-Ganka area of Manzala Lake, while TBCs were 5.00 ± 0.58 and $3.00 \pm 1.03 \times 10^4$ CFU/mL in El-Boughaz and Domiette, respectively [7]. Water samples from Manzala Lake revealed high bacterial counts of *Staphylococcus sciuri*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Aeromonas veronii*, *Aeromonas caviae*, and *Vibrio alginolyticus* [60]. Also, 100 pathogenic bacterial isolates, representing nine genera, have been identified in different sites of the lake, including *E. coli* (15%), *K. pneumoniae* (13%), *Pseudomonas aeruginosa* (12%), *Pseudomonas fluorescens* (9%), *Salmonella choleraesuis* (11%), *Shigella* sp. (7%), *Serratia liquefaciens* (8%), *P. vulgaris* (8%), *Acinetobacter* sp. (8%), and *Chryseomonas lutecla* (9%) [61].

15.6.2 Edku Lake

Data in Table 15.2 address the TB and coliform group in water at different sites of Edku Lake. The highest values of total bacterial count and coliform group were recorded in the summer at Edku Pumps station and Abu Hummus drain as 6317 and 2717×10^3 CFU/mL and 107.7 and 53.5×10^3 CFU/mL, respectively [62]. According to the guideline standers for fecal indicator organisms of WHO [64] which accepts the count values of the exanimated bacteria up to 500/100 mL for total coliform (TC) and 100/100 mL for both fecal coliform and fecal streptococci, we can conclude that Edku Pumps station and Abu Hummus drain are heavily polluted. The lowest values of TB and coliform group were 210

Table 15.1 Seasonal count of total bacteria and fungi in water.

Study area		Season	Bacteria CFU × 10^3							
			TBC	FCC *E. coli*	TF	*Staphylococci*	*Aeromonas* sp.	*Vibrio cholera*	Coliform	References
Manzala Lake		Winter	19.5	10.1	–	–	–	–	–	[9]
		Spring	3.6	2.2	–	–	–	–	–	
		Summer	37	46.6	–	–	–	–	–	
		Autumn	36.5	33.5	–	–	–	–	–	
El-Roda city in Damietta		Winter	3	–	0.06	0.015	0.2	–	0.0	[12]
		Spring	4400	–	22000	1760	66	–	1210	
		Summer	39	–	22500	1	2	–	36	
		Autumn	0.0	–	0.3	0.0	0.1	–	0.0	
Manzala Lake, 2014	**Kapoty**	Autumn	1.2	–	–	–	–	–	0.2	[59]
		Winter	1.3	–	–	–	–	–	0.1	
		Spring	5.6	–	–	–	–	–	1.5	
		Summer	10	–	–	–	–	–	3.8	
	Bashtier	Autumn	1.0	–	–	–	–	–	0.003	
		Winter	5.0	–	–	–	–	–	0.1	
		Spring	4.0	–	–	–	–	–	0.05	
		Summer	3.0	–	–	–	–	–	0.1	
	Gamil outlet	Autumn	1.5	–	–	–	–	–	0.03	
		Winter	2.75	–	–	–	–	–	0.1	
		Spring	3.0	–	–	–	–	–	0.05	
		Summer	0. 1	–	–	–	–	–	0.1	
	Mataryia	Autumn	1.4	–	–	–	–	–	0.2	
		Winter	4.0	–	–	–	–	–	0.1	
		Spring	5.6	–	–	–	–	–	0.05	
		Summer	7.2	–	–	–	–	–	0.1	

Manzala	Autumn	290	250		0.7	0.5	0.3	350	[60]
El-Tawila	Winter	260	–	–	–	–	4.0	–	[62]
	Spring	288	–	–	–	–	5.1	–	
	Summer	550	–	–	–	–	8.7	–	
	Autumn	479	–	–	–	–	6.6	–	
El-Shlachel	Winter	275	–	–	–	–	4.3	–	
	Spring	311	–	–	–	–	5.7	–	
	Summer	497	–	–	–	–	9.3	–	
	Autumn	387	–	–	–	–	7.8	–	
Abu Hummus drain	Winter	1455	–	–	–	–	16.6	–	
	Spring	1711	–	–	–	–	27.1	–	
	Summer	2717	–	–	–	–	53.5	–	
	Autumn	2189	–	–	–	–	37.9	–	
El-Kanaess	Winter	210	–	–	–	–	3.3	–	
	Spring	399	–	–	–	–	6.7	–	
	Summer	545	–	–	–	–	16.3	–	
	Autumn	431	–	–	–	–	9.4	–	
Edku Pumps	Winter	3555	–	–	–	–	44.4	–	
	Spring	4314	–	–	–	–	61.6	–	
	Summer	6317	–	–	–	–	107.7	–	
	Autumn	5418	–	–	–	–	80.2	–	
Nakhnookh	Winter	377	–	–	–	–	7.4	–	
	Spring	488	–	–	–	–	13.3	–	
	Summer	709	–	–	–	–	29.7	–	
	Autumn	575	–	–	–	–	20.2	–	

(*Continued*)

Table 15.1 (Continued)

Study area	Season	Bacteria CFU × 10^3							
		TBC	FCC *E. coli*	TF	*Staphylococci*	*Aeromonas* sp.	*Vibrio cholera*	Coliform	References
El-Boughaz	Winter	50.00	1.3	–	–	–	–	0.20	[7]
El-Ganka		60.70	40.00	–	–	–	1.06	12.67	
Domiette		30.0	18.00	–	–	–	0.17	0.47	
Mariout	February 2018–January 2019	180–31200	0.04–28.30	–	–	–	0.01–1.8	180–12670	[63]

TBC, Total bacterial count; FCC (*E. coli*), fecal coliform count; *TF*, total fungal; *V. cholera* = *Vibrio cholera*.

Table 15.2 Microbial incidence among studied fishes in Egyptian northern lakes.

Study area	Fish species	Bacteria	Percentage (%)	References
Manzala Lake	*Tilapia* sp.	*Yersinia ruckeri*	20	[65]
		Aeromonas hydrophila	10	
		Vibrio anguillarum	13	
		Streptococcus pyogenes	2	
		Other organisms	5	
	Cat fish	*Yersinia ruckeri*	5	
		Aeromonas hydrophila	3	
		Vibrio anguillarum	7	
		Streptococcus pyogenes	3	
		Other organisms	–	
	Lates niloticus	*Yersinia ruckeri*	4	
		Aeromonas hydrophila	3.7	
		Vibrio anguillarum	2	
		Streptococcus pyogenes	5	
		Other organisms	3	
Manzala Lake	*Oreochromis niloticus*	*E. coli*	36	[66]
		Proteus mirabilis	30	
		Klebsiella pneumoniae	7	
		Citrobacter freundii	7	
		Providencia stuartii	7	
		Erwinia sp.	7	
		Aspergillus niger	All organs, gills, intestine, skin	
		Aspergillus terreus		
		Penicillium cyclopium		
		Cladosporium cladosporioides		
Kapoty, Bashtier, Mataryia, and Gamil areas (Manzala Lake)	Intestine and gills of Tilapia spp.	*Erwinia* sp.	8	[59]
		S. maltophilia	4	
		Aeromonas spp.	10	
		Chryseomonas lutcola	2	
		Flavobacterium odoratum	2	

(*Continued*)

Table 15.2 (Continued)

Study area	Fish species	Bacteria	Percentage (%)	References
		Flavobacterium maningosepticum	2	
		Serratia sp.	2	
		Vibrio sp.	2	
		Pseudomonas sp.	6	
		Pasteurella sp.	4	
		Klebsiella sp.	6	
		Citrobacter freundii	4	
		Sphingomonas paucimobilis	2	
		Proteus mirabilis	18	
		E. coli	20	
		Enterobacter amnigenus	4	
El Bashtier and El Mataryia area (Manzala Lake)	Fish	*Stenotrophomonas maltophilia*	2.2	[67]
		Aeromonas hydrophila	17.7	
		Aeromonas sobria	16.6	
		Klebsiella sp.	3.3	
		Citrobacter freundii	2.2	
		Sphingomonas paucimobilis	1.1	
		Proteus mirabilis	10	
		E. coli	11.1	
		Enterobacter amnigenus	1.1	
	Water	*Acinetobacter*	1.1	
		Erwinia sp.	4.4	
		Chryseomonas lutcola	1.1	
		Flavobacterium odoratum	1.1	
		Flavobacterium maningosepticum	1.1	
		Flavobacterium oryzihabitans	2.2	
		Bacillus sp.	8.8	
		Serratia sp.	1.0	
		Vibrio sp.	1.1	
		Pseudomonas sp.	1.1	
		Pasteurella sp.	1.1	
		Strepotococcus sp.	3.3	

(*Continued*)

Table 15.2 (Continued)

Study area	Fish species	Bacteria	Percentage (%)	References
El-Roda city Damietta, Manzala Lake.	*O. niloticus* and water	*Micrococcus* sp. *Aeromonas* sp. *Escherichia* sp. *Pseudomonas* sp. *Aspergillus alliaceus* *Aspergillus niger* *Aspergillus flavus* *Penicillium* sp.	Bacteria Fungi	[12]
El-Manzal	*O. niloticus* and *Clarias gariepinus*	*Vibrio alginolyticus* *Aeromonas veronii* *Aeromonas caviae* *Enterococcus faecalis*	32.3 14.7 23.5 29.4	[60]

and 3.3×10^3 CFU/mL, respectively; in addition, the highest values were observed in the summer in all studied stations while the lowest values were reported in winter [62].

15.6.3 Burullus Lake

Bacteriological examination of three different sites of Lake Burullus revealed that total bacterial count and total coliform count were much higher in the case of aquacultural wastewater discharge site. The total fecal count was higher in the agricultural drainage site of the lake [68].

15.6.4 Mariout Lake

Farouk [63] indicated that Mariout Lake is now one of the most heavily polluted lakes in Egypt. The bacteriological examination of three basins of the lake showed that the main basin (the largest area; 6000 feddan) had the highest bacterial load (TBC, CF, *E. coli*, and *V. cholera*) in water, sediment, and *O. niloticus* organs, where TBC, CF, *E. coli*, and *V. cholera* recorded higher values in sediment and water than in *O. niloticus* organs (Table 15.1). However, the abundance of bacteria in water and *O. niloticus* organs exceeds the permissible limits which can cause a health risk for fish and consumers.

15.7 Microbial isolates and their prevalence in northern Delta lake fishes

The microbial isolates and their abundance percentage in fish and water of northern lakes are shown in Table 15.2. Abo El Gheit [65] reported the bacterial incidence among different moribund and freshly dead fishes, such as Tilapia spp., catfish, and *Lates niloticus* in Manzala Lake, and showed higher infection with *Yersinia* and *Aeromonas*, *Vibrio* spp., and *Streptococcus* spp., respectively. Zaky and Ibrahim [66] isolated several bacteria belonging to six species, *E. coli and P. mirabilis*, which account for 36% and 30%, respectively, of the total number of bacteria that were isolated from *O. niloticus* from Manzala, while each of other four species, *K. pneumoniae*, *C. freundii, Providencia stuartii*, and *Erwinia* sp., showed only a fraction of 7%. Also, four species of fungi, *Aspergillus niger, Aspergillus terreus, Cladosporium cladosporioides*, and *Penicillium cyclopium*, have been isolated from organs, skin, gills, and intestine of *O. niloticus*. In addition, several pathogenic bacteria, such as *S. sciuri*, *S. aureus*, *E. faecalis*, *A. veronii*, *A. caviae*, and *V. alginolyticus*, were isolated from *O. niloticus* and African catfish (*Clarias gariepinus*) of the Manzala fishes in the autumn of 2020 [60].

Isolated bacteria from the gills and intestine of *O. niloticus*, which were collected from four sites of Manzala Lake, namely, Kapoty, Bashtier, Mataryia, and Gamil areas (Table 15.2) showed that *E. coli* is the most abundant and accounted for 20% of the total isolates, while *Chrysomonas lutcola, Flavobacterium odoratum, Flavobacterium maningosepticum, Serratia* sp., *Vibrio* sp., and *Sphingomonas paucimobilis* showed only 2% of recorded isolates [59]. In addition, *A. hydrophila* and *Aeromonas sobria* have been recorded as two dominant pathogenic bacterial species in Lake Manzala [67]. Also, several bacterial genera have been isolated from Manzala Lake water samples including *Aeromonas, Bacillus, Proteus, Pseudomonas, Streptococcus, S. epidermidis, S. aureus, Micrococcus, Vibrio*, and *E. coli* [12]. Moreover, fungal isolates, *A. niger, Aspergillus flavus, Aspergillus ochraceus*, *Aspergillus oryzae*, *Geotrichum candidum*, and *Penicillium* sp., have been isolated from the gastrointestinal tract of fish as *O. niloticus*, *C. gariepinus*, *Scomber scombrus* [69–73].

Different fish organs such as skin, gill, and intestine have been surveyed for fecal coli infection at various locations of Egyptian northern Delta lakes. Table 15.3 illustrates the summary of these surveys. El-Fadaly [12] collected Nile tilapia samples, seasonally in 2014, from El-Roda area, Manzala Lake, to study the microbial community in fish organs. The

Table 15.3 Microbiological values (CFU/g $\times 10^3$) of fish taken from investigated lakes at different seasons.

Study area/references	Season	Organs	CFU $\times 10^3$							
			TB	*E. coli*	TF	St.	Pse.	Aer.	*Vibrio cholera*	Coliform
El-Rodaarea (Manzala) [12]	Spring	Muscles	17.6	–	1.87	198	–	0.275	–	0.0
		Intestine	46200	–	13200	33	–	2530	–	1210000
		Surface	1980	–	46.2	77	–	1.01	–	12100
	Summer	Muscles	6000	–	1.2	0.0	–	800	–	0.0
		Intestine	1000	–	12000	0.0	–	0.0	–	930
		Surface	500	–	68	0.0	–	0.0	–	160
	Autumn	Muscles	0.06	–	0.7	0.01	–	0.07	–	110
		Intestine	0.0	–	40	0.0	–	0.0	–	0.0
		Surface	0.2	–	0.0	0.7	–	1	–	0.0
	Winter	Muscles	45	–	6.0	0.01	–	0.2	–	0.0
		Intestine	10	–	20	1.5	–	30	–	1
		Surface	20	–	0.0	0.0	–	0.50	–	0.0
(Manzala) [74]	Winter	Intestine	2050	2.2	–	–	7.6	–	–	170
		Gills	460	4.3	–	–	4.6		–	120
		Muscle	10	0.2	–	–	0.07	–	–	2.0
	Summer	Intestine	2220	6.8	–	–	18.5	–	–	425
		Gills	1440	9.0	–		17.8	–	–	361
		Muscle	20	0.2	–	–	0.4	–	–	3.0

(*Continued*)

Table 15.3 (Continued)

Study area/references		Season	Organs	CFU × 10^3							
				TB	*E. coli*	TF	St.	Pse.	Aer.	*Vibrio cholera*	Coliform
Edku Lake [64], Nile tilapia	El-Tawila	Winter	Skin	3.33	–	–	–	–	–	–	0.74
			Muscle	0.47	–	–		–	–	–	31
		Spring	Skin	4.19	–	–	–	–	–	–	0.96
			Muscle	0.69	–	–			–	–	0.78
		Summer	Skin	7.97	–	–	–	–	–	–	1.77
			Muscle	1.13	–		–	–	–	–	1.33
		Autumn	Skin	6.08	–	–	–	–	–	–	1.17
			Muscle	0.89	–		–		–	–	0.91
	El-Shlachel	Winter	Skin	4.75	–	–	–	–	–	–	1.02
			Muscle	0.56	–	–	–	–	–	–	0.11
		Spring	Skin	5.35	–	–		–	–	–	1.77
			Muscle	0.89	–	–	–	–	–	–	230
		Summer	Skin	7.73	–	–			–	–	2.99
			Muscle	1.83	–	–	–	–	–	–	0.55
		Autumn	Skin	6.11	–		–	–	–	–	2.15
			Muscle	1.05	–	–	–	–	–	–	0.43
	Abu Hummus drain	Winter	Muscle	21.75	–		–		–	–	2.37
			Skin	3.88	–	–	–	–	–	–	0.78
		Spring	Muscle	27.17	–	–	–	–	–	–	3.33
			Skin	4.79	–	–		–	–	–	1.25
		Summer	Muscle	39.01	–	–	–	–	–	–	5.16
			Skin	7.40	–	–			–	–	2.66

		Autumn	Muscle	33.13	–	–	–	–	–	–	4.24
			Muscle	6.07	–		–	–	–	–	1.87
	El-Kanaess	Winter	Muscle	3.55	–	–	–	–	–	–	0.71
			Skin	0.49	–		–		–	–	0.25
		Spring	Muscle	4.61	–	–	–	–	–	–	1.11
			Skin	0.67	–	–	–	–	–	–	0.44
		Summer	Muscle	6.36	–	–		–	–	–	2.75
			Skin	1.19	–	–	–	–	–	–	0.78
		Autumn	Muscle	5.11	–	–			–	–	2.02
			Skin	0.93	–	–	–	–	–	–	0.58
	Edku Pumps	Winter	Muscle	51.11	–		–	–	–	–	6.14
			Skin	6.77	–	–	–	–	–	–	1.78
		Spring	Muscle	61.6	–		–		–	–	8.14
			Skin	8.32	–	–	–	–	–	–	3.14
		Summer	Muscle	88.1	–	–	–	–	–	–	13.0
			Skin	14.04	–	–		–	–	–	5.47
		Autumn	Muscle	70.07	–	–	–	–	–	–	10.0
			Skin	10.14	–	–			–	–	4.09
	Nakhnookh	Winter	Muscle	5.09	–	–	–	–	–	–	1.08
			Skin	0.64	–		–	–	–	–	0.37
		Spring	Muscle	6.88	–	–	–	–	–	–	1.11
			Skin	0.65	–		–		–	–	2.11
		Summer	Muscle	9.19	–	–	–	–	–	–	4.12
			Skin	2.29	–	–	–	–	–	–	1.34
		Autumn	Muscle	7.62	–	–		–	–	–	3.17
			Muscle	1.77	–	–	–	–	–	–	0.87

(*Continued*)

Table 15.3 (Continued)

Study area/references	Season		Organs	CFU × 10^3							
				TB	*E. coli*	TF	St.	Pse.	Aer.	*Vibrio cholera*	Coliform
Manzala [66]	Nile tilapia		Intestine	310	29.0	–	–	–	–	–	–
			Gills	62.0	5.0	–	–	–	–	–	–
			Skin	2.9	0.5	–	–	–		–	–
Manzala [7]	Winter 2016	Nile tilapia	Muscles	3.33	0.0	–	–		–	0.0	0.97
			Skin	9.77	2.33	–	–	–	–	0.30	2.5
			Gills	80.0	41.0	–	–	–	–	60.3	17.0
		Catfish	Muscles	14.33	0.0	–	–		–	0.0	1.5
			Skin	7.53	8.56	–		–	–	0.43	0.63
			Gills	28.33	15.3	–	–	–	–	65.3	15.6
Mariout [62]	Annual average	Tilapia	Skin	20–36	0.18–19.9*	–	–	–	–	0.7–5.5*	9.9–12.5
			Gills	23–46.6	0.2–16.9*	–	–		–	0.3–0.7*	21.0–28.3
			Muscle	0.41–15.3	0.08–4.4*	–	–	–	–	0.2–0.38*	8.3–11.3

Total bacterial count (TBC), coliform group (CF), fecal coliform (*E. coli*), *Vibrio cholera* (*V. cholera*), total fungi (TF), *Streptococci* (St), *Pseudomonas* (Pse), *Aeromonas* (Aer), – not detected.
*Range between.

highest values of TB in fish organs were observed in summer and spring, but the lowest value was in autumn and winter, and the highest abundance of bacteria has been detected in intestine. The highest values of the fungal count have been recorded in spring and summer, while the lowest fungal counts were during winter and autumn. Zaky [67] reported that the highest count of bacteria has been observed in the mucus of the skin of tilapia fish. The pathogenic bacteria, such as *Pseudomonas, Vibrio, Streptococcus*, and the Enterobacterales, such as *Escherichia*, *Serratia*, and *Salmonella*, have been isolated from tilapia skin mucus [67].

The bacterial counts of *O. niloticus* organs that were collected from Lake Manzala varied from one organ to another. While the intestine exhibited a mean count of TB is 3.1×10^5, gills revealed a mean count of 6.2×10^4 and skin 2.9×10^3 [66].

Pseudomonas spp. had high distribution in tilapia organs, gills, and intestines [74]. In the tilapia intestine, *Pseudomonas* sp. counted 7.9×10^3 CFU/g in winter and 18.5×10^3 CFU g in summer [74]. In the gills of tilapia, the *Pseudomonas* sp. counts were 4.6×10^3 CFU/g and 17.8×10^3 CFU/g in winter and summer, respectively, while in flesh, the bacterium counted 70 CFU/g in winter and 400 CFU/g in summer [75].

15.8 Clinical signs and histological changes in diseased *O. niloticus* isolated from Manzala Lake

Diseased Nile tilapia collected from Manzala Lake in summer of 2021 showed clinical signs and mortality due to infection with *Streptococcus* sp., *Aeromonas* sp., and *Micrococcus* sp. (unpublished data by author). These clinical signs were ulcer and hemorrhage on the skin and exophthalmia (Fig. 15.2A–C), due to *Aeromonas* sp. infection, while *Streptococcus* sp. infection was represented by severe ulcer on the skin (Fig. 15.2C and D). The infection by *Micrococcus* sp. showed severe body swellings (Fig. 15.2E). Moreover, the complicated bacterial infections showed some internal signs such as enlargement of the liver and gall bladder, congestion in the kidney and liver, and hemorrhage in the abdominal cavity of infected Nile tilapia (Fig. 15.2F).

Samples of diseased Nile tilapia collected from Manzala Lake in summer of 2021 showed histopathological alterations caused by the pathogenic bacteria *A. hydrophila* (unpublished data by author) which is recorded in Fig. 15.3A–F as focal necrotic areas between the hepatic cells (Fig. 15.3A), dilation and congestion of sinusoids and nuclear and

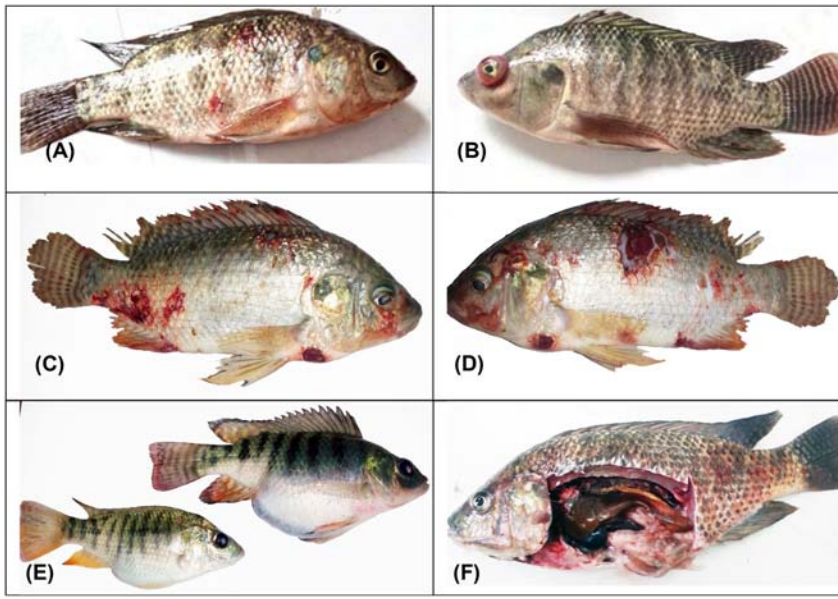

Figure 15.2 Clinical signs of *Aeromonas hydrophila* infected *Oreochromis niloticus* which were collected from Manzala Lake showed ulcer and hemorrhage on the skin and exophthalmia (A,B), severe ulcer on skin of *Streptococcus* sp. infected fish (C,D), severe body swellings of *O. niloticus* infected by *Micrococcus* sp. (E), and enlargement of liver and gall bladder and congestion in kidney and liver of *O. niloticus* (F).

cytoplasmic degeneration (Fig. 15.3B and C), with severe fatty changes, besides pyknotic nucleus hepatocytes (Fig. 15.3C) in the liver. Moreover, the spleen showed intense hyperplasia of melanomacrophage centers and hemolytic areas in between red pulps in the spleen (Fig. 15.3D), while gills showed congestion and dilation of primary gill blood vessels (Fig. 15.3E and F) with a fusion of the secondary lamellae and desquamation, particularly at the tips (Fig. 15.3F).

15.9 Effects of lake microbial fish diseases on human

Many of the recorded fish pathogenic bacteria have toxigenic characteristics as well as multidrug resistance, such as *A. hydrophila, A. sobria, P. aeruginosa, P. fluorescence*, and *V. anguillarum*, which infect gills, intestines, and flesh, resulting in the risk of diarrheal diseases among human populations, who may feed on infected fishes [74,76–79]. Moreover, the presence of *E. coli* in fish may indicate a possible cause of gastrointestinal diseases.

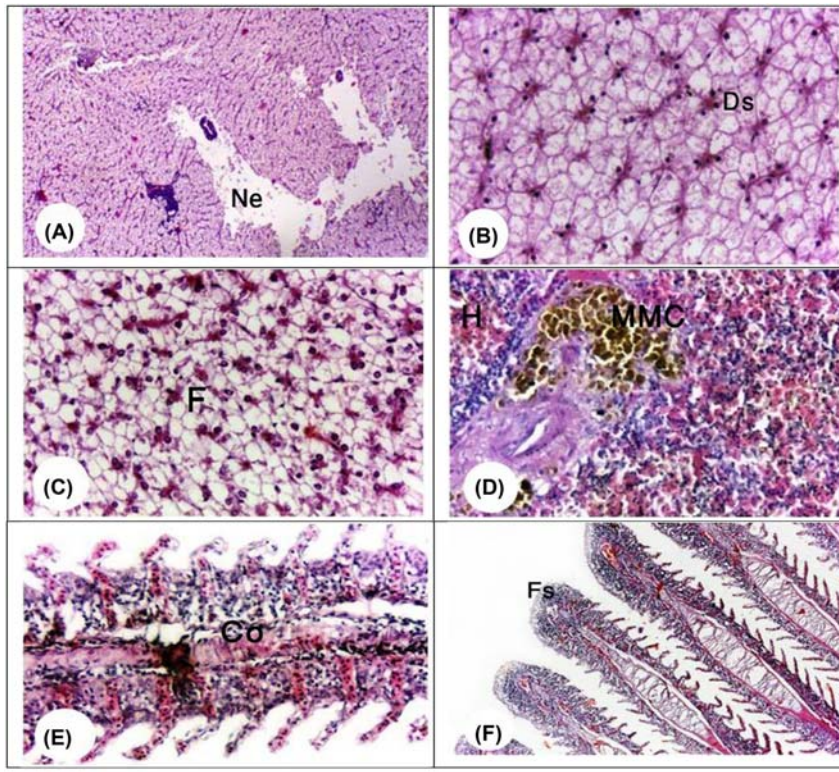

Figure 15.3 (A–F) Histopathological changes in the liver of *Aeromonas hydrophila* infected *Oreochromis niloticus* stained with hematoxylin–eosin (H&E); (A) focal necrotic areas between the hepatic cells (× 100), (B) dilation and congestion of sinusoids, (× 200), (C) fatty changes, besides pyknotic nucleus hepatocytes (× 200), (D) hyperplasia of melanomacrophage centers and hemolytic between red pulps of the spleen (× 250), (E) congestion (Co) and dilation of primary gill blood vessels (× 400), (F) fusion of the secondary lamellae (Fs) and desquamation (× 100). *Ne*, Focal necrotic area; *Ds*, dilation of sinusoids; *F*, fatty changes; *MMC*, melanomacrophage; *H*, hemolytic; *Co*, congestion; *Fs*, fusion of the secondary lamellae.

Also, *Pseudomonas* sp. is among bacterial communities, which infect humans [80,81].

15.10 Challenges facing the Egyptian northern Delta lakes and their relationship with microbial fish diseases

The main challenges facing Egyptian northern lakes are the deterioration of lake areas and complicated pollution from different sources, leading to

serious decline in lake fish productivity. For example, the area of Manzala Lake has decreased from more than 1400 km^2 in the early 1970s to less than 700 km^2 in 2003 [21]. Pollution causes poor water quality, which is a major stress factor that has led to an increase in the risk of fish microbial diseases.

15.11 Recommendations

Great efforts are really needed for the recovery of the fishes at northern Delta Lakes. The efforts include:

1. Providing a monitoring system and a concrete database for water quality and microbial fish diseases that help decision-makers to develop plans for the proper management of the lakes.
2. Great efforts and cooperation between different authorities are needed to protect the lakes from pollution and reduce environmental risks.

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CHAPTER 16

Microbial dynamics within Lake Victoria Basin in relation to human activities

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16.1 Introduction

African inland lakes have been a positive influence on the livelihoods and income of a multitude of riparian communities living in and around them since time immemorial [1,2]. The lakes are contributing to poverty reduction and boosting nutrition and food security [3,4]. However, pollution and increased eutrophication have been known to occur due to anthropogenic activities around the African inland lakes [5]. They are mainly attributed to agricultural activities, industrial effluents, and urban waste management due to urbanization, cage culture and aquaculture wastes, wetland reclamations, and sedimentation [6]. These anthropogenic uses have made most of the once clear, life-filled African lakes to eutrophic [1,7]. The streams and rivers contribute expressively toward the lakes and small water bodies (SWBs) contamination [8,9] since they are regularly subjected to receiving and flowing some of the afore-highlighted pollutants specifically agricultural, industrial and domestic wastes into SWBs and the lakes [10]. The reduction of a wide range of aquatic contaminants derived from anthropogenic activities is therefore essential to advance the sustainable growth of humanity with low undesirable ecological impact [8,10]. Furthermore, climate change impacts are occasioning changes in abiotic factors for instance temperature and precipitation consequently affecting the normal function of aquatic ecosystems by changing the habitats of aquatic flora and fauna [11,12].

Microbial contamination in African lakes is additionally heightened by the economic challenges that are blamable for the lack of adequate sanitary and phytosanitary measures primed in most developing countries [13]. On the other hand, apparent biological changes such as the water

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hyacinth invasion, increasing levels of algal blooms as well as emerging undesirable traits, for example, the paradigm shift from large-sized to smaller-sized fish are testimonies of deteriorating water quality and other related consequences [14,15]. In addition to physicochemical variables and nutrient levels, pollution impacts consequences present themselves in the occurrences, prevalence, shifts in abundance, and distribution of diverse biota. This is especially true of macrophytes, fish species, plankton, and micro-contaminants such as the coliform bacteria [16].

Lake Victoria, Africa's largest lake and the second in the world, basin is experiencing increased contamination [17]. The general anthropogenic features of Lake Victoria Basin are the ever-increasing number of cages, encroachment of SWBs, sewage discharges, and emerging aquaculture firms [5,18]. These functions of aquatic systems are known to deteriorate water quality and are likely to exacerbate lake pollution and its linkages to aquatic systems and affect biota occurrence and increase the incidences of water-borne human diseases. Whereas several physicochemical parameters and water quality indicators such as fish, for example, [15,16], benthic organisms, for example, [19], plankton, for example, [20], and nutrients, for example, [6] have been assessed in the region. Little information is known on the microbial water quality in terms of diversity and abundance.

However, bioindicators naturally occurring in environments are used to evaluate their health and are important tools for recognizing changes within the environment, either positive or negative, and their resultant impacts on humans [19,21]. Among the bioindicators, microorganisms are regularly utilized as health pointers for aquatic environments due to their abundance, ease to test, and availability [16,22,23]. They can be used to indicate variations in the aquatic environment as well as depict negative or positive impacts based on their numbers and presence or absence [24]. The state of the environment is efficiently monitored or examined by the use of bioindicator organisms owing to their resistance to ecological changes. The coliform bacteria are the most commonly used indicator organism to the anthropogenic uses of water [22]. Pollution is one of the biggest issues confronting the African lakes, and as such, management approaches to such systems have tended to focus on fisheries to obtain a specific quantity of catch and with patchy data on microbiological contaminants such as total and fecal coliforms [18].

Whereas coliform bacteria are not well documented in the region [16], they are utilized as the key criterion for determining the quality of water [22,23]. They are good indicators of pollution since they are found

in the feces of all warm-blooded animals and humans, as well as in the environment (nutrient-rich waterways, soil, and decaying plant material) and drinking water in low concentrations [22]. Coliform bacteria are clustered in three diverse groups consisting of *Escherichia coli*, fecal coliform, and total coliform [25]. Total coliform bacteria are common in the environment and are usually harmless. If only total coliform bacteria are found in drinking water, the source is likely to be environmental [23]. Fecal coliform bacteria are a subgroup of total coliform bacteria that can be in large numbers in both human and animal intestines and feces [26]. The presence of fecal coliform bacteria in a water sample frequently suggests recent fecal contamination, implying that pathogens are more likely to be present if simply total coliform bacteria are identified [27]. *E. coli* bacteria are found in the intestines and gut of some animals. Most types of *E. coli* are harmless but some strains can cause diarrhea when drinking foul water [11].

Microbial contamination in the aquatic environment is one of the essential issues concerning the sanitary state of the aquatic system utilized for domestic water supply, recreational undertakings, and fishing activities due to potential pollution by pathogenic microorganisms [13,28]. While there are global suggestions that different human activities result in varying concentration levels of coliforms in water quality assessments [23], there is patchiness of microbial information in African lakes and their basins to rely on in making such conclusions. Therefore, the current study assessed the total and fecal coliform concentrations as well as the physicochemical parameters [temperature, dissolved oxygen (DO), pH, conductivity, Secchi depth, depth, and size] in relation to the existing human use of aquatic systems in the Lake Victoria Basin. The assessment of the microbial water quality issues and related physicochemical parameters will aid in the creation of catchment management measures to reduce the negative effects related to the aquatic use and fishery in African lakes and their environments.

16.2 Methods

16.2.1 Study area

This study was undertaken in the Lake Victoria Basin, Kenya (Fig. 16.1) which constitutes a catchment area of 42,480 km^2 (Kenyan side) of the lake's total catchment of 194,000 km^2 extending up to Rwanda and Burundi [29]. There are many rivers, which drain the study basin, and pour their waters into Lake Victoria with the major ones being Gucha-Migori, Sondu-Miriu, and Nyando found in the southern basin, whereas

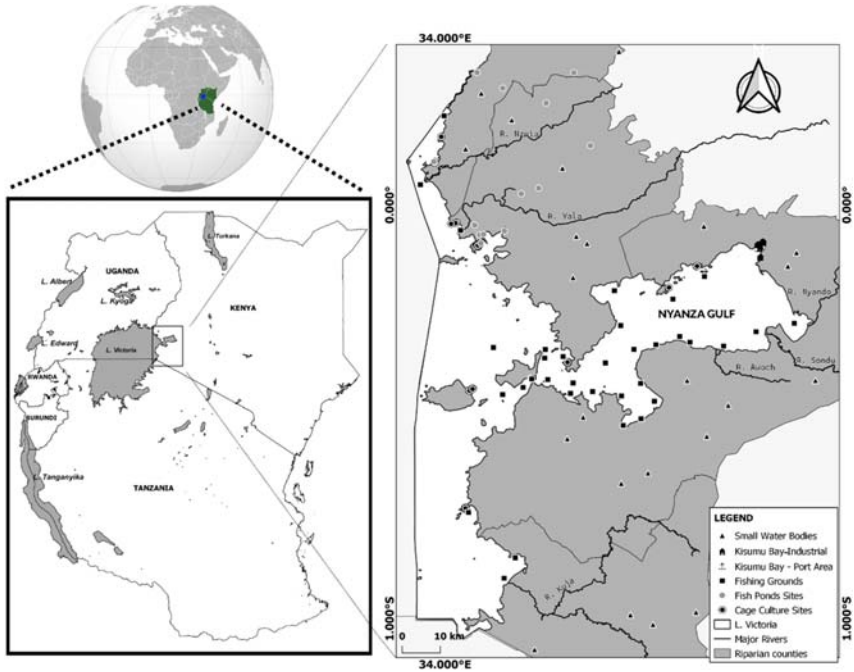

Figure 16.1 Sampled sites represented by hotspot areas for coliform occurrence in the Lake Victoria Basin, Kenya. *Redrawn from KMFRI-generated Shapefiles.*

Nzoia and Yala drain the northern Kenyan basin. Over 40 million people in the three riparian countries (Kenya, Tanzania, and Uganda) benefit from Lake Victoria's environmental services [20]. These include fisheries, cage culture, treated sewage discharges, linkage to SWBs, transport, and water for the home, agricultural, and industrial uses [30]. The lake yields roughly one million tons of fish worth USD 400 million per year, employing 200,000 fishermen and up to 700,000 people along the value chain [17].

Lake Victoria with a surface area of 68,000 km^2 is the world's largest tropical and the second-largest freshwater lake. The lake touches the equator on the northern side, and is generally shallow for its surface area, with a maximum depth of 79 m and an average depth of 40 m. The lake is shared by Tanzania (51%), Uganda (43%), and Kenya (6%) (47). However, the cumulative stresses affecting Lake Victoria are numerous, and intricately interwoven, posing a threat to all the lake's fisheries, resource utilization, ecology, and overall ability to provide support services. Indeed, pollution and eutrophication have degraded the entire ecosystem [31], which has impoverished the lake by driving an irreparable

decline in biodiversity [32]. Also, these stresses may have resulted in a more widespread collapse of fish stocks [33], as well as the spread of aquatic weeds, like water hyacinth and algal blooms [34].

16.2.2 Approach to coliform status in the lake basin

Fig. 16.2 shows a schematic diagram linking dominant anthropogenic activities in the Lake Victoria Basin with microbial indicators associated with contamination levels. The approach involves the use of anthropogenic characteristics, selected physicochemical and morphological parameters, and their interactions to serve as a decision support tool for monitoring factors affecting the various socioecological uses of a basin.

16.2.2.1 Data collection

To better understand the microbial status of the lake basin, data and information in the current study were obtained from resource monitoring programs that included Lake Victoria Environment Management Project (LVEMP II) surveys from 2015 to 2018 on fishing grounds monitoring; Kenya Marine and Fisheries Research Institute (KMFRI) cage culture data and weekly Kisumu Bay monitoring from 2017 to 2020; Aquaculture Business Development Programme (ABDP) for SWBs monitoring from 2019 to 2020; Kenya Climate Smart Agricultural Programme (KCSAP) for monitoring of fish ponds from 2019 to 2020; and

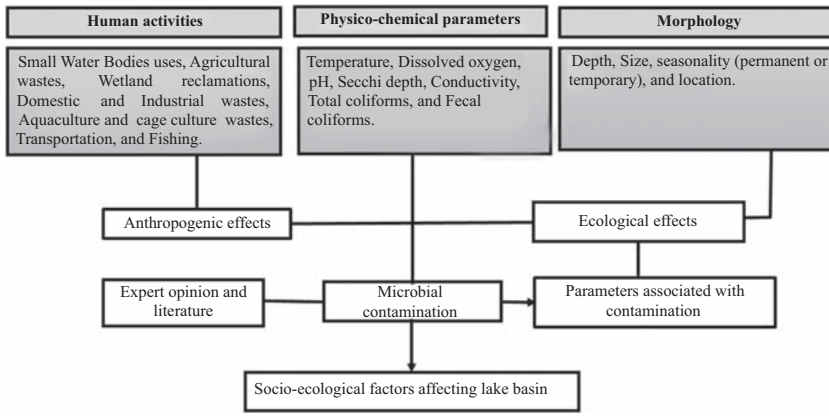

Figure 16.2 Schematic representation toward linking dominant anthropogenic activities in the Lake Victoria Basin (Kenya) with microbial indicators associated with contamination levels to establish socioecological factors affecting characteristics of inland lakes. *Drawn by the authors.*

KMFRI—Mango Tree Project for the Kisumu Bay area monitoring from 2019 to 2021. Although there is a huge amount of data on the aforementioned projects, the use of data herein was based on relevance, availability, and consistency.

The sampled data for the total and fecal coliform as well as selected physicochemical parameters were based on the dominant anthropogenic activities in the lake basin. The sampling sites were purposively chosen to account for the representations of SWBs, Kisumu Bay—Industrial Area (KBI), Kisumu Bay—Port Area (KBPA), Fishing Grounds (FGs), Fish Ponds Sites (FPS) and Cage Culture Sites (CCS) (Table 16.1). Dominant fish species in the selected sampling sites were recorded. Before sampling for the microbial assessments, the selected physicochemical parameters were evaluated using established procedures for in situ data collection. Temperature (°C), DO (mg/L), pH, and conductivity (μS/cm) were among them. A portable electronic water quality meter (a multiparameter field probe (YSI Incor.550, United States) was used to measure the physicochemical parameters. Water transparency (photic depth) measured as Secchi depth was determined using a standard Secchi disk [39]. The average sizes and depth of the water body under intensive use were estimated using a tape measure and depth finder, respectively.

16.2.3 Determination of coliforms bacteria

To determine microbial water quality, total and fecal coliform counts were carried out according to general microbiological principles [39]. Water samples were collected in the field using a sterile water sampling cup on the surface water at three points per sampling site. The three samples taken per site were composite into one which was used for analysis. Samples were analyzed in triplicate and reported as colony-forming units. Using a portable incubator test kit Wagtech Potalab + (M), the samples were instantly examined in triplicate. The membrane filtration technique was used to determine total and fecal coliforms at 37°C and 44°C after 24 h of incubation under aerobic conditions, correspondingly. Using coliform selective agar and MacConkey's agar as differential culture media, total and fecal coliforms were detected and quantified. The organisms were cultured in lauryl Sulfate broth, and the composite samples were evaluated in triplicates for each sampling site. The sample dilution factor depended on the water turbidity. The depth and sizes of SWBs were determined using a depth finder and tape measure accordingly.

Table 16.1 Characteristics of sampling sites that were selected based on the dominant human activities in Lake Victoria Basin, Kenya.

No.	Sampling site	Characteristics	References
1.	Small Water Bodies (SWBs)	Associated with high concentrations of agriculture, water use, fish farming, and production and an evolving sectoral infrastructure (processing, marketing and research); Sampled SWBs are permanent with water throughout the year. Dominant fish species recorded were *Procambaru* ssp (Crayfish), *Oreochromis niloticus* (Nile tilapia), *Oreochromis leucostictus* (Tilapia), *Coptodon zillii* (Tilapia), *Clarias gariepinus* (Catfish), *Enteromius pleurogramma* (Redfinedbarbus), *Gambusia affinis* (Mosquito fish), *Labeo victorianus* (Labeo), *Enteromius paludinosus* (Barbus), *Labeo altianalis* (Labeo) *Protopterus aethiopicus* (Mudfish), and Haplochlomines.	KMFRI-ABDP-SWBs 2020, 9
2.	Kisumu Bay—Industrial Area (KBI)	Consist of industrial and domestic waste discharges from Kisat River Mouth, Slaughterhouses, Cocoa cola, Sugar factory, Water treatment plant, tourist site, and densely populated areas including mushrooming unplanned settlements. Dominant fish species recorded were *C. gariepinus* (Catfish), *Lates niloticus* (Nile perch), *O. niloticus* (Nile tilapia), *O. leucostictus* (Tilapia), Haplochromines, *Schlibemystus* (Schlibe), *Protopterusaethiopicus* (Mudfish), *Labeo victorianus* (Labeo), and *Synodontisvictoriae* (Synodontis).	[35]
3.	Kisumu Bay—Port Area (KBPA)	A sheltered Kisumu Bay area that is under finalization for port services with increased water transport with possibilities of oil spill. Dominant fish species recorded were *C. gariepinus* (Catfish), *L. niloticus* (Nile perch), *O. niloticus* (Nile tilapia), *Oreochromisleucostictus*(Tilapia), Haplochromines, *Schlibemystus* (Schlibe), *Protopterusaethiopicus*(Mudfish), *Labeo victorianus* (Labeo), and *Synodontisvictoriae*(Synodontis).	[18,36]

(*Continued*)

Table 16.1 (Continued)

No.	Sampling site	Characteristics	References
4.	Fishing Grounds (FGs)	Associated with annual mixing, wind induces strong shear forces at the bottom of the lake and vigorous vertical mixing within the water column, especially around the Mid Gulf area. Dominant fish species recorded were *C. gariepinus* (Catfish), *L. niloticus* (Nile perch), *O. niloticus* (Nile tilapia), *Oreochromis leucostictus* (Tilapia), Haplochromines, *Schlibemystus* (Schlibe), *Protopterus aethiopicus* (Mudfish), *Labeo victorianus* (Labeo), *Synodontis victoriae* (Synodontis), and *Rastrineobola argentea* (Omena).	[37]
5.	Fish Ponds Sites (FPS)	Very active fishponds with production throughout the year, with influences from catchment activities. Dominant fish species recorded were *O. niloticus* (Nile tilapia) and *C. gariepinus* (Catfish).	ABDP Aquaculture Blue Book 2021
6.	Cage Culture Sites (CCS)	Very active tilapia cage culture sites of Homabay and Siaya, Kenya, with possibilities of discharge of particulate and dissolved nutrients. Dominant fish species recorded was *O. niloticus* (Nile tilapia).	[38]

Source: Prepared by the authors.

16.2.3.1 Data analyses and interpretation

Microsoft Excel 2016 (Microsoft Inc. Redmond, Washington—United States) was used for data entry and cleaning while SPSS version 21 (SPSS Inc., Chicago, IL, United States) and R version 4.0.0 [40] were used for statistical analyses. The physicochemical data were compared using the non-parametric Kruskal–Wallis one-way ANOVA to examine the uncertainty of values and variations through pair-wise comparisons. The lack of significant variations in physicochemical data between sampling stations within sites led to the pooling of data into categories of SWBs, KBI, KBPA, FGs, FPS, and CCS as the major independent variables. The correlation between microbial indicator organisms (total and fecal coliforms) and conductivity that was associated with water quality contamination was determined using the Pearson's correlation test (Student's t-test) in SPSS. The correlation scatter-plots for case-wise MD deletion were used to show relationships between the SWBs parameters that showed significant variations to varied ($P < .05$) contaminant indicators. The least significant difference (LS means) was used to compare the means of coliform concentrations between sites.

16.3 Results

The commonest fish species recorded during the study was *Oreochromis niloticus* (Nile tilapia) which was recorded among the dominant species in all sampled sites (Table 16.1). The species was followed by *Lates niloticus* (Nile perch) which was dominant in the Lake Victoria sites with the exception of the CCS that recorded *O. niloticus* to be the only dominant species. The other fish species' dominance varied depending on the environment (lake, pond, and SWBs) and the size of the water body. However, fish species dominance results were not correlated nor compared during analysis with the microbial results as well as physicochemical parameters to avoid biases since sites such as ponds, SWBs, and cage culture were stocked with specific species and at different densities. Other than water quality attributes, fish population and diversity are influenced by many factors among them is fishing pressure. More so, the study did not establish fish species density in the studied sites but concentrated on identifying the most dominant species to characterize the site while utilizing the total and fecal coliforms as bioindicators of pollution.

The results from this study showed conductivity, depth, and size to be significantly different ($P < .05$) between sampled sites (Table 16.2). On the other hand, though insignificantly different ($P > .05$), the DO levels were generally higher in FGS as compared to other sampled sites. The other parameters

Table 16.2 Physicochemical parameters (mean ± SE) for various sites selected based on dominant anthropogenic influences of Lake Victoria Basin, Kenya. F and p represent data comparison using the non-parametric Kruskal-Wallis one-way ANOVA at $P < .05$.

Parameter	SWBs	KBI	KBPA	FGs	FPS	CCS	F; p
Temperature (°C)	25.57 ± 0.36	24.74 ± 0.36	24.60 ± 0.36	24.80 ± 0.70	26.91 ± 0.4	24.30 ± 0.30	6.68; 0.08
Dissolved oxygen (mg/L)	5.13 ± 0.35	6.10 ± 0.20	5.13 ± 0.35	6.50 ± 0.50	6.32 ± 0.20	5.20 ± 0.10	15.32; 0.06
pH	7.40 ± 0.10	8.18 ± 0.00	7.44 ± 0.10	7.60 ± 0.04	7.80 ± 0.11	8.00 ± 0.20	6.99; 0.09
Conductivity (μS/cm)	225 ± 7.21	310 ± 7.21	210 ± 3.50	153 ± 12.0	98 ± 4.0	170 ± 4.20	7.34; 0.04
Secchi depth (m)	0.32 ± 0.05	0.42 ± 0.01	0.50 ± 0.03	1.2 ± 0.01	0.20 ± 0.08	0.50 ± 0.01	1.16; 0.06
Depth (m)	2.14 ± 0.18	4.64 ± 0.18	5.24 ± 0.10	12.34 ± 1.1	1.5 ± 0.20	6.60 ± 0.02	7.66; 0.02
Size (ha)	5.92 ± 0.92	0.005 ± 0.001	0.04 ± 0.001	0.0002 ± 0.0001	0.0003 ± 0.001	0.00005 ± 0.00001	1.8; 0.001

CCS, Cage culture sites; *FGs*, fishing grounds; *FPS*, fish ponds sites; *KBI*, Kisumu Bay—Industrial Area; *KBPA*, Kisumu Bay—Port Area; *SWBs*, small water bodies.
Source: Prepared by the authors.

(temperature, pH, and Secchi depth) recorded no significant differences ($P > .05$) and did not depict a particular trend in variations to sampled sites.

Concerning microbial assessments, the current study recorded significant variations ($F = 19.56$; $P = .00$) in both total and fecal coliforms between sampled sites (Fig. 16.3). Both total and fecal coliforms were highest in KBI, followed by KBPA, and SWBs. The sites with the least concentrations were CCS, FPS, and FGs.

Correlation analysis was undertaken to gain an overview of the association of total and fecal coliforms versus conductivity that is associated with water quality contamination (Fig. 16.4). Generally, an increase in

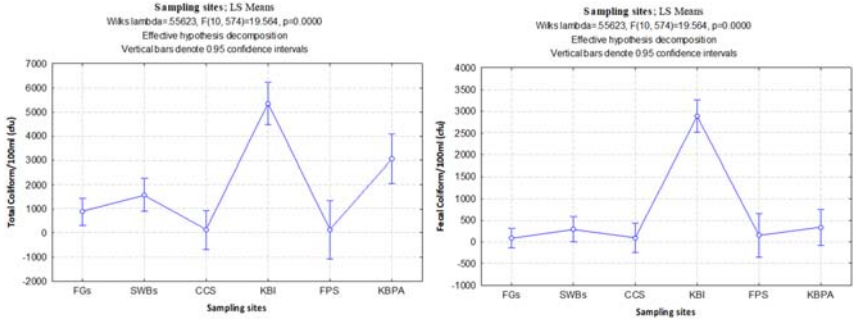

Figure 16.3 Total and fecal coliforms (mean ± SE) concentrations in various sites selected based on dominant anthropogenic influences of Lake Victoria Basin, Kenya. *CCS*, Cage culture sites; *FGs*, fishing grounds; *FPS*, fish ponds sites; *KBI*, Kisumu Bay—Industrial Area; *KBPA*, Kisumu Bay—Port Area; *SWBs*, small water bodies. *Redrawn from KMFRI data archives.*

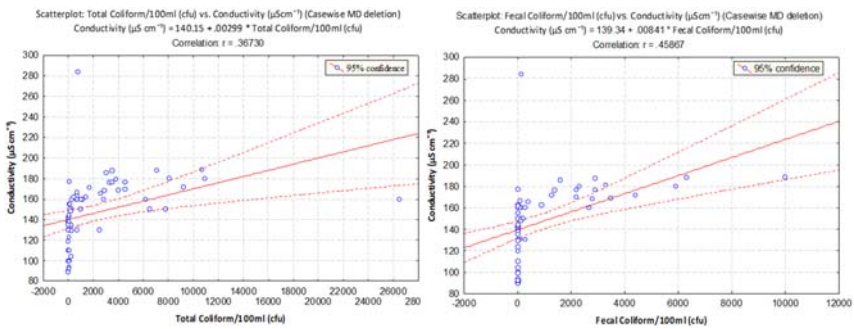

Figure 16.4 Correlation scatterplots of total and fecal coliforms versus conductivity ($P < .05$) that are associated with water quality contamination for various sites due to selected dominant anthropogenic influences of Lake Victoria Basin, Kenya. *CCS*, Cage culture sites; *KBI*, Kisumu Bay—industrial area, *KBPA*, Kisumu Bay—port area, *FGs*, fishing grounds, *FPS*, fish ponds sites, and *SWBs*, small water bodies) *Redrawn from KMFRI data archives, 2015–21.*

conductivity was linked to a decrease in the concentration levels of total and fecal coliforms. There was a weak but significant relationship between conductivity versus total coliforms ($r = 0.37$; $P = .002$) and fecal coliforms ($r = 0.46$; $P = .000$). Notably, most of the correlation points were outside the 95% confidence level.

16.4 Discussion

The current study gives preliminary findings on socioecological system actors' interaction and discharge influences on microbial contaminants. In determining microbial contaminations, total and fecal coliforms were assessed in water in Lake Victoria Basin, Kenya, vis-à-vis selected dominant anthropogenic influences, owing to their ease and low cost of detection as compared to other pathogens [12,16,41]. Although microbial communities are naturally present in the aquatic environment, the presentation of pathogenic microorganisms originating from excreta is of most concern [42]. Therefore, the presence of fecal coliform in aquatic environments shows water to have been sullied with fecal matter from humans or other animals [12,41,42]. However, in aquatic systems, contamination concentration is influenced by water body size and horizontal transport of contaminants that are compelled by inflows and basin-scale circulation patterns, such as wind-driven currents and internal waves [43]. Evidence shows that the aquatic system can be self-cleaning off pollutants due to high dilution and water exchange if pollution is reduced to a manageable level [44].

The findings herein are expected to trigger the upscaling of research, management, and enforcement activities in the lake basin. This is because human activities determine the microbial contaminants in aquatic systems since many of the pathogens in water originate from human excrement and other animal sources [12,41]. Moreover, financial challenges may be boosting microbial contamination of water in most developing countries [42,44], conceivable due to meager investment in waste treatment systems and policy implementation [42]. Hence, the findings of this study may stimulate the need for investment or financial commitment by respective authorities toward sustainable lake basin management. This would enhance the provision of lake basin ecosystem services including contributing to poverty reduction and boosting nutrition and the food security of the riparian communities [3,4].

The dominant aquatic uses in the basin to account for anthropogenic activities formed qualitative and quantitative results that were linked to

microbial contaminant indicators. This approach could be applied in the management of various waterways in the African lakes basin since they are manifest and would rely more on threats and uses that are reported by the stakeholders. This streamlined approach could be used in managing various inland systems that are managed by various authorities, which has resulted in a large administrative burden [45].

The use of total and fecal coliforms as indicators of contamination and selected physicochemical parameters (temperature, DO, pH, conductivity, Secchi depth, depth, and size), was to assess the pollution and degradation status due to various dominant water uses in the lake region since their water quality characteristics are strongly influenced by local conditions [46]. Because of the small size of these water bodies, which have little water exchange and are very susceptible to the effects of land and the atmosphere, physical and chemical parameters in inland African lakes and systems are highly variable [47]. As would be anticipated, the sampled sites examined within the lake basin varied considerably in depth and size since the sites ranged from fish ponds, SWBs, and distinct locations within the sheltered bay on Lake Victoria's Kenyan side. Therefore, if pollution that is prompted, among others, by runoff from agricultural land, inputs of industrial effluent, urban sewage discharges, and mushrooming unplanned urban settlements inflows is not controlled, the normal function of the studied ecosystem (SWBs, ponds, and lake) may be affected by changing the habitats of aquatic flora and fauna [11,12], thereby, compromising the basin's ecosystem service provision potential.

The differences in conductivity levels and slight variations in other physicochemical parameters could be attributed to the usual pattern of change in SWBs, FPS, and Lake Victoria's physicochemical parameters that are extremely variable and unpredictable. This may be attributed to shallow mean depth and sizes as well as the landscape context of the lake basin, which is strongly influenced by extremely variable seasonal wind patterns and shear as well as runoff from agricultural land, inputs of industrial effluent, their relatively urban settings, and the nature of their inflows, in addition to natural processes [37]. The same pattern is linked to the Kisumu Bay which had high conductivity and total and fecal coliforms which are considered a direct impact of urban and industrial development around the Kisumu urban center. This might have been exacerbated by the sheltered nature of the bay, especially in the fishing ground, due to the minimal water mixing in the area [34,48]. It may as well be ascribed to the discharge of semitreated sewage from the Kisat

sewage treatment plant (the only sewage treatment plant serving Kisumu city with a population of about 600,000 residents), which, during the period, was not functioning to its full capacity due to poor state of maintenance.

The slightly high conductivity and microbial contaminants in SWBs could be explained based on the features of water bodies. SWBs and fish pond sites in this study are frequently small bodies of water with limited ability to dilute and retain pollution. As a result, they are particularly vulnerable to even modest levels of pollutants from their surroundings, such as pesticides from agriculture [49]. The SWBs in the study were located mostly in the catchment areas where agricultural activities are rampart, and in addition, dry periods and water abstraction can greatly reduce their water flow and water level [50]. Their natural physical state is often deteriorated. In the lowlands, many SWBs have been altered from natural, meandering channels into straight drains to enhance the draining of agricultural fields, and many barriers are affecting the connectivity [51]. Notwithstanding, SWBs and inland systems are experiencing the effects of acceleration in the rate of land cover change, population growth, and ecosystem changes. These effects are impacting the long-term sustainability of the lake basin's ecosystem services including poverty reduction [3], boosting nutrition and food security [4], and water and energy [52]. However, fish pond sites may have had low levels of microbial contaminants as the system has outlets and are artificially controlled. Nonetheless, the presence of microbial contaminants portrays that there are still challenges in reducing point and nonpoint source pollution in the lake basin. For instance, agricultural activities and fecal matter from the unplanned settlements in the basin end up in the SWBs and lake. Climate change consequences arising from changes in abiotic elements such as precipitation and temperature levels also have an impact on the normal function of aquatic ecosystems, such as aquatic flora and fauna habitats [11,12]. The abovementioned impact of climate change could be more severe on SWBs than on large aquatic systems.

Sites in the lake environment consisting of cage culture and FGs recorded the least microbial contaminant levels due to the high dilution and water exchange effects of the lake water, which could be related to their size and depth. Though low, the presence of a microbial contaminant in sites with cages could depict a possible negative impact of cage culture on the environment. Cage culture is associated with the discharge of particulate and dissolved nutrients such as fecal matter and excretory

products to the aquatic ecosystem [53–55]. Generally, the scenario (cage culture and FGs) is explained further in the relationship between conductivity and microbial contaminants in the current study that is linked to the processes of dispersion, dilution, and horizontal and vertical transport [43].

16.5 Conclusion and recommendations

The current study noted that the impact of human activities concerning microbial contaminants is potentially greater in industrial and urban discharges (KBI and KBPA) and SWBs than in lake water and fishponds (i.e., CCS, FGs and FPS). This was linked to the escalations of dispersion, dilution, and vertical and horizontal transport. It is crucial to develop a structural framework to systematically include socioecological system actors' interaction association with microbial contaminants into spatially integrated management plans. To safeguard inland waterways, there is a pressing need to raise public awareness about their increasing deterioration as well as their numerous societal benefits including contributing to poverty reduction and boosting nutrition and food security. The awareness creation will boost the political acknowledgment of their importance. Furthermore, the coordinated activities with the protected habitats under the citizen science perspective would be of value in the conservation, utilization, and management of African inland aquatic systems. This study recommends further research in the field, management, and enforcement activities in the lake basin.

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CHAPTER 17

Egyptian lakes as sources of bioactive materials

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17.1 Introduction

Microalgae are the main food source for mollusks, zooplankton, and crab larvae, and they are still necessary for fish production [1,2]. The importance of phytoplankton as a primary source of nutrition for fish is widely understood, and it is vital to research phytoplankton and the factors that influence its biomass, nutritional quality, and productivity to manage the fish economy [3]. Furthermore, phytoplankton's nutritional quality is determined by chlorophyll-a and biochemical contents [4]. Algal nutritional compositions are significant as live food because they can influence aquatic animal growth and reproduction [5]. The two key elements limiting primary productivity are phosphorus (P) and nitrogen (N), and their availability can modify the biochemical constitution of algae [6,7]. Biochemical patterns have recently been employed to track changes in phytoplankton physiological conditions as a result of climate change [8]. Algal growth and biochemical composition are influenced by nutrient availability in the environment [9]. The empirical relationship that predicts chlorophyll concentration is an example of how this nutrient supply well incorporates into phytoplankton biomass [10]. This method has offered an adequate foundation for phytoplankton biomass and lake management evaluations [11]. The present study's goal is to use the den's development of some economically important algae in Egyptian lakes to produce biodiesel and bioactive materials.

17.2 Nasser lake

One of the largest synthetic lakes in the world is Lake Nasser, which lies between 22°00′N and 23°58′N in Egypt, the main body, and two Khors: Tushka and Dahmeit (Fig. 17.1B & Tables 17.1–17.3) [4].

Lakes of Africa
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(A)

(B)

Figure 17.1 (A) Nasser Lake (ar.wikipedia.org). (B) Main body and two Khors; (Tushka and Dahmeit) in Lake Nasser [4].

Table 17.1 Section of the main body of Nasser Lake [4].

Section main body	Lat.	Long.
Up-Stream	23°56′11.61″N	32°52′7.00″E
Wadi-Abyad	23°20′43.57″N	32°56′9.43″E
El Madiq	22°55′21.23″N	32°36′43.69″E
Tushka	22°36′15.29″N	31°55′16.00″E
Abu-Simble	22°20′21.04″N	31°38′42.52″E

Table 17.2 Section of Tushka Khor of Nasser Lake [4].

Stations Tushka	Lat.	Long.
St.1	22°32′1.51″	31°47′3.32″
St.2	22°34′25.82″	31°44′44.18″
St.3	22°37′50.12″	31°41′35.19″
St.4	22°36′0.97″	31°40′42.09″
St.5	22°33′14.10″	31°43′17.78″

Table 17.3 Section of Dahmeit Khor of Nasser lake [4].

Stations Dahmeit	Lat.	Long.
St.1	23°44′55.98″N	32°57′31.73″E
St.2	23°45′29.31″N	32°59′2.32″E
St.3	23°44′51.30″N	32°59′52.12″E
St.4	23°45′4.39″N	33° 1′6.49″E
St.5	23°43′51.66″N	33° 2′0.44″E

In the main body, chlorophyll-a and biochemical constituents (Table 17.4) showed highly significant differences between the two seasons ($P < .003$). In Khor Tushka, seasonal changes in chlorophyll-a and protein content were observed (Fig. 17.2B), but there were no significant differences in the lipid and carbohydrate content. In Khor Dahmeit, between seasons, substantial differences in total protein ($P < .0005$), fat ($P < .005$), and carbs ($P < .01$) were discovered, but no significant differences in chlorophyll-a were discovered (Fig. 17.2C). Generally, chlorophyll-a, carbohydrate, lipid, and protein levels did not differ significantly between locations of Lake Nasser but differed considerably between seasons. The biochemical components of phytoplankton in Lake Nasser were similar to those found in many other lakes of Egypt, however, chlorophyll levels were lower than those found in most other lakes [4].

In general, in the main body, the average chlorophyll-a, carbohydrate, lipid, and protein were 4.27, 2.89, 0.2, and 38.91 mg/L, respectively (Table 17.4). In Khor Tushka, 7.86, 1.74, 0.16 and 30.68 mg/L, respectively (Table 17.5), and they were 4.2 μg/L, 1.34 mg/L, 0.28 mg/L and 39.36 mg/L, respectively, in Khor Dahmeit (Table 17.6). The results of the principal components analysis and correlation showed that biochemical composition and chlorophyll-a responses to changes in nutrient concentrations differed depending on the location and time of sampling,

Table 17.4 Biochemical contents of phytoplankton in the Main body [4].

Stations	Autumn				Spring			
	Chlorophyll μg/L	Carbohydrate mg/L	Lipid mg/L	Protein mg/	Chlorophyll μg/L	Carbohydrate mg/L^2	Lipid mg/L^3	Protein mg/4
M1 ES	1.24	1.2	0.24	34.09	2.34	6.15	0.34	102.27
M1 WS	1.72	1.2	0.08	45.45	2.55	6	0.27	14.21
M1 MS	13.32	2.25	0.08	50	3.52	5	0.24	18.75
M1 EB	2.15	2.2	0.09	49.43	1.87	3.3	0.24	26.14
M1 WB	2.56	2.8	0.06	44.89	5.59	5.5	0.27	11.93
M1 MB	1.05	1.2	0.1	47.16	3.31	5.75	0.18	6.82
M1 MM	1.84	0.9	0.2	51.14	2.78	1.8	0.34	40.34
M1%	2.69	2.9	0.08	35.8	3.31	4.6	0.39	17.61
M2 ES	2.35	3	0.25	48.3	8.42	5.5	0.24	26.71
M2 WS	2.28	2	0.18	41.48	6.6	5.75	0.53	5.68
M2 MS	2.22	2.6	0.24	36.93	4.7	4.6	0.27	47.16
M2 EB	3.52	0.6	0.19	68.18	11.65	4.8	0.24	16.48
M2 WB	2.22	2.8	0.2	48.3	4.23	5	0.92	3.98
M2 MB	2.71	0.2	0.18	46.59	2.67	6	0.22	9.66
M2 MM	2.96	0.75	0.15	35.23	3.33	4	0.11	8.52
M2 M1%	2.83	1.2	0.26	34.66	5.13	5.75	0.18	5.11
M3 ES	7.23	2.85	0.12	39.2				
M3 WS	7.52	3.4	0.18	48.3	1.92	4.6	0.15	63.07
M3 MS	5.11	1	0.25	32.95	2.38	5.6	0.35	6.82
M3 EB	3.94	0.7	0.1	64.77				
M3 WB	9.43	2.2	0.17	36.93	5.33	2.8	0.15	5.68
M3 MB	2.12	1.6	0.2	76.7	1.51	5	0.44	9.66
M3 MM	5.71	3.9	0.14	52.27	2.66	4.6	0.39	6.82

M3 M1%	4.53	1	0.06	54.55	2.96	4.2	0.06	8.52
M4 ES	6.39	1.6	0.21	64.2	2.61	2.15	0.23	50.57
M4 WS	10.25	0.6	0.21	46.59	4.61	2.9	0.24	32.39
M4 MS	7.55	1.2	0.92	50	2.93	0.6	0.21	17.61
M4 EB	4.77	0.95	0.45	28.98	3.5	3.35	0.22	51.7
M4 WB	7.46	1	0.09	45.45	4.91	1.4	0.22	53.98
M4 MB	5.14	1.8	0.25	76.7	0.73	2.2	0.17	53.98
M4 MM	6.26	0.8	0.25	7.39	1.27	2.8	0.17	52.84
M4 M1%	5.14	2	0.35	21.59	3.92	2.6	0.31	52.27
M5 ES	6.91	4	0.21	46.02	1.2	2.2	0.27	52.27
M5 MS	7.39	2.8	0.19	49.43	2.87	2	0.27	53.98
M5 EB	6.16	2.2	0.22	48.3	3.99	0.4	0.53	48.3
M5 MB	5.47	2.6	0.13	40.34	3.12	0.8	0.26	48.3
M5 MM	6.75	1.2	0.36	42.61	4.26	2	0.26	53.98
M5 M1%	6.13	4.8	0.11	43.75	4.5	1	0.25	50.57

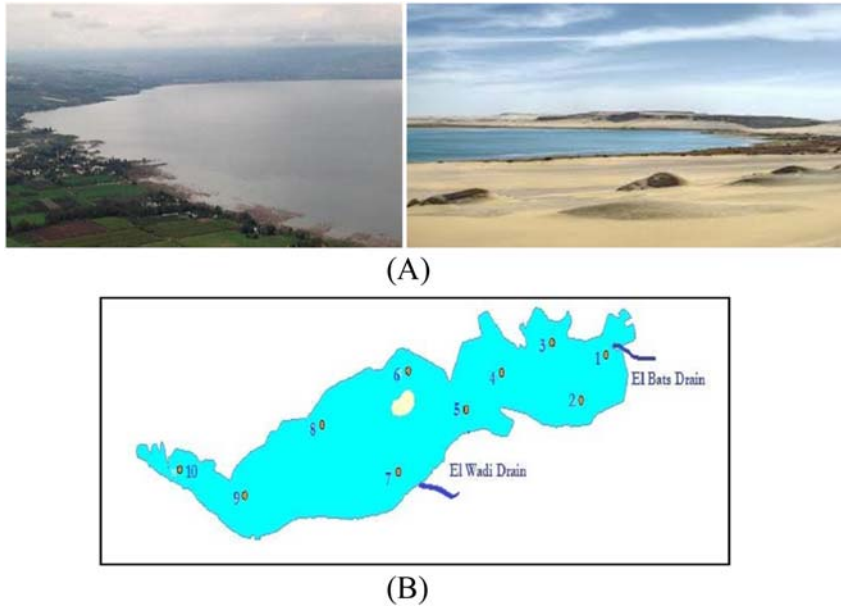


Figure 17.2 (A) Qarun and Wadi El-Rayan Lakes (ar.wikipedia.org). (B) Map of Lake Qarun [12].

indicating that many other factors, in addition to nutrients, regulate chlorophyll-a and biochemical contents in Lake Nasser [4].

17.3 Qarun and Wadi El-Rayan lakes

Lake Qarun is a natural reservoir in the Fayoum depression that receives water from two main drains: El-Bats (northeastern corner) and El-Wadi (southeastern corner) (Fig. 17.2A, B & Table 17.7) [12].

Winter had the highest protein, carbohydrate, and lipid concentrations, with average seasonal values of 10.13, 1.3, and 0.27 mg/L, respectively. Spring, on the other hand, had the lowest seasonal average value, at 3.28, 0.29, and 0.02 mg/L, respectively [12]. During the four seasons, there is a wide range of biochemical content levels in phytoplankton communities, depending on species and location. The density of protein, carbohydrate, and fat was found to differ significantly between seasons and stations using ANOVA [12]. In addition, there are considerable differences in phytoplankton phyla and dominating species. Canonical correspondence analysis revealed a strong positive relationship between phytoplankton and all of its biochemical components and many environmental variables [12]. Discriminant analysis

Table 17.5 Biochemical contents of phytoplankton in Tushka Khor [4].

	Autumn				Spring			
	Parameters				Parameters			
Stations	Chlorophyll μg/L	Carbohydrate mg/L	Lipid mg/L	Protein mg/L	Chlorophyll μg/L	Carbohydrate mg/L	Lipid mg/L	Protein mg/L
S1	7.64	0.1	0.13	25				
S2	7.89	0.16	0.14	26.71	4.77	2.8	0.08	34.09
S3	35.78	0.6	0.16	27.27	4.08	1.2	0.32	39.77
S4	8.74	0.4	0.14	27.84	3.92	3.4	0.06	32.39
S5	6.43	2.8	0.11	28.98	5.5	5	0.14	22.73
S6	6.5	1.2	0.17	29.55	3.01	0.5	0.22	22.73
B1	8.27	0.8	0.19	6.82	9.74	0.5	0.19	34.09
B2	7.69	1.2	0.11	7.96	10.02	2	0.06	80.68
B3	8.82	0.4	0.42	6.25	2.01	3.4	0.11	68.18
B4	7.74	0.1	0.11	13.64	1.92	3.4	0.23	53.41
B5	9.04	2.35	0.21	10.23	9.13	4.4	0.14	46.59
B6	10.5	2.8	0.14	10.8	1.69	0.6	0.14	50

Table 17.6 Biochemical contents of phytoplankton in Dahmit Khor [4].

	Autumn				Spring			
Stations	**Chlorophyll μg/L**	**Carbohydrates mg/L**	**Lipid mg/L**	**Protein mg/L**	**Chlorophyll μg/L**	**Carbohydrates mg/L**	**Lipid mg/L**	**Protein mg/L**
S1	4.7	0.5	0.2	21.02	1.99	0.7	0.16	58.52
S2	4.58	0.65	0.34	11.36	2.19	0.33	0.18	49.43
S3	4.76	1	0.27	11.93	1.88	3.4	0.14	52.27
S4	4.7	1.2	0.28	30.11	4.9	0.5	0.17	56.82
S5	3.73	0.1	0.24	30.68	4.77	1.4	0.26	52.27
S6	4.13	0.65	0.28	38.07	5.15	4.4	0.27	56.25
S7	3.53	0.3	0.38	33.52	3.79	0.1	0.25	54.55
S8	3.75	0.4	0.27	35.23	3.8	3.4	0.28	48.3
S9	2.86	0.6	0.31	35.8	2.83	0.5	0.18	51.7
B1	6.28	0.7	0.44	14.21	8.06	0.5	0.06	68.18
B2	6.57	0.4	0.34	19.89	5.6	1.2	0.26	59.66
B3	3.3	0.6	0.27	18.75	2.18	1.2	0.09	58.52
B4	4.19	0.35	0.5	21.59	3.24	3.4	0.21	59.66
B5	2.38	0.2	0.48	18.75	3.83	4.4	0.26	48.3
B6	4.52	1.2	0.68	22.16	4.3	5	0.12	52.27
B7	4	0.4	0.55	11.36	6.54	3.4	0.16	55.11
B8	4.11	0.1	0.56	18.18	6.35	4.4	0.1	68.75
B9	4.96	0.2	0.34	13.07	4.51	0.5	0.19	60.8

Table 17.7 Description of sampling stations from Lake Qarun [12].

Stations	Features of stations	Average of depth (m)	Longitude	Latitude
1	Opposite to El-Bats Drain	2.00	30° 48′ 47.2″	29°31′ 04.1″
2	Opposite to El-Operg	3.00	30° 47′ 23.1″	29° 28′ 58.1″
3	Far North-East of Lake	4.00	30° 44′ 58.1″	29° 30′ 56.5″
4	Opposite to Abou Nema lasn	5.00	30° 42′ 53.9″	29° 29′ 11.4″
5	Hkor Maeiouf (Middle lake)	5.00	30° 40′ 57.4″	29° 29′ 37.4″
6	North of El-Karn Island (Middle lake)	7.50	30° 37′ 10.9″	29° 29′ 36.8″
7	Opposite to El-Wadi Drain	2.50	30° 37′ 43.4″	29° 26′ 49.4″
8	Opposite to Maser for reconstruction	5.50	30° 34′ 51.3″	29° 27′ 41.0″
9	West Lake	4.00	30° 31′ 09.6″	29° 25′ 42.4″
10	Malahet Mizar (Far West of Lake)	4.00	30° 26′ 08.4″	29° 26′ 37.1″
11	El-Bats Drain	1.50	30° 49′ 20.8″	29°32′ 52.4″
12	El-Wadi Drain	1.50	30° 38′ 08.4″	29° 30′ 23.5″

showed that the maximum counts of Cryptophyta, Cyanophyta, and Ochrophyta exhibited positive values in the summer, whereas maximum lipid and protein values indicated positive values in the winter (Fig. 17.3A). In Lake Qarun, there is a seasonal change in phytoplankton species, phyla, and biochemical components such as chlorophyll (a), carotenoid, protein, lipid, and carbohydrate, indicating that phytoplankton species and phyla are diverse throughout the year (Fig. 17.4A and B) [12]. Changes in water temperature throughout the year affect the amount and quality of phytoplankton, as well as their biochemical content, according to Flefil and Mahmoud [12]. According to Flefil and Mahmoud [12], high quantities of protein and lipid content of phytoplankton observed during the winter season could be regarded as a growth-enhancing element for hydrobionts present in Lake Qarun's aquatic environment.

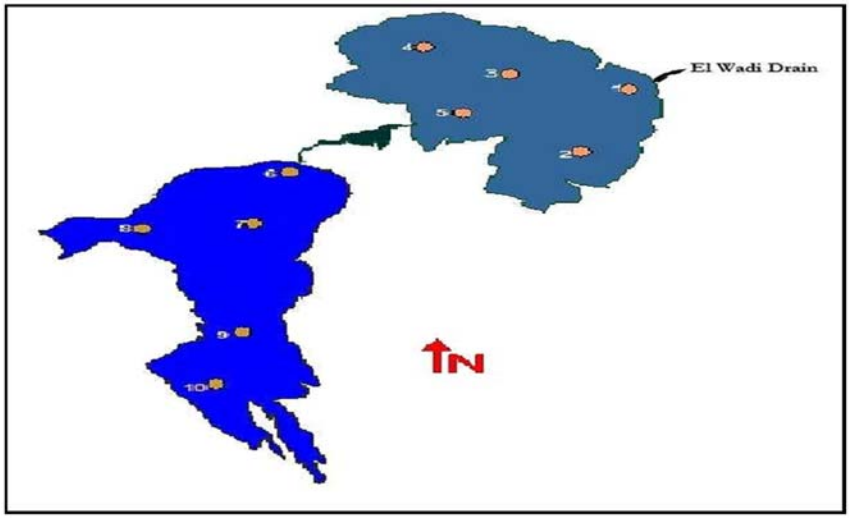
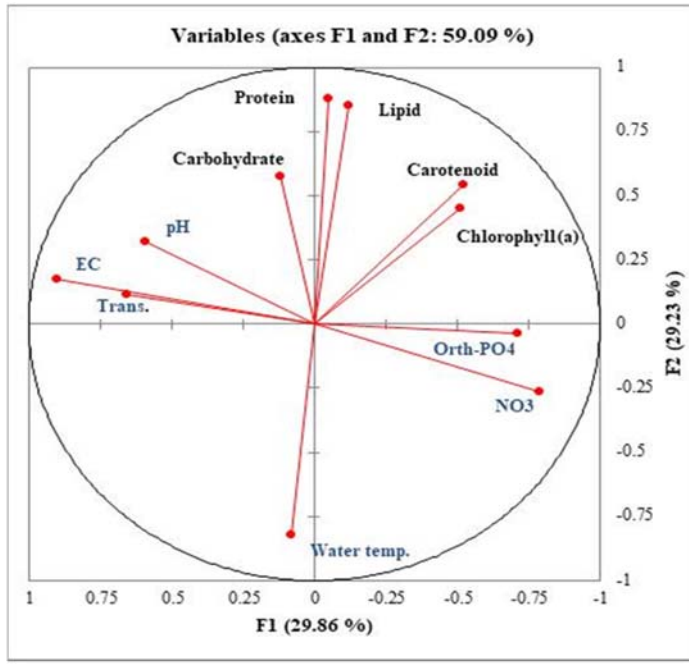


Figure 17.3 Map of Wadi El-Rayan Lakes [13].

Wadi El-Rayan Lakes are a natural protected area and an important supply of irrigation water and fisheries. Two humanmade lakes in the Wadi El-Rayan depression: the upper and lower lakes (southwest of Cairo in Egypt's Western Desert) receive wastewater drainage from the El-Fayoum depression. They are located between 30°20′−30°25′E and 29°05′−29°20′N (Fig. 17.5 & Table 17.8) [13].

In the Wadi El-Rayan Lakes, seasonal and geographical variations alter the nutritional quality of food available in the aquatic system by causing changes in the total protein, carbohydrate, and fat content of phytoplankton (Fig. 17.6A) [13]. According to principal component analysis (PCA), the biochemical composition of the phytoplankton varied greatly between species and locales throughout the seasons (Fig. 17.4B) [13]. The progressive increase in the concentrations of salts, heavy metals, pesticides, and other contaminants, according to evaporation of water from the Wadi El-Rayan Lakes, is changing their water quality and likely impacting aquatic life [14,15]. As a result, the Wadi El-Rayan Lakes' physicochemical and biological features have been intensively researched [16−19]. Biochemical patterns have recently been employed to track changes in phytoplankton physiological conditions as a result of climate change [8]. These biochemical constituents are critical indications of the physiological status and nutritional value of algae species [20,21]. Mahmoud [21] discovered a direct link between biochemical contents and physicochemical and



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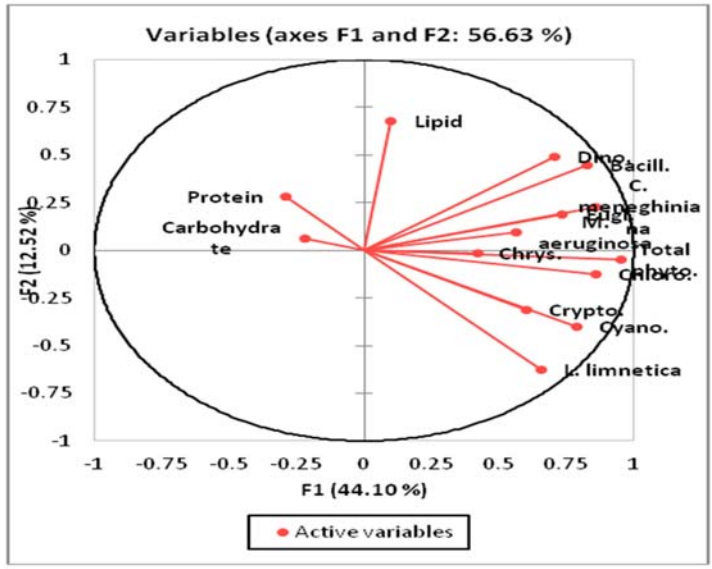
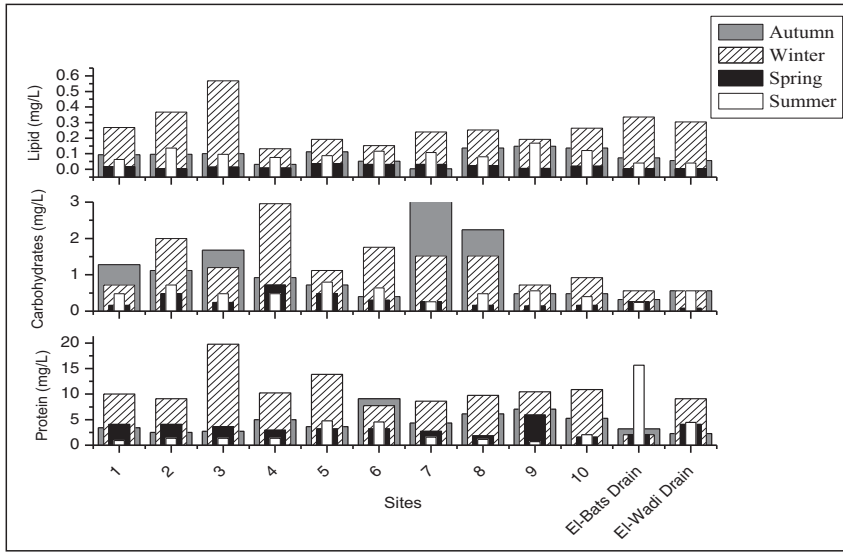


(B)

Figure 17.4 (A) PCA performed between physicochemical variables and phytoplankton biochemical contents in Lake Qarun [12]. (B) Principal component analysis of biochemical and biological variables at the various stations of Wadi El-Rayan Lakes [13].



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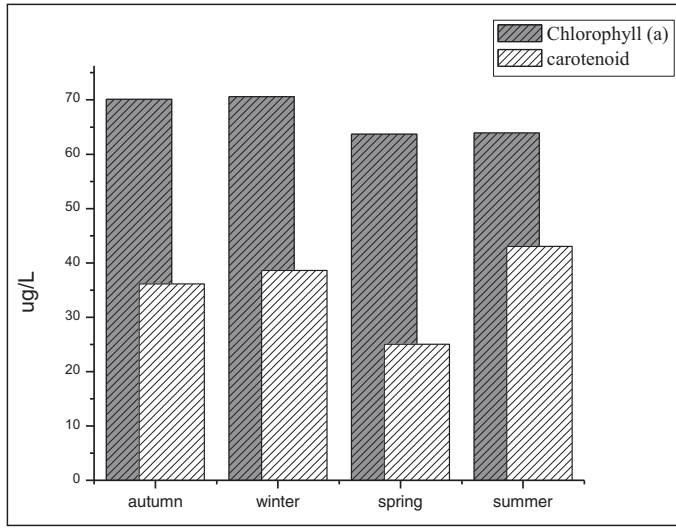


(B)

Figure 17.5 (A) Biochemical contents of phytoplankton in Lake Qarun during four seasons [12]. (B) Seasonal average of chlorophyll (a) and carotenoid (μg/L) in Lake Qarun [12].

Table 17.8 Description of stations of Wadi El-Rayan Lakes [13].

Wadi El-Rayan lakes	Station	Description
Upper lake	1	In front of Wadi drain
	2	East of upper lake
	3	Middle of upper lake
	4	West of upper lake
	5	In front of conductive canal
Lower lake	6	In front of the water entrance
	7	Middle of lower lake
	8	East of lower lake
	9	South of lower lake
	10	Far south at sandy islands

environmental conditions in the Nile River, including nutrients, particularly nitrates and phosphates. Proteins are important biochemical components that play a role in enzymatic catalysis and phytoplankton community performance [22]. Lipids and carbohydrates are key components of all cell membranes, and in phytoplankton bodies, they serve as larger energy reserves [23]. As a result, in a nitrogen-deficient environment, protein production is reduced while fat and carbohydrate production is increased [24]. Protein synthesis is heavily reliant on the nitrogen substrates available at the time of photosynthesis, hence, low protein levels are frequently the result of insufficient nitrogen nutritional circumstances [25]. Lipids and carbohydrates, on the other hand, are non-nitrogenous components, and their amounts are unaffected by the nitrogenous nutrient supply [26]. Seasonal and regional fluctuation affects the nutritional quality of the aquatic system by changing the biochemical composition of phytoplankton populations [27]. The upper lake of the Wadi El-Rayan Lakes has a more dense phytoplankton population than the lower one [28]. Sabae and Mahmoud [13] discovered that the biochemical composition of the phytoplankton varied greatly between species and sites throughout the seasons (Fig. 17.4A). The phytoplankton density was substantially higher in the upper lake than in the lower lake, according to Sabae and Mahmoud [13] (Fig. 17.4B). This was likely owing to the high nutrient concentrations received by the upper lake from drainage water via the El-Wadi Drain, which is comparable to what Konsowa [29] discovered.

The biochemical composition of the phytoplankton could be a good predictor of their nutritional content and a valid integrator of the

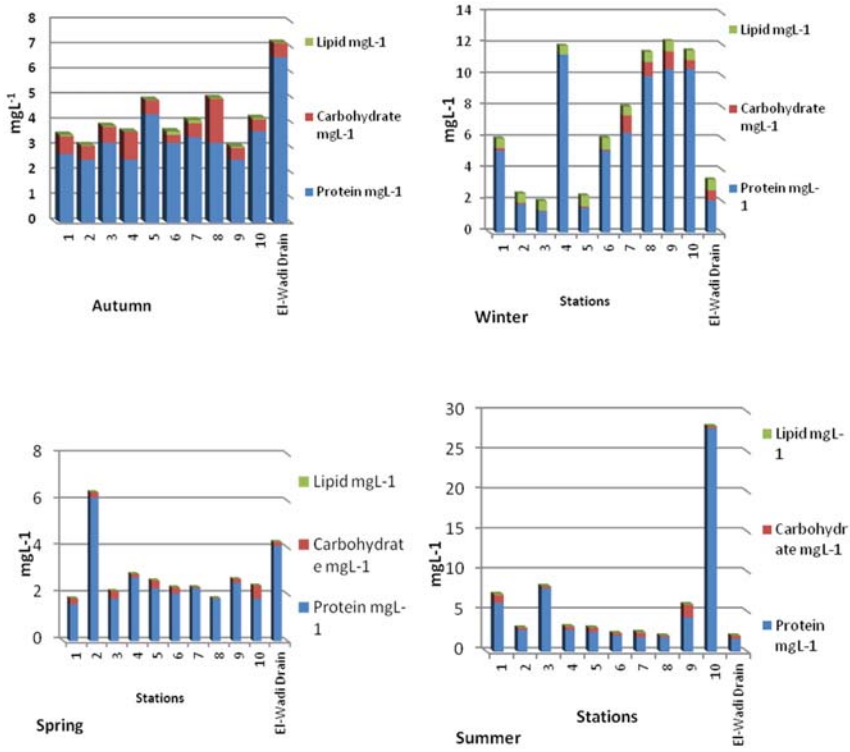


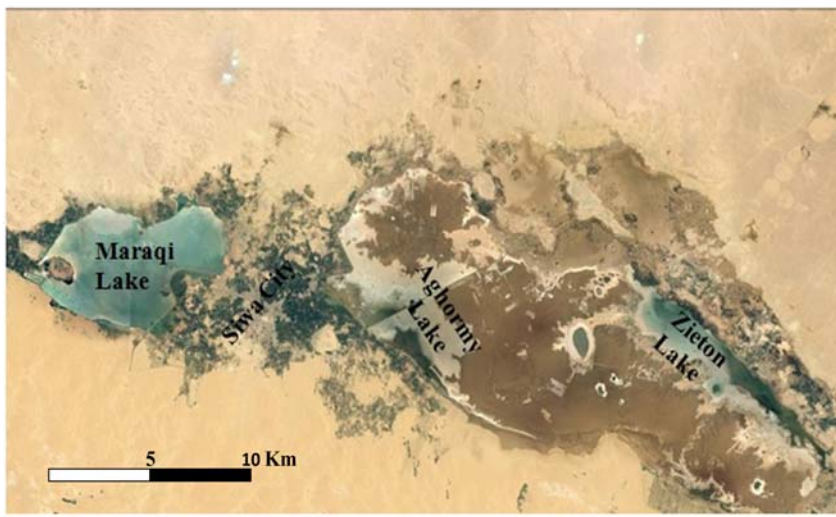
Figure 17.6 (A) The biochemical content of phytoplankton in Wadi El-Rayan Lakes across the seasons [13]. (B) Seasonal variation in total phytoplankton density ($\times 10^4$ Cells/L) in Wadi El-Rayan Lakes [13].

surrounding ecosystems in the Qarun and Wadi El-Rayan Lakes. Seasonal and regional variations cause changes in the phytoplankton's total protein, carbohydrate, and lipid levels, which influence the nutritional quality of food available in the Qarun and Wadi El-Rayan Lakes' aquatic systems (Fig. 17.4A and B) [13].

17.4 Siwa Oasis lakes

One of the primary aquifer systems in northeast Africa is the Siwa Oasis Lakes: Aghormy, Zieton, and Maraqi (Fig. 17.7A, B) [30]. The lakes

(A)



(B)

Figure 17.7 (A) Image of Siwa Lakes (ar.wikipedia.org). (B) Image of Siwa Lakes from Prof. Dr. Abd El-Karim [30].

stretch east-west at a depth of 23 m below sea level. Also, there are over 146 springs and over 1000 wells on the oasis's surface, all of which are naturally flowing [31]. The northerly boundary limestone plateau and the steep escarpment running E-W are distinguished, as are sections of mobile sand dunes to the south and closed flat depressions with cultivated land, playas, and saline lakes [32].

17.4.1 Cyanobacterial mats

Cyanobacteria have a lot of natural compounds that could be useful [33]. In the bioindustry, cyanobacteria possess a variety of pigments that are employed as natural colors, antioxidants, nutritional, and medicinal additives [34,35]. Cyanobacterial lipids are rich in essential fatty acids such as the C18 linoleic and Y-linolenic acids and their C20 derivatives [36]. Mahmoud and Abd El-Karim [30] investigate how to commercially exploit the dense growth of cyanobacterial mats in the three lakes of the Siwa Oasis (Fig. 17.8).

17.4.2 Microalgae and biodiesel

Microalgae are better for biofuel generation because of their high lipid content, adaptability to a wide range of climates, and ability to grow in saltwater [37]. The physical and chemical qualities of biodiesel made from algae oil are identical to those of petroleum-based diesel [38]. On an annual basis, oil production from certain algae strains can be 300 times higher than corn, 130 times higher than soybeans, 30 times higher than jatropha, and roughly 10 times higher than oil palm [39]. Microalgae can also produce useful coproducts, such as proteins and pigments, which can be used as animal feed, pharmaceuticals, or fertilizers following oil extraction [38]. Mohamed et al. [40] examined the effects of β-carotene and phycocyanin derived from *Spirulina platensis* on Nile tilapia (*Oreochromis*

Figure 17.8 Cyanobacterial mats (ar.wikipedia.org).

niloticus) development, serum biochemistry, digestive enzymes, antioxidant defense, and immunological responses. Some microalgae can already meet the high needs of the food and pharmaceutical industries and are crucial in the production of high-value items like vitamins [41]. The remaining biomass from these procedures can be used as fertilizers, soil supplements, or fish or livestock feed [42].

Algae may be utilized to make a variety of biofuels; transesterification of algal oil yields biodiesel, sugar fermentation, and distillation yield bioethanol (C_2H_6O). Biobutanol ($C_4H_{10}O$) is an alcohol that can be made from the green waste left over after oil extraction, and SVO (straight vegetable oil) is an algae oil that is utilized directly as a fuel.

Most of the early work on biofuels from microalgae was focused on biogas (methane) production when they were primarily evaluated for their applications in wastewater treatment [43]. On a commercial level, microalgal biofuels have a great future, but much more research is needed on various fronts to make these fuels a success [44].

The fatty acid spectrum discovered in Mahmoud and Abd El-Karim's [30] study is ideal for usage as biodiesel, especially in the Aghormy Lake, where fatty acids have high unsaturation and a high proportion of palmitic and oleic fatty acids. Seven biodiesel quality characteristics were estimated based on the fatty acid profile: Cetane Number, Iodine Mass (IV), Saponification Value, Cold Filter Plugging Point, Long-Chain Saturated Factor, Solid Phase Formation Temperature (CP), and Degree of Unsaturation [30]. The best biodiesel was found in the Aghormy Lake, according to the biodiesel quality standards [30].

17.4.3 Biorefinery of microalgae

Biorefinery is a manufacturing process that converts biomass into a variety of biochemical materials and energy products. Wijffels et al. [45] recommend that microalgae strains utilized for biorefining of important chemicals have the following metabolic and physiological characteristics: fast growth, high biomass, high production of a valuable compound, able to grow heterotrophically using cheap carbon substrates, valuable substances excreted from the cells and thin cell walls in large cells (to facilitate product extraction).

The selection of appropriate strains and the installation of optimal growing conditions are critical components of biofuel production's overall success [46,47]. Posadas et al. [48] investigated integrated microalgae biorefinery and discovered that *Scenedesmus* sp. had a lower lipid content and higher

carbohydrate and protein content, resulting in less oil production and more microalgae oil-free cake manufacturing (for substitution of soybean meal).

The lipids taken from microalgal cells may primarily be transformed into biodiesel, while the carbohydrates, such as starch and cellulose, can be fermented into bioethanol. Through aerobic digestion, carbohydrates, proteins, and lipids in microalgae tissues can be transformed into methane and biohydrogen [47]. The carbohydrate/lipid ratio was utilized as a measure of plankton chemical quality [49]. Anaerobic organisms organize the conversion of algal biomass (oil and/or starch removal) into bio-H_2 via dark fermentation. Enterobacter and Clostridium strains are well-known for producing bio-H_2 and being able to use a variety of carbon sources [50–52]. Hydrogen is created in cyanobacteria by a light-dependent mechanism catalyzed by nitrogenase or by hydrogenase in dark anaerobic circumstances [53,54]. Cyanobacteria, formerly known as "blue-green algae" and "nitrogen-fixing" bacteria, may thrive in air, water, and mineral salts using light as their sole source of energy for photobiological H_2 synthesis [55,56]. Cyanobacteria are the most cost-effective biological producers, as they only require air (N_2 or CO_2), water, mineral salts, and light for energy. Because some microalgae have a high starch content, they have a significant potential for producing bioethanol [57,58]. Microalgae such as *Chlorella, Dunaliella, Chlamydomonas, Scenedesmus*, and *Spirulina* contain substantial amounts ($>50\%$) of starch and glycogen, which are excellent as raw materials for ethanol synthesis, according to Ueda et al. [59]. Microalgae can absorb cellulose, which can then be fermented to produce bioethanol [60]. *Chlorococum* sp., microalgae, has also been investigated as a feedstock for ethanol production [61]. When compared to biogas from maize, the methane content of microalgae biogas is 7%–13% greater according to Sialve et al. [62]. Microalgae species with a high degree of decomposition and a low number of indigestible leftovers should be used for biogas production [63]. According to Das [64], wastewater-grown algal biomass played a critical role in the biomethanation process improvement. Many microalgal species have significant lipid, carbohydrate, and protein content, which have prompted research into a wide range of applications for human consumption. They are utilized as tablets and capsules, and are also added to sauces, candies, and drinks [65]. Cyanobacteria are important in agriculture because of their ability to metabolize molecular nitrogen; in a rice field, the application of chemical fertilizers at the recommended level or lower levels stimulated cyanobacterial population development and nitrogenase activity, whereas higher

fertilizer levels inhibited growth [66]. Vitamins A, B1, B2, B6, B12, C, and E, nicotinate, folic acid, pantothenic acid, and ß-carotene, as well as minerals, may be abundant in algal biomass [67]. Microalgae could be a new source of bioactive chemicals in the future. They may also include significant probiotic components that are beneficial to anyone's health [68]. Skjånes et al. [69] discovered that microalgae have particular carbohydrate-binding proteins called lectins that are extremely selective for changed complex oligosaccharides, glycoproteins, or glycolipids during illness. Phycocyanin, which is mostly obtained from *Spirulina*, has potential diagnostic applications in medicine and biotechnology. In immunolabelling research, phycocyanin's strong and very sensitive fluorescence characteristics can be used to label antibodies, receptors, and other biological molecules [70]. Because of their excellent molecular absorption, strong fluorescence ability, and photostability, carotenoids are widely employed in clinical and immunological research laboratories. ß-carotene is converted to vitamin A in the human body, allowing the immune system to function [71].

At the three lakes in the Siwa Oasis, the contents of pigments and biochemicals in cyanobacterial mats are illustrated in Table 17.9 [30]. The maximum phycocyanin content was recorded in winter in the Aghormy Lake.

The protein content was 284.09 wwt.% in Aghormy and ß-carotene reached 41 times more than in carrots (Table 17.9). Phycocyanin PC values in Aghormy and Maraqi, which were 4.99 and 4.6 wwt.% in winter and summer, respectively, were identical to those found in optimal dry mass production (Table 17.9). ß-Carotene was an essential biochemical substance with a high economic value. The highest concentration of ß-carotene was found in winter in the Maraqi Lake, reaching 608.97 wwt%, while the lowest concentration was recorded in autumn in the Aghormy Lake at 85.47 wwt% [14]. Glycerol, the base of esterified saturated or unsaturated fatty acids, makes up algal lipids. In winter, the Aghormy Lake's total lipid level peaked at 23.46 wwt%, whereas in autumn, the Maraqi Lake's total lipid content fell to 5.07 wwt% (Table 17.9). Mahmoud and Abd El-Karim's [14] data revealed a link between carbohydrate and glycerol levels. The carbohydrate produced during photosynthesis was used for glycerol synthesis, which was obvious in the Zieton Lake (Table 17.9). At the three lakes (Aghormy, Zieton, and Maraqi Lakes) in the winter, Mahmoud and Abd El-Karim [30] discovered 34 fatty acids in the cyanobacterial mats (Table 17.10). In the cyanobacterial mats of the Siwa Lakes, the lipid biomarker profiles demonstrated a

Table 17.9 Contents of pigments and biochemicals in cyanobacterial mats [30].

Parameters	Autumn Aghormy	Zieton	Maraqi	Winter Aghormy	Zieton	Maraqi	Summer Aghormy	Zieton	Maraqi
Chlorophyll-a (μg/g wwt)	300.65	700.74	700.67	300.5	800.2	1100.5	500.72	700.44	1000.92
ß-Carotenes (wwt.%)	85.47	192.31	90.5	149.57	239.09	608.97	146.52	269.23	341.88
Phycocyanin (mg /g wwt)	1.85	1.08	1.84	4.99	2.55	2.85	3.5	2.65	4.6
Protein (wwt.%)	189.39	197.63	218.53	222.33	202.92	216.45	284.09	195.9	218.53
Lipid (wwt.%)	10.53	7.87	5.07	23.46	12.93	12.8	16	10.66	12.14
Carbohydrates (wwt.%)	52.23	40.15	38.02	51.71	43.06	33.17	52.05	40.86	88.24
Glycerol (wwt.%)	0.33	0.78	0.41	0.44	0.85	0.39	0.52	0.59	0.42
Ash (%)	25.8	38.01	12.62	27.14	13.25	16.03	19.34	18.3	19.08
Water contents (%)	46.58	56.78	44.69	63.44	36.99	36.97	44.97	43.76	44.41

Table 17.10 Fatty acids (μg/g dry wt.) of cyanobacterial mats in Siwa Lakes [30].

Fatty acid	Aghormy Lake	Maraqi Lake	Zieton Lake
Caproic acid methyl ester (C6)	0	0	0.221
Caprylic acid methyl ester (C8)	2.292	2.274	2.268
Capric acid methyl ester (C10)	2.812	3.286	3.525
Undecanoic acid methyl ester (C11)	0.617	0.277	0.277
Lauric acid methyl ester (C12)	0.78	0.828	1.499
Tridecanoic acid methyl ester (C13)	0.383	0.398	0.385
Myristoleic acid methyl ester (C14)	1.177	1.965	0.824
Myristic acid methyl ester (C14)	1.846	2.824	3.941
Cis-10-Pentadecenoic acid methyl ester (C15)	0.959	1.031	1.08
Pentadecanoic acid methyl ester (C15)	0.774	1.094	1.316
Palmitoleic acid methyl ester (C16)	1.433	7.421	4.781
Palmitic acid methyl ester (C16)	20.802	59.555	56.409
Cis-10-Heptadecenoic acid methyl ester (C17)	45.614	5.907	3.366
Heptadecanoic acid methyl ester (C17)	1.062	1.291	1.639
Gama-Linolenic acid methyl ester (C18)	1.67	1.701	1.696
Linolenic acid methyl ester (C18)	1.674	1.825	1.721
Oleic acid methyl ester (C18)	3.066	17.553	11.875
Elaidic acid methyl ester (C18)	1.059	1.115	1.035
Stearic acid methyl ester (C18)	7.832	18.126	17.929
Arachidonic acid methyl ester (C20)	1.917	1.68	
Cis-5,8,11,14,17-Eicosapentaenoic acid methyl ester (C20)	1.583	1.941	1.97
Cis-8,11,14-Eicosatrienoic acid methyl ester (C20)	1.703	1.689	1.69
Cis-11,14-Eicosadienoic acid methyl ester (C20)	1.507	1.522	1.52
Cis-11-Eicosenoic acid methyl ester (C20)	1.368	1.317	1.242
Cis-11,14,17-Eicosatrienoic acid methyl ester (C20)	1.523	1.524	1.525
Arachidic acid methyl ester (C20|)	0.954	1.053	1.011
Heneicosanoic acid methyl ester (C21)	1.397	1.347	1.166
Cis-4,7,10,13,16,19-Docosahexaenoic acid methyl ester (C22)	2.442	1.921	1.851
Cis-13,16-Docosadienoic acid methyl ester (C22)	1.748	1.723	1.804
Eruoic acid methyl ester (C22)			
Behenoic acid methyl ester (C22)	2.308	2.034	2.031
Cis-13,16-Docosadienoic acid methyl ester (C22)	1.378	2.235	2.076
Nervonic acid methyl ester (C24)	1.681	1.817	1.734
Lignoceric acid methyl ester (C24)	3.021	3.111	2.918

surprising range of organic matter sources. Cluster analysis identified two groups when the Siwa Lakes were compared based on fatty acid profiles, saturation and unsaturation levels, and biodiesel quality criteria. The Aghormy Lake, which was isolated from the Maraqi and Zieton groups, reflected the Aghormy oil's specific components. ANOVA analysis revealed a significant difference ($P < .01$) in glycerol content compared to the lakes with a notable rise in Maraqi Lake. Generally, summer and winter had the highest biochemical content and pigments, with no significant differences between lakes or seasons [30].

17.5 Conclusion

Phytoplankton is a key component of many aquatic ecosystems' equilibrium. In Lake Nasser, the biochemical content and chlorophyll (a) responses to nutrient concentration variations varied depending on the sampling site and time. In Lake Qarun, there is a seasonal change in phytoplankton species, phyla, and biochemical components such as chlorophyll (a), carotenoid, protein, lipid, and carbohydrate, indicating that phytoplankton species and phyla are diverse throughout the year. According to correlation and PCA analyses, many other parameters associated with nutrients, such as zooplankton grazing, lake morphometry, and phytoplankton biochemical contents, are often a result of phytoplankton biomass and biochemical composition responses to different environmental conditions and seasons. In several areas in the Wadi El-Rayan Lakes, phytoplankton groups and their biochemical content can be used as ecological indicators. The biochemical composition of phytoplankton could be a good predictor of their nutritional content and a good mediator of the water body in which they develop. The cyanobacterial mats of the three Siwa Lakes are regarded as renewable sources for the manufacture of pharmaceutical, industrial, and liquid fuels. So the cyanobacterial mats in the Siwa Lakes are considered a natural resource for a variety of economically useful natural products.

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CHAPTER 18

African salt lakes: distribution, microbial biodiversity, and biotechnological potential

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18.1 Introduction

Over the past decade, interest in extreme environments from all over the world has attracted the attention of scientists since these ecosystems host great biotechnological potential. Salt lakes are considered an important ecosystem to humans and biodiversity. Salt lakes' salinity range from 3 to 300 g/L, with a large variation in their chemical composition [1].

Africa is endowed with numerous salt lakes both thalassohaline and athalassohaline. They range from small ponds to large water bodies extending over hundreds of kilometers. Moreover, in some African countries, the precise number of salt lakes is difficult to determine. North Africa hosts the largest lakes called sebkha, chott, or garaet. Chott Djerid in Tunisia is the largest of all North African salt lakes [2].

Microorganisms including the three majors domain Bacteria, Archaea, and unicellular eukaryotic organisms are present in the saline and hypersaline ecosystems. Microbial diversity in African salt lakes is composed especially of halophilic Archaea and Bacteria. Many novel species of microbes have been reported from African salt lakes such as *Halanaerobium sehlinense* [3], *Haloarcula sebkhae* [4], *Melghirimyces algeriensis* [5], *Halanaerobaculum tunisiense* [6], *Halanaerobacter jeridensis* [7], and *Halopiger djelfamassiliensis* [8]. Such microorganisms have adapted biochemical pathways which are of great interest for biotechnological applications. They produce enzymes and other molecules to survive in harsh conditions [9]. Halophiles produce unique metabolites that can be exploited for biotechnological purposes, for example, exopolysaccharides (EPS), hydrolytic enzymes, antimicrobial peptides, and

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others. This chapter describes the most important African salt lakes with an emphasis on the northern part of Africa and provides an overview of the microbial diversity with its biotechnological potential application.

18.2 Salt lakes: classification and characteristics

Salt lakes are wetlands found in all worldwide inland regions. They are usually limited to subhumid, arid, and semiarid environments. Salt lakes account for almost half of the total volume of aquatic ecosystems (about 44%) [10]. They occupy around 30% of the planet's land surface [11]. These wetlands include the Caspian Sea, which is the largest lake in the world, and many other large lakes which are located between 400 m below sea level as the Dead Sea and above 3000 m altitude for Altiplano in South America [12].

Salt lakes can be classified according to their nature, salt concentration, and origin. Hammer [1] considered water from lakes with salinity ranging from 0.5 to 3‰ as subsaline (Table 18.1), in which halophilic and freshwater microbes can coexist. Water is considered hypersaline when salinity is above 50‰ to saturation. The water salinity of some North African salt lakes can reach 250 to 350 g/L [13–15].

Lakes situated in arid and semiarid zones are filled with water during the rainy season. It is the case of the Eyre Lake in Australia [16] and some hypersaline lakes from northern part of Africa like Algerian chotts. Otherwise, in extremely arid environments, several lakes are dried out by evaporation and become saltier. Salt lakes can be classified according to their origins and the nature of salts to thalassohaline and athalassohaline [16].

Lakes that arise from seawater evaporation are called thalassohaline. They are characterized by a cation ratio very close to seawater, such as lagoons. In contrast, athalossohaline lakes, which are located in closed basins have a different chemical composition in comparison to seawater. These waters derive salts dissolution from the continental regions.

Table 18.1 Classification of lakes according to their salinity.

Water classification	Salinity ‰
Freshwater	0.5
Subsaline	0.5–3
Hyposaline	3–20
Mesosaline	20–50
Hypersaline	50 to saturation

Hypersaline ecosystems show a high variation in pH, chemical composition, and salt concentration. Sodium and chloride are the principal dissolved cation in most salt lakes. Otherwise, for anion composition, there are three major brines, carbonate (HCO_3), sulfate (SO_4^{2-}), and chloride (Cl). Table 18.2 gives some chemical composition for some African saline and hypersaline lakes.

18.3 North African salt lakes

18.3.1 Sebkhas and chotts of Algeria

In Northern Africa, salt lakes are called chotts, sebkhas, garaet, salines, or lakes which have sometimes the same signification (closed depressions). However, chott may describe the area surrounding sebkhas. The Arabic word sebkha designates saline subject to periodic flooding in depressions. Strong evaporation leads to the formation of evaporite crust which lines the bottom of these depressions [2].

Algeria has a large number of chotts and sebkhas. Their geographical distribution is very wide. Salt lakes in Algeria are located mainly in the northern part of the country. They are located between Tellian Atlas to the north, the Saharan Atlas to the south, Western Erg to the east, and Oriental Erg to the West [25,26].

In the east highlands, we find chotts of Oum el Bouaghi. To the center Chott Hodna, Zahrez Chergui, Zahrez Gherbi and Sebkha of Naâma in the West; Sebkha of Oran and Saline of Arzew in coastal plains. In the northeast of the Algerian Saraha lies Chott Melghir and Chott Merouane, the latter one is located 31 m below sea level. It is considered the lowest location in northwest Africa [27]. To the south, in the region of Ouargla, there is Chott of Ain Beida, Oum Raneb, Sidi Amrane, and Safioune. The rest of the salt lakes are located in the Great Western Erg area, such as Sebkhat el Melah (Fig. 18.1).

The most important sebkhas and chotts in Algeria are Sebkhet El Melah, Sebkha of Oran, Sebkhet Ezzmoul, Chott Chergui, Chott El Hodna, Chott Melghir, Chott Merrouane, Zahrez Chergui, and Zahrez Gherbi. Most of them are located in the northeastern part of Algeria. Among 50 Ramsar sites with an area of about 3,032,813 ha, approximately 24 salt lakes have been designed to date, which represent 45% of the total protected sites in Algeria [28].

Chott Chergui, in the Saida province, is the largest salt lake in Algeria and the second largest chott in North Africa, after Chott Djerid in Tunisia. Chott Chergui has an area of about 855,500 ha and the main depth is about

Table 18.2 Chemical and physical properties of some African salt lakes compared to others worldwide saline and hypersaline natural water.

Salt lake	pH	Salinity ‰	Na^+	K^+	Mg^{2+}	Ca^{2+}	Cl^-	SO_4^{2-}	HCO_3	References
Sidi Ameur salt lake (Algeria)	7.2–7.5	200–350	40–67	0.13	3	0.85	111–158	2.1–25	0.19	Yaiche Achour et al. [13] and Boutaiba et al. [17]
Himalatt salt lake (Algeria)	7.2	17	24.5	0.12	1.6	0.22	63.8	3.1	n.d.	Boutaiba et al. [17]
Sebkhat Wadi El Malah (Algeria)	6.5–8.2	n.d.	0.24	n.d.	n.d.	0.13	0.370	0.385	n.d.	Akmoussi-Toumi et al. [18]
Lake Assal (Djibouti)	n.d.	158–277	93	4.73	11	2.56	185.23	4,35	n.d.	Houssein [19]
Gaet'ale Pond (Ethiopia)	1.7	433	1.3	2.4	34.9	109	281	n.d.	n.d.	Pérez and Chebude [20]
Lake Magadi (Kenya)	9.61	70–140	17.7	0.29	0.02	n.d.	4	0.39	14.2	Kambura et al. [21]
Sehline salt lake (Tunisia)	8.77	266	101	6.6	31.75	1.04	100.5	40.21	0.25	Abdeljabbar et al. [22]
Great salt lake (USA)	7.7	333	105	6.7	11	0.3	181	27	0.72	Post [23]
Dead sea	7.8	340	40	7.6	44	78	225	0.44	0.26	Gavrieli [24]

Ions concentration is represented as g per liter. *n.d.*, not determined.

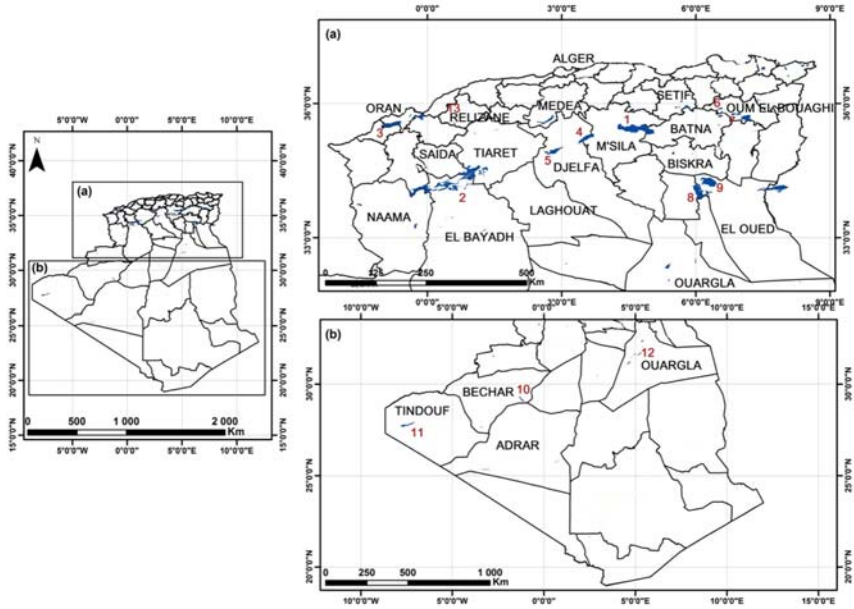

Figure 18.1 Geographical localization of the main Algerian salt lakes. 1: Chott El Hodna. 2: Chott Chergui. 3: Sebkha of Oran. 4: Zahrez Chergui. 5: Zahrez Gherbi. 6: Chott Tinsilt. 7: Sebkhet Ezzmoul. 8: Chott Merouane. 9: Chott Melghir. 10: Sebkhat el Melah. 11: Sebkha of Tindouf. 12: Sebkhat Oum Raneb. 13: Sebkhat Sidi Bouziane. (a) North and (b) South Algeria.

10 cm. Chott Melghir and Chott Merouane are some other large ones in the northeast Algerian Sahara. During summer, water salt lake evaporation leads to strong fluctuations in areas, depths, and salinity.

18.3.2 Sebkhas and chotts of Tunisia

Tunisia has several hypersaline environments of varying size, physical and ecological characteristics. These salt lakes extend from the Tunisian south coast to the Atlas mountains in Algeria [29]. The Tunisian salt lakes represent 29% of the total wetland and include 54 coastal sebkhas and 17 continental chotts (Fig. 18.2). Chott Djerid or Chott El Jerid, in the southwest, is the largest salt lake in Tunisia by surface area (approximately 500,000 ha). During summer, water loss by evaporation increases dissolved ions concentration, and consequently salt covers the depression [30]. Chott Djerid contains similar ions as seawater with salinity varying between 250 and 330 g/L [31]. Chott El Gharsa, located at the Algerian border, is also an important wetland [32].

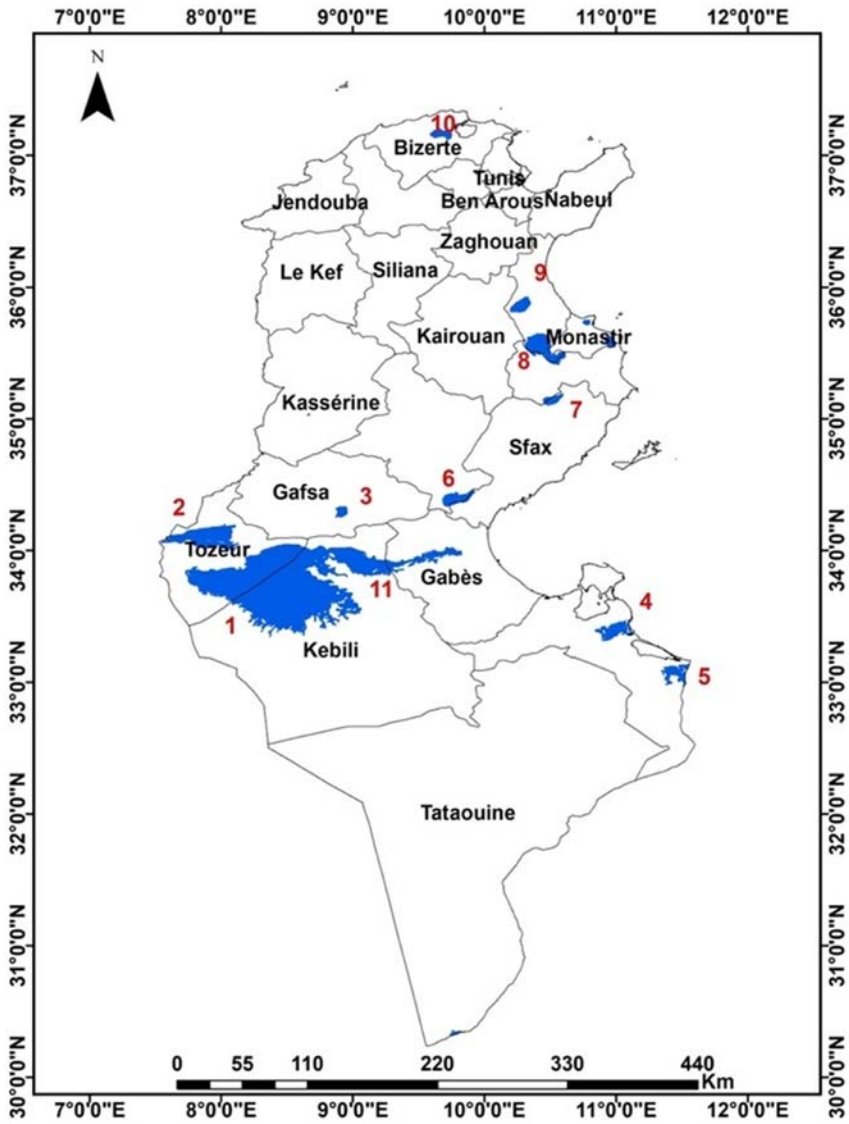

Figure 18.2 Distribution of the main Tunisian salt lakes. 1: Chott El Djerid. 2: Chott El Gharsa. 3: Chott El Guettar. 4: Sebkhat el Melah. 5: Sebkhet Tader. 6: Sebkhet Noual. 7: Sebkhat Mta Al Rherra. 8: Sebkha Sidi El Hani. 9: Sebkhat El Kelbia. 10: Lagoon of Bizert. 11: Chott El Fejej.

The Tunisian coastline of the Cap Bon peninsula has the largest and the most complex wetlands and lagoons. The most important are Sebkha Bou Zid (North of Kélibia), Sebkhas of Tegdimane, Klibia, Bit El Assa,

Tafekhsite, El Henchir, Dar Rebiah, Lebna, Bou Jemil, Korba, and Sidi Ahmed Ben Daoued (in the east coast of Cap Bon) [33].

18.3.3 Salt lakes of Egypt

The Egyptian Mediterranean coast hosts five salt lakes (lakes or lagoons). These salt lakes extend from the east in North Sinai to the west in Alexandria. These are Bardawil, Manzala, Burullus, Edku, and Mariout lakes. Manzala is the largest (1200 km^2) and the widest (49.0 km) lake of the Mediterranean Egyptian northern lakes. These lakes are separated from the sea by very narrow strips of land and are connected with the sea by narrow outlets. Taking into account lake salinity, all these lakes are brackish, except hypersaline Bardawil Lake [34].

In the Egyptian western desert is located the major depression of Wadi El Natrun. It contains several shallow lakes, for example, Lakes Gabara, Muluk, Hamora, Zugm, Gaar, and Rizunia. These lakes are rich in sodium and potassium and are considered soda lakes (pH around 11). Moreover, the salinity of Wadi El Natrun lakes ranges from 9% to 39%. High microbial biodiversity is observed in this lake, including purple bacteria, Cyanobacteria, and halophilic archaea [35].

18.4 Salt lakes from East Africa

Salt lakes from East Africa are limited in the Eastern Rift valley including Uganda, Kenya, and Ethiopia. Salt lakes from these regions are small in area compared to sebkhas and chotts from the North African desert. The largest inland salt lakes are located in northern Kenya. Lakes from the Rift Valley were formed by a combination of volcanic and tectonic activities. Most of them are rich in solutes and are considered soda lakes (pH $>$ 10), with carbonates as a dominant anion. However, ionic concentrations depend on seasons. It is highest during the dry season in comparison to the wet season [36].

18.5 African soda salt lakes

Alkaline environments can be of natural or anthropogenic origin. In the latter case, they are the results of commercial processes, such as the manufacture of cement or paper. Lakes and soda deserts are the main types of natural alkaline environments.

Soda lakes or alkaline lakes are aquatic alkaline environments and are distributed worldwide. Van Lake is the largest soda lake in the world, which is located in the Eastern Anatolian region, Turkey. Soda lakes have an elevated pH value (9 and above). A high concentration of carbonate, especially sodium carbonate, is responsible for water alkalinity [37]. A soda lake contains also a high concentration of sodium chloride and other salts, making it a saline or hypersaline lake. They occur naturally in arid and semiarid areas.

The pH of the water in the depression increases due to evaporation of the lake, which requires a suitable climate such as the desert climate to balance the inflow and evaporation [38]. A particular combination of geographical, geological, and climatic conditions is required for lakes to become alkaline. Some lakes become mesosaline and alkaline, while other lakes evaporate and remain hypersaline and highly alkaline.

Most African soda lakes are located in the East African Rift System (EARS), including Kenya, Ethiopia, Djibouti, and Tanzania. Lake Natron situated in Tanzania is one of the most remarkable soda lakes in Africa because of the high pH, which can reach up to 12 (Fig. 18.3). Soda lakes in the EARS vary widely in salinity, ranging from < 0.1 to 277‰.

18.6 Microbial communities in saline and hypersaline systems of Africa

Halophiles are microorganisms that require salt (NaCl) for their growth. They can survive in saturated salt concentrations, thanks to their capacity to adapt themselves to balance the osmotic pressure [39]. Halophilic microorganisms are divided into two main groups based on salt concentration. We can find moderate halophiles, which can grow optimally in media with 0.5–2.5 M NaCl, and extreme halophiles, which can grow optimally in media with 2.5–5.2 M NaCl. Hypersaline habitats are a typical example of the extreme environments in which a considerable and unique diversity of halophilic microbial species can be found [40], ranging from eukaryotic organisms to heterogeneous groups of prokaryotes (bacteria and archaea) which constitute the predominant microflora. However, most halophiles are prokaryotic [41].

18.6.1 Archaea

Halophilic archaea are found in various hypersaline ecosystems. The main factors determining their distribution in nature are total salt concentration,

Figure 18.3 Google Earth image of some African soda lakes. 1: Lake Abiata and 2: Lake Shala, Ethiopia. 3: Lake Katwe, Uganda.4: Nakuru lake, Kenya. 5: Lake Natron and 6: Balangida lake, Tanzania. 7: Chitu lake, Ethiopia.

ionic compositions of salts, and nutrient availability [42]. High archaea densities in hypersaline environments can be observed with the naked eye due to the bright red, orange, or purple coloration. Archaeal strains are a promising

natural source of carotenoids, which is why some water in hypersaline lakes such as the Magadi Lake in Kenya are colored bright red. The red archaea of the family Halobacteriaceae dominate the hypersaline systems [43].

In African salt lakes, several halophilic archaea have been isolated and characterized, such us *Natronococcus occultus*, *Halorubrum vacuolatum*, and *Natrialba magadii* from the Magadi Lake in Kenya, *Haloferax* from Salt Lakes Chott Tinsilt, and El Malah in Algeria [44,45]. Hacěne et al. [46] have investigated the El Golea salt lake, the strains isolated have been affiliated with seven archean genera *Halobacterium*, *Halococcus*, *Natronobacterium*, *Haloferax*, *Natronococcus*, and *Haloarcula*. The genera *Haloferax*, *Halorubrum*, *Halalkalicoccus*, *Haladaptatus*, *Halobacterium*, and *Halosarcia* have been reported from the sebkhas of Sidi Ameur and Himalatt [17]. Members of the genus *Halobacterium* are extreme halophile archaea. They have been largely reported from different North African hypersaline salt lakes [17,46].

18.6.2 Bacteria

The domain of bacteria contains the greatest diversity of halophiles that are mainly represented by moderate halotolerant and halophilic species as extreme halophiles. They are identified in many phyla distributed in a large number of very heterogeneous phylogenetic groups, such as Actinobacteria, Bacteroidetes, and Cyanobacteria. However, most moderate halophilic bacteria can be either gram-positive, gram-negative, heterotrophic, aerobic, or facultative anaerobic [47]. A lot of new species have been isolated and described from the African salt lakes (Table 18.3).

18.6.3 Actinobacteria

Actinobacteria are one of the main groups in the domain of Bacteria. A very heterogeneous specific phylogenetic diversity of halophilic actinobacteria has been described and classified into various genera [53]. Due to their salt tolerance, actinobacteria can be found in marine environments, salt lakes, lake sediments, saline soils, and hypersaline environments. Many novel halophilic actinobacteria have been described from different African saline systems: *Actinopolyspora mzabensis*, *Prauserella isguenensis* (saline soil from Algerian Saharan) [54,55], *Bogoriella caseilytica* (saline soil from Bogoria soda lake, Kenya) [56], *Kocuria aegyptia* (saline soil, Egypt) [57], *Actinopolyspora egyptensis* (Qarun salt lake, Egypt) [58] and *Nocardiopsis* sp. (saline soil from the Sebkha of Ain Salah, Algeria) [59]. As can be seen, most of the halophilic actinobacteria are isolated from terrestrial saline

Table 18.3 New halophilic species, isolated from diverse salt lakes in Africa.

Halophilic species	Sources	References
Halanaerobium sehlinense sp. nov.	Sebkha of Sehline, Tunisia	Abdeljabbar et al. [3]
Haloarcula sebkhae sp. nov.	Sebkha of Ouargla, Algeria	Barreteau et al. [4]
Salicola salis sp. nov.	Sebkha of Ezzemoul, Algeria	Kharroub et al. [48]
Melghiribacillus thermohalophilus gen. nov.	Chott Melghir, Algeria	Addou et al. [49]
Melghirimyces algeriensis gen. nov.	Chott Melghir, Algeria	Addou et al. [5]
Halonatronum saccharophilum gen. nov.	Magadi lake, Kenya	Zhilina et al. [50]
Natronococcus amylolyticus sp. nov.	Magadi lake, Kenya	Kanai et al. [51]
Halanaerobaculum tunisiense gen. nov.	Chott El Djerid, Tunisia	Hedi et al. [6]
Halanaerobacter jeridensis sp. nov.	Chott El Djerid, Tunisia	Mezghani et al. [7]
Virgibacillus natechei sp. nov	Saline lake located in Taghit, Algeria	Amziane et al. [52]
Halopiger djelfamassiliensis sp. nov.	Zahrez Gharbi, Algeria	Hassani et al. [8]

sources, but many of them are isolated also from saline water mainly from salt lakes and marine sources.

18.6.4 Cyanobacteria

Cyanobacteria represent an important part of the phototrophic biota of hypersaline environments, including several halotolerant and extreme halophilic species. Unicellular or filamentous microorganisms have been isolated from the sediment surface of hypersaline environments where they form microbial mats, represented mainly by Cyanobacteria and anoxygenic purple bacteria. The most common species of filamentous Cyanobacteria found in hypersaline environments are *Microcoleus chthonoplastes* and *Halospirulina tapeticola*. Cyanobacteria are a component of the microbiota of saline and hypersaline lakes, single-celled species "*Aphanothece halophytica*" and other

filamentous such as *Phormidium*, *Oscillatoria*, *Microcoleus*, *Spirulina*, and *Nodularia* are found in shallow sediments of salt lakes [60].

The physical and chemical characteristics of East African saline soda lakes can change considerably which affects microbial diversity. The East African saline soda lakes comprise a few taxa of Cyanobacteria with a high growth rate and high biotechnological potential [61]. When salinity is low (< 50‰), the dominant Cyanobacteria from Bogoria and Nakuru lakes is *Arthrospira fusiformis* [62]. Currently, the Cyanobacteria *A. fusiformis* is present in high densities only in a few lakes, such as Lake Chitu (Kenya) and Lake Bororia (Kenya). In other saline soda lakes, this taxon is found in low densities and is associated with other Cyanobacteria such as the *Cyanospira* and *Anabaenopris* [63].

18.6.5 Halophilic eukaryotes

In the Eukarya domain, halophilic microorganisms are rare. Most halophilic eukaryotes are moderate or halotolerant, but some extreme halophilic species have been identified [64]. Filamentous fungi of the genus *Hortaea*, *Wallemia*, and *Aureobasidium*, the yeast *Debaryomyces*, and microalgae of the genus *Dunaliella* and *Asteromonas* can be found in saline systems [65]. In addition, *Dunaliella* is the most ubiquitous microalgae in hypersaline environments [66]. It is a unicellular, eucaryotic, and green halotolerant microalga. The genus *Dunaliella* comprises almost 30 species, throughout fresh, marine, and hypersaline waters. The species *Dunaliella salina* is the most cultivated among the genus *Dunaliella*, for its high concentration (up to 10% of its dry cell weight) of β-carotene. When salt lakes dry out, salinity increases. These changes help the species *D. salina* to produce large amounts of β-carotene, which can turn the color of the lakes into red color [67,68]. During summer, several sebkhas and chotts from North Africa turn red, for example, Zahrez Chergui and Zahrez Gherbi (Algeria), Chott Djerid (Tunisia), Saline of Tissa (Morocco), and the Bardawil Lake (Egypt) [13,15,17,69–71]. Otherwise, little information is available about the microalgae diversity from the salt lakes in Africa (Table 18.4).

18.7 Biotechnological potential of halophiles from African salt lakes

Halophilic microorganisms can survive in diverse environments at high salt concentrations such as salt lakes, saline soils, and other hypersaline ecological niches [76]. These microorganisms produce enzymes and other

Table 18.4 Microalga isolated from saline and hypersaline African salt lakes.

Microalga	Salt Lake	Medium	References
Dunaliella salina *Dunaliella viridis*	Sidi Ameur salt lake, Algeria	F/2	Yaiche Achour et al. [13,15]
Dunaliella sp.	Saline Azla, Morocco	Semenenko and F/2 media	Charioui et al. [72]
Dunaliella sp.	Saline Idao Iaza, Morocco	Semenenko and F/2 media	
Chlorella sp.	Sebkha of Sahline, Tunisia	Conway medium	Jazzar et al. [73]
Micractinium sp.		Conway medium	
D. salina	Sebkha of Sidi El Hani, Tunisia	F/2 medium	
Dunaliella sp.	Chott El Djerid, Tunisia	F/2 medium	Elleuch et al. [74]
D. salina	Sfax Solar Saltern, Tunisia	–	Dahmen-Ben Moussa et al. [75]

biomolecules to survive in extreme environmental conditions. Halophiles produce unique metabolites that can be exploited for biotechnological purposes, for example, biopolymers, hydrolytic enzymes, EPS, antimicrobial peptides, and others. Here, we expose a prominent investigation of the bioactive molecules from African salt lakes with potential application in biotechnology.

18.7.1 Hydrolytic enzymes

The halophilic microorganisms contain enzymes that maintain their activity at high salt concentrations. Few halophilic enzymes have found applications in biotechnology, compared with enzymes from other extremophiles, for example, thermophiles and alkalophiles. Halophilic bacteria are more metabolically active than archaea, and their enzyme activities are more diversified (lipases, proteases, amylases, cellulases, nucleases, etc.) [64]. These enzymes are good candidates for industrial applications because of their ability to be active in the presence of high salt concentrations, and tolerate relatively high temperatures and pH variations [77].

18.7.2 Lipases and esterases

Enzymes hydrolyzing carboxylic esters are ubiquitous and have been found in all three domains of life (Bacteria, Archaea, Eucarya). These enzymes can act as hydrolases that catalyze the hydrolysis of triglycerides to fatty acids and glycerol [78]. In an organic solvent, they can catalyze the reverse reaction or transesterification. They are widely used as biocatalysts because of their ability to produce pure compounds. Esterases are distinguished from lipases by their preference for short carbon chains. These enzymes have a wide range of applications including the production of polyunsaturated fatty acids for food and energy industries, thanks to their properties in organic synthesis, mainly for flavors, detergents, and biodiesel [79].

Several studies have investigated the production and characterization of lipases and esterases mainly from the halophilic archaea. For example, the screening for extracellular halophilic enzymes of 68 strains of *Haloarchaea* isolated from different salt lakes in Algeria (Chott El Beïdha−Hammam Essoukhna, Sebkha Medghacen, Chott Kralla, Sebkha El Hamiet, Sebkha Djendli, Sebkha Oumache, and Chott Tinsilt) has been shown to have a high potential, 89% of strains produced at least two hydrolytic enzymes. In addition, 72% of the isolates are esterase-producing strains. They have been identified mainly for strains affiliated with the genus *Haloferax* [80]. Similarly, Akmoussi-Toumi et al. [45] studied the diversity of extreme halophiles from the Tinsilt and El Malah Salt Lakes in Algeria, concluding that lipase was one of the predominant enzymes from halophilic Archaea and Bacteria. Halophilic enzymes from Archaea are not employed on an industrial scale. However, the biotechnological interest of these enzymes has been widely studied in halophilic bacteria.

Among 44 bacterial strains from five distinct saline environments in southern Tunisia, 17 are lipase-producing strains. The majority of the producers are affiliated with *Halomonas* and *Bacillus* genera [81].

It was also reported that fungi strains isolated from Sebkha of Oran have exhibited high enzymatic activities and about 46% of the strains are lipase producers. The highest lipolytic activity was observed in *Penicillium vinaceum, Ustilago cynodontis*, and *Wallemia* sp. [82].

In contrast, only a few halophilic lipases have been characterized. Akmoussi-Toumi et al. [18] have characterized for the first time an extracellular lipase (HML) from the Haloarchaea *Haloferax mediterranei* strain ATS1 isolated from the Sebkha of Medea, Algeria. The lipase HML is active over a broad pH (2 to 13), with maximum activity at pH 7.

18.7.3 Amylases

Amylases are ubiquitous enzymes synthesized by plants, animals, and microbes. They play an important role in biotechnology. Amylases are classified into α, β, and γ subtypes and the first two are the most studied. Amylases are hydrolytic enzymes that catalyze the hydrolysis of α-1−4 glycosidic bonds of amyloidosis, amylopectin, starch, and glycogen, into glucose, maltose, and α-dextrin [83]. These enzymes are produced by different microorganisms, but the most used in commercial, or industrial application, are extracted from the *Bacillus* species [84]. In addition, several bacterial species affiliated with the genera *Halobacillus*, *Halothermothrix*, *Marinobacter*, *Nesterenkonia*, *Thalassobacillus*, and halophilic archaea (*Haloferax*, *Haloarcula*, and *Haloterrigena*) have been characterized for their amylolytic activities. Isolation and screening of enzyme production by the archaea from Algerian salt lake reported a predominance of amylolytic activity [85]. Twenty-one amylase archaea producers represented by the genus *Haloferax*, *Haococcus*, *Haloarcula*, *Haloterrigina*, and *Natrialba* were isolated from the northeastern salt lakes in Algeria [80]. In saline and hypersaline African environment, limited studies on the characterization of amylase from halophilic bacteria have been conducted.

Microbial amylases are used in foods, pharmaceuticals, detergents, and textile industries. Their application in the food industry concerns baking, glucose syrups, juice, and maltose syrups [86]. Table 18.5 gives some amylase-producing halophiles isolated from African salt lakes.

Table 18.5 Amylase-producing halophiles from African salt lakes.

Isolate	Location	References
Natronococcus amylolyticus	Magadi lake, Kenya	Kanai et al. [51]
Amphibacillus sp. NM-Ra2	Wadi An Natrun, Egypt	Mesbah, Wiegel [87]
Bacillus sp. BCHS3	Chott El Beïdha−Hammam Essoukhna, Algeria	Menasria et al. [88]
Bacillus sp. BSDJ5	Sebkha Djendli, Algeria	Menasria et al. [88]
Oceanobacillus spp. BSMD20	Sebkha Medghacen, Algeria	Menasria et al. [88]

18.7.4 Proteases

Proteases are the most important enzymes for biotechnology and their global markets have been growing drastically. Currently, microbial proteases enzymes are widely used in feed, food, textile, cosmetology, medical, and pharmaceutical industries. Moreover, proteases are universal and are found in plants, animals, and microbes including viruses and bacteria [89]. Microorganisms producing halophilic proteases belong to bacteria, archaea, and eukaryotes thriving in saline or hypersaline environments [90]. Most of the extracellular proteases synthesized by Haloarchaea and bacteria are serine enzymes [91].

An extracellular protease was characterized from *N. magadii* haloalkaliphilic archaea isolated from Lake Magadi [44]. This protease has an optimum temperature of 60°C at 1.5 M NaCl and requires a high salt concentration to act in an organic medium [92]. Otherwise, according to Karray et al. [93], who conducted a study on the screening of hydrolytic enzymes produced by bacteria and archaea strains isolated from chott El Djerid, there were no archaea strains that could produce protease, unlike halophilic bacteria.

Chamekh et al. [82] performed a study focused on the screening of fungi protease producers from the Sebkha of Oran. Among the isolated strains, 67% synthesized the enzyme protease. The highest proteolytic activity has been detected for the species *Gymnoascus halophilus* and *U. cynodontis*. These data are in agreement with another finding performed on the hydrolytic enzymes from fungi in Chott Merouane, Chott Melghir, and Chott Tighdidine (Algeria), where 61% of the total isolates are protease producers [94]. However, it is important to characterize these enzymes to use them on an industrial scale.

18.7.5 Cellulase

Cellulases catalyze the hydrolysis of the β-1,4 bonds of glucans, producing shorter polysaccharides and oligosaccharides or monosaccharides such as β-glucose. Cellulases are produced by a large number of microorganisms, for example, bacteria, actinobacteria, and fungi. These enzymes are mainly used in the textile industry and show a wide range of applications in the food, biomedical, and chemical industries. They have also increased interest in the production of bioethanol [95].

Among all cellulase producing microorganisms, the best-characterized ones are filamentous fungi, especially species affiliated to the genus

Trichoderma and *Aspergillus*. Enzymes from these microorganisms are produced on a large scale for agricultural use [96].

The screening of extracellular cellulase from archaea strains isolated from arid and semiarid ecosystems in Algeria showed that 35% of the total strains had an interesting cellulase activity [80]. Another study conducted on the enzymatic activity of halophilic and halotolerant fungi from the Sebkha of Oran has shown that almost all strains produce cellulase. Strains affiliated with the species *G. halophilus* exhibited the highest activity [82].

Halobacillus sp. QLS 31 isolated from the sediment of Lake Qarun in Egypt exhibited a cellulase activity yield ranging from 1.49 to 48.08 U/mg depending on several factors, such as carbon source, pH, temperature, NaCl concentration, and time. Cellulase producer *Halobacillus* sp. QLS 31 has been proposed for commercial production [97]. Several other cellulase producing bacteria have been isolated from the soda salt lakes Wadi El Natrun [98].

18.7.6 Exopolysaccharides from halophiles

Bacterial EPS are an interesting source with several proprieties and potential applications, for example, in the food industry as gelling agents and emulsifiers. This is can be made easier thanks to their resistance to salt and thermal degradation. The archaea affiliated with the species *H. mediterranei* are considered potential producers, but unfortunately, several EPS from archaea did not lead to commercial applications.

Under optimum cultural conditions (15% NaCl), EPS-K2 production by *Halomonas smyrnensis* K2 was 74 mg/L after incubation at 30°C. EPS-K2 was revealed to be a hetero-polysaccharide, with a high percentage of mannose [99]. This enzyme has several potential applications in the food, cosmetics, and medical industries. The examples of EPS from African salt lakes are given in Table 18.6.

18.7.7 β-Carotene from the microalga *Dunaliella salina*

Dunaliella is unicellular, eukaryotic, and halophilic microalgae. *D. salina* is the most important β-carotene producer from hypersaline lakes. Others pigments (lutein and chlorophylls) can be produced by this and other *Dunaliella* species. The cultivation of *D. salina* is considered a successful application of halophilic microorganisms. Natural β-carotene from *D. salina* has found several applications in various forms: biomass powder as feed

Table 18.6 Characteristics and potential applications of some microbial exopolysaccharides from African saline and hypersaline lakes.

Species/EPS	Location	Characteristics	EPS production	Potential applications	References
Halomonas smyrnensis K2 « 3EPS-K2 »	Solar saltern of Kerkennah, Tunisia	High thermostability (degradation temperature of about 260 °C)	0.74 mg/L	Functional ingredients in food, biomedicine, and pharmaceutical industries	Joulak et al. [99]
Halomonas maura S-30 « Mauran »	Saltern in Asilah, Morocco	High viscosity displays pseudoplastic, viscoelastic, and thixotropic behavior	3.8 g/L	Pollution remediation and Treatment of waste waters	Arias et al. [100]
Halobacillus sp. EG1HP4QL	Lake Qarun, Egypt	Emulsifying activity	5.9 g L	Bioremediation of oil-polluted environments	Ibrahim et al. [101]
Halomonas sp. NASH	Wadi El-Natran, Egypt	Antioxidant activity Anti-inflammatory Emulsifier	4 g/L	Food and pharmaceutical industries	Youssif et al. [102]

coloring and cosmetics applications. Several other carotenoids are found in *D. salina* cells, for example, zeaxanthin, violaxanthin, and neoxanthin [103].

Only a few studies have been conducted on the investigation of the African salt lakes for the isolation of *D. salina* strains [13,15,74].

During the hot season, some African hypersaline water bodies, especially from extremely arid environments, dried out by evaporation and become saltier. These water bodies are pink, orange, or dark red. This coloration is due to the presence of halophiles archaea, carotenoid-rich prokaryotes, and the microalga *D. salina*. Zahrez Chergui and Gherbi are some of the Algerian salt lakes which turn orange to red during hot seasons.

18.8 Conclusion

African salt lakes remain largely unexploited and unexplored. There have been just a few reports about microbial biodiversity and their potential applications, especially from those of eastern and southern Africa. However, many sebkhas, chotts, and lagoons from North Africa were investigated, but still, most of them are unexplored. Most studies have focused on archaea and bacteria. It is rare to find a complete study on the biodiversity of the microalgae in these saline waters. To our knowledge, there are no industrial applications of halophilic molecules from the African salt lakes. However, it is important to thoroughly study these molecules to use them in biotechnological processes.

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CHAPTER 19

Microbial modeling in African lakes

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19.1 Different distribution patterns of aquatic microorganisms

Prokaryotic microbes play critical roles in the water and sediment of different natural bodies of water where they are important colonizers. They can significantly affect its preservation in sediments by involving the degradation of organic matter. Also, they have played important roles in sulfur cycles, nitrogen, and phosphorus in both sediment and water [1].

Eukaryotic microbes, including unicellular fungi, are also playing an important role in different ecological niches in sediment and water, for instance, they participated in the above biogeochemical cycles and food interactions [2]. However, there is a distinct difference between microorganisms in water bodies either in sediment or the water column that may have obstructed the previous studying of their ecological distributions in these habitats.

Both sediment components and water columns are the most important and closely related aquatic systems components. Sediments are generally considered the main nutrient source of water. Therefore, it is logical to presume that the aquatic macrobiotia exchange their nutrients between the water and sediment, resulting in the similarity of the communities of microorganisms between the two ecosystems. General bacterial and fungal member taxa were isolated and identified from the water column and sediment samples. Sediments are found to be a very important bacterial and fungal source [3].

Definite taxa and patterns of bacterial, archaeal, and fungal distributions between water column and sediment have been studied [4], resulting in complex microbiological interactions between marine water and sediment. Various microbial types prefer water and sediment habitats. For instance, aerobic chemoheterotrophic and phototrophic microorganisms

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are found to be widespread in the water while those sharing organic matter decomposition and sulfur transformation cycles are often detected in sediment [5].

Furthermore, many environmental factors figure out the microbial distributions in sediment and water, that is, the temperature of the water, pH, dissolved oxygen (DO), nutrient level, and sedimentary organic matter. Besides, interactions among different microbial communities are considered an important factors in sharing their distribution patterns in water and sediment. Understanding all these factors in microbial distribution patterns is very important for elucidating the microbial relationships between marine water and sediment. One of these aquatic environments is the lakes that were scarcely studied. Regarding a wide spectrum of water bodies of environmental and trophic gradients, lakes are considered a core factor for different microbial niches. Sequences using 16S and 18S rRNA genes according to taxonomic assignment from phylum to species showed that microbial diversities in the water bodies (lakes) were markedly diverse and distinguished by the higher richness and more varied taxonomical structure [6,7].

In this chapter, we deal with the bacterial, archaeal, and fungal communities distributions (autotrophic and heterotrophic populations) in the most known African lakes where, in water columns, the dominant bacterial community composition were α- and β-Proteobacteria, Actinobacteria, Bacteroidetes, Cyanobacteria, and Thaumarchaeota phyla and the dominant methanogens strain in the layer of the sediment [8]. The archaeal domain was considered the lower distribution; however, the African soda lakes showed their highest archaeal distribution. Regarding fungal distribution, Ascomycota represented the major fungal communities, besides, the minor existence of Basidiomycota. This study was furnished by modeling of these microbial communities that were analyzed and discussed concerning their influence on habitats as well as the specific different taxa relationships. Useful data for microbial distributions evaluating the main African lakes were provided by this study, which may also be a new domain for predicting their distribution in the future.

19.2 General microbial biodiversity in the lakes

Microbes are ubiquitous on earth, inhabiting soil, air, water, and even other organisms. They also inhabit extreme environments including hot

springs and saline environments. The extremophiles have also been associated with harsh habitats and difficult environmental conditions [9].

Geographic position and tropical status affected the studies of comparison between the microbial community compositions in the ecosystems of the lake, whereby changes in the physicochemical parameters of the sediment and water column are the main factors that affect the microbial communities distribution in the lakes [10].

It is well understood that fresh and saline water lakes have a few limited microbial species compared with their counterpart microorganisms. Salt (Soda) lakes are defined as an aquatic environment that represents high productivity due to the high intensities of light, high ambient temperatures, rich in phosphates, and amount of CO_2 in the carbonated water. Visible soda lake coloration is a result of different and dense microbial communities in the water of the lake. [11].

19.3 Bacterial diversity in the lakes

Molecular mechanisms of alkaliphilic microbes were first known by [12] who investigated the Yellowstone National Park hot springs (Wyoming, USA), which inhabited a large number of archaeal communities. The archaea are considered the dominating microorganisms in hot springs sites. The bacterial diversity analysis in these hot spring sites resulted in a unique bacterial community with 12 new division ancestries. The authors showed that strains from the bacterial domain were higher than the archaea in this hydrothermal environment.

Keller and Zengle [13] subsequently studied microbial diversity in the Yellowstone National Park in United States, and indicated that despite the close geographical proximity of all the hot springs, regarding the same temperatures (between 90°C and 100°C) and pH values (8–9), they differed noticeably concerning their diversity of microorganisms. This statement indicated that geochemical variations affect microbial biodiversity and integrated measurements of these geophysicochemical characteristics will help to predict and understand microbial diversity.

Zhiyu et al. [14] isolated two endospore-formers, gram-positive, alkaliphilic bacteria from the sediment and water samples of the Okuhida hot area, Japan. The isolated bacteria were morphologically and molecularly identified. Depending on the phylogeny and phenotypic characterization, a novel species of *Bacillus okuhidensis* sp. nov. was suggested with GTC 854T (JCM 10945TDSM 13666T) strain type.

Yanhe et al. [15] studied the Mongolia Soda Lake, China, and indicated that using 16S rDNA molecular analysis, different bacterial communities inhabit this soda lake that could be identified depending on the phenotypic and molecular characterization methods. Fifty-three alkaliphilic microorganisms were found and isolated from the sediment samples; 20 were subjected to 16S rDNA sequence analysis. The authors found that a minor number of some clones was correlated to the isolated alkaliphilic bacteria from the studied soda lakes such as *Thioalcalovibrio denitrificans, Alkalispirillum mobile*, and *Halomonas campisalis*, while the major clones were correlated to nonalkaliphilic identified species ($>97\%$ similarity). These isolates were identified as *Alkalibacterium, Amphibacillus, Bacillus, Cyclobacterium, Exiguobactrium, Gracilibacillus, Halomonas, Marinospirillum, Pseudomonas*, and *Salinicoccus*. Out of the 30 isolates, the predominant gram-positive and four gram-negative isolates were obtained. However, most of these clones obtained from this soda lake were correlated to *Proteobacteria*, with only about 10% of the obtained clones associated with gram-positive bacteria [16].

Based on the 16S rRNA gene sequence and DNA–DNA hybridization data, *Anaerobranca californiensis* sp. nov., a novel, alkalithermophilic, chemo-organotrophic, obligatory anaerobic bacterium was isolated from the alkaline hot spring sediment of the Mono Lake, USA. This rod-shaped bacterium is motile via peritrichous flagella and can reduce ferric and selenium due to the presence of organic matter. The G + C content of the DNA of the strain is about 30 mol.% [17].

In the northern Egypt desert, Wadi Natrun was represented by many alkaline soda lakes depending on the low surface elevation, which are fed by underground Nile water. They flourished through large microbial flora and represent the isolation source of many meso-alkaliphilic strains. *Alkalilimnicola halodurans*, a new aerobic and alkaliphilic bacterium, was isolated from the sediments of these lakes which were represented as a member of the Ectothiorhodospiraceae family. The knowledge of saline lakes in Africa has been related to the research on their biodiversity. The isolation of alkalithermophilic microorganisms from the large and warm soda lakes of the Rift Valley of East Africa (Tanzania, Ethiopia, and Kenya)have high concentrations of Na_2CO_3 and high pH values of 10–11. These lakes are characterized by hot alkaline springs below and tropical sun heating above. They represent reasonably stable water columns of the lakes on the scale of geological time [18].

The Rift Valley of the East African soda lakes contains a massive and multiple populations of autotrophic, alkaliphilic, alkali-tolerant, halophilic,

heterotrophic, and organotrophic representatives of major bacterial, archaeal, and fungal phyla. Alkaliphilic Cyanobacteria (*Anabaenopsis, Arthrospira, Cyanospira, and Spirulina*) are responsible for nitrogen fixation and the primary production in these soda lakes [19].

These microbes are considered as the main new biomolecule source with biotechnological applications and also for studying the mechanisms of adaptation to extreme and difficult environmental conditions such as pH and temperature. Many of these soda lakes inhabit microorganisms. They are not only alkaliphilic but at least highly alkali-tolerant [20].

Microbial diversity in two different subregion soda lakes, Brazil, was studied using the metagenomic sequencing method to study the functions and compositions of the bacterial communities patterns. These two lakes had different permanent cyanobacterial blooms (Salina Preta, Salina Verde, green-water lake). In the Salina Verde, the dominant bacterial species bloom was *Anabaenopsis elenkinii*. This cyanobacterium made alternations in some abiotic parameters such as turbidity, DO, and pH, and thus, the overall microbial distribution. In Salina Preta, the community of microorganisms had a more specific and structured taxonomy, regarding their metabolic functions, where this microbial community contained a large number of taxa, while, in Salina Verde, the studying of the functional potential was understood by a specific group of taxa. The abundance of specific genes is related to the nitrogen, carbon, and sulfur cycles. It was found that the genes associated with arsenic (As) metabolism resistance were associated with the cyanobacterial bloom and presented at higher abundance in Salina Verde [21].

The Van Soda Lake in Turkey has the highest level of microbialites among the various endemic fish species. This high level of bacterial diversity was analyzed using 16S rRNA gene metabarcoding. The samples of the direct water were inhabited by Cyanobacteria. Bacteroidota and Proteobacteria, however, the samples of the preenriched water were inhabited by Firmicutes and Proteobacteria at the phylum level. In the samples of the sediment, both Proteobacteria and Firmicutes were found at the highest level. The samples of preenriched fish were dominated by Firmicutes and Proteobacteria at the level of the phylum. [22,23].

19.3.1 Estimation and identification of bacteria inhabiting the lakes

Generally, the abundance of planktonic bacteria is around 10^6–10^7 cells/mL in the soda lakes and they mainly belong to the Actinobacteria,

Bacteroidetes, and Proteobacteria phyla. Archaea represent a small fraction (~ 10% on average) of the different planktonic prokaryotic. Two types of bacterial community composition were found in a turbid pan and a colored soda pan based on the 16S rRNA sequencing data indicated by Bedics et al. [24]. The uncultured groups' acIII-A1, acSTL, acTH1, and *Nitriliruptor* and *Ilumatobacter* genera (Fig. 19.1) are the most abundant distinctive planktonic Actinobacteria in the shallow water of soda pans; using lower taxonomic level, where their abundance can reach the highest values. It was reported that small-sized bacteria with a protective structure of cell wall are the most survivors of high pressure during summer–spring [24]. The planktonic proportion Betaproteobacteria (e.g., Hydrogenophaga and Limnohabitans) is well identified in freshwater lakes considered the highest in periods with the lowest salinity. Other most important planktonic bacteria such as members of the classes *Flavobacteria*, *Cytophagia* (Fig. 19.1), and the order Alphaproteobacteria (Rhodobacterales), are related to the blooms

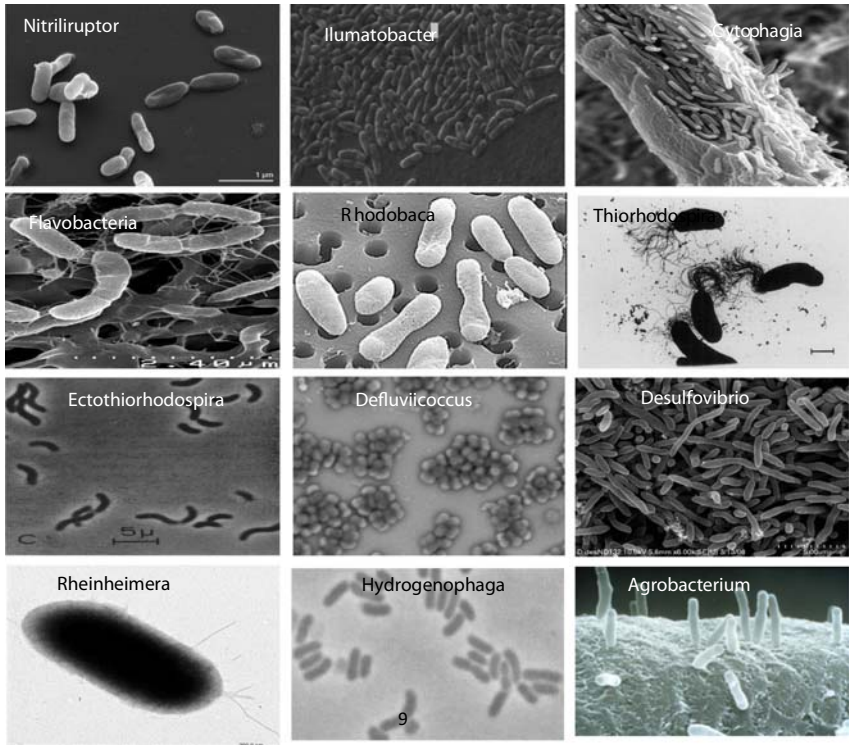

Figure 19.1 Scan electron microscope (SEM) of the most common bacterial strains in soda lakes.

of algae. Using the metagenomic method of data genes, these genes are responsible for the uptake of high molecular weight organic matter derived from phytoplankton. This plankton is the most abundant in the community gene pool in a turbid pan [25].

It is rare to observe in dual bloom, under the surface layer of the green algae, dense community of purple bacteria: *Rhodobaca* (Rhodobacterales), Thiorhodospira, or *Ectothiorhodospira* (Hromatiales, Gamma-proteobacteria) (Fig. 19.1) which inhabit just above the sediment layer. Probably, such blooms can come out in warm weather, sunny and calm. Nevertheless, the photoheterotrophic bacteria characterize a significant portion of the total community of planktonic bacteria in the pans and soda lakes. The isolation of *Aeromonas, Pseudomonas*, and *Bacillus* species denotes only a trivial part of bacterioplankton. In soda pans, the sediment is dominated by bacterial communities of the Proteobacteria, Actinobacteria, Bacteroidetes, Gemmatimonadetes, and Chloroflexi phyla which have a critical contribution. Similar to the planktonic bacteria, different notable diversity is observable in the colored and the turbid pan. It seems that the most abundant genus, *Defluviicoccus*, have the anaerobic biodegradation ability of organic material within the sediment resulting in glycogen accumulation. Lactate-utilizing sulfate-reducing bacteria including genera *Desulfovibrio*, *Desulfotomaculum*, and *Desulfobulbus* (Fig. 19.1) were of higher magnitude order in the surrounding area of the organic carbon matter source derived from macrophyte (reed rhizosphere) than in the lake sediment and this was detected in Lake Velence [26]. Additionally, many moderately alkaliphilic and halophilic microorganisms with diverse metabolic characterization have been isolated from the reed periphyton. The most dominant identified phyla are Proteobacteria (e.g., genera Hydrogenophaga, *Rheinheimera*, *Agrobacterium*) and Bacteroidetes (e.g., *Flavobacterium*) (Fig. 19.1) that have been detected in the samples of these reed periphyton in cultured-independent studies.

19.4 Fungal diversity in the lakes

The lakes that were extensively studied were the Great Salt Lake (USA), Wadi Natrun alkaline brines (Egypt), Magadi Lake in Kenya, and the Dead Sea. Remarkably, the taxonomic biodiversity of microorganisms is very low in all these soda lakes doubtless due to the high concentration of salt. Fungi are most extensive in these lake ecosystems due to their usual colonization of different types of substrates. The highest eukaryotic fungi distribution is detected in tropical areas such as tropical forests around the

world. In Puerto Rico, many reports on fungal diversities have concentrated on coastal ecosystems and forests [27].

Most fungi are capable of adapting to these harsh conditions from pH, temperature, water, and even salinity. Most of the fungi that accommodated these extremes are related to Ascomycota, the fungi imperfect stage, which have been isolated from marine sediments, salt marshes, seawater, and mangroves. The isolation of fungal species and strains from natural hypersaline habitats has been studied and described [28].

Fungal distribution and population studies within such difficult ecosystems have been conducted in the latitudes of the north, in and around the slatterns along the Mediterranean Sea coast, the Red Sea coast, in the region between the Dead Sea and Russia, the Adriatic coast, Great Salt Lake, Gulf of California, the Atlantic coast, Utah, and the Indian West Coast. Imran et al. [29] reviewed fungal isolation from many natural and artificial hypersaline environments detected in Dominican Republic, Namibia, France, Slovenia, Portugal, and Spain. Therefore, great interest invoked many reports for the presence of eukaryotic fungi in the Dead Sea hypersaline waters by 340 g/L total dissolved salts that support fungal life meaning for their survival spores and high salinity in this extreme environment.

Moreover, the gene represented high osmolarity for glycerol (HOG) obtained from *Eurotium herbariorum*, the fungus which has been identified from the Dead Sea as tolerant to thawing and freezing. A further study was conducted on the production the HOG gene of a recombinant yeast *Saccharomyces cerevisiae*. The genetically transformed yeast was capable of opposing high salinity, extreme cold, and heat conditions, where high salt concentration tolerance is supported by many neighbor genes which is considered the first step to the genetic engineering of salt-tolerant agriculture crops.

Fungal diversity fauna was detected in aquatic ecosystems with salinities ranging between 15% and 32%, where it was supposed to be related to bacterial growth only. The first fungus that was isolated from hypersaline waters in Slovenia was identified as *Secovlje salterns* and followed by the salterns of Bonmatí (Santa Pola, Valencian Community, Spain) and La Trinitat (Ebro Delta, Catalonia, Spain), with the presence of the same dominant strains. Also, major species were isolated, and belonged to yeast-like fungi and melanized meristematically, but a few filamentous fungal genera were identified and studied. Among the identified halophilic and halotolerant dematiaceous Ascomycetales, mycobiota, of these

genera were isolated: *Alternaria, Aureobasidium, Cladosporium, Phaeotheca, Hortaea* and *Trimmatostroma*. Later, Jean-Luc Legras [30] isolated five melanin-producing species from the La Trinitat salt lakes (Spain) and then were grown in cultures. These melanized species had unique morphological aspects in a culture medium that began by black, clump-like colonies and then end in dividing cells in the water which acts as a response to multistress conditions and factors to support the melanized fungus to tolerate high salinity, temperatures, and low activity of the water by optimizing the surface-volume ratio [31].

Moreover, the Nieves-Rivera [27] studied the coastal mycology in Puerto Rico including different aspects of fungi in marine environments. Ruiz-Suarez [32] studied the filamentous fungi of arenicolous in the Bay of Mayaguez shoreline and indicated the existence of *Dreschlera, Aspergillus, Geotricum, Cladosporium, Fusarium, Trichoderma, Penicillium, Rhizopus*, and *Mucor*, where, of the total fungal abundance, *Aspergillus* represented about 80%. The data recommended that high salt concentration may restrain the presence of filamentous fungi on the bay shoreline.

Fungal capability in the decomposition of salt marsh grasses is a characteristic feature of halotolerant fungi that inhabit a moderate salt marshes environment. In Europe, many mycorrhizal species had been detected on the surfaces of salt marshes halophytes that were represented by large quantities of spores; 80% of them were identified as *Glomus geosporum*. A study by Landwehr et al. [33] suggested that these filamentous fungi benefit plants' salt tolerance depending on the existence of *Glomus caledonium* and *G. geosporum* spores in high salt marshes. This indication was later maintained by Carvalho et al. [34] who illustrated that the filamentous fungi in high salt marsh plants might not only have the ability to confer the tolerance of high salt concentration in plants but also may affect their vegetative distribution. This evidence was guided to the Portugal salt marsh indicating that the adaptation of fungi is one of the probable reasons for the presence of mycorrhizal filamentous fungi in the salt marshes.

The first record of a novel species, filamentous fungi *Gymnascella marismortui* (Ascomycota) was reported in the Dead Sea. This fungus was an obligate halophile that propagated at a salinity optimum range of 10%–30% in the water of the Dead Sea. The same authors isolated new fungal species *Penicilium westlingii* and *Ulocladium chlamydosporum* with tolerance to high salt concentration ranging from 5% to 25% NaCl at 30°C. Isolates belonging to *Chaetomium aureum*, *Chaetomium avigenum*, *Eurotium amstelodami*, and *Emericella nidulans* from the Dead Sea have been successively studied.

Later, Kis-Papo et al. [35] detected the presence of *Aspergillus versicolor*, *E. herbariorum, Chaetomium globosum, E. amstelodami, G. marismortui*, and *E. rubrum* in the Dead Sea waters and tested their mycelia and spores survival in the water of the Dead Sea for an extended time. After the first evidence of these fungi from the water of the Dead Sea, Kis-Papo et al. [36] reported a study on *A. versicolor* genomic diversity and their data submitted that the diversity of the genome was accurately related to stress. A recent report by Perl et al. [37] includes *C. globosum* isolation from the saline lakes of Wadi El-Natrun and the Dead Sea.

Many species including *Candida glabrata* and *Candida atmosphaerica*-like strain, *Rhodotorula larynges*, and *Trichosporon mucoides* were isolated from these lakes, where *C glabrata* were unknown for their tolerance for high salinity and *C. atmosphaerica* was confirmed by its association with other extreme environments—the hydrothermal systems of the deep sea of the rift of the Mid-Atlantic.

Sarocladium kiliense fungal isolates from Lake Sonachi in Kenya were studied by Francis and Ndwigah [38] Recently, Orwa et al. [39] illustrated 18 fungal genera distribution, namely *Acremonium*, *Aniptodera*, *Aspergillus*, *Biatriospora, Chaetomium*, *Cladosporium, Juncaceicola*, *Paradendryphiella Penicillium*, *Phaeosphaeria Phoma*, *Pyrenochaeta*, *Sarocladium*, *Septoria*, *Septoriella*, *Talaromyces*, and *Zasmidium* from Lake Magadi in Kenya.

The alkaline, hypersaline, and closed basin of the Mono Lake in California was the studied site reported where these conditions permit the formation of a mineral called tufa (carbonate minerals precipitate). Thus, the most recommended fungal species were of the genera *Achaetomium, Aspergillus, Acremonium, Chaetomium, Alternaria, Cunninghamella, Embellisia, Curvularia, Fusarium, Papulaspora, Geotricum, Penicillium, Phaeoramularia, Phialophora, Phoma, Sporothrix, Mucor, Sporormiella, Ulocladium*, and *Thelebolus*. However, it was interesting that all previous species are not able for being cultured; however, the authors proposed that the more the pH and salinity the best conditions favorable for fungal growth [40].

19.4.1 Estimation and identification of fungi inhabiting lakes

Many studies on extremophiles have been attentive to prokaryotes, on the other hand, many reports were published on alkali-tolerant and alkaliphilic fungi isolated from soda lakes and soda water columns and sediments [39]. Many species of eukaryotes yeast have been found isolated from high salinity waters of solar salterns, and many genera, including

Alternaria, Acremonium, *Aspergillus, Cladosporium*, and *Penicillium*, have existed as either weakly or moderately tolerant species for high alkalinity in hypersaline environments.

High-product sequencing permits rapid identification and estimation of microorganisms by using an uncultivable method. By using this method, a high eukaryotic microbial community has been recorded from many alkaline lakes such as the hypersaline Tibetan Plateau in Central Europe, Ethiopian soda, Magadi in Kenya, Turkey, and the Dead Sea.

As a result, a sequence-based point of view allows the understanding structure and diversity of the microbial population in different eco-lakes. Many of the outcomes sequencing approaches used in the study of fungal diversity have a step of amplification. Earlier, PCR primers received large acceptance in many fungal studies. They were designed depending on the constant 18SrRNA gene. Then, this was modified by Schoch et al. [41]. Thus, many primers of the 18S rRNA gene have been designed [42]. However, phylogenetic analysis and the coverage to reach the lower levels of taxonomy are always the target, especially with the presence of less explored and extreme habitats.

19.5 Modeling of microbial distribution in the lakes

The computational modeling and analysis methods can be used to describe the dynamics of the communities of microorganisms in the complex lakes which are not possible by the conventional models of correlation. The microbial composition changes throughout the year and so the study of these dynamic changes is very important to determine the functionality of these lakes. It has been revealed that higher diversity of microbial species is associated with resilient and robust marine ecosystems [43].

For example, some studies capture the rare and abundant microbial community in the African lake, supporting data on microbial distribution and diversity in correlation to different environmental conditions. Because of the nature of meromictic, there is a variation in the oxygen availability and also the electron acceptors and donors play a very important role in the prokaryotes and eukaryotes' distribution and diversity.

The microbial community PCR analysis showed that the archaeal community is a minor microbial component in the freshwater compared to bacterial and fungal communities and also the high abundance of uncultured bacterial, fungal, and archaeal species in anoxic water depth. This evidence highlights the lack of data on different microbial

communities in water depth environment which requires additional studies in the future [44].

19.6 Salinity, pH, temperature, and microbial diversity in the African lakes

Hypersaline ecosystems are found worldwide such as in Utah, Great Salt Lake, the alkaline hypersaline soda lakes of Wadi El-Natrun (Egypt), Big Soda Lake, the Dead Sea, the Mono Lake in California, and the soda lakes of Antarctica. The African lakes are represented as very important reservoirs for both micro-prokaryotes and micro-eukaryotes that have been able to colonize and flourish under extreme or unique conditions, which are represented by high/low pH, salt, temperature, or pressure, and extreme habitats such as soda lakes. Soda lakes are widely distributed in semiarid and arid regions, such as the African Rift Valley. Despite the extreme conditions in these soda lake environments, high microbial diversity has been recorded. These ecosystems may also display higher microbial diversity than freshwater habitats [45].

"Soda" was named regarding the chemical composition of alkaline waters, due to the high concentration of dissolved inorganic carbon and sodium as the main cation, so nearly water evaporation the soda lake could accumulate and precipitate Na_2CO_3 leading to an increase in the pH values (10−12) and increasing the salinity of the lake water (>50 psu). Therefore, in such drastic conditions, soda lakes are populated by different microorganisms which comforts to high alkalinity and salinity. These adaptations relied on molecular mechanisms, including membrane structure modification, the synthesis of osmoregulatory molecules, and the use of proteins for transportation. In Kenya, for example, Magadi, Bogoria, and Elmenteita as soda lakes represent naturally occurring highly alkaline environments where the alkalinity with high pH values range between 10 and 12. Salinity is the most important environmental factor that creates the structure and composition of marine microbial diversity on a large scale [46]. Therefore, the microbial communities in soda lakes are tolerant to high salt concentrations and have a key role in those ecosystems' biogeochemical cycles (e.g., nitrogen carbon and sulfur cycles). Table 19.1 represents the major lakes in the African continent regarding their pHs and salinity%.

Soda lakes are the most throughput aquatic environment, especially in African high temperature and tropical areas with high-incident solar

Table 19.1 Salinity and pH levels in studied major African lakes.

Name of lake	Salinity%	pH	Country
Lakes of Wadi El-Natrun	28.3–54.0	9.5–12	Egypt
Arenguadi lake	0.25	9–10	Ethiopia
Shala lake	1.8	9.9	
Chitu lake	5.8	10.5	
Abijatta lake	3.4	9.8	
Magadi lake	>10	10.5	Kenya
Bogoria lake	35	10.9	
Turkana lake	0.25	8.5–9.5	
Logipi lake	2–5	9.8–10.8	
Natron lake	>10	9.5–10.5	Tanzania
Eyasi lake	0.5	9.5	
Kivu lake	0.25	8.5	Congo
Rombou lake	2	10.5	Chad
Himalatt lakes	12	7.5–8.0	Algeria
Sidi Ameur lakes	20	7.5–8.0	

radiations. Cyanobacteria are associated in this environment with prodigious rates of photosynthetic primary production, where the most common genera are *Arthrospira*, *Cyanospira*, *Geitlerinema*, *Leptolyngbya* or *Anabaenopsis* or generally named anoxygenic phototrophic bacteria. Hot springs are disbanded in the world. These results govern the geothermally heated groundwater, with extreme temperatures beginning from 45°C and above [47]. Temperature is considered one of the most important factors affecting the evolution and the activity of microorganisms.

19.7 Culture-independent and dependent methods for microbial diversity in the African lakes

Several microorganisms have been isolated from the East African Rift Valley soda lakes using both culture-independent and dependent approaches. The culture-dependent method includes the isolation of microorganisms from the collected samples (water sediments) using media for cultivation. These methods are very important in understanding and studying the physiological characterization of isolated microorganisms.

However, culture-based methods do not give complete data on the microbial communities' composition of the studied lakes, so an additional method is required (culture-independent methods). Culture-independent approaches depend on the analysis of the DNA of the microbial

community to indicate the microbial diversity of a certain sample from the collection sites. Novel organisms with their new properties could be verified using culture-dependent studies, whereas the culture-independent methods give a more extensive assessment of microbial communities [48].

Many culture-independent results have described hot spring microbial communities, such as those present in Tengchong, Iceland, and China. Earlier culture-independent studies on Kenyan soda lakes analyzed microorganisms of the libraries of -amplified (rDNA) clones. However, this method is not suitable within the specific microbial community regarding low coverage and speed of sequencing and cloning-dependent methods. These methods gave a low number of sequences compared to the high number of sequences reaching millions produced by high-product sequencing methods such as Illumina Sequencing and 454 pyrosequencing [49].

In the twenty-first era, Margulies and his coworkers [50] have emerged with an alternative efficient method to the conventional sequencing method which is used in both the whole sequence of genome and metagenomics which has given high-product sequencing considered an easy tool for discovering many novel microorganisms and new applications.

19.8 Case studies on microbial diversity and ecology in some African lakes

19.8.1 Kenyan soda lakes

The Rift Valley of East Africa is considered the most substantial, active zone on the earth. It is the most studied area containing a large number of soda lakes. The Kenyan soda lakes' salinity formed ranged from 10% to 30% total salts (w/v) and pH values ranged from 9.5 to 12. The Kenyan soda lakes include Elmenteita, Olbolosat, Magadi, and Bogoria. Microbial diversity inhabits these soda lakes. Tallar and Suen [51] studied these soda lakes as the main source of alkalithermophilic microorganisms.

The Kenyan soda lakes are still a fragile environment due to low water evaporation levels and pollution which resulted from different human activities in the areas of catchment, industrial, agricultural wastes, and domestic effluent. This led to changes in the microbial diversity of these lakes as a result of human activities, which may reduce specific microbial species. The Kenyan soda lakes are characterized by a high productivity rate of extremophiles due to the temperatures, high light intensities, high phosphates availability, and unlimited supplies of CO_2 [51].

The first microbial study of the environments of the soda lakes that described the taxonomic presence of the isolates was done by Duckworth et al. [52], who isolated many types of aerobic, haloalkaliphilic, and alkaliphilic organography strains from the East African Rift Valley soda lakes. Although, culture-independent research done on the Kenyan soda lakes depended on the PCR-amplified rDNA analysis methods. This may not give a clear image of the microbial diversity due to the low speed and coverage of sequencing and cloning-dependent method [53].

Two soda lakes in Kenya: Elmenteita and Bogoria are also marked by hot springs which represent a good host for both haloalkalithermophilic and hyperthermophilic microorganism growth. However, salinity is also considered a key factor in these alkaline lakes. In contrast, to dilute lakes, which have high salinity approaching saturation, the microbial community composition of hypersaline and alkaline lakes, such the Magadi Lake, differs significantly. Many organotrophs and aerobic strains have been found and isolated from the soda lakes of the rift Valley on different media. About 100 strains have been examined chemotaxonomically and phenotypically for the numerical taxonomy study [53].

Many studies of microbial communities have been carried out on different Kenyan natural environments. Bacteria and archaea are the most unique taxon groups of microbial communities that are important in studying lake ecosystem functioning [54]. The microorganisms in Kenyan lakes play a very important role in the decomposition of the organic material into simple nutrients taken by other organisms as food and controlling the lake water quality [53]. They are also significant in balancing the processes of photosynthesis and respiration in the natural carbon, sulfur, oxygen, and other metals cycles [54]. However, many abiotic and biotic factors influence the abundance, diversity, composition, distribution, and processes of microbial communities in these marine ecosystems. The microbial diversity has been promoted by many environmental factors. The tropical lakes exhibit hydrogeology variation as a result of climatic change. These lakes were flooded with freshwater to slightly salinity caused by water evaporation and anthropogenic actions [55].

19.8.1.1 Bogoria lake

The Bogoria Lake is well known for its hot springs. The microorganisms which were isolated from Lake Bogoria have a great biotechnological application due to their ability to tolerate and grow in harsh conditions such as high temperature and high pH. Many alkaliphile microorganisms

have been isolated and identified from this lake including anaerobic alkalithermophiles: *Anaerobranca gottschalkii* and *Thermosyntropha lipolytica*, and some other unidentified ones. Lake Bogoria, similar to Lakes Elementaita, Nakurn, Magadi, and Lake Logipi, is a Ramsar place and has been protected. Lake Bogoria also contains high geysers concentration in Africa; about 19 are identified.

The lake water is saline and alkaline reaching 150 g/L of TDS. The salinity of the water is due to the evaporation process since it is high in this region. Although this hypersaline lake is high in salt concentrations, it is also highly Cyanobacteria-productive (*Arthrospira fusiformis*). Cyanobacteria are considered the main food of pelicans and flamingoes, which also mainly inhabit this hypersaline lake. Lake Bogoria is one of the largest homes for the inhabiting flamingo population, which are the main attraction for tourists and contribute significantly to the economy of Kenya [56].

19.8.1.2 Elmenteita lake

Culture-independent study results on Lake Elmenteita indicated that the microbial diversity was lower than the other studied lakes like the Wadi al Natrun Lake in Egypt. Like other ecosystems, Lake Elmenteita has been influenced by climatic changes and long drought periods which led to water level fluctuation. Lake Elmenteita is considered an important reservoir for flamingos during drought periods [57].

The Magadi Lake is one of the most stable and alkaline lakes among the soda lakes of the East African Rift Valley, with pH ranging from 10.5 to 12. Extreme ecosystems are inhabited by extremophilic microorganisms that are adapted to grow in extreme conditions. High salt concentration can reach 30% saturation in the Magadi Lake. In the Magadi Lake, salts are supplied mostly by a large number of alkaline hot springs with temperatures up to 80°C. Using traditional cultivation methods, microorganisms were isolated and identified from Magadi Lake and indicated low microbial diversity levels in these extreme environments. The previous studies using both culture-independent and culture-dependent methods on this lake have illustrated different groups of aerobic, halophilic, alkaliphilic, organotrophic, alkali-tolerant, and haloalkaliphilic microorganisms which represent the major bacterial and archaeal phyla [58].

19.8.1.3 Olbolosat lake

The Olbolosat Lake is one of the rare freshwater lakes present in Africa. It is lake of drainage. It is one of the Kenyan lakes found in the outer rift

valley. The water evaporation in this lake leads to a high loss of water but the lake water is rapidly raised as a result of rainfall. The Olbolosa Lake is a highly rich ecosystem with availability of conditions and resources required for microbial growth [59]. Studies on the lake microbial communities are very important in understanding the diversity and composition of microfiches', microorganisms patterns, the microbial diversity functional role, and microbial diversity regulation [60].

Microbial communities of the Olbolosat Lake water and sediments have a key role in the soda lakes. However, due to culture-dependent method's complexity, only a small number of microorganisms have been studied [61]. PCR amplification and sequencing of conserved genes is a fast technique to study lake microbial taxonomic distribution. Also, the microbial distribution can be related to the metadata obtained from the investigation of sampling. High-throughput sequencing method is used extensively to study the prokaryotic communities' composition and diversity. Bacterial and archaeal phylogenetic analysis is frequently performed using the method of Illumina sequencing. Callahan et al. [62] indicated that the Amplicon Sequence Variants method detected the microbial sequences in the collected sample before the sequencing and amplification errors introduction and distinguishing between sequence variants. This is the first record of microbial composition using a culture-independent method within Lakes Oloiden and Olbolosat.

19.8.2 Congo soda lake

19.8.2.1 Kivu lake

Kivu Lake is located in the volcanic area between the Democratic and Rwanda of the Congo and has a stable vertical layer that separates the mixed and complex layer with 65 m depth from the constant anoxic area which is rich in dissolved CO_2, salts, and methane (CH_4). The Kivu Lake has received attention as a specific and unique habitat that contains the largest world CH_4 reservoirs. However, the oxic zone CH_4 concentrations are low compared to the other worldwide soda lakes. This might be due to strong microbial oxidation resulting in CH_4 diffusing within the lake from the deep to the surface. Furthermore, Lake Kivu has high vertical water stability and physicochemical changes. The vertical position variation of both the anoxic – oxic interface is driven by different wind speeds between dry (June – September) and rainy (October – May) seasons [63].

This lake received several groundwater sources at various depths, which explains the vertical profiles of temperature, salinity, and dissolved gas concentrations' strong gradients. Hence, these different conditions might influence the vertical microbial abundance and distributions, with very little information obtainable on the composition, diversity, and distribution of the archaeal and bacterial communities found in the lake water [64].

Moreover, these studies mainly focus on the most abundant microbial communities' members due to the limitations of their molecular tools. Now the lake microbial diversity is consisting of two fractions of species: abundant one [65,66] and rare one [66]. A set of analyses was used to explain the patterns of rare and abundant taxonomic units (OTUs) and to study the microbial processes' potential functional roles in controlling the lake biogeochemical cycles such as carbon and sulfur cycles in the Kivu Lake.

19.8.3 Algerian lakes

Bou Saâda is located in the north of Algeria at 280 km south of the Algerian coast between the Saharan Atlas Mountains and el-Hodna Depression. This oasis is closest to hypersaline lakes including Himalatt and Sidi Ameur Salt Lakes. These two alkaline and hypersaline lakes, which are separated by a distance equal to 80 km, have received great interest not only in studying the microbial diversity and distribution of extreme habitats but also in studying human activity's impact on the water of these extreme environments. High microbial diversity levels, especially among the Himalatt Salt Lake bacteria and the Sidi Ameur Lake archaea, were isolated from these extreme ecosystems. All representatives identified extreme halophilic bacterial taxa as well as more than five genera of extreme halophilic archaea were isolated and identified. Moreover, many new types of bacteria and archaea were found and isolated. Haloarchaea remain the dominant halophilic microorganisms that live in extreme hypersaline habitats and are uniquely adapted for survival in high salt life [67].

Hypersalinity and human pollution are the major factors affecting the biodiversity of microorganisms in these Algerian hypersaline lakes and this may support the novel species and genera identification. Many studies depend on culture-independent methodology and physicochemical analyses to survey the diversity of halophilic microorganisms and further understand these two salt lakes in the Algerian Sahara [68].

19.8.4 Egyptian soda lakes

19.8.4.1 Siwa and Sebkha

Brines are one of the most interesting habitats that support and understand the diversity of the microbial community in extreme environments and studying their adaptation under different chemical and physical conditions [69]. The origin of the hypersaline habitats may be either marine origin (thalassohaline) or inland aquatic saline environments (athalassohaline). The Siwa Oasis at the depression Egyptian Western between latitudes 29° 50′N and 29°250′N and longitudes 25°50′E and 265°60′E is with a region of about 1200 km^2. The deepest parts of the Siwa Oasis are occupied by salty lakes which are surrounded by salt marshes. The Siwa Oasis Lakes are the areas which naturally discharge water from abundant springs and cultivated places. An athalassohaline Aghormy Lake is located 18 m below the level of the sea and is flooded by springs.

This lake is characterized by the concentration of TDS reaching 230.00 g/L and pH up to 8 compared with the other lakes in Egypt. The Aghormy Lake's chemical composition is characterized by the presence of many metals as Na + (55 g/L), Mg^{2+} (52 g/L), K^+ (11.4 g/L), and Ca^{2+} (10 g/L) cations, in addition to the SO_4^{2-} (10.7 g/L) and Cl^- (246.8 g/L) anions [69]. The sediments of this lake are extensively enriched with various heavy metals, for example Cd, Cu, Co, Se, Mn, Pb, and Zn. Seasonal microbial mats along the margins of the lake have been documented in both spring and early summer [70].

The hypersaline lagoon represents nearly 600 km^2 and is joined to the Mediterranean Sea by two inlets, one artificial and the other natural. The pH values of the lagoon water fluctuate between narrow ranges of 7.94 to 8.79 on the alkaline side [71]. The salinity of the lagoon increases from 50 g/L in the north to 80 g/L in the south [70]. The salinity increase in the south direction is due to the high-water evaporation rate which reaches 2190 mm/year [70]. This water evaporation leads to the formation of halite minerals and gypsum. Hence, the salts that cover the eastern and southern parts of the hypersaline lagoon are commonly illustrated as "Sabkhas." Sebeaka Sabkha is considered an example of a thalassohaline environment. Sebeaka Sabkhas is distinguished by different salt precipitation. These different types of salts start from $CaCO_3$, followed by the accumulation of gypsum on the bottom of the pond [70].

Finally, the precipitation of NaCl reaches above 300 g/L, resulting in different metals concentrated in the water such as K, Cl, Mg, and sulfate ions, with pH values ranging from 8.5 to 9.5. The halophilic microorganisms represent different groups of archaea and bacteria, their abundance, distributions, and

metabolic activities refer to the final salt concentration. The variety in the halophiles' salinity tolerance affects their diversities in these brines and allows them to be candidates for many biotechnological potentials [72].

The PCR amplification technique has been considered an essential approach for studying the diversity of halophiles, by introducing novel uncultured prokaryotic and diverse taxonomical species. The high-throughput molecular method has been used to estimate the taxonomic presence and the diversity of the communities of the extreme halophilic microorganisms. The analysis of V1−V3 has shown the prevalence of Proteobacteria, Planctomycetes, Bacteroidetes, Cyanobacteria, and Actinobacteria in South Africa [73]. Very little data about the biodiversity of hypersaline habitats in Egypt lead to difficulty in studying the structure, ecological role, and dynamics of the microbial ecosystem in these ecosystems.

19.8.4.2 Wadi El-Natroun lakes

The Wadi El-Natrun is a depression located in the Sahara Desert in Egypt, about 80 km northwest of Cairo. The valley bottom is 23 m below the level of the sea and 38 m below the branch of the Rosetta of the Nile River. The valley contains seven hypersaline and alkaline lakes. The water of these lakes is supplied by underground water from the Nile River and rainfall. High evaporation rates and the changes in climate during the summer season lead to the salinity rising above 30% (w/v).

The lakes of Wadi El- Natrun are extreme in more than one aspect: the concentrations of TDS ranges between 90.0 and 390.0 g/L and have been shown in all Wadi El-Natrun lakes. Also, all lakes have pH values of up to 11. The lakes in the valley are eutrophic environments due to the presence of high organic and inorganic nutrients, the estimated phosphate reaches 116 mM, dissolved organic carbon concentration ranges between 136 and 1,552 mg/L, ammonia concentration ranges between 2 and 461 mM, and nitrate concentration between 53 and 237 Mm. The lakes of Wadi El-Natrun are inhabited by large haloalkaliphilic microorganisms communities. The colors of the lake water become purple, red, and green due to the presence of a large amount of extreme haloalkaliphilic archaea, Cyanobacteria, and photosynthetic red bacteria. Mats of haloalkaliphilic microorganisms grow along the floors and the margins of the lake. They consist of thin layers of red photosynthetic bacteria and red extreme haloalkaliphilic archaea, and subsequently, thick layers of black sulfide minerals and decayed organic matter [74].

Abd-el-Malek and Rizk [74] reported the important role of sulfate-reducing bacteria in the alkalinity increase of the lake and also showed

that the ($Na_2CO_3H_2O$) deposition in the lakes is due to the sulfate-reducing bacteria activity. However, they cannot notice sulfate-reducing bacteria in most hypersaline lakes' bottom. Sulfide oxidation is also done by large photosynthetic sulfur bacteria communities such as chemoautotrophic sulfur-oxidizing bacteria, *Ectothiorhodospira* spp, and *Halorhodospira*.

The Wadi El-Natrun lakes contain a large number of new microbial strains, bacteria, as well as archaea. These halophilic microorganisms participate in anaerobic and aerobic carbon, sulfur, and nitrogen cycles in the ecosystem. Both cultured- and molecular-based approaches have been used to study the diversity of the microbial communities in hypersaline lakes. Microbial diversity understanding in hypersaline lakes is still incomplete in comparison with the understanding of microbial diversity of fresh and marine water habitats. In addition, the studies related to the sediments of the hypersaline lake are very low. Numerous recent pieces of research have been concerned with studying the column of water lakes. The previous culture-dependent studies on the three largest lakes in Wadi El-Natrun were done by the phylogenetic composition analysis of the communities of microorganisms in both sediments and water of these lakes and compared to similar environments [75].

19.9 Modeling on microbial diversity in some African lakes

Modeling on bacteria, archaeal, and fungal diversity was carried out to realize the environmental niche considering the range of tolerance of these taxa in 11 African lakes: Bogoria, Elmenteita, Magadi, Little Magadi, Olbolosat, Oloiden, Kivu, Himalatt, Sidi Ameur, ElHamra, and Aghormi.

Bacterial and archaeal diversity at the phylum level was analyzed using modeling design through assigned taxonomy within 11 African lakes, where different diversities in the phylum levels were detected in the Kenyan lakes. However, only Cyanobacteria and Actinobacteria were the most dominant phyla in the Kivu Lake, Congo. Moreover, Cyanobacteria, Firmucites, Planctomyces, and Bacteroitedes in the bacterial domain and Euryaycheato in the Archaeal domain were the most abundant and dominant phyla represented by the Algerian and Egyptian lakes (Fig. 19.2).

Depending on the family level, we noted the dissimilarity of bacterial and archaeal diversity in the Kenyan lakes, while Salinibacteriacae, Bacilliaceae, Pseudomonadaceae (as bacteria), and Halobacteriaceae and Methanocaldococcaceae (as archaea) were considered the most abundant families in both the Algerian and Egyptian lakes (Fig. 19.3).

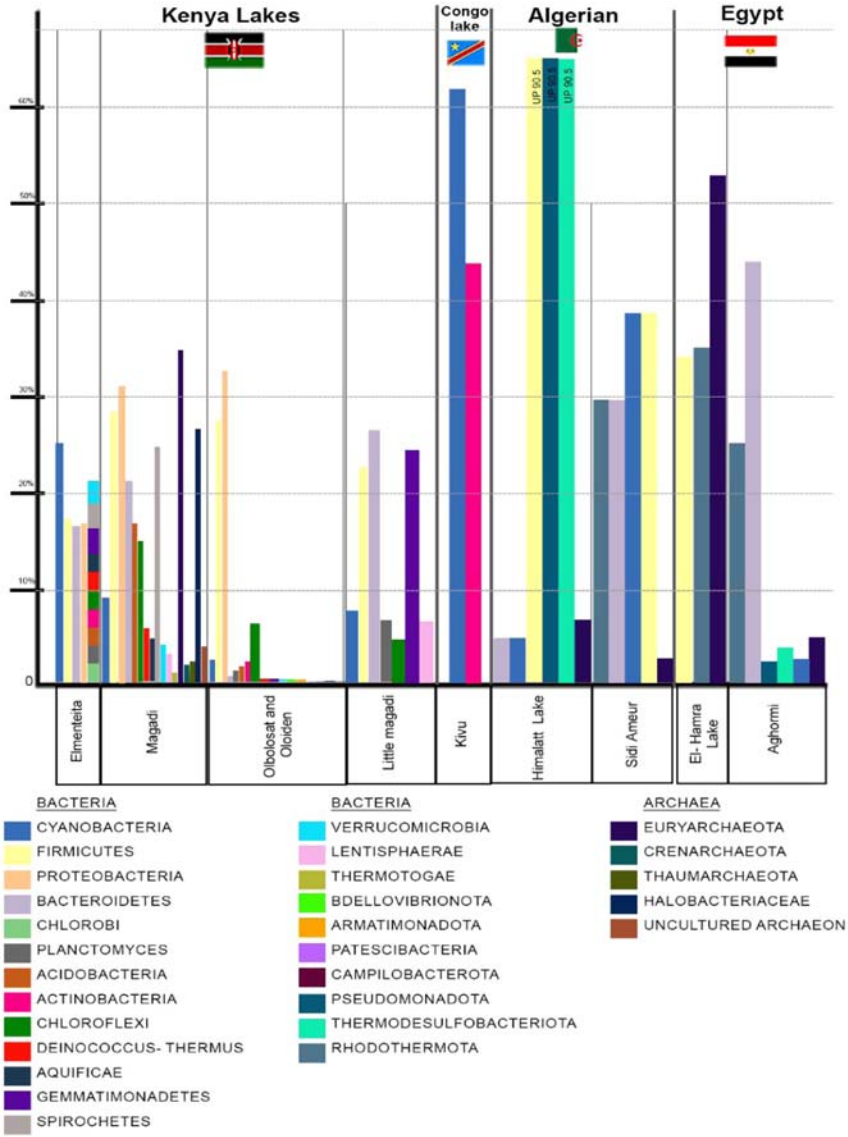

Figure 19.2 Modeling of bacterial and archaeal communities at the phylum level in some African lakes: Bogoria, Elmenteita, Magadi, Little Magadi, Olbolosat, Oloiden, Kivu, Himalatt, Sidi Ameur, ElHamra, and Aghormi.

Fungi grow well in acidic to neutral conditions, however, many halophilic and alkaliphilic fungal strains have been isolated from the soda lakes such as the Magadi Lake in Kenya, considering pH ranging from 11 to 12.

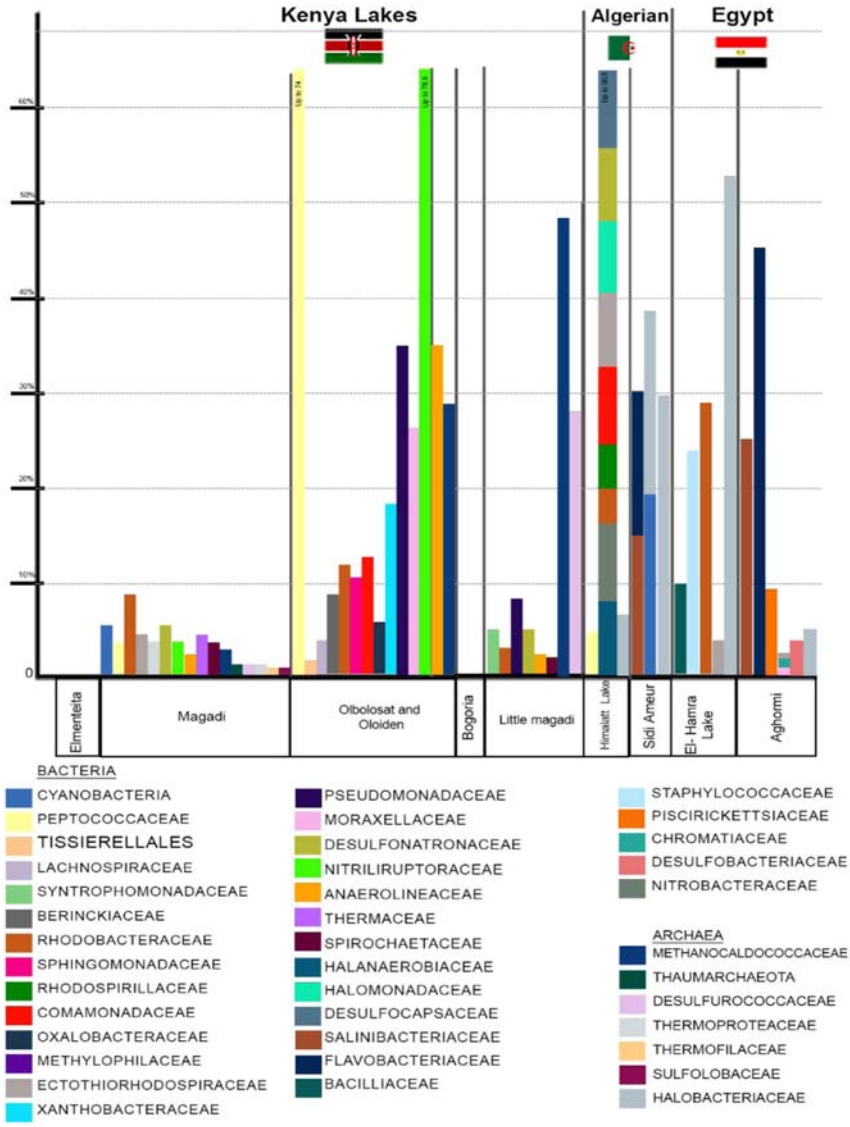

Figure 19.3 Modeling of bacterial and archaeal communities at the family level in some African lakes: Bogoria, Elmenteita, Magadi, Little Magadi, Olbolosat, Oloiden, Kivu, Himalatt, Sidi Ameur, ElHamra, and Aghormi.

Therefore, modeling fungal diversities in the Kenyan lakes was designed. Based on phylum level, Ascomycota followed by Basidiomycota showed the major phyla distributed across the three lakes (Bogoria, Elmenteita,

Magadi) while on the strains level, data showed a great difference for fungal diversity (Phoma, Sclerotina, Cladosporium, Cheatomium, Fusaruim, and Monodictys) (Fig. 19.4).

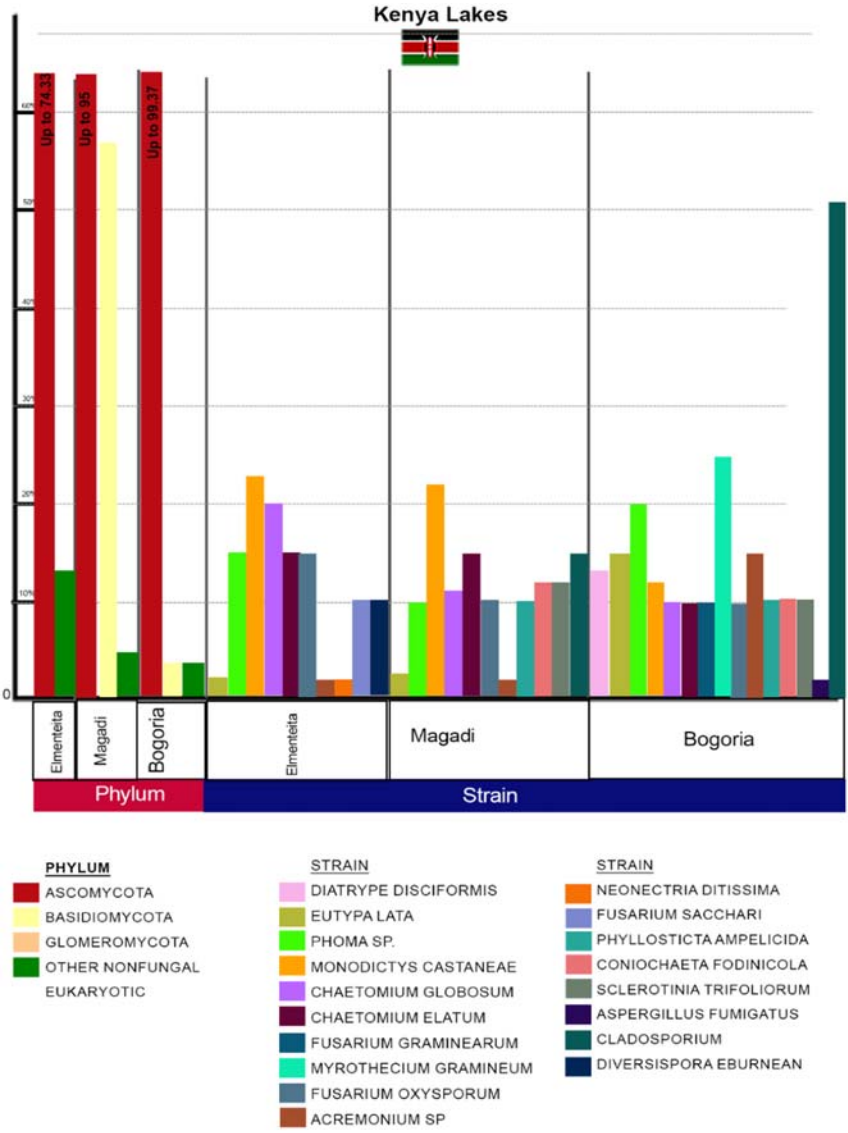

Figure 19.4 Modeling of fungal communities at the phyla and strains level in Kenyan lakes: Bogoria, Elmenteita, and Magadi.

19.10 The perspective future on the microbial role in African lakes

In lake ecosystems, prokaryotic and eukaryotic microbes are major in the transformation of complex organic compounds into simple nutrients that are taken by other organisms as food resulting in controlling the quality of water in lakes [76]. In extreme soda lake conditions, these microorganisms also have a crucial role in restoring and then remineralizing these nutrients which affect the circulation of the material during the biogeochemical process. In addition, under the harsh conditions of pH, salinity, and temperature, more than 50 phyla of bacteria, archaea, and fungi are responsible for the decomposition of dissolved organic matter and production of useful and active byproducts in the lake water.

Evaluation of dominant microbial groups of alkaliphilic and halophilic nature in these lakes is very important because these microbes dissimilate the organic matter dissolution and contribute to other processes such as cycling of the matter and energy production in the environment. The study of microbial community composition in these lakes is also essential to recognize the active microbial cells in the environment [77].

From our perspective, microbes inhabiting these lakes may play the role of our tiny natural scavengers which are widely distributed in such environments for their ability to manage anthropogenic activities, and ecological balance maintenance. As these microorganisms are well tolerated and adapted and expanded in most lakes, it easy to use as water quality indicator [78].

Microorganisms in these lake ecosystems are also of great interest in their extracted useful chemicals byproducts in this alkaliphilic and high salinity environment which is considered a wealthy source of new types of hydrolytic enzymes: lipases, proteases, amylases, phospholipase, catalases, and other industrial useful enzymes. These microbial enzymes have wide biological applications in medicinal formulations, detergents, food industries, and the treatment of wastewater [79].

Also, it is very important to apprehend genetic resources of microbial distribution, their diversity, functional interpretation, and external factors affecting their diversity in this aquatic environment. Thus, learning about these microbial communities within lakes is major regarding the following:

1. To gain knowledge about the resources of microbial genes in the lake ecosystem.

2. To study the patterns of microbial distribution in the lakes.
3. To study microbial diversity and its functional roles in the lakes.
4. To study the regulation of microbial biodiversity in the lakes.
5. Last, but not least, to study the modeling of microbial diversity.

19.11 Conclusions

Lake water bodies with unique innate environmental conditions and different habitats result in their distinctive bacterial, archaeal, and fungal communities and composition. Nowadays, the use of a culture-independent approach has a better understanding of the microbial communities in the lakes that vanishes the thought of microorganisms inhabiting terrestrial areas similar to these aquatic habitats. Lakes with extreme conditions like high pH, salinity, and temperature are attaining great importance to comprehend microbial evolution and determine the ecological and technological impact of specific niches and climatic change on microbial diversity and distribution as they share the lake biogeochemical cycles and decompose organic materials into simple nutrients which control the water quality in these environments.

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LAKES OF AFRICA

Microbial Diversity and Sustainability

Edited by
Mostafa El-Sheekh and Hosam Easa Elsaied

Lakes of Africa: Microbial Diversity and Sustainability consists of 19 chapters, forming four sections, which cover almost all fields of studying and benefit from microbial ecosystems inhabiting African lakes. The first section includes background chapters, describing the history and formation of African lakes. The second section includes chapters that describe how environmental stresses, including seasonal variations, climate changes, and anthropogenic activities, affect microbial ecosystem dynamics in African lakes and the microbial responses to these stresses. The third section includes chapters that deal with exploring and evaluating of extremophiles in the desert and harsh African lakes, and how to benefit from these microbes in the term of industrial biotechnology. Finally, the fourth section concludes by highlighting the challenges facing by the microbial ecology in African lakes and the designing of models for solving these problems, along with the prediction of the future of lake microbial ecosystem succession and sustainability.

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