



ASSESSMENT ON BACTERIAL COMMUNITY STRUCTURE WITH SEASONAL TRENDS AND MICROBIAL WATER QUALITY OF THE SELECTED RESTRICTED WATER BODIES AS SANCTUARIES FOR INDIGENOUS AND MIGRATORY BIRDS

*¹Shamima Nasrin Jolly, ²Nazia Afrin, ¹Chandrima Das and ²Rasheda Yeasmin Shilpi

¹Laboratory of Phycology and Limnology, Department of Botany, Faculty of Biological Sciences, Jahangirnagar University, Savar, Dhaka, Bangladesh.

²Laboratory of Microbiology, Department of Botany, Faculty of Biological Sciences, Jahangirnagar University, Savar, Dhaka, Bangladesh.

*Corresponding authors' email: jolly06_ju@yahoo.com

ORCID ID: <https://orcid.org/0009-0002-2473-6445>

ABSTRACT

Jahangirnagar University campus is a hub of several water bodies making it as a heaven for native and migratory birds. This research focused on the microbial quality of three water bodies of this campus where human interference is restricted. Isolation and identification of heterotrophic bacteria, fecal coliform and other pathogenic bacteria were carried out in this study. In the present investigation, Heterotrophic bacterial count varied from 17-100 cfu/ml for Site-1, 19-45 cfu/ml for Site-2 and 17-85 cfu/ml for Site-3. Seasonal trends in bacterial concentrations were also present, where highest concentration was found during winter and lowest one was during monsoon. In case of monthly variation, the highest average was recorded in the month of February for Site-1 and Site-2 and January for Site-3 whereas the lowest mean was recorded in the month of July in all studied sites. No coliform bacteria had been found in the studied water bodies. Bacterial colonies were isolated according to standard protocol and identified on the basis of morphological and biochemical characteristics. This study showed that the isolated bacteria were *Bacillus* sp. and *Staphylococcus aureus* that forbidding human activities like swimming or domestic use though water samples were lack of fecal pollution. It may be suitable enough for the indigenous and migratory birds.

Keywords: Bacterial Identification, Biochemical Test, Fecal Coliform, Heterotrophic Bacteria, Seasonal Variation

INTRODUCTION

The most rudimentary and prime component amongst the natural resources is water for the ultimate existence of every single living organism in the world. On the earth, water bodies are the most fecund ecosystem. Wetlands contain greater biodiversity of flora and fauna that have native, national and biogeographical significance (Bhuiyan *et al.*, 2010a, 2010b). According to Ramsar convention, wetlands may be occupied more than two third (7-8 million ha) of total land of Bangladesh (Akonda, 1989).

In developing countries, one of the most public health issues is the microbiological safety of inland water. Pollutants that are harmful for living organisms and human as well, contaminate water of streams, rivers, ponds, lakes or oceans resulting unpleasant in looking, smelling and swimming. Severe microbial pollution may cause killing of a large number of fish, birds and other animals in an affected area. Presence and activity of aquatic microorganisms play significance role in many ways. Since they supply rich nutrition to the next higher level of life and affect human and animal health, aquatic microorganisms occupy a key position in the food chain (Munshi *et al.*, 2012, Acharjee *et al.*, 2013, Okonko *et al.*, 2008 and Pelczer, 1988). According to Obi *et al.*, 2002 and Sharma *et al.*, 2005, unprotected water bodies may be contaminated by agricultural inputs, sewage effluents and faeces of wild lives along with rainfall run-off.

During winter season, the lakes of Jahangirnagar University campus act as an important sanctuary for migratory or guest birds migrated from Mongolia, China and Siberia. Around 69 species of migratory with 126 native bird species were recorded from the campus. Bacteriological studies of water bodies are essential to assess the quality of water in accordance to microbiological standard for the living

organism in aquatic ecosystem and for the surrounding environment as well. Physico-chemical analysis may not provide as accurate result of water quality as bacteriological examination can do (Hirsch, 1958 and Hussainy & Abdulappa, 1967).

Therefore, the bacteriological survey was undertaken since they play a major role to determine the extent of pollution. Moreover, they are able to respond quickly to the environmental changes and are key factor in biogeochemical cycle.

MATERIALS AND METHODS

Description of the Study Area

The present investigation was carried out in three (3) different water bodies of Jahangirnagar University campus. The selected water bodies are designated as Site-1, Site-2 and Site-3 with varying water depth, size, dimension, age and ecological variabilities. All the sites are reserved water bodies without human interferences.

Duration of the Study

The duration of the research was one year (June, 2017- May, 2018). Four seasons were taken into consideration according to Rashid, 1991 and those are Summer (March- May), Monsoon (June – early October), Autumn ((Late October- November) and Winter (December- February).

Sample Collection

The sampling was carried out from the littoral zone of the three selected sites at 50 cm depth during day time (10.00 am. - 3.00 pm) using sterilized bottles. Samples were immediately taken to the laboratory of Microbiology, Department of

Botany of Jahangirnagar University. Then they were preserved at 4°C and analyzed within 24 hours.

Culture Media

Bacterial culture media like Nutrient agar (NA), Mannitol Salt Agar (MSA), Eosin Methylene Blue Agar (EMBA), MacConkey Agar (MacA), Cetrimide Agar (CA), Bouillon Agar (BA), Brilliant Green Agar (BGA), Salmonella Shigella Agar (SSA), Simmon Citrate Agar (SCA) and Motility Indole Urease (MIU) media were used in this investigation and prepared by the proposed methods of manufacturers.

Bacteriological Analysis

Aerobic heterotrophic bacterial enumeration and isolation was carried out using nutrient agar medium while enteric and related bacteria were on MacConkey agar medium. For the enumeration and isolation of bacteria two different techniques were used namely serial dilution plate (APHA, 1998), spread plate (Sharp and Lyles, 1969). After 24-hour incubation at 37°C temperature bacterial colonies were recorded. Bergey's was followed for the identification of Gram-positive bacterial isolates were identified according to the manual for Systematic Bacteriology (Sneath *et al.*, 1986). A mercury thermometer was used to record the temperature of air and water at the period of sampling.

Determination of Bacterial Load

It determines the total number of bacteria present in each dilution of every samples. Isolated colonies were measured in colony formation unit (CFU/g) according to the following formula:

$$\text{Number of CFU/ (Volume plated ml x total dilution used)} = \text{Number of CFU/ ml}$$

Collection and analysis were done each month of the studied year and seasonal changes in heterotrophic bacteria was observed.

Morphological Studies

Size, color and shape of bacterial colony were studied in ten different media (NA, MSA, EMBA, MacConkey, MSA, CA, BA, BGA, SSA and SCA).

Biochemical Test for Bacterial Isolation

Catalase Test

The formation of bubbles (O₂) via contact of bacterial colony with Hydrogen per oxide is the evidence of catalase activity. As a differential test, the catalase test is used to distinguish between *Streptococci* (catalase negative) and *Staphylococci* (catalase positive).

Carbohydrate Fermentation Test

Carbohydrate fermentation tests demonstrate fermentation of sugars like glucose, lactose or sucrose. The fermentation is noted by acid and gas production by bacterial cells.

Indole Test

It is important in the identification of Enterobacteria. Most strains of *E. coli*, *Pseudomonas vulgaris*, *P. rettgeri* and *Providencia* species break down the amino acid tryptophan with the release of indole. It is used as part of the IMViC procedures, a test designed to distinguish among members of the family Enterobacteriaceae.

Starch Hydrolysis Test

It is a biochemical test, also known as amylase test is used to determine the ability of bacteria in producing and utilizing

starch as carbon source. This test differentiates species of *Bacillus*, *Pseudomonas*, *Enterococcus*, *Clostridium*, *Corynebacterium* and *Streptococcus* genus.

Motility Test

It is used in determination of motility of pathogenic microorganisms (such as the typhoid *Bacillus*) by slide techniques. For this test MIU medium (Motility Indole Urease medium) is used which is a combination of differential medium that tests three different parameters, Urea Production, Indole Production and Motility.

Methyl Red test (MR test)

It is used to differentiate members of the Enterobacteriaceae family and consecutively followed by the VP test.

Voges-Proskauer (VP) Test

The VP test is used primarily to separate *Escherichia coli* (VP-negative) from the *Klebsiella-Enterobacter* groups (VP-positive).

Endospore Staining

It is a technique used in bacteriology to identify the presence of endospores in a bacterial sample. Special techniques for endospore staining include the Schaeffer-Fulton stain and the Moeller stain.

Gram Staining

It is a differential staining procedure that classify bacteria to either Gram positive or Gram negative

Coagulase Test

To identify primarily *Staphylococcus aureus*, by detecting the presence of the enzyme coagulase through the coagulase test.

RESULTS AND DISCUSSION

Heterotrophic Bacterial Count along with Seasonal Variations

The variation of air and water temperature were recorded throughout the study period (Fig. 1). During the study period, variation of microbial load among the three water bodies found significant. Heterotrophic bacterial count varied from 17-100 cfu/ml for Site-1, 19-45 cfu/ml for Site-2 and 17-85 cfu/ml for Site-3. The highest monthly average of heterotrophic bacterial count was recorded in the month of February for Site-1 and Site-2 and January for Site-3 whereas the lowest mean heterotrophic bacterial count was recorded in the month of July for Site-1, Site-2 and Site-3 (Fig. 2). Bacterial counts were highest during winter and lowest during monsoon for all the counts (Fig. 3). In this investigation, the reduction of microbial concentration during monsoon might be because of extensive rainfall and high temperature (Table 2) that is similar to the finding of the research carried by Sikdar *et al.*, 2019. They observed a significant reduction of surface water microbiota of river and lake water of Dhaka city. While, heterotrophic bacterial count was found to be increased during rainy season in another investigation that might be due to the runoff (Saha *et al.*, 2009). In winter, both temperature and rainfall decrease and water concentration increases resulting the elevation of microbial load in water bodies. Bacterial count was comparable due to the spatial distribution of water bodies. Additionally, fluctuation of count with seasons throughout the year was noticeable in this investigation and also reported by that was reported by Sikdar *et al.*, for Banani and Dhanmondi lake of Dhaka city in 2018.

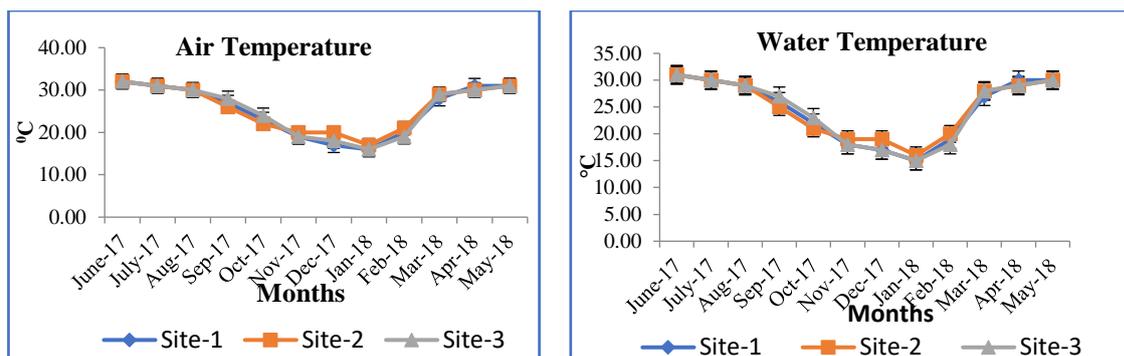


Figure 1: Graph Showing Monthly Variation of Mean Air and Water Temperature of the Study Sites

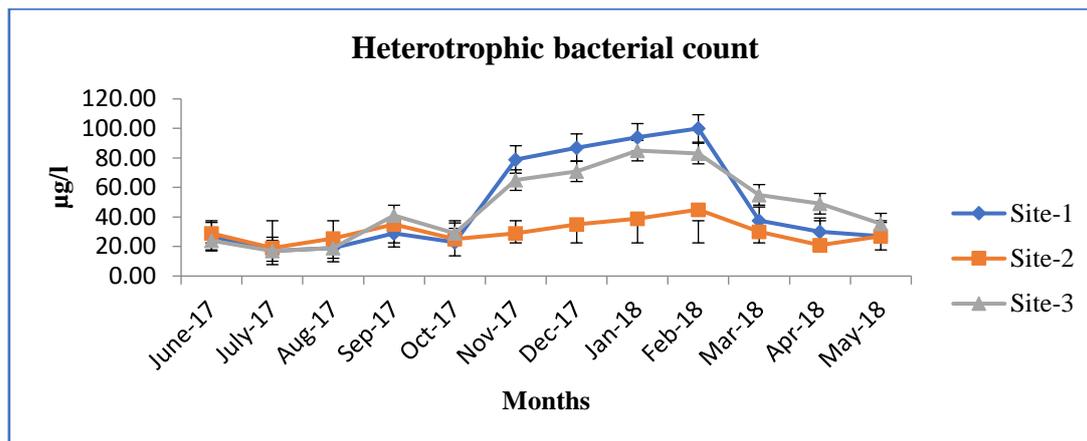


Figure 2: Graph Showing Monthly Variation of Heterotrophic Bacterial Count for the Site-1, Site-2 and Site-3

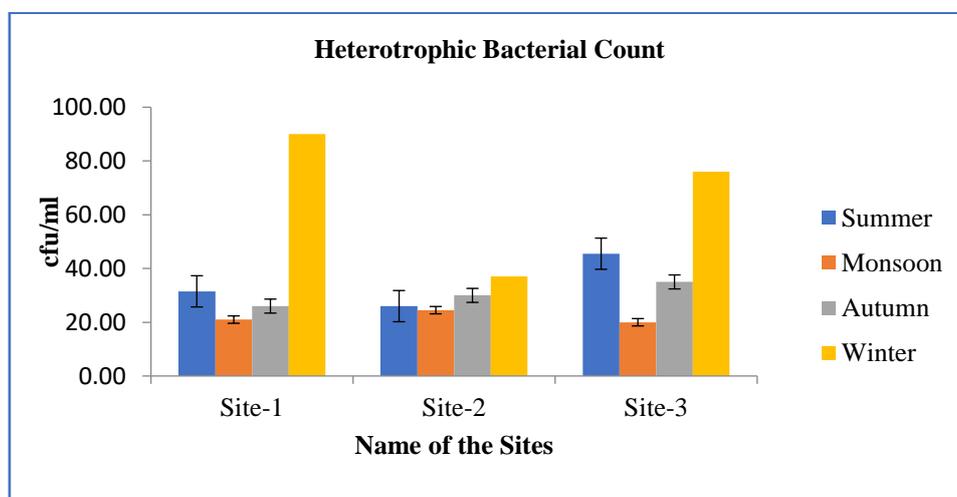


Figure 3: Seasonal Variation of Heterotrophic Bacterial Count for the Site-1, Site-2 and Site-3.

Table 1: Seasonal Mean Air Temperature, Water Temperature and Microbial Load

Year	Site-1			Site-2			Site-3		
	Mean AT (°C)	Mean WT (°C)	Microbial load (cfu/ml)	Mean AT(°C)	Mean WT(°C)	Microbial load (cfu/ml)	Mean AT(°C)	Mean WT(°C)	Microbial load (cfu/ml)
2017-2018									
Summer	30	30	31.50	30	30	26.00	30	30	45.50
Monsoon	31	31	21.00	31	31	24.50	31	31	20.00
Autumn	26	25	26.00	27	27	30.00	26	26	35.00
Winter	18	21.5	90.00	19.5	19.5	37.00	18	18	76.00

Coliform Count

In the present study, the total coliform count in Mac Conkey media was nil for all the studied sites (Table 2 & Photograph-d) indicating the water of study sites were free of fecal

contamination and potential pathogenic organisms. The water bodies under present investigation are reserved and the water has minimal impact of sewage disposal or agricultural runoff. Absence of fecal coliform might be due to zero human

interference. Similarly, fecal coliform contamination was absent at Kajaga site of Burundian coast of Lake Tanganyika (Niyoyitungiye *et al.*, 2020). According to the present study (absence of coliform bacteria), it is not confirmed that there is

zero contamination and water is potable since bacteria are highly sensitive to disinfection of laboratory equipment (Payment *et al.*, 1997).

Table 2: Morphological Characteristics of Bacterial Colonies Isolated from Mac Conkey Medium

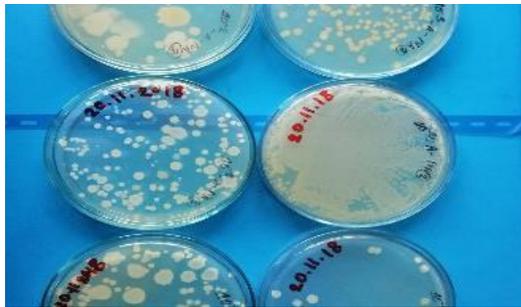
Features	Bacterial isolates							
	J1	J2	J3	J4	J5	J6	J7	J8
Colorless	-	-	-	-	-	-	-	-
Pink	-	-	-	-	-	-	-	-
Fade Pink	-	-	-	-	-	-	-	-
Growth	-	-	-	-	-	-	-	-

Isolation and Characterization of Aquatic Bacteria

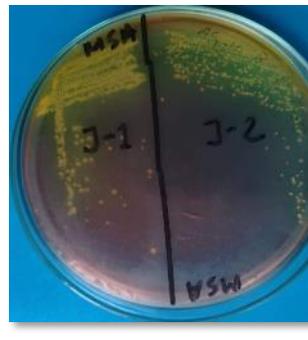
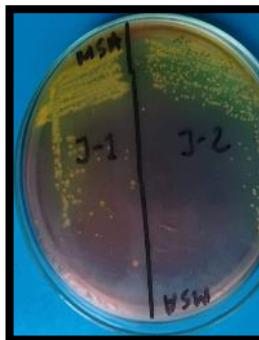
Morphological Characterization of Bacterial Isolates

Primarily 20 isolates were selected and 8 were finalized and identified on the basis of morphological characteristics, biochemical tests and Gram staining reaction. (Table 2 to Table 9). Most common color of the bacterial isolates was

found white but off white, yellow and orange colored colony were also abundant. The common size was moderate whether large and small sizes were also present. Most of the colonies gave shiny appearance, smooth texture and opaque optical density (Table 3 Photograph a).



Nutrient Agar (NA) Media (a)



MSA medium (b)

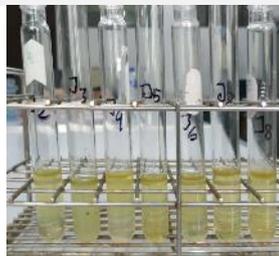
Bouillon Agar medium (c)

Mac Conkey medium (d)

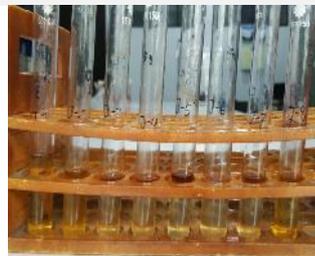
Simmon Citrate medium (e)



Fermentation test (f)



Indole test (g)



Methyl Red test (h)



Voges Proskaur test (i)



Starch Hydrolysis test (j) Motility indole Urease test (k) Catalase test (Bubble formation) (l) Endospore staining (m)

Figure 4: Characterization of Bacterial Isolates in Selected Media and through Biochemical Tests

Table 3: Morphological Characterization in Different Media

Isolates	MacConkey	MSA	EMB	Bouillon Agar	Cetrimide Agar	SSA	BGA	Simmon Citrate
J-1	---	Yellow colony	--	--	--	--	--	--
J-2	--	Yellow colony	--	-	--	--	--	--
J-3	--	--	--	White colony	--	--	--	--
J-4	---	--	---	White colony	--	--	--	--
J-5	--	Yellow colony	--	Yellow colony	--	--	--	--
J-6	--	Yellow colony	--	Yellow colony	--	--	--	--
J-7	--	--	--	--	--	--	--	--
J-8	--	--	---	--	--	--	--	--

'-' means no growth

Table 4: Response to Different Biochemical Tests

Bacterial isolates	Biochemical tests							
	Catalase test	Motility test	Fermentation test	Indole test	Endospore staining	Starch hydrolysis	MR test	VP test
J1	+ve	-	-	-	-	-	-	-
J2	+ve	-	-	-	-	-	-	-
J3	+ve	+ve	-	-	+ve	-	-	-
J4	+ve	+ve	-	-	+ve	-	-	-
J5	+ve	-	-	-	-	-	-	-
J6	+ve	-	-	-	-	-	-	-
J7	+ve	+ve	-	-	+ve	-	-	-
J8	+ve	+ve	-	-	+ve	-	-	-

Table 5: Morphological Characteristics of Gram Staining

Features	Bacterial isolates							
	J-1	J-2	J-3	J-4	J-5	J-6	J-7	J-8
Staining color	Purple	Purple	Purple	Purple	Purple	Purple	Purple	Purple
Shape	Round, grape-like clusture	Round, grape-like clusture	Rod, chain-like structure	Rod, chain-like structure	Round, grape-like clusture	Round, grape-like clusture	Rod, chain-like structure	Rod, chain-like structure
Identification	Gm +ve	Gm +ve	Gm +ve	Gm +ve	Gm +ve	Gm +ve	Gm +ve	Gm +ve

Biochemical Characterization of Bacterial Isolates

In the present study, 4 among 8 isolates were identified as *Staphylococcus aureus* and rest of the 4 were as *Bacillus* sp. through their typical colony characteristics onto specific culture media and several biochemical tests Table 3&4, Photograph b-1). *S. aureus* gave yellow colored colony on MSA media (Table 3 & photograph b). *Bacillus* sp. gave white colored colony on Bouillon agar media (Table 3. Photo. c). Results of biochemical tests of different isolates revealed that

all 8 isolates were Gram positive (Table 5.) They were both rod and cocci shaped.

All the isolates were catalase positive (Table 4 & photograph l) and negative in both fermentation and indole test (Table 4 and photo. F & g). Out of 8 isolates, only 4 isolates showed positive result in motility test (Photograph k) and endospore staining (Photograph m) which indicates the presence of *Bacillus* sp. Among 4 cocci shaped bacteria all were positive for coagulase test which confirmed the presence of *S. aureus*. This study was in agreement with Panneerselvam and

Arumugam (2012) who isolated *S. aureus* and other pathogenic bacterial species from lake water samples around Ranipet area of Vellore District (Panneerselvam and Arumugam, 2012). Pelletier *et al.*, (2014) also isolated *Staphylococcus* sp. from water sources in and around San Salvador Island, Bahamas. A study conducted by Douglas and Isor (2015) showed the presence of *E. Coli*, *Salmonella*, *Streptococcus*, *Bacillus*, *Pseudomonas*, *Micrococcus*, *Shigella*, *Enterobacter*, *Klebsiella*, *Proteus* and *Staphylococcus aureus* from pond water of Ogoniland, Nigeria. *Bacillus* sp. was also isolated from water samples in current study. A study by Shaha *et al.*, 2009, out of 23 isolates, 5 were Gram-positive and among them 4 isolates were rod, spore former and members of the genus *Bacillus* (*B. fastidiosus* and *B. alvei*), clearly indicated that among the Gram-positive bacteria, spore former *Bacillus* was the dominant genus. Among 24 Gram-positive isolates, 17 were rod, spore former and members of the genus *Bacillus* dominated four ponds in Dhaka metropolis, Bangladesh (Saha *et al.*, 2012). No *E. coli*, *Salmonella* sp., *Shigella* sp., *Enterobacter* sp. and *Pseudomonas* sp. was present in the samples of present research, indicating relatively good quality of the water. On the contrary, Gram-negative bacterial isolates belonged to the genus *Sphingomonas*, *Escherichia*, *Enterobacter* and *Klebsiella* were found from the four ponds of Dhaka metropolis. According to Hu *et al.*, (2018) and Zhao *et al.*, (2022) water contamination is correlated to improper land use and sewage disposal. key factors driving contamination include fecal pollution, nutrient-rich sediments, and organic waste accumulation, which provide an ideal environment for bacterial growth. *Escherichia coli*, *Salmonella* spp., *Klebsiella* spp., and other pathogens underscores the risks aquaculture poses to aquatic ecosystems and human health. Due to the direct contamination through human and animal activities *Vibrio* spp., *Salmonella* spp., *Aeromonas* spp. contaminated the water of fish pond in the Osun state (Omotoso *et al.*, 2025).

CONCLUSION

Bacteria are considered as a reliable indicator of water contamination. Some of them play an important role in decomposing organic materials to nutrients and supplying to different parts of aquatic ecosystem. Thus, they help in nutrient cycling processes. The studied water sample contained a good number of heterotrophic bacteria. Absence of fecal coliform indicate zero fecal pollution. It may be safe for birds and suitable for activities like swimming but not for drinking without further study. On the contrary, presence of *Bacillus* and *Staphylococcus aureus* do not permit human activities in the studied water bodies.

REFERENCES

Acharjee, M., Jahan, F., Rahman, F., & Noor, R. (2013). Bacterial proliferation in municipal water supplied in Mirpur locality of Dhaka city, Bangladesh. *CLEAN- Soil Air Water*, 41, 1-8.

Akonda, A.W. (1989). Bangladesh. In: A directory of Asian Wetlands, Scott DA (Ed), 541-581. IUCN, Switzerland and Cambridge.

APHA (1998). Standard methods for the examination of water and waste water. American Public Health Association, Water Pollution Control Federation, Washington D.C., 20th edition, 10-161.

Bhuiyan, M..A.H, Khondker, M., & Begum, Z. N. (2010b). Other side of the Ashulia Wetland: A limnological preview. *Dhaka University Journal of Biological Sciences*, 19 (1), 21-26. <https://doi.org/10.3329/dujbs.v19i1.8940>

Bhuiyan, M..A.H., Khondker, M., & Begum, Z.N. (2010a). Diversity in the pelagic plankton of wetland Ashulia. *Journal of Taxonomy and Biodiversity Research*, 4, 09-16.

Douglas, S.I., & Isor F 2015. Bacteriological Investigation of Pond Water Quality from Ogoniland, Nigeria. *IOSR Journal of Environmental Science, Toxicology and Food Technology*, 9(2), 36-41.

Hirsch, A. (1958). Biological evaluation of organic pollution in New Zealand streams, *New Zealand Journal of Science*, 1, 500-533.

Hu, J., Zhao, F., Zhang, X. X., Kan, L., & Mei, L. (2018). Metagenomic profiling of ARGs in airborne particulate matters during a severe smog event. *Science of the Total Environment*, 615, 1332-1340. <https://doi.org/10.1016/j.scitotenv.2017.09.222>

Hussainy, S.W., & Abdulappa, M.K. (1967). Expression of biological data in water pollution research. *Environment. Health*, 9(3), 210-219.

Munshi, S. K., Rahman, M.M., & Noor, R. (2012). Detection of virulence potential of diarrheagenic *Escherichia coli* isolated from surface water of rivers surrounding Dhaka city. *Journal of Bangladesh Academy of Sciences*, 36 (2), 109-121.

Niyoyitungiye, L., Giri, A., & Ndayisenga, M. (2020). Assessment of Coliforms Bacteria Contamination in Lake Tanganyika as Bioindicators of Recreational and Drinking Water Quality. *Academic Leadership*, 2020, Article no. *South Asian Journal of Research and Microbiology*, 57764, 6 (3), 9-16. [ff10.9734/SAJRM/2020/v6i330150ff](https://doi.org/10.9734/SAJRM/2020/v6i330150ff). fhal02880918

Obi, C.L., Potgieter, N., Bessong, P.O., & Matsaung, G. (2002). Assessment of the microbial quality of river water sources in rural Venda communities in South Africa. *Water SA*, 28, 287-292.

Okonko, I. O., Ogunnusi, T.A., Adejoye, O.D., & Shittu, O.B. (2008). Microbiological and physicochemical analysis of different water samples use for domestic purposes in Abeokuta, Ogun State and Ojota, Lagos State, Nigeria. *African Journal of Biotechnology*, 7 (5): 617-621. 19.

Omotoso, A. J., Solomon, O. A., & Opasola, O. A. (2025). Bacteria Isolated from Fish Pond Water and Sediment in Selected Fish Pond Ecosystems in the Osun State: Multidrug Resistance Profiles. *Fountain Journal of Basic Medical and Health Sciences (FUJBMHES)*, 1(1), 114 – 130.

Panneerselvam A and Arumugam G 2012. Isolation and Identification of Bacteria from Lake Water in and Around Ranipet Area, Vellore District. *International Journal of Pharmaceutical & Biological Archives*, 3(4):1008-1011.

Payment, P., Siemiatycki, J., Richardson, L., Renaud, G., Franco, E., & Prevost, M. A. (1997). Prospective epidemiological study of gastrointestinal health effects due to the consumption of drinking water. *International Journal of Environmental Health Research*, 7, 5-31.

- Pelczar, M.J., Chan, E.C.S., & Krieg, N.R. (1988). *International Journal of Hygiene and Environmental Health*, 208(5), 425–433.
- Pelletier, M., Haynes, J. M., Dungan, A.M., & Kroeckel, J. (2014). Identification of the microbial population found in water sources in and around San Salvador Island, Bahamas. *The International Journal of Bahamian Studies*, 20(1), 27-37. <https://doi.org/10.15362/ijbs.v20i1.196>
- Rashid, H. Er. (1991). *Geography of Bangladesh*. Univ. Press Ltd. Dhaka, 529.
- Saha, M. L., Nessa, M., Khan, M. R., Islam, M. N., & Hoque, S. (2012). Bacteriological and Physicochemical Water Quality of Four Ponds of Dhaka Metropolis. *Bangladesh Journal of Botany*, 41(1), 55–60. <https://doi.org/10.3329/bjb.v41i1.11083>
- Saha, M.L., Khan, M.R., Ali, M., & Hoque, S. (2009). Bacterial load and chemical pollution level of the river Buriganga, Dhaka, Bangladesh. *Bangladesh Journal of Botany*, 38, 87-91.
- Sharma, A., Dubey, N., & Sharan, B. (2005). Characterization of aeromonads isolated from the river Narmada, India.
- Sharp, M.S., & Lyles, S.T. (1969). *Laboratory Instruction in Biology of Microorganism*. C. V. Mosley Company. 23-25. pp.
- Sikdar, M. S. S., Abony, M., Zerín, T., Banik, A., & Datta, S. (2019). Seasonal variation of bacterial load in river and lake waters of Dhaka city, Bangladesh. *Bangladesh Journal of Microbiology*, 35(2), 116–121. <https://doi.org/10.3329/bjm.v35i2.42640>
- Sneath, P.H.A., Mair, N.S., Sharpe M.E., & Holt, J.G. (1986). *Bergey's Manual of Systematic Bacteriology* (9th edn. Vol. 2). The Williams and Wilkins Co., Baltimore, USA. 1599.
- Zhao, R., Yu, K., Zhang, J., Zhang, G., Huang, J., Ma., L. (2020). Deciphering the mobility and bacterial hosts of antibiotic resistance genes under antibiotic selection pressure by metagenomic assembly and binning approaches. *Water Research*. 186:116318. doi: <https://doi.org/10.1016/j.watres.2020.116318>

