

Preliminary Assessments of Composition and Diversity of Bacterioplankton in Two Tropical Man-Made Lakes, Southwestern Nigeria

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Abstract

*Lakes Eleyele and Asejire are tropical man-made lakes (reservoirs) in southwestern Nigeria created for domestic water supply and fisheries. The abiotic and biotic features of the two lakes have been studied by various researchers. However, there is little or no study on the bacteria community despite being of ecological and public health concern. In this article, the bacterioplankton composition and diversity of Eleyele and Asejire Lakes were investigated by sequencing 16S rRNA gene clones. Our results showed that proteobacteria was the dominant phylum in Eleyele Lake, while actinobacteria phylum dominated in Asejire Lake. In both lakes, bacteria that contribute to prokaryotic primary production (*Limnohabitans*, *Methylobacterium*, and *Methylotenera*) and biogeochemically significant bacteria were encountered. *Polynucleobacter* was the predominant genus in Lake Eleyele and this could be related to the physicochemical parameters. Large number of bacterioplankton in the Eleyele and Asejire Lakes could not be classified into known taxonomic unit indicating largely unknown bacterial composition.*

Keywords: Bacteria composition; Clone library; 16S rRNA; Asejire and Eleyele Lakes; Freshwater lake.

1. Introduction

Bacterioplankton are an extremely diverse and highly dynamic group whose activities directly influence the water conditions in their immediate environment as well as having profound effects on biospheric biogeochemical cycling [1]. The bacterioplankton community composition (BCC) of aquatic environment contributes substantially to the biogeochemical cycle and this may have important implications for the functioning of aquatic environments and the ecosystem services they provide [2]. Reservoirs (like natural and man-made lakes) act as important sinks for organic material that are from their natural catchment and from human activities, and the resident microbiota consume major proportions of such inflows [3], [4], [5], making them essential factors directly affecting stored water quality. Also, some bacteria in recreational freshwaters, such as *Escherichia coli* O157:H7, *Legionella*, *Pseudomonas*, and *Shigella* have

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caused public health concerns due to their associations with waterborne illnesses [6]. Despite these ecological and public health concerns, only in the last two decades have studies begun to give some insight into the freshwater bacterioplankton, by using culture dependent and independent methods and this include research by [7]- [15].

Eleyele and Asejire Lakes are man-made reservoirs constructed by the Nigerian government for water supply and fisheries in the southwestern region of Nigeria. Eleyele Lake lies north to northwest of Ibadan town, Nigeria (7° 26'1"N, 3°52'1"E) at an altitude 125 m above sea level with an average depth of 6.0 m. The lake has a length of 240 m, catchments area of 323.7 km² and an impoundment area of 156.2 ha with a storage capacity of 29.5 million liters of water. Eleyele Lake receives wastewater from non-point sources in the surrounding watersheds including residential areas, small food industries, mechanic workshops, cement/ block making factories and farmland. Asejire Lake is in Egbeda Local Government Area, Ibadan (07° 21'N, 04° 07'E) at an altitude of 137m above sea level. Lake Asejire could be influenced by run-off from cropland and forestland, also wastewater from bottling company and fish farm. The climate of the study areas is tropical and seasonal. The dry season occurs from November to April and rainy season from May to October.

A variety of investigations have been carried out on the abiotic and biotic features of Eleyele and Asejire Lakes including [16]-[21]. However, there is a dearth of information on the profiles of bacteria in both lakes; hence this study on the composition and diversity of bacterioplankton in Eleyele and Asejire Lakes using 16S rRNA clone library.

2. Materials and Methods

2.1 Water sampling

Surface water samples (0 – 0.5 m) were collected in triplicate from each lake (Asejire and Eleyele) in dry season using sterilized 1L polycarbonate bottles. The samples of water were kept on ice and transported to the laboratory. All water samples were processed within 4hours of collection. Water samples (200 ml) were passed through 5 µm pore size filters to remove larger plankton and particles. The filtrates were then passed through 0.22 µm pore size polycarbonate membrane filters (Millipore) to concentrate the bacterioplankton biomass [13]. Filters were stored at -80°C until further analyzed. Temperature of the surface water was determined using a mercury-in-glass thermometer. Unfiltered water samples were used to measure conductivity, total dissolved solids (TDS), phosphate, nitrate, P^H, and dissolved oxygen (DO) according to [22].

2.2 DNA extraction and purification, PCR amplification, cloning and sequencing

The total genomic DNA was purified using a soil DNA extraction kit (Q Biogene). It involved a bead beating step and filter that contained the concentrated bacteria cut into small pieces to represent the 'soil' [11]. Total extracted genomic DNA was quantified using spectrophotometry and the quality of the DNA was revealed through Agarose gel electrophoresis on 1% gels followed by ethidium bromide staining and visualization by UV transillumination [11]. PCR amplification of the gene 16S rRNA of the obtained total genomic DNA was carried out using universal primer pair FD1(5'-AGAGTTTGATCCTGGCTCAG-3'), and RP2(5'ACGGCTACCTTGTTACGACTT-3') [23]. Gel electrophoresis was used to determine the amplification products and molecular cloning of environmental 16S rRNA genes via TOPO cloning (Invitrogen) was done. After the amplification product was cloned into the plasmid vector, the 16S rRNA gene insert

was reamplified with primers M13 Forward (-20) (5' GTA AAA CGA CGG CCA GTG) and M13 Reverse (-27) (5' GGA AAC AGC TAT GAC CAT G) targeting the M13 cloning site. The amplified insert was verified visually by agarose gel electrophoresis (1% gels) and purified using the Qiagen MinElute purification kit following the manufacturer's instruction (Qiagen). Purified PCR amplicon (typically 5 to 125 ng μl^{-1}) was eluted in 10 l EB buffer (10 mM Tris-Cl, pH 8.5) [11]. Automated sequencing of clones with correct - sized insert was accomplished at the sequencing facility MCLAB Molecular Cloning Laboratories located in San Francisco, CA. Identification of each clone was by identifying its nearest neighbour using the sequence match and classifier tools at the Ribosomal Database Project (RDP) (<http://rdp.cme.msu.edu/>). The following cutoff values were used for taxonomic assignment: species ($X \geq 97\%$), genus ($94 > X \geq 97\%$), family ($94\% > X \geq 90\%$), order ($90\% X \geq 85\%$), class ($85\% X \geq 80\%$), and phylum ($80\% X \geq 75\%$) [24], [25].

2.3 Statistical Analysis

Shannon-Wiener diversity index (H') [26], Pielou Evenness (E) [27] and Simpson index of diversity(D) [28] were used to analyze the community structure of the microbes. Community similarities were determined by Sorenson's coefficient [29].

3. Results

3.1 Physicochemical parameters of Lake Eleyele and Lake Asejire

The physico-chemical parameters of the Eleyele and Asejire reservoirs are shown on Table 1. The pH of the two reservoirs ranged between 7.5 – 8.34, thus were alkaline. The pH of Lake Asejire (8.34 ± 0.61) exceeded the National Environmental Standards and Regulations Enforcement Agency (NESREA) limit. The nutrient concentrations (nitrate, 15.17 mg/L; PO_4 , 1.74 mg/L) of Eleyele Lake were higher than Asejire Lake (nitrate, 4.61 mg/L; 0.41 mg/L). The nitrate level of Lake Eleyele exceeded the NESREA limit. The dissolved oxygen concentration of Lake Asejire was 9.14 ± 3.41 mg/L and higher than Lake Eleyele (5.75 ± 2.56 mg/L).

Table 1: Physico-chemical Parameters (mean \pm sd) of Eleyele and Asejire Lakes, southwestern Nigeria.

Physico-chemical Parameters	Lake Eleyele	Lake Asejire	NESREA Limits
Temperature ($^{\circ}\text{C}$)	26.45 ± 1.32	27 ± 0.94	35.00
pH	7.47 ± 0.20	8.34 ± 0.61	6.50 – 7.50
Dissolved Oxygen(mg/L)	5.75 ± 2.56	9.14 ± 3.41	7.50
Conductivity($\mu\text{s}/\text{cm}$)	190.03 ± 59.2	102.4 ± 20.63	N/A
Total Dissolved Solids(mg/L)	100.95 ± 31.4	54.6 ± 10.7	N/A
Nitrate(mg/L)	15.17 ± 1.97	4.61 ± 0.32	10.00
Phosphate(mg/L)	1.74 ± 0.35	0.41 ± 0.07	<05.00

3.2 Bacterial community composition of Lake Eleyele

Ninety – two 16S rRNA gene clones were obtained from the library of bacteria from Lake Eleyele. Of these clones, 60 representatives (approximately 65%) of each set of distinct same-length band were chosen as Operational Taxonomic Units (OTUs) and were sequenced.

Sequenced clones were identified and belonged to Proteobacteria, Actinobacteria and Bacteroidetes divisions and the Alpha- and Betaproteobacteria, Actinobacteriae, Sphingobacteria and Flavobacteria subdivisions. The contribution of these bacterial groups and subgroups to the sequenced OTUs is shown on Figs. 1 and 2. The bacterial group that were most represented in the clone library were Proteobacteria (55%) and Actinobacteria (35%) Fig. 1. The Betaproteobacteria (48.3%), Actinobacteria (35%) and Alphaproteobacteria (6.7%) were the predominant classes in the Lake Eleyele sample Fig. 2. At the order level, bacteria in Lake Eleyele belonged predominantly to Burkholderiales (28.3%), Actinomycetales (20%), Acidimicrobiales (11.7%), Methylophilales (8.3%) and Rhodocyclales (5%) Table 2. The bacteria community of the Lake Eleyele comprised predominantly of the Burkholderiaceae (13.3%), Comamonadaceae (11.7%), Methylophilaceae (8.3%) and Acidimicrobiaceae (5%) families Table 3. At the genus level, the Betaproteobacteria OTUs were closely related to *Polynucleobacter* (11.7%), *Curvibacter* (1.7%), *Limnohabitans* (1.7%) and *Methylothera* (1.7%) Table 4. The Actinobacteriae and Sphingobacteria OTUs, were closely related to *Ilumatobacter* (1.7%), *Conexibacter* (1.7%) and *Terrimonas* (1.7%), respectively. A significant proportion (78.3%) of the clones had low similarity to known sequences on the database.

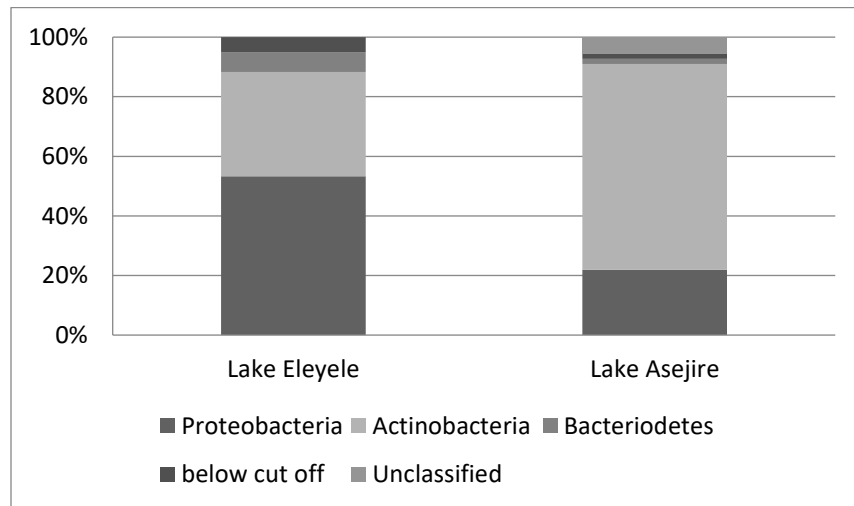


Fig. 1. Percentage (%) contribution of different bacterial Phyla to Lakes Eleyele and Asejire Clone Library.

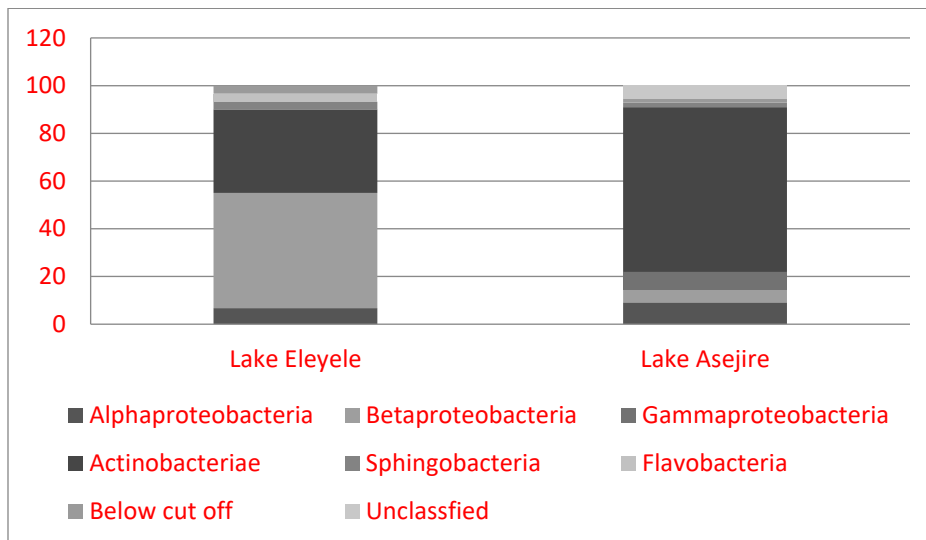


Fig. 2. Percentage (%) contribution of different bacterial classes to Lakes Eleyele and Asejire Clone Library.

Table 2: Taxonomic Composition of Bacterial (order level) From Eleyele and Asejire Lakes.

Taxonomy	Eleyele Lake Frequency (%)	Asejire Lake Frequency (%)
Actinobacteria_Actinobacteriae_Actinomycetales	12(20)	26(47.3)
Actinobacteria_Actinobacteriae_Acidimicrobiales	7(11.7)	12(21.8)
Actinobacteria_Actinobacteriae_Solirubrobacteriales	1(1.7)	0(0)
Bacteroidetes_Flavobacteria_Flavobacteriales	2(3.3)	0(0)
Bacteroidetes_Sphingobacteria_Sphingobacteriales	2(3.3)	1(1.82)
Proteobacteria_Alphaproteobacteria_Rhizobiales	1(1.7)	5(9.1)
Proteobacteria_Betaproteobacteria_Burkholderiales	17(28.3)	2(3.6)
Proteobacteria_Betaproteobacteria_Rhodocyclales	3(5)	0(0)
Proteobacteria_Betaproteobacteria_Methylophilales	5(8.3)	1(1.82)
Proteobacteria_Gammaproteobacteria_Legionellales	0(0)	1(1.82)
Proteobacteria_Gammaproteobacteria_Xanthomonadales	0(0)	1(1.82)
Below cut-off	10(16.7)	6(10.9)

Table 3: Relative Abundance of Bacterioplankton (Family Level) From Eleyele and Asejire Lakes.

Taxonomy	Lake Eleyele Frequency(%)	Lake Asejire Frequency (%)
Actinobacteria_Actinobacteriae_Actinomycetales_Microbacteriaceae	1(1.7)	2(3.6)
Actinobacteria_Actinobacteriae_Acidimicrobiales_Acidimicrobiaceae	3(5)	7(12.7)
Actinobacteria_Actinobacteriae_Solirubrobacteriales_Conexibacteriaceae	1(1.7)	0(0)
Bacteroidetes_Flavobacteria_Flavobacteriales_Cryomorphaceae	1(1.7)	0(0)
Bacteroidetes_Sphingobacteria_Sphingobacteriales_Chitinophagaceae	1(1.7)	1(1.82)
Bacteroidetes_Sphingobacteria_Sphingobacteriales_Cytophagaceae	1(1.7)	0(0)
Proteobacteria_Alphaproteobacteria_Rhizobiales_Methylobacteraceae	0(0)	1(1.82)
Proteobacteria_Betaproteobacteria_Burkholderiales_Burkholderiaceae	8(13.3)	1(1.82)
Proteobacteria_Betaproteobacteria_Burkholderiales_Comamonadaceae	7(11.7)	0(0)
Proteobacteria_Betaproteobacteria_Burkholderiales_Oxalobacteraceae	0(0)	1(1.82)
Proteobacteria_Betaproteobacteria_Methylophilales_Methylophilaceae	5(8.3)	1(1.82)
Proteobacteria_Betaproteobacteria_Rhodocyclales_Rhodocyclaceae	2(3.3)	0(0)
Proteobacteria_Gammaproteobacteria_Legionellales_Legionellaceae	0(0)	1(1.82)
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae	0(0)	1(1.82)
Below cut-off	30(50)	39(70.9)

Table 4: Relative Abundance of Bacterioplankton Taxa (Genus Level) Encountered in Lakes Eleyele and Asejire.

Taxonomy	Lake Eleyele Frequency(%)	Lake Asejire Frequency(%)
Actinobacteria_Actinobacteriae_Acidimicrobiales_Acidimicrobiaceae_Illumatobacter	1(1.7)	3(5.45)
Actinobacteria_Actinobacteriae_Solirubrobacteriales_Conexibacteriaceae_Conexibacter	1(1.7)	0(0)
Bacteroidetes_Sphingobacteria_Sphingobacteriales_Chitinophagaceae_Terrimonas	1(1.7)	1(1.82)
Proteobacteria_Alphaproteobacteria_Rhizobiales_Methylobacteraceae_Methylobacterium	0(0)	1(1.82)

Proteobacteria_ Betaproteobacteria_ Burkholderiales_ Burkholderiaceae _ <i>Polynucleobacter</i>	7(11.7)	1(1.82)
Proteobacteria_ Betaproteobacteria_ Burkholderiales_ Comamonadaceae _ <i>Limnohabitans</i>	1(1.7)	0(0)
Proteobacteria_ Betaproteobacteria_ Burkholderiales_ Comamonadaceae _ <i>Curvibacter</i>	1(1.7)	0(0)
Proteobacteria_ Betaproteobacteria_ Methylophilales_ Methylophilaceae _ <i>Methylostenobacter</i>	1(1.7)	0(0)
Proteobacteria_ Gammaproteobacteria_ Legionellales_ Legionellaceae _ <i>Legionella</i>	0(0)	1(1.82)
Below cut-off	47(78.3)	48(87.3)

3.3 Bacterial Community Composition of Lake Asejire

Eighty – one 16S rRNA gene clones were obtained from the library of bacteria from Lake Asejire. Of these clones, 55 representatives (approximately 68%) of each set of distinct same-length band were chosen as OTUs and were sequenced.

The identified sequenced clones belonged to Actinobacteria, Proteobacteria, and Bacteroidetes divisions and the Gamma-, Alpha- and Betaproteobacteria, Actinobacteriae and Sphingobacteria subdivisions Figs 1 & 2. Actinobacteria phylum (69.1%) was the dominant group followed by Proteobacteria (21.9%) Fig.1. At the class level, Actinobacteriae (69.1%), Alphaproteobacteria (9.1%), Gammaproteobacteria (7.3%) and Betaproteobacteria (5.5%) were the most frequently encountered. The bacterioplankton community composition of the lake at the order level was predominated by Actinomycetales (47.3%), Acidimicrobiales (21.8%) and Rhizobiales (9.1%). At the family level, Acidimicrobiaceae (12.7%) and Microbacteriaceae (3.6%) were more frequently encountered in Lake Asejire. The Actinobacteria OTUs were closely related to *Ilumatobacter* (5.45%) Table 4. The Alpha- and Betaproteobacteria OTU were closely related to *Methylobacterium* (1.82%) and *Polynucleobacter* (1.82%), respectively. A significant proportion (87.3%) of the clones had low similarity to known sequences on the database, while three were unclassified.

3.4 Diversity Index

The Simpson diversity index and Evenness obtained for bacterioplankton of the Asejire Lake was $D=3.79$ and $E= 0.93$, and were higher than Lake Eleyele ($D = 3.03$; $E = 0.80$). However, Shannon Weiner Index of Lake Eleyele was 1.55 and higher than Asejire Lake ($H' = 1.48$) Table 5. Sorenson's coefficient used for determining community similarities was 0.50 indicating quite a bit of species overlap/similarity between the two lakes.

Table 5: Diversity Indices of Bacterioplankton in Lakes Eleyele and Asejire.

Diversity Index	Lake Eleyele	Lake Asejire
Shannon (H')	1.55	1.48
Evenness (E)	0.80	0.93
Simpson (D)	3.03	3.79
Sorenson's coefficient	0.5	

4. Discussion

4.1 Physicochemical Parameters of Lake Eleyele and Lake Asejire

The nitrate level of Lake Eleyele that exceeded the acceptable limits could have resulted from wastewater of various anthropogenic activities in the catchment area that entered the lake. High nitrate levels in water have serious health implications and can result in several diseases. At concentration levels greater than 10 mg/L, there is an increased risk of babies developing infant methemoglobinemia, a disease commonly known as 'blue baby' syndrome [30]. The mean dissolved oxygen concentration of Eleyele Lake was 5.75 ± 2.56 mg/L and below the NESREA limit. Previous reports have shown that physicochemical factors have impact on bacterial composition in various habitats, in soil [31], [32] and freshwater [32].

4.2 Bacteria Community Composition of Lake Eleyele and Lake Asejire

Members of phyla Proteobacteria, Actinobacteria and Bacteroidetes were encountered in samples from both Lakes Eleyele and Asejire and this agreed with previous freshwater studies [33]-[37]. However, the proportion of each phylum was different in the two libraries, with Proteobacteria (55%) and Actinobacteria (69.1%) dominated in Lakes Eleyele and Asejire, respectively. This observed difference could have resulted from the differences in physicochemical parameters of the two lakes especially nitrate concentration in Lake Eleyele that exceeded the standard limit. According to [38], N nutrient (nitrate and ammonia) is an important environmental factors to alter the microbial community structure significantly by serving as essential nutrients for the growth of river microorganism, which corroborate the finding that trophic types have profound effects on microbial communities [39], [40]. The three and two subdivisions of Proteobacteria encountered in the Lake Asejire (α , β , and γ -proteobacteria) and in Lake Eleyele (α and β -proteobacteria) samples are commonly detected in marine and freshwater plankton [33], [11], [38]. The differences in the abundance of the Proteobacteria subdivisions between the two libraries have been reported in previous studies including 33; 36. Betaproteobacteria, the dominant class in the library of Eleyele Lake are abundant in most freshwater environments; [38] reported that 74.1% of sequenced bacteria clones in Dongjiang River were related to Betaproteobacteria. This result also agrees with other studies on reservoirs [41], [42] and lakes [43], [44], [11]. The wide distribution of Betaproteobacteria in freshwater habitats may be due to the adaptation capacity in most [42]. Betaproteobacteria are believed to share the ability to degrade complex organic macromolecules along with *Bacteroidetes* [45]. Various anthropogenic activities (small food industries, fish processing, mechanic workshop, cement industry, etc) that occurred in the catchment area of Lake Eleyele introduced waste water and organic matter into the water body which may have supported the growth of microbes belonging to Betaproteobacteria subdivision. In addition, some members of the Betaproteobacteria were reported to respond quickly to nutrient additions in freshwater mesocosm and isolation studies [46], [47], and [42] and act as autotrophic ammonia removal [48]. Four [Comamonadaceae (betI), Burkholderiaceae (betII), Methylophilaceae (betIV) and Oxalobacteraceae (betVII)] and three (Burkholderiaceae, Oxalobacteraceae and Methylophilaceae) of the Betaproteobacteria families in Eleyele and Asejire Lakes, respectively contain the "bet" lineages in the Freshwater Lake Bacteria database [49]. Comamonadaceae (betI), an abundant taxa encountered in the Lake Eleyele is a fast-growing and nutrient-loving bacterial group [38]. Rhodocyclaceae family was detected only in Lake Eleyele and had no lineages included in the freshwater bacterial database [49], [50].

Representatives of phylum Actinobacteria dominated the Asejire clones (69.1%) and agreed with previous findings e.g. [5] reported Actinobacteria are among the dominant members of nearly all freshwater data sets they examined, constituting sometimes nearly half of the total community. Other previous studies that reported Actinobacteria as a most abundant group of total bacteria in freshwater include [7] in Lake Gossenköllesee; [51] in Gossenköllesee, Piburgersee, Fuchskuhle and Cadagno Lakes; [52] in upper Parana River. Actinobacteria can degrade the complex mixture of organic matter derived from plant biomass. Their capacity for efficient uptake of nutrients, enhances the performance of these bacteria under oligotrophic or nutrient-depleted conditions. Also, the surface area-to-volume ratio is increased by their small size and this leads to efficient nutrient uptake [53]. The low nutrient level of Asejire Lake during this study could have led to the dominance of the Actinobacteria since they are capable of nutrient uptake namely phosphorus (e.g. exopolyphosphatases, inositol acquisition), nitrogen (cyanophycin degradation) and carbon (use of plant xylan, lignin breakdown by-products) [5]. In addition, Actinobacteria possess an ability to remove pesticides, heavy metals, and other soil contaminants [54] [55]. However, in some cases, harmful effects known as actinobacterial plant, animal, and human diseases can also be caused by Actinobacteria. The majority of phytopathogenic features were found in *Corynebacterium*, whereas *Actinomyces*, *Mycobacterium*, *Dermatophilis*, *Renibacterium*, and *Rhodococcus* are responsible for human and animal diseases [56].

Polynucleobacter, the major genus detected in Lake Eleyele is a cosmopolitan genus that often dominates planktonic freshwater communities [47]. It produces extremely small cells that can grow aerobically on a wide range of complex media. According to [14], *Polynucleobacter* possesses genes related to the degradation of pesticides used in agriculture. [57] determined polychlorinated biphenyls (chemicals used in making pesticides) in the Eleyele Lake water from December 2013 to February 2014 and reported 493.90 –732.55 $\mu\text{g L}^{-1}$ and 52.00–390.03 $\mu\text{g L}^{-1}$ for the dry and wet seasons, respectively. These values were higher than USEPA permissible levels (500 ng L^{-1}) for PCBs in drinking water. Thus, the predominance of the *Polynucleobacter* genus could have resulted from the need to degrade these chemicals. *Limnohabitans* was encountered in Lake Eleyele and a great metabolic versatility has been suggested for *Limnohabitans* species when [58], obtained a complete photosynthesis gene cluster, RuBisCO, carbon monoxide dehydrogenase, ammonia monooxygenase, and sulfur-oxidizing genes from two *Limnohabitans* isolate from Rímov reservoir (Czech Republic). The genus *Methylobacterium* found in Lake Asejire are widespread in natural environments including freshwater, soil, air and they have an important ecological role in carbon cycle because of being able to metabolize different plant decomposition compounds. They often also become highly resistant to chlorine in man-made environments like drinking water supplies [59]. Bacteria of the *Methylobacterium* genus are facultative methylotrophs capable of growing on one-carbon compounds such as formate, formaldehyde, and methanol as the sole source of carbon and energy, as well as on a wide range of multicarbon substrates [60], [61]. *Methylotenera* found in Eleyele Lake is a new genus within the family Methylophilaceae [62]. All known members of this family are obligate methylotrophs, i.e. they are specialized in degradation of organic compounds containing no carbon-carbon bonds (C1 compounds), most prominently methanol and methylamine [63]. Thus, methylotrophy was achieved in both environments however via different organisms (Alpha- and Betaproteobacteria). *Limnohabitans*, *Methylobacterium*, and *Methylotenera* seemed to contribute to the prokaryotic primary production of the Lake Asejire and Eleyele, respectively.

Ilumatobacter belonging to the family Acidimicrobiaceae identified in our study as the dominant genus in Lake Asejire is described in the literature database, as a mesophilic, neutrophilic, aerobic, Gram-positive bacterium having enzymes required for biosynthesis of vitamins (K, B6) [64]. Members of the genus *Terrimonas* are generally characterized as strictly aerobic, Gram-negative, non-motile, non-gliding and non-filamentous bacteria that are oxidase-positive and weakly catalase-positive. These bacteria usually contain iso-C15:0, iso-C15:1 G, iso-C17:0 3OH and summed feature 3 as major fatty acids, menaquinone-7 (MK-7) as the predominant respiratory quinone and have DNA G+C contents of 47.0–48.9 mol% [65]. *Terrimonas* species recovered from both studied lakes have been found in other environments including garden soil, a freshwater spring, polluted farmland, bulking sludge, tundra and Arctic glacier till [66]. *Legionella* genus was encountered only in Asejire sample and they have also been found in watery soils, natural or man-made aquatic environments, such as rivers, lakes, ponds, mud, and cooling towers or water distribution systems [67]. *Legionella* species have ability to cause disease in susceptible humans, thus are of public health interest.

The 5.5% 16S rRNA clones in the Lake Asejire sample that could not be classified into any phylum under the Bacteria domain and the 87.3% and 78.3% clones read of the Lakes Eleyele and Asejire, respectively that could not be grouped into genus reveal the largely unknown bacterioplankton composition of these lakes. This could be since most of the previous studies were carried out in temperate ecosystems, the unusual bacterioplankton community of the studied sites could be due to their tropical locations. [68] made the same observation on the microbial community of the Lake Tangayinka and [9], reported that temperature influences bacterial composition. Although microorganisms have been detected to have global distribution by previous studies including [69] and [35], the result from this study may suggest more localized distribution patterns for the microbial organisms in the ecosystems. Thus, more studies are required in tropical ecosystems to enhance comparison and confirm the peculiarity of the bacterial composition.

5. Conclusion

This is the first report on the bacterioplankton composition and diversity of Lakes Eleyele and Asejire. Proteobacteria was the dominant phylum in Eleyele Lake, while Actinobacteria phylum dominated in Asejire Lake. The bacterioplankton composition of both lakes could be related to the physicochemical parameters. In both lakes biogeochemically significant bacteria and bacteria that contribute to prokaryotic primary production (*Limnohabitans*, *Methylobacterium*, and *Methylotenera*) were encountered. Large number of bacterioplankton in the Eleyele and Asejire Lakes are unknown/ unidentified, and further research may be required to determine the novelty of their classification lineage.

6. Acknowledgements

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7. Authors' Contributions

AAA conducted the research, did statistical analysis and wrote the manuscript. NSA supervised the research and corrected the manuscript.

8. Conflict of Interest

The authors declare that there is no conflict of interests regarding the publication of this article.

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