



International Journal of Fisheries and Aquatic Studies

E-ISSN: 2347-5129

P-ISSN: 2394-0506

(ICV-Poland) Impact Value: 5.62

(GIF) Impact Factor: 0.549

IJFAS 2020; 8(3): 478-483

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www.fisheriesjournal.com

Received: 19-03-2020

Accepted: 21-04-2020

Omondi A Owino

Department of Aquatic and
Fisheries Sciences, Kisii
University, P.O Box 408-40200,
Kisii, Kenya

Ogendi G Mokua

Department of Natural
Resources Management and
Environmental Science, Kisii
University, P.O Box 408-40200,
Kisii, Kenya

Onchieku M James

Department of Natural
Resources Management and
Environmental Science, Kisii
University, P.O Box 408-40200,
Kisii, Kenya

Oduor S Omondi

Department of Biological
Sciences, Egerton University,
Njoro, P.O Box 536, Nakuru,
Kenya

Reuben Omondi

Department of Aquatic and
Fisheries Sciences, Kisii
University, P.O Box 408-40200,
Kisii, Kenya

Omweno J Ombiro

Department of Aquatic and
Fisheries Sciences, Kisii
University, P.O Box 408-40200,
Kisii, Kenya

Corresponding Author:

Omondi A Owino

Department of Aquatic and
Fisheries Sciences, Kisii
University, P.O Box 408-40200,
Kisii, Kenya

Phytoplankton community structure and ecology in Lake Naivasha, Kenya

**Omondi A Owino, Ogendi G Mokua, Onchieku M James, Oduor S
Omondi, Reuben Omondi and Omweno J Ombiro**

Abstract

The phytoplankton community structure and ecology of L. Naivasha was studied for a period of six months on a monthly basis between February 2019 and July 2019. The main objective was to determine the phytoplankton species diversity, distribution, and abundance from the seven sampling points in L. Naivasha. A total of one hundred and twenty four (124) species belonging to six (6) taxonomic group were identified. Chlorophyceae was represented by 43 species consisting of 34.68% by species composition, Bacillariophyceae was represented by 38 species consisting of 30.65% by species composition. Cyanophyceae was represented by 24 species leading to 19.35% species composition. Other taxonomic groups included Zygnematophyceae, Euglenophyceae, and Dinophyceae represented by 9 (7.26%), 7 (5.65%) and 3 (2.42%) species respectively. Cyanophyceae recorded the highest abundance in cells/litre, followed by Chlorophyceae and Bacillariophyceae. The total number of algal species was highest in Hippo point with 72 (16.59%) species, followed closely by 68 (15.67%) species in Crescent Island, followed by 66 (15.21%) species in Oserian Bay. Mouth of R. Malewa recorded 59 (13.59%) species, Sher Bay had 58 (13.36%) species, this was followed by Mid Lake station with 56 (12.90%) species, and Sewage Discharge Point had 55 (12.67%) species. Shannon-wiener diversity (H) index ranged from 2.0455 (Mouth of R. Malewa) to 2.7077 (Oserian Bay). In conclusion, Lake Naivasha depicted a higher diversity of phytoplankton species. Results from this study showed the state of L. Naivasha trophic status based on phytoplankton ecology.

Keywords: Diversity, ecology, phytoplankton, relative abundance, Lake Naivasha

1. Introduction

Phytoplankton are the primary source of energy transferred to all trophic levels in aquatic ecosystems^[1], which helps to sequester atmospheric carbon (iv) oxide and oxygenate the earth. The measurement of primary productivity indicates the fishery potential of an aquatic ecosystem^[2]. Besides primary production, the phytoplankton are sensitive to changes in water bodies caused by natural and anthropogenically mediated activities. Therefore, they can be used as bio-indicators of water pollution during water quality monitoring and assessment. Their rapid reproduction in eutrophic waters can sometimes result in algal blooms, which upon decomposition deprive dissolved oxygen, affect pH and are a nuisance to aquatic life, navigation and recreation. Some species of phytoplankton such as cyanobacteria easily form algal blooms because of their ability to migrate vertically in the water column and also fixation of atmospheric nitrogen into nitrates^[3]. Since 1963, Lake Naivasha has been characterized by complex ecological and environmental changes which result from human activities in the lake and the surrounding catchment^[4]. These include siltation and nutrient loading, which have resulted in proliferation of free floating and emergent macrophytes and a higher phytoplankton biomass^[5]. The nutrient enrichment of Lake Naivasha water as well as changes in fish community can be associated with reduction, overproduction, growth, distribution and composition of phytoplankton which consequently affect the phytoplankton community structure, abundance and diversity. The knowledge of plankton dynamism is important in understanding ecosystem resilience to increased human activities and the effects of global warming^[6]. However, there is limited information on community structure, abundance and diversity of phytoplankton in Lake Naivasha. Therefore, this study seeks to determine the phytoplankton community structure, abundance and diversity from the different sampling to provide crucial information for ecosystem monitoring, management and conservation of L. Naivasha.

2. Materials and Methods

2.1 Study area

Lake Naivasha (approx. 153.2 km²) is the second-largest freshwater lake in Kenya [7], located on the eastern arm of the Great Rift Valley at an altitude of 1895 m above sea level. Geographically, the lake lies at latitude 00 45' S and longitude 36^o 20' E, between Kinangop Plateau and Eburru Hills. The lake comprises of three separate water bodies; Lake Sonachi, Lake Oloiden and the main lake itself as shown in figure 1.

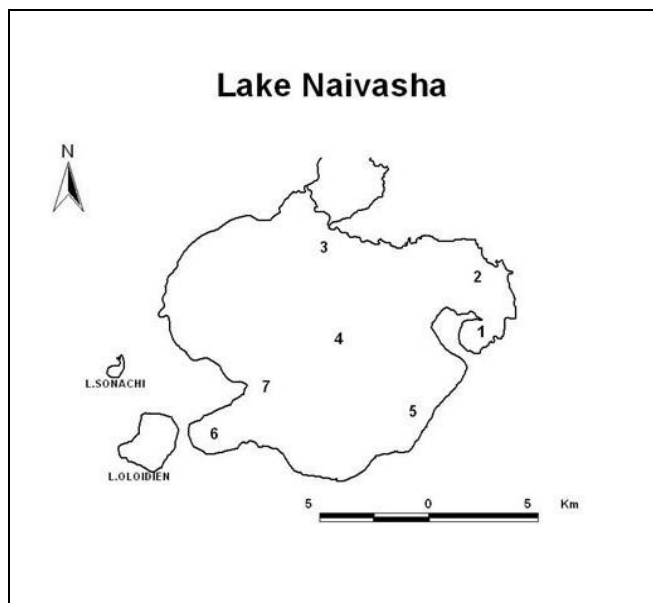


Fig 1: Map of Lake Naivasha showing the sampling points (Crescent Island (1), Sewage Discharge Point (2), Mouth of R. Malewa (3), Mid Lake (4), Sher Bay (5), Oserian Bay (6) and Hippo point (7)

2.2 Sampling and analysis for phytoplankton groups

The seven sampling stations were sampled once per month between February 2019 and July 2019. Water samples for the determination of phytoplankton community structures were collected by use of plankton net of 20 microns at the water surface (10 cm depth). The net was then rinsed using deionized water in order to wash off the remaining algal cells attached to the net. The plankton net content was then poured into a well-labelled pre-rinsed acid wash algal bottles at each station. The samples were then preserved by adding 2-3 drops of 1% Lugol’s solution. The samples were stored at 4 degrees Celsius cooler box for laboratory analysis. At the laboratory, each station sample was poured into a 250 ml measuring cylinder and topped to 100 ml level. 1 ml of 1% Lugol’s solution was later added to each of the sample to enhance the sedimentation process of the algal cells. The sedimentation cylinders were then covered with stoppers or protective film or foils. A minimum of 24 hours was given to the phytoplankton cells to sediment at the bottom of the cylinder. Such a sedimentation time also settled ‘difficult’ species such as *Cylindropermopsis* and *Planktolyngbysa* [8].

After the elapse of the sedimentation time, the top 90 ml of the volume was carefully siphoned out using a calibrated micropipette without disturbing the bottom volume of the algal cells. The remaining 10 ml was later poured into labelled algal vials for the respective sampling stations in readiness for microscopy. Quantitative analysis of the phytoplankton cells and enumeration was done by use of Sedgewick-Rafter counting chamber. From the 10 ml concentrated sample volume, 2 ml of sub sample was pipetted

out after shaking for 2 minutes and placed into the counting chamber and left to settle on the microscope for 15-20 minutes so that the algal cells could settle. Enumeration of the algal cells was done using the Zeiss Axioinvert 35 inverted microscope model at 100X and 400X magnification. The identification and classification of the algae species was based on the guide provided by the Algae Identification according to Huber-Pestalozzi [8] and Cocquyt *et al.* [9].

2.3 Determination of phytoplankton abundance and relative abundance

According to Eyo *et al.* [10] and Rahman *et al.* [11] abundance and relative abundance (species composition) was determined using the formulae below;

• Abundance (N) = (A* 1000* C)/ (V*F*L)..... Equation 1

Where

- N = Number of phytoplankton in cells per litter
- A = Total number of phytoplankton cells counted
- C = Volume of final concentrate of samples in ml,
- V = Volume of a field in ml
- F = Number of the fields counted
- L = Volume of original water in L

• %RA =n (100)/N.....Equation 2

Where

- n = total number of phytoplankton species in each taxonomic group
- N = the total number of phytoplankton species in all taxonomic group

2.4 Determination of Phytoplankton Diversity

With the limited resources for identification of Phytoplankton, identifications was primarily considered at the genus or species level. To determine the diversity and abundance of Phytoplankton, three diversity indices (Shannon-Wiener, Margalef’s Index (d), and species evenness) were computed using the following formulas according to [12] and Eyo *et al.* [10].

• **Shannon-Wiener Index** $H' = -\sum_i p_i \ln_i p_i$ Equation 3

Where, p_i is the proportion (n/N) of all the Phytoplankton which belongs to the i^{th} species, \ln is natural log and \sum is the sum of the calculation.

The Shannon-Wiener Diversity Index assumes that all species are represented in a sample and that they are randomly selected. It accounts for both abundance and evenness of the species present.

- **Margalef’s Index (d)** determined as;

$$d = \frac{S - 1}{\ln(N)} \dots\dots\dots \text{Equation 4}$$

Where;

- S = the total number of species
- \ln = the Natural log
- N is the total number of individuals.

- **Evenness (E)**

Evenness (E) was given as:

$$E = \frac{H}{\log S} \dots\dots\dots \text{Equation 5}$$

Where;

H = the Shannon-wiener index

S = the total number of species.

3. Results

3.1 Phytoplankton Species Composition and Abundance in Lake Naivasha

The phytoplankton species identified in this current study are shown below (Table 1). A total of one hundred and twenty four (124) species belonging to six (6) taxonomic group were identified from Lake Naivasha. Chlorophyceae was represented by 43 species consisting of 34.68% by species composition, followed by Bacillariophyceae, which was represented by 38 species consisting of 30.65% by species composition. Bacillariophyceae was closed followed by Cyanophyceae that was represented by 24 species leading to 19.35% species composition. Other taxonomic groups included Zygnematophyceae, Euglenophyceae, and Dinophyceae represented by 9 (7.26%), 7 (5.65%) and 3 (2.42%) species respectively (Table 2). Among the Chlorophyceae family, *Monoraphidium* sp, *Tetraedron* spp, *Scenedesmus* spp, *Botryococcus* sp, *Oocystis* spp, and *Pediastrum* spp. were the dominant species, while *Anabaena* spp, *Chroococcus* spp, *Microcystis* spp, *Planktolyngbya* spp and *Aphanocapsa* spp. dominated the family of Cyanophyceae. The family of Bacillariophyceae was dominated by *Amphora* spp, *Aulacoseira* spp, *Navicula* spp, *Synedra* spp, and *Nitzschia* spp while *Euglena* spp, *Phacus*

spp and *Trachelomonas* spp dominated the family of Euglenophyceae. *Cosmarium* spp and *Closterium* spp dominated the family of Zygnematophyceae while the family of Dinophyceae was dominated *Ceratium* sp. In this current study, Cyanophyceae family recorded the highest abundance of 1045×10^6 cells/L, this was followed by Chlorophyceae family with 511×10^6 cells/L and Bacillariophyceae family with 473×10^6 cells/L. The family of Dinophyceae recorded the least cell density of 4×10^6 cells/L in terms of abundance (Table 3). In terms of spatial variation, Mid Lake and Crescent Island stations had the highest abundance of 610×10^6 cells/L and 374×10^6 cells/L respectively. Low abundance was recorded in Oserian Bay (132×10^6 cells/L) and Sher Bay (161×10^6 cells/L) (Table 4).

3.2 Phytoplankton species diversity in Lake Naivasha

Various phytoplankton diversity indices were considered in this present study and they included Shannon-wiener (H), Species evenness (E), and Margalef's diversity (d) indices (Table 5). Phytoplankton diversity indices in L. Naivasha were high in three sampling stations. Shannon-wiener diversity (H) index ranged from 2.0455 (Mouth of R. Malewa) to 2.7077 (Oserian Bay). Margalef's diversity (d) index was high at Oserian Bay (7.8522) and lowest at Mid Lake station (5.6041). Evenness (E) ranged from 0.6463 (Oserian Bay) to 0.5014 (Mouth of R. Malewa). Shannon-wiener diversity index was higher in the month of July.

Table 1: Phytoplankton Species of Lake Naivasha

Chlorophyceae	Bacillariophyceae	Cyanophyceae
<i>Ankistrodesmus fusiformis</i>	<i>Achnanthes</i> sp.	<i>Anabaena flos-aquae</i>
<i>Ankistrodesmus falcatus</i>	<i>Amphora</i> sp.	<i>Anabaena limnetica</i>
<i>Ankistrodesmus</i> sp.	<i>Amphora ovalis</i>	<i>Anabaena spiroides</i>
<i>Botryococcus braunii</i>	<i>Aulacoseira ambigua</i>	<i>Anabaenopsis circularis</i>
<i>Chlamydomonas ovalis</i>	<i>Aulacoseira nyassensis</i>	<i>Aphanocapsa pulchra</i>
<i>Chlorella vulgaris</i>	<i>Aulacoseira schroidera</i>	<i>Aphanocapsa rivularis</i>
<i>Chlorella</i> sp.	<i>Aulacoseira ulna</i>	<i>Aphanothece</i> sp.
<i>Coelastrum reticulatum</i>	<i>Cyclotella kutzingiana</i>	<i>Chroococcus limnetica</i>
<i>Coelastrum microporum</i>	<i>Cyclotella ocellata</i>	<i>Chroococcus</i> sp.
<i>Crucigenia rectangularis</i>	<i>Cymbella cistula</i>	<i>Chroococcus turgidus</i>
<i>Crucigenia quadrata</i>	<i>Cymbella solea</i>	<i>Coelomoron</i> sp.
<i>Crucigenia</i> sp.	<i>Cymbella</i> sp.	<i>Coelomoron vestitus</i>
<i>Crucigenia tetrapedia</i>	<i>Diatoma elongatum</i>	<i>Cylindrospermopsis africana</i>
<i>Kirchineriella contrata</i>	<i>Diatoma hiemale</i>	<i>Lyngbya</i> sp.
<i>Kirchineriella lunaris</i>	<i>Diatomella hustedtii</i>	<i>Merismopedia convoluta</i>
<i>Kirchineriella obesa</i>	<i>Fragillaria capucina</i>	<i>Microcystis aeruginosa</i>
<i>Monoraphidium</i> sp.	<i>Gomphonema acuminatum</i>	<i>Microcystis wasenbergii</i>
<i>Oocystis nageri</i>	<i>Gomphonema</i> sp.	<i>Oscillatoria tenuis</i>
<i>Oocystis borgei</i>	<i>Navicula granatum</i>	<i>Plankolyngbya tallingii</i>
<i>Oocystis lucastris</i>	<i>Navicula mutica</i>	<i>Planktolyngbya limnetica</i>
<i>Oocystis parva</i>	<i>Navicula scutelloides</i>	<i>Planktolyngbya circumcreta</i>
<i>Oocystis pusilla</i>	<i>Navicula</i> sp.	<i>Planktolyngbya contrata</i>
<i>Oocystis solitaria</i>	<i>Nitzschia sub-acicularis</i>	<i>Planktolyngbya</i> sp.
<i>Pediastrum boryanum</i>	<i>Nitzschia dissipata</i>	<i>Spirulina subsalsa</i>
<i>Pediastrum duplex</i>	<i>Nitzschia lucastris</i>	
<i>Pediastrum simplex</i>	<i>Nitzschia palea</i>	Zygnematophyceae
<i>Pediastrum tetrans</i>	<i>Nitzschia recta</i>	<i>Closterium leibleinii</i>
<i>Scenedesmus acuminatus</i>	<i>Nitzschia</i> sp.	<i>Closterium navicular</i>
<i>Scenedesmus bijugatus</i>	<i>Pinnularia major</i>	<i>Cosmarium depressum</i>
<i>Scenedesmus crassus</i>	<i>Pinnularia viridis</i>	<i>Cosmarium cunningtonii</i>
<i>Scenedesmus curvatus</i>	<i>Stephanodiscus astrea</i>	<i>Cosmarium retusiforme</i>
<i>Scenedesmus longus</i>	<i>Stephanodiscus</i> sp.	<i>Cosmarium</i> sp.
<i>Scenedesmus maximus</i>	<i>Surirella linearis</i>	<i>Staurastrum paradoxum</i>
<i>Scenedesmus obliquus</i>	<i>Surirella ovalis</i>	<i>Staurastrum lunatum</i>
<i>Scenedesmus quadrata</i>	<i>Surirella</i> sp.	<i>Staurastrum</i> sp.

<i>Scenedesmus</i> sp.	<i>Synedra acus</i>	Euglenophyceae
<i>Scenedesmus tenuispina</i>	<i>Synedra nyassae</i>	<i>Euglena acus</i>
<i>Schroederia Africana</i>	<i>Synedra ulna</i>	<i>Euglena viridis</i>
<i>Schroederia setigera</i>		<i>Phacus longicauda</i>
<i>Tetraedron arthrodesmisforme</i>	Dinophyceae	<i>Phacus pleuronectes</i>
<i>Tetraedron inflatum</i>	<i>Ceratium branchyceros</i>	<i>Phacus</i> sp.
<i>Tetraedron minimum</i>	<i>Ceratium hirundinella</i>	<i>Trachelemonous armata</i>
<i>Tetraedron triangulare</i>	<i>Glenodinium perardii</i>	<i>Trachelemonous volvocina</i>

Table 2: Total Number of Species and Relative Abundance of Phytoplankton Species in L. Naivasha

Taxonomic group	Total no. of species	Relative Abundance (%)
Chlorophyceae	43	34.68
Bacillariophyceae	38	30.65
Cyanophyceae	24	19.35
Zygnematophyceae	9	7.26
Euglenophyceae	7	5.65
Dinophyceae	3	2.42
Total	124	100.00

Table 3: Phytoplankton family abundance expressed as Cells per Litre in Lake Naivasha

Taxonomic group	No. of species	Abundance (cells/L x 10 ⁶)
Chlorophyceae	43	511 x 10 ⁶
Cyanophyceae	24	1045 x 10 ⁶
Bacillariophyceae	38	473 x 10 ⁶
Dinophyceae	3	4 x 10 ⁶
Euglenophyceae	7	23 x 10 ⁶
Zygnematophyceae	9	19 x 10 ⁶

Table 4: Spatial variation of Phytoplankton family abundance expressed as Cells per Litre in Lake Naivasha

Sampling stations	No. of species	Abundance (cells/L x 10 ⁶)
Crescent Island	68	374 x 10 ⁶
Hippo Point	72	291 x 10 ⁶
Mouth of R. Malewa	59	248 x 10 ⁶
Mid Lake	56	610 x 10 ⁶
Oserian Bay	66	132 x 10 ⁶
Sewage Discharge Point	55	289 x 10 ⁶
Sher Bay	58	161 x 10 ⁶

Table 5: Phytoplankton Diversity indices in L. Naivasha in relation to sampling stations

	Sampling Stations						
	Sewage Discharge point	River Malewa Mouth	Hippo Point	Oserian Bay	Sher Bay	Mid Lake Point	Crescent Island
Taxa (s)	55	59	72	66	58	56	68
Individuals	7753	7439	8720	3936	4805	18291	11215
Margalef's index (d)	6.0296	6.5063	7.8251	7.8522	6.7237	5.6041	7.185
Shannon-wiener index (H)	2.0787	2.0455	2.1676	2.7077	2.4925	2.1483	2.3241
Evenness (E)	0.5187	0.5017	0.5068	0.6463	0.6139	0.5337	0.5508

4. Discussion

Phytoplankton play a vital role in any aquatic ecosystems^[13] both as pollution indicators and source of primary production, hence provide understanding of ecosystem functioning. This study recorded a total of one hundred and twenty four (124) phytoplankton species. This was lower than the phytoplankton species identified by Kitaka^[14]. The low number of species can be attributed to lower number of sampling stations (3) compared to the seven (7) sampling stations of the current study. However, this study recorded fewer number of phytoplankton species compared to the number identified by Hubble & Harper^[1] (170 species) and^[12] (143 species). Chlorophyceae, Bacillariophyceae, and Cyanophyceae families dominated the phytoplankton species in this study. The dominance of Chlorophyceae family collaborates the study done by Njuguna^[15] and Kitaka^[14]. On the contrary, the dominance of Chlorophyceae in this study differs from what was reported by^[16, 12, 9]. Bech *et al.*^[12] and Ballot *et al.*^[16] found out that Cyanophyceae dominated the phytoplankton species of L. Naivasha while Bacillariophyceae family dominated the study done by Hubble & Harper^[1]. Chlorophyceae, Cyanophyceae, and Bacillariophyceae mainly dominate the phytoplankton community structures of L. Naivasha as evident in this study

and the previous studies. Chlorophyceae family comprised of *Monoraphidium* sp, *Pediastrum* with four dominant species, *Pediastrum duplex*, *Pediastrum simplex*, *Pediastrum tetras*, and *Pediastrum boryanum*. The genera of *Scenedesmus* with *S. acuminatus*, *S. longus*, *S. maximus*, *S. quadrata*, *S. curvatus* and *S. obliquus*. *Botyococcus braunii*, *Tetraedron* genera (*T. arthromisforme*, *T. minimum*, and *T. triangulare*), *Oocystis* genera (*O. solitaria*, *O. parva*, *O. borgei* and *O. lucastri*) also dominated Chlorophyceae family. Bacillariophyceae family was dominated by the *Aulacoseira* genera (*A. ambigua*, *A. nyassensis*, *A. schroidera* and *A. ulna*), *Amphora ovalis*, *Navicula* genera (*N. granatum* and *N. mutica*), genera of *Nitzschia* (*N. lucastris*, *N. palea*, *N. recta*, *N. sub-acicularis* and *N. dissipata*) and genera of *Synedra* (*S. cunningtonii* and *S. ulna*). Cyanophyceae family was dominated by genera *Anabaena* of *A. circinalis*, *A. flos-aquae*, *A. limnetica*, genera of *Chroococcus* by *C. turgidus*, *C. limnetica*, *Aphanocapsa* spp, and *Microcystis aeruginosa*. *Cosmarium* spp, *Closterium* spp, and *Staurastrum* spp dominated the Zygnematophyceae family. *Ceratium* spp dominated Dinophyceae family while the genera of *Euglena* (*E. acus* and *E. viridis*), *Phacus longicauda*, and *Trachelemonous* spp dominated the Euglenophyceae family. The most copious phytoplankton species recorded at the seven sampling stations belonged to

the genera *Aulacoseira*, *Pediastrum*, *Monoraphidium*, *Scenedesmus*, and *Chroococcus*. *Euglena* genera (*E. acus* and *E. viridis*), *Phacus longicauda*, and *Trachelemonous* spp mainly dominated Sewage Discharge Point. This can be attributed to the pollution status of the station from sewage effluents, municipal waste, organic matter, and higher nutrients levels from the point sources of pollution.

The high prevalence of Bacillariophyceae especially the genera *Aulacoseira* at Crescent Island, Mid Lake and Hippo point can be related to elevated silicates levels, higher concentrations of nutrients, favourable temperatures and reduced turbidity resulting from high transparency. Increased prevalence of *Anabaena* spp at the Mid Lake station and Mouth of R. Malewa can be credited to their tolerance to low dissolved oxygen, sensitivity to mixing and the fact that they belong to a group of algae that can fix nitrogen. Occurrence of *Microcystis* spp at Sewage Point and R. Malewa mouth has been associated with higher mixing rates leading to upwelling of bottom nutrients, nutrient rich waters, lake depth, and their buoyancy characteristics. These observations and findings corroborate the findings observed by Sitoki *et al.* [17] in the Nyanza gulf of L. Victoria. The low occurrence of Dinophyceae family especially the genera of *Ceratium* can be linked to lower salinity (0.09-0.13 ppt) levels of Lake Naivasha hence low reproductive rates. Kitaka [14], also observed this from her study on phytoplankton productivity in the Lake Naivasha. The Chlorophyceae in this study had higher species composition of 34.68%. This can be associated with favourable environmental factors like light regime and availability of essential nutrients (TP, TN, SRP, Ammonium nitrogen & Nitrate nitrogen). Studies have also shown that Chlorophyceae depict a positive correlation to shallow water, favourable temperature, and good tidal exposure (mixing). Some aspects of feeding ecology of Nile tilapia, *Oreochromis niloticus* in Lake Naivasha have also been studied. This has shown some effect of variations in the distribution, abundance and diversity of phytoplankton. This study has shown that the *O. niloticus* has spatial variation in their diet more so in the near shores and open water habitat. The study by Outa *et al.* [18] revealed that algae contributed the biggest proportion among its diverse diet with majority of its feeding being on the open waters. Straus Linear index of food selection also shows that Nile tilapia preferred Chlorophyceae but avoided algae in the other genera (Bacillariophyceae and Cyanophyceae). This could be attributed to the fact that diatoms have tough cell walls that are harder to digest as compared to green algae.

Cyanobacteria are filamentous and hence more difficult to handle during feeding and can lead to clogging of fish gills. Some Cyanobacteria are also known to produce toxins. This could explain the avoidance of some of them by the fish in their diet hence the higher abundance of blue-green algae and diatoms in this study. The higher abundance of Cyanophyceae in this study can also be attributed to the favourable lake conditions. High organic loading, higher temperatures, increased nutrients loads, higher competition rates, polymictic nature of the lake and favourable light regime also explains their high abundance. These findings corroborate the observation made by Ogendi *et al.* [19] in Lake Victoria on the effects of point sources of pollution on water quality and phytoplankton community structures. For instance, cyanobacteria can also fix atmospheric nitrogen and have ability to move up and down in water column hence have got a greater advantage over other phytoplankton taxa [3].

Increased climate change has also favored the proliferations of certain phytoplankton families like the Cyanophyceae that has been recorded to bloom during periods of high temperatures [5, 20, 14]. The low abundance of Euglenophyceae, Dinophyceae, and Zygnematophyceae families can be linked to the harsh environmental conditions of the lake. Phytoplankton species composition and their abundance showed spatial and temporal variation. Various phytoplankton diversity indices were considered in this present study and they included Shannon-wiener (H), Species evenness (E), and Margalef's diversity (d) indices. Phytoplankton diversity indices in L. Naivasha were high in three sampling stations. Shannon-wiener diversity (H) index ranged from 2.0455 (Mouth of R. Malewa) to 2.7077 (Oserian Bay). Margalef's diversity (d) index was high at Oserian Bay (7.8522) and lowest at Mid Lake station (5.6041). Evenness (E) ranged from 0.6463 (Oserian Bay) to 0.5014 (Mouth of R. Malewa). High phytoplankton diversity at Sher Bay, Oserian Bay and Crescent Island can be attributed to favourable temperatures, nutrients availability, trace elements and light conditions. High temperatures influence the solubility rates of DO and the metabolic processes of the species. The higher species diversity recorded in July can be attribute to favourable environmental conditions of nutrients influx and lake mixing. Njuguna [15] and Kitaka [14] also attributed the high species diversity in Lake Naivasha to its polymictic nature due to wind action and convection without persistent stratification. This mixing makes algal cells to undergo vertical circulation continuously exposing them to prevailing light regime. Phytoplankton abundance and diversity has been influenced by seasonal fluctuations in nutrient availability and concentrations. Phytoplankton abundance and diversity in L. Naivasha according to the study conducted by Hubble & Harper [1] has been influenced by the recent anthropogenic impacts and higher nutrients loads from the lake's catchment. Chin [21] states that a species is favored when both absolute concentrations of nitrogen and phosphorus and their ratio in the environment conforms to that particular species' requirements. Addition of nitrate-nitrogen to Phosphorous-rich water favors most algae community structure. At present, most evidence shows that freshwater eutrophication ultimately arises from persistent increase in Phosphorous influx from urban and other anthropogenic source according to Njuguna [15].

5. Conclusion

In conclusion, Lake Naivasha depicted a higher diversity of phytoplankton species. Results from this study showed the state of L. Naivasha trophic status based on phytoplankton ecology. A total of one hundred and twenty four (124) species belonging to six (6) taxonomic group were identified from Lake Naivasha. Chlorophyceae was represented by 43 species consisting of 34.68% by species composition, followed by Bacillariophyceae, which was represented by 38 species consisting of 30.65% by species composition. Bacillariophyceae was closed followed by Cyanophyceae that was represented by 24 species leading to 19.35% species composition. Chlorophyceae, Bacillariophyceae, and Cyanophyceae families dominated the phytoplankton species in this study. Cyanophyceae family recorded the highest abundance, this was followed by Chlorophyceae family and Bacillariophyceae family. The family of Dinophyceae recorded the least cell density in terms of abundance. In terms of spatial variation, Mid Lake and Crescent Island stations

had the highest abundance. Low abundance was recorded in Oserian and Sher Bay.

6. References

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