MICROBIAL PROFILING OF A FRESH WATER AQUACULTURE POND WITH EMPHASIS ON BACTERIA AND FUNGI IN TAMIL NADU, INDIA

ABSTRACT

As an agriculture has almost reached its saturation level, the contribution of fish in fighting hanger and nutritional security has come to be widely recognized as fish is a low cost and high quality animal protein which can be consumed by all cadres of individuals regardless of their religious beliefs and nutritional preferences. However, it is now well known that fishes and the environment can harbour potential pathogenic microbes including bacteria and fungi and hence the present study. During the presummer season 7 species of bacteria were isolated from the water and 6 species bacteria in the skin of ***Catla catla*** while the summer season recorded only 5 bacterial species in water and 4 in the skin of *Catla catla*. The post summer and rainy seasons recorded 6 and 9 bacterial species both in water, and the skin of *Catla catla* respectively. Regarding the fungal species the presummer and rainy season recorded 8 species in water while the summer seasons recorded 6 species and the post summer season recorded only 5 species in water. The skin of *Catla catla* recorded 6 fungal species during presummer and rainy season whereas only 5 species were recorded in postsummer and 4 species in summer season in the skin of *Catla catla*. All the species recorded in the skin of *Catla catla* were also found in water. The system and the skin of *Catla catla* recorded both beneficial and harmful microbes. The study clearly suggests the need for the constant monitoring of microbes so that the health of fishes can be maintain by the use of appropriate therapeutic measures as and when necessary.

Keywords:

Microbes, Bacteria, Fungi, *Catla catla,* Fresh water aquaculture, Seasonality

INTRODUCTION

With India's fast-developing population, the need for maximizing all possible means of food production is a prerequisite. Based on reports by the National Health and Family Survey and the World Health Organization, rates of malnutrition among adult women, expectant and nursing mothers, and children continue to be alarmingly high in India. Since agriculture has almost reached its saturation level, the contribution of fish in fighting hunger and nutritional security has come to be widely recognized, as fish is a low-cost and high-quality animal protein source. Fish is preferred as a protein source as it can be consumed by all cadres of individuals regardless of their religious beliefs and nutritional preferences (**Agwaranze *et al.,* 2024**). Thus has resulted in the preference of fish over other sources of animal proteins such as pork or red meat (Njoku *et al.,* 2015). In addition, fish can be processed for commercial purposes or preserved so that it can remain unsplit for a long time or can be eaten fresh, dry or smoked (**Agwaranze *et al.,* 2020**).

India has an impressive range of inland water bodies ranging from tiny temporary pools to large perennial reservoirs and wetlands of varying sizes. These water bodies cover an area of about 4.5×10^6 hectares, and these water bodies are providing enormous scope for aquaculture development for increased food production.

It is now well known that fishes and their environment can harbor pathogenic microbes including bacteria and fungi. If not properly treated, this condition can cause extensive loss to aquaculturists besides transmitting these pathogens to handlers and consumers. Hence, it is pertinent to include microbial analysis in culture systems to monitor and provide suitable remedies.

With the global population projected to reach 9 billion by the middle of the century and challenges such as climate change and environmental degradation threatening food security, aquaculture is expected to play a pivotal role in ensuring sustainable food production on a global scale (Forsberg, 1982; Bais & Agarwal, 1990; Morris & Mischke, 1999; Petchey, *et al.,* 1999; Meerhoff *et al.,* 2007; Suseela, 2009; Ismael, 2019; Ahmed, *et al.,* 2013; Kather, *et al.,* 2015; FAO, 2016; **Annamali, *et al.,* 2023**). In this context, the present study was conducted in a perennial pond in Swamimalai, located in Thanjavur District, Tamil Nadu, India.

MARTIALS AND METHODS

Location and Sample collection

For the present investigation, the samples were collected from the pond at Kumbakonam District, Tamil Nadu, during the year 2024 and 2025. The water samples were taken in plastic containers kept in an ice box and brought to the laboratory.

Bacterial Analysis and Its Identification

Water samples for microbiological analysis were aseptically sampled in sterile 500 ml bottles and delivered to the laboratory, where they were examined within 1 to 2 hours from sampling time. The examination involved the determination of total and fecal coliforms, fecal Streptococci, and pathogenic Salmonella using the most probable number (MPN) method as described by the **American Public Health Association (2005).** For determination of the total viable count (TVC) of the heterotrophic bacteria, nutrient agar was utilized, and plates were incubated at 28°C for a period of 48 hours.

For the qualitative identification of bacterial species in both water and fish samples (scientific name of studied fish species must be mentioned), we inoculated M-FC agar in duplicate and incubated them for 24 hours at 37°C. After the incubation period, we identified distinct colored bacterial colonies that appeared on the plates, following the methodologies described by Edwards and Ewing (1972), Cowan (1974), Martin and Washington (1980), Brenner (1984), Cheesbrough (1989), and Cabral (2010).

Identification and Colony Counting of Fungi

Fungi are known for their relatively slow growth rates, often taking several days to weeks to fully develop. They produce spores on vibrant, colorful aerial hyphae and generally prefer room temperature (around 25°C) over the warmer 35°C. The PDA medium is used for growing fungi.

After sterilizing the medium, it was carefully poured into sterile petri dishes under aseptic conditions. Each dish was labeled as either a control or a sample plate. To keep bacterial contamination at bay, a small amount of streptomycin was mixed into the medium before it was poured into the plates. The sample preparation followed the serial dilution method.

Inoculation

Seven petri plates filled with solidified agar were labeled as control, 10^{-1}, 10^{-2}, 10^{-3}, 10^{-4}, 10^{-5}, and 10^{-6} dilutions. Inoculation took place using a micropipette inside an inoculation chamber. The diluted sample was carefully transferred onto the culture plates with a microculture medium. Each plate was gently rotated to ensure the organisms were evenly distributed while avoiding any splashing. This process was repeated for all six dilution plates.

Additionally, another set of seven petri plates containing solidified PDA medium was labeled as control and sample plates. Diluted samples from the 10^{-4} dilution were transferred onto these PDA plates using a micropipette. The plates were then placed in the culture chamber at room temperature (25°C) for 6–7 days to encourage fungal growth. The same procedure was applied to all other samples.

Colony Counting

Once the fungal colonies had fully developed, they were counted directly using a counting chamber. The average number of fungal colonies in each sample was recorded for further analysis.

Isolation of Fungi

A small portion of fungal growth was carefully transferred from the culture to a microscope slide using a dissecting needle, followed by staining to aid in identification.

Staining of Fungi

Lactophenol cotton blue stain was used to stain Fungi and identified by the help of available literature (Gerba & Mcleod, 1976).

RESULTS AND DISCUSSION

Bacterial Studies

Bacterial count in water during the period of study was found to vary from 2×10^3 to 9.2×10^5 Cfu/ml with the minimal level being recorded in May, with the maximum observed in November (Table 1-2).

Season wise identification of the different bacterial species disclose that during the presummer season, 7 bacterial species could be identified in the water samples (*Escherichia*

coli, *Pseudomonas aeruginosa*, *Enterobacter aerogenes*, *Salmonella typhi*, *Staphylococcus aureus*, *Vibrio alginolyticus* and *Streptococcus faecalis*). The skin of *Catla* recorded the presence of 6 bacterial species. All the six bacterial species found in fish were also recorded in water. However, *S. aureus* which was present in water could not be detected in the skin samples of *Catla* (Table 2).

The summer season recorded the presence of 5 species. Of these, 4 species (*E. coli*, *S. aureus, P. aeruginosa* and *S.faecalis*) were also recorded in the presummer season. The new species that was recorded in the summer season, *Proteus vulgaris* was not found during the presummer season. The skin of *Catla* showed the presence of 4 bacterial species; in which 3 were recorded in the water sample (*E. coli*, P. *vulgaris* and *P. aeruginosa*). The 4th species, *E. aerogenes* that was recorded in fish skin was not recorded in the water samples (Table 1-2).

The post summer season, recorded the presence of six bacterial species in the water samples. Of these, 4 species (*S. aureus, E. coli*, *P. aeruginosa* and *S. faecalis*) were recorded during the presummer and summer seasons also in the water samples. *E. aerogenes* which was recorded in the post summer and presummer seasons was not recorded in the water sample of the summer season. Similarly, *P. vulgaris* which was recorded in the post summer and summer seasons was not observed during the presummer season. The skin of *Catla* recorded 5 bacterial species. Of these, all the species except for *P. vulgaris* that were recorded in water were also found in the skin of the fish (Table 2).

The rainy/winter season recorded the presence of 9 bacterial species in water. Of these, only 4 species (*S. aureus, E. coli*, *P. aeruginosa*, and *S.faecalis*) were recorded during all the four seasons. The remaining species (*E.aerogenes*) was recorded during the presummer and post summer season while *P.vulgaris* was recorded during the summer and post summer season and *S. typhi* along with *V.alginolyticus* was recorded only in the presummer season along with the rainy/ winter season. However, *Klebsiella pneumoniae* was recorded in the water samples only during the rainy/winter season and was absent in all other seasons in the water samples. The skin of *Catla* was represented by 7 species. All the species that were recorded in the water samples except for two species (*E. aerogenes* and *K.pneumoniae*) were recorded in the skin of the fish (Table 2).

Variability in bacterial density seen in the present study concurs with the evidence reported by Antony and Renuga (2012), who determined that bacterial contamination sources include surface run-off, animal waste-contaminated pasture areas, leakage from septic tanks,

and naturally occurring plant and soil bacteria. Further, Gerba and McLeod (1976) hypothesized that organic matter in the presence of aquatic bacteria will facilitate the survival of aquatic bacteria, which would contribute to increased bacterial concentration (Sugita, *et al.,* 1985; Surendraraj, *et al.,* 2009).

Apun *et al*. (1999) obtained a positive correlation between fish and pond water Total Plate Count (TPC), whereas other workers have also observed both positive and negative correlations with temperature, salinity, and the overall quality of the pond microbial population. Bacterial count in this study had a positive correlation with temperature (r = 0.68; r = 0.72)

Various investigators (Sharma & Hobson, 1985; Eva *et al.,* 2014; Barker & Brown, 1994; Baldy *et al.,* 2002; Chauhan *et al.,* 2009; Pawar *et al.,* 2023) have also documented a direct correlation between bacterial counts and the trophic status of an environment. When resources are plentiful, competitive species will prevail, pushing less competitive species aside, which has a subsequent impact on the total bacterial community structure. In this research, the maximum bacterial load was noticed during the rainy season. Literature suggests that similar reports have also been reported by others (Kistemann *et al*., 2002; Rajkumar & Sharma, 2013). According to Kistemann *et al*. (2002) during rainfall, microbial loads would increase in the system as a result of the entry of runoff water which would have brought microbes from afar. This would be the reason in the present study also resulting in increased load during the rainy season.

In this work, a total of a 9 bacterial species could be identified. An deep analysis of literature disclose that the species recorded in the system are common as they have been observed in many other acquatic systems also. According to Madigan *et al*. (1997) and Michaud *et al*. (2012) the members of the genus *Pseudomonas* are most adaptive in nature with exceptional metabolic activity and hence are able to **colonise** a variety of niches while Rajkumar and Sharma (2013) attributed the presence of *Pseudomonas* in all seasons in aquatic systems to human activities and sewage discharge. Turner *et al*. (2009) reported variations in *Vibrio* populations with seasons and planktonic composition. The presence of *Klebsiella pneumoniae* can probably be attributed to its entry into the system as a result of runoff water as it was noticed only during the rainy season and was not recorded in other seasons.

Microbial analysis of the skin of *Catla* revealed the presence of 8 bacteria. A comparison of the water and skin microbes disclose that the skin recorded all the bacteria that were observed in water except for the presence of *K. pneumoniae*. This clearly suggests that

the bacterial content in the skin of fish is a reflection of what is found in water. Similar observations were also recorded by others (Liston, 1980).

A perusal of literature discloses that Sinha *et al*. (1991) recorded the presence of *Salmonella*, *Staphylococcus*, *Aeromonos*, *Pseudomonas*, *Proteus*, and *Klebsiella* was observed in rohu. Several workers have reported the bacterial load in *L. rohita* / freshly harvested fish to range between 10^3-19^5/g (Nair *et al.,* 1971; Bandyopadhyay *et al.,* 1985; Surendran *et al.,* 1989; Ali *et al*., 1992; Jeyasekaran & Ayyappan, 2003) reported that the initial flora of *Tilapia* consisted of *Psendomonas, Vibrio, Acinetobacter Moraxella, Micrococcus, Alcaligenes, Entero bacteriaceae, Flavobacteria, Bacillus, Streptococcus* and others while Ali *et al*. (1992) reported freshly harvested *L.rohita* to consist of *Staphylococcus, Acineto bacter, Micrococcus, Enterobacteriaceae, Aeromonas, Moraxella* and *Pseudomonas* while Lilabati and Vishwanath (1998) detected coliforms, *Staphylococcus, Streptococcus, Pseudomonas Moraxela, Acinetobacter, Lactobacillus, Bacillus, Aeromonas, Flavobacterium* and *Micrococcus* from fresh water fish. Jeyasekaran and Ayyappan (2003) reported the presence of *Staphylococcus, Lactobacillus, Micrococcus* and *Bacillus* in *L.rohita*. Thus, the presence of various bacterial species recorded in the skin of fish is in line with those reported by others.

Variability in bacterial concentration noted in this research is consistent with observations by Antony and Renuga (2012), who attributed origin of bacterial contamination to include surface runoff, pasture area animal waste, leakage from septic tanks, sewage treatment facilities, and naturally occurring soil and plant bacteria. Gerba and McLeod (1976) further mentioned that the presence of organic matter facilitates the survival of aquatic bacteria, leading to higher concentration of bacteria (Sugita, *et al.,* 1985; Surendraraj, *et al.,* 2009).

Apun *et al*. (1999) found a positive correlation between fish and total plate count (TPC) of pond water, whereas other workers have observed positive and negative correlations with temperature, salinity, and general pond microbial quality. In the current study, bacterial count was positively correlated with temperature ($r = 0.94$, $r = 0.72$).

A number of researchers (Sharma & Hobson, 1985; Eva *et al.,* 2014; Barker & Brown, 1994; Baldy *et al.,* 2002; Chauhan *et al.,* 2009; Pawar *et al.,* 2023) have also identified a direct correlation between bacterial abundance and the trophic level of an environment. In a rich resource environment, more competitive species will predominate over less tolerant species, ultimately shaping the overall bacterial community structure.

Fungal Studies

Fungal count in the water samples of the system was found to range between 1.7 to 3.4 × 10^2 Cfu/ml. The minimum count was recorded in May and the maximum during November (Table 2).

During the period of study, 8 species of fungi could be isolated in the system during the different seasons of the year. The **presummer** season recorded the presence of all the 8 species (*Aspergillus niger,Fusarium oxysporum, Aspergillus flavus, Pencillium notatum, Aspergillus terreus, Achlya apiculata, Trichoderma viride and Saprolegnia diclina*). The skin of *Catla* also showed the presence of all the 8 species of fungi that were found in the water samples (Table 2).

The summer season on the other hand, recorded only 6 species of fungi. All the species of fungi that were recorded in the water samples during the **presummer** season was also recorded in this season except for the presence of two species (*A. flavus* and *T.viride*) that were not recorded. The skin of *Catla* also recorded all the six species of fungi that were observed in water during this season (Table 2).

The post summer season recorded the presence of only 5 species in the water sample. Thus *A. flavus*, *F. oxysporum* and *S. diclina* were not recorded in this season while all the other species that were noticed in the post summer season were observed in this season also. The skin of *Catla* also recorded all the 5 species of fungi that were recorded in water in this season.

The rainy/winter season again recorded all the 8 species that were noticed in the water samples during the **presummer** season. The skin of *Catla* also recorded all the 8 species of fungi that were recorded in this season (Table 2).

Thus an overall comparison of all the four seasons discloses that 4 out of the 8 species (*A.niger, A. terreus, P.notatum* and *A.apiculata*) were perennial as they were noticed in all the four seasons (Table 2).

The fluctuation in fungal species seen in this research seems to be consistent with results from other studies. Temperature has been recognized as a critical environmental parameter that affects microbial metabolism, growth, and survival by Madigan *et al*. (2009). Likewise, temperature variations can greatly influence patterns of abundance at seasonal and regional scales and fungal community composition by **Barlocher (1992)**. In addition, Barlocher (1992) also indicated that aquatic hyphomycete richness is found to be increased within a range of moderately wide pH of 5 to 7, but richness decreases if outside this. In addition to that,

environmental conditions with low pH, alkalinity, and calcium content augment the sensitivity of aquatic hyphomycetes towards heavy metal toxicity (Abel & Barlochert, 1984). Several other studies have also established that human-acidification of aquatic ecosystems can result in a significant decline in fungal diversity and activity (Chamier, 1985; Chamier & Tipping 1997; Baudoin *et al.,* 2008) Sridhar (2009) observed a positive relationship between fungal diversity and nitrates and phosphates while Krauss *et al*. (2011) reported that stress factors like nitrate, heavy metal, sulfate and low oxygen concentrations are connected to reduced fungal diversity and biomass. In the present study, there was a positive correlation between pH., alkalinity, Ca, NO_3 SO_4 PO_4 thus revealing their inter relationship ($r = 0.64$; $r = 0.72$). This could be the reason why maximum fungal count was recorded in November in the present study.

Analysis of literature regarding fungi identified in this study disclose that many workers have reported the presence of these fungi in various aquatic systems in India (Sudheep & Sridhar, 2011; Nizamydeen *et al.,* 2014; Hestrin *et al.,* 2019, Mehboob *et al.,* 2021).

In this study, there was a relative abundance of the Family Trichocomaceae which includes *Aspergillus* and *Penicillium*. In this study, 3 species of *Aspergillus* were recorded along with a species of *Penicillium.* Potekhina *et al*. (2020) suggested that water hardness and increased NO_2 and NO_3 content in water contribute to the growth of *Aspergillus* sp. In this study also, there was a positive correlation between fungi and NO_2 and NO_3 ($r = 0.42$; $r = 0.94$). Houbraken and Samson (2011) have reported members of this family have a diverse metabolic potential and secrete several pharmacologically important secondary metabolites. Ramya Urs *et al*. (2012) suggested that members of this group have a significant correlation with faecal pollution. Khallil *et al*. (2020) reported that *Achlya* sp is one of the most common genera in aquatic systems while Kiziewicz (2004) opined that *Aspergillus* and *Achlya* sp are dominant colonisers on aquatic submerged plants.

A perusal of the fungal flora in the skin of *Catla* revealed that it was the same as that was recorded in water samples. Literature disclose that fungi are known to attack all the life stages of fish right from egg to adults (Bangyeekhum & Sylvie, 2001) in both wild and commercial fish farms. Werren and Neil (1997) opined that every fresh water fish is exposed to **atleast** one species of fungi during the life time.

According to Kalaria *et al*. (2024), most fungal infections noticed in carp culture are those caused by *Saprolegnia*, *Achlya* and *Aphanomyces* species. In this study also, species belonging

to *Saprolegnia* and *Achlya* were identified, thus complementing the observations made by Kalaria *et al*. (2024). According to Mukherjee (2022) the oomycetes fungi are commonly acknowledged as saprophytic entities. Kalaria *et al*. (2024) also suggested that saprolegniasis is more prevalent in cage culture systems and typically lower in pond culture systems except in cases of significant mismanagement.

Thus the system under study had both beneficial and harmful microbes. As disease prevention and mitigation in aquculture is crucial for increasing productivity and diminishing economic losses (Kalaria *et al.,* 2024; **Thanga Kiruba, 2025**) the present study clearly shows the need to take ideal and immediate steps by suggesting constant monitoring of the physio chemical characteristics of the water and health of fishes and the immediate use of therapeutics as and when the need arises.

Table 1

Monthly Occurrence of Microbilogical studies

of a Freshwater Pond at Swamimalai, Tamil Nadu

S.No	Month	Bacterial Count (Cfu/ml)		Fungal Count (Cfu/ml)	
		2024	2025	2024	2025
1.	January	6.6×10^4	6.2×10^3	2.8×10^2	2.2×10^2
2.	February	5.1×10^4	5.4×10^3	3.0×10^2	2.6×10^2
3.	March	4.4×10^4	4.6×10^3	2.1×10^2	2.4×10^2
4.	April	3.7×10^4	3.1×10^3	1.9×10^2	2.0×10^2
5.	May	2.2×10^4	2.0×10^3	1.8×10^2	1.7×10^2
6.	June	2.9×10^4	3.1×10^3	2.2×10^2	2.1×10^2
7.	July	4.4×10^4	4.3×10^3	2.5×10^2	2.4×10^2
8.	August	6.1×10^4	5.5×10^3	2.7×10^2	2.6×10^2
9.	September	7.2×10^5	6.7×10^4	2.8×10^2	2.9×10^2
10.	October	8.4×10^5	7.2×10^4	2.9×10^2	3.1×10^2
11.	November	9.2×10^5	8.3×10^4	3.1×10^2	3.4×10^2
12.	December	7.9×10^4	7.1×10^3	2.9×10^2	3.1×10^2

Table 2

Bacterial and Fungal Species isolated during the

Different Seasaons from the Pond at Swamimalai, Tamil Nadu

	Seasons / Species Details	Pre-Summer Season January – March		Summer Season April – June		Post Summer Season July – September		Rainy/Winter Season October – December	
	Bacterial Species	**Water**	**Fish**	**Water**	**Fish**	**Water**	**Fish**	**Water**	**Fish**
1	*Escherichia coli*	+	+	+	+	+	+	+	+
2.	*Enterobacter aerogenes*	+	+	-	+	+	+	+	-
3.	*Proteus vulgaris*	-	-	+	+	+	-	+	+
4.	*Salmonella typhi*	+	+	-	-	-	-	+	+
5.	*Pseudomonas aeruginosa*	+	+	+	+	+	+	+	+
6.	*Staphylococcus aureus*	+	-	+	-	+	+	+	+
7.	*Klebsiella pneumoniae*	-	-	-	-	-	-	-	-
8.	*Vibrio alginolyticus*	+	+	-	-	-	-	+	+
9.	*Streptococcus faecalis*	+	+	+	-	+	+	+	+
	Total Count	**7**	**6**	**5**	**4**	**6**	**5**	**9**	**7**
	Fungal Species								
1.	*Aspergillus niger*	+	+	+	+	+	+	+	+
2.	*Aspergillus flavus*	+	+	-	-	-	-	+	+
3.	*Aspergillus terreus*	+	+	+	+	+	+	+	+
4.	*Fusarium oxysporum*	+	+	+	+	-	-	+	+
5.	*Penicillium notatum*	+	+	+	+	+	+	+	+
6.	*Achlya apiculata*	+	+	+	+	+	+	+	+
7.	*Trichoderma viride*	+	+	-	-	+	+	+	+
8.	*Saprolegnia diclina*	+	+	+	+	-	-	+	+
	Total Count	8	8	6	6	5	5	8	8

Fish: *Catla catla* skin, I Year 2024, II Year 2025; - Not Found

CONCLUSION

The study showed that the freshwater aquaculture pond at Swamimalai contained culturable bacterial and fungal communities that varied across seasons. Higher bacterial and fungal counts were recorded during the rainy/winter period, while lower counts were observed during summer. Several bacterial and fungal species detected in pond water were also found on the skin of *Catla catla*, suggesting a close relationship between pond-water microbial occurrence and fish-surface microbiota. The presence of potential opportunistic or pathogenic microorganisms indicates the need for regular microbial monitoring in

aquaculture ponds. Improved pond hygiene, water-quality management and periodic microbial assessment may help support fish health and reduce possible risks during culture.

Declaration of AI Use

This manuscript was prepared through the combined contributions of all author(s), including contributions to the study design, data, content development, results, interpretation, and related scholarly work. The author(s) acknowledge the use of Grammarly and ChatGPT to assist with grammar checking, language refinement, reference formatting. These AI-assisted tools were not used as authors and did not replace the intellectual contributions or scholarly judgment of the author(s). All AI-assisted outputs, including content, references, and interpretations, were carefully reviewed, revised, verified, and approved by the author(s). The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

COMPETING INTERESTS DISCLAIMER:

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper.

REFERENCES

Abel, T.H. & Barlochert, F. (1984). Effects of cadmium on aquatic Hyphomycetes Botanical Institute, University of Basel, Applied and Environmental Microbiology, 48(2): 245-251.

Agwwaranze, D.I., Gabriel, U.P. & Ukeachu, N.F. (2024). Microbiological analysis of some fish pond water in Wukari metropolis, Journal of Research in Agriculture and food Sciences., 1(3): 115-120.

Agwwaranze, D.I., Ogodo, A.C., Nwaneri, C.B. & Agyo, P. (2020). Bactriological examination of well water in Wukari, Nigeria. Int J Sci Res Environ Sci., 5(5): 0042-6.

Ahmed, M., Singh, A.K., Mondal, J.A. & Sarkar, S.K. (2013). Water in the hydration shell of halide ions has significantly reduced fermi resonance and moderately enhanced Raman cross section in the OH stretch regions. The Journal of Physical Chemistry B, 117 (33): 9728-9733.

Ali, A., Karunasagar, I. & Karunasagar, I. (1992). Bacteriological changes during iced storage of the tropical freshwater carp, Labeo rohita. Fish. Res., 13: 189-197.

Annamalai, A., Radhakrishnan, K., Gunasekaran, C. & Narasimman, M. (2023). Temporal changes in plankton diversity in relation to hydrographical diaracteristics at

Perumal lake, Cuddalore District, Tamil Nadu, India. The J. Basic and Appl. Zool., 84: 13.

Antony, R.M. & Renuga, F.B. (2012). Microbiological analysis of drinking water quality of Ananthanar Channel of Kanyaakumari District, Tamil Nadu, India. Ambiente Agua-An Interdisciplinary Journal of Applied Science, 7: 42-48.

APHA, AWWA, WEF. (2005). Standard Methods for the Examination of Water and Wastewater (21st ed.). American Public Health Association, Washington, DC.

Apun, K., Yusof, A.M. & Kumbag, J. (1999). Distribution of bacteria intropical freshwater fish and ponds. Int. J. Environ. Hlth Res., 9: 285-292.

Bais, V.S. & Agarwal, N.C. (1990). Seasonal variations of nitrogen contents in the sediment and water of the Sagar Lake. Bulletin of Environmental and Scientific Research, 8: 21-24.

Baldy, V., Chauvet, E., Charcosset, J.V. & Gessner, M.O. (2002). Microbial dynamics associated with leaves decomposing in the mainstem and floodplain pond of a large river, Aquatic Microbial Ecology, 28: 25-36.

Bandyopadhyay, J.K., Chattopadhyay, A.K. & Bhattacharyya, S.K. (1985). Studies on the ice storage characteristics of commercially important freshwater fishes. In: Harvest and Post-harvest Technology of Fish, pp. 120.

Bangyeekhun, E. & Sylvie, M.A. (2001). Characterization of *Saprolegnia* spp. isolates from channel catfish. Dis. Aquat. Org., 45(1): 53-59.

Barker, J. & Brown, M.R.W. (1994). Trojan horses of the microbial world: protozoa and the survival of bacterial pathogens in the environment. Microbiology, 140(6): 1253–1259.

Bärlocher, F. (1992). Community organization. In the ecology of aquatic hyphomycetes. F. Bärlocher (ed.). Berlin, Germany: Springer-Verlag, 38 – 76.

Baudoin, J., Guérold F., Felten, V., Chauvet, E., Wagner, P. & Rousselle, P. (2008). Elevated aluminium concentration in acidified headwater streams lowers aquatic hyphomycete diversity and impairs leaf-litter breakdown. Microb Ecol., 56: 260-269.

Brenner, D.J. (1984). Enterobacteriaceae. In: Bergey's Manual of systematic Bacteriology. Vol. 1. (ed. N. R. Kreig), Williams and Wilkins, Baltimore, M. D. pp. 408-516.

Cabral, J.P.S. (2010). Water Microbiology. Bacterial Pathogens and Water, Int J Environ Res Public Health, 15;7(10): 3657-3703.

Chamier, A. & Tipping, E. (1997). Effects of aluminium in acid streams on growth and sporulation of aquatic hyphomycetes. Environ Pollut. 96: 289-298.

Chamier, A.C. (1985). Cell-wall-degrading enzymes of aquatic hyphomycetes: a review. Bot. J. Linn. Soc., 91: 67-81.

Chauhan, A., Cherrier, J. & Williams, H.N. (2009). Impact of sideways and bottom-up control factors on bacterial community succession over a tiday cycle, Proc. Nati. Acad. Sci. USA, 106: 4301-4306.

Cheesbrough, M. (1989). Medical laboratory manual for tropical countries. Vol. II. Microbiology. Butterworth Heinemann, London. pp. 198.

Cowan, S.T. (1974). Cowan and Steel's Manual for the identification of Medical Bacteria. 2nd ed., Cambridge Univeresity Press, Cambridge. pp. 168.

Edwards, P.R. & Ewing, W.H. (1972). Identification of Enterobacteriaceae. 3rd ed. Burgess Publishing Co., Minneapolis, pp. 240.

Eva, S., Lindström, E. & Lindstrom, M. (2014). Gabriel Zwart distribution of typical freshwater bacterial groups is associated with pH, Temperature, and Lake Water Retention Time, Applied and Environmental Microbiology, 71(12): 11-14.

FAO, (2016). The State of food and agriculture climate change, agriculture and food security, Food and Agriculture Organization of the United Nations Rome, 1-194.

Forsberg, C. (1982). Limnological research can improve and reduce the cost of monitoring and control of water quality. Hydrobiologia, 86(1): 143-146.

Gerba, C.P. & Mcleod, M. (1976). Effect of sediments on the survival of *Escherichia coli* in marine waters. Applied and Environmental Microbiology, 6:11-17.

Hestrin, R., Hammer E.C., Mueller, C.W. & Lehmann, J. (2019). Data from: synergies between myccorhizal fungi and soil microbial communities increase plant nitrogen acquisition, 2: 233.

Houbraken, J. & Samson, R.A. (2011). Phylogeny of *Penicillium* and the segregation of *Trichocomaceae* into three families Studies in Mycology, 70: 1-51.

Ismael, E.S. (2019). Mediterranean Sea fry; a source of isopod infestation problem in Egypt with reference to the effect of salinity and temperature on the survival of *Livoneca redmanii* (Isopoda: Cymothoidae) juvenile stages. J. Egypt. Soc. Parasitol., 49(1): 235-242.

ISO, (2024). Water Quality, Sampling – Part – 3, Preservation and handling of water samples, pp. 1-7.

Jeyasekaran, G. & Ayyappan, S. (2003). Study of Microbiology in fishes. Fisheries College and Research Institute Tamil Nadu Veterinary and Animal Sciences University, Tuticorin, India. Division of Aquatic Microbiology, Central Institute of Freshwater Aquaculture, ICAR, Bhubaneswar -751 002, India, Indian J. Fish., 50(4): 455-459.

Kalaria, K.K., Piyushbhai, M.K., Narendra, P., Saxena, M., Dhruve, D. & Vaghabhai, T.P. (2024). Diseases of freshwater fishes in India and its treatment: A review, International Journal of Advanced Biochemi stry Research, SP-8(1): 634-648.

Kather, B., Chitra, S.J. & Malini, E. (2015). Studies on plankton diversity and water quality of Ambattur Lake, Tamilnadu. International Journal of Pure and Applied Zoology, 1(3): 31-36.

Khallil A.M., Ali E.H., Hassan E.A. & Ibrahim S.S. (2020). Biodiversity, spatial distribution and seasonality of heterotrophic stramenopiles and true zoosporic fungi in two water bodies exposed to 176 Czech Mycology, 74(2): 153-179.

Kistemann, F., Classen, T. & Koch, T. (2002). Microbial load of drinking water reservoir tributaries during extreme rainfall and runoff. Applied and environmental Microbiology, 65: 251-264.

Kiziewicz, B. (2004). Occurrence of parasitic and predatory fungi and fungus-like organisms in different water reservoirs of Podlasie Province of Poland. – Mycologia Balcanica 1: 159-162.

Krauss, J., Wuerzburg, I.G. & Steffan-Dewenter, I. (2011). Decreased functional diversity and biological pest control in conventional compared to organic crop fields. Journal of pest control. pp. 136.

Lilabati, H. & Vishwanath, W. (1998). Biochemical, nutritional and microbiological quality of ice stored *Notopterus chitala* of Imphal market, Manipur. Indian J. Fish., 45: 441-446.

Liston, J. (1980). Microbiology in fishery science. In: Connell JJ, editor. Advances in Fish, Science and Technology. Farnham, Surrey, U.K.: Fishing News Books. p 138-157.

Madigan, M., Martinko, J. & Bender, K. (2009). Brock Biology of Microorganisms (14th edn.), Pearson, USA, pp. 126.

Madigan, M.T., Martinko, J.M. & Parker, J. (1997). Brock Biology of Microorganisms. 8th Edition, Prentice Hall International, Inc., New York.

Martin, W.J. and Washington, J.A. (1980). Enterobacteriaceae. In: The Manual of Clinical microbiology. 3rd edition. (E.H. Lennette, A. Belows, W.J., Hausler and J.P. Truant, eds.), pp. 195-219.

Meerhoff, M., Clemente, J.M., De Mello, F.T., Iglesias, C., Pedersen, A.R. & Jeppesen, E. (2007). Canada warm climate-related structure of littoral predator assemblies weaken the clear water state in shallow lakes, Global Change Biology, 13: 1888-1897.

Mehboob, A., Ganie, A.H., Dar, A.R. & Soni, K.K. (2021). Studies in Fungi, Aquatic fungal diversity in two freshwater ecosystems of Madhya Pradesh, India, 6(1): 116-137.

Michaud, K., Vera-Llonch, M. & Oster, G. (2012). Mortality risk by functional status and health-related quality of life in patients with *Rheumatoid Arthritis*. The Journal of

Rheumatology, 39(1): 54-59.

Morris, J.E. & Mischke, C.C. (1999). Plankton management for fish culture ponds, Environmental Science, Technical bulletin series 114. Ames, lowa, pp. 24.

Mukherjee, P.K., Mendoza-Mendoza, A., Zeilinger, S., Horwitz, B.A. (2022). Mycoparasitism as a mechanism of *Trichoderma-mediated* suppression of plant diseases. Fungal Biology Reviews, (39): 15–33.

Nair, R.B., Tharmanai. P.K. & Lahiry, N.L. (1971). Studies on chilled storage of freshwater fish – I. Changes during iced storage. J. Food Sci. Technol., 8: 53-56.

Nizamydeen, N., Santhiya, T., Ambika, R. & Sengottaian, N. (2014). Department of Microbiology, Urumu Dhanalakshmi College, Trichy, Tamilnadu. Pelagia Research Library Advances in applied Science Research, 5(2): 55-58.

Njoku, O.E., Agwa, O.K. & Ibiere, A.A. (2015). An investigation of the microbiological and physicochemical profile of some fish ponds water within Niger Delta of Nigeria. Afri J Food Sci., 9(3): 155-62.

Pawar, K.S., Singh, P.N. & Singh, S.K. (2023). Fungal alkaline proteases and their potential applications in different industries, Review article Front. Microbiol., 30 Sec. Microbiotechnology 14: 30.

Petchey, O.L., McPhearson, P.T., Casey, T.M. & Morin, P.J. (1999). Environmental warming alters food-web structure and ecosystem function. Nature, 02: 69-72.

Potekhina, R.M., Tarasova, E.Y. & Tanaseva, S.A. (2020). Biodiversity of mycelial fungi in fresh water in the territory of the park mari chodra of the Russian Federation. Systematic Reviews in Pharmacy, 11(12): 1464-1472.

Rajkumar, B. & Sharma, G.D. (2013). Seasonal bacteriological analysis of Barak River, Assam, India. Applied Water Science, 3: 625-630.

Ramya Urs, S.K., Ajith, S., Chauhan, J.B. & Santa Ram, A. (2012). Pathogenic bacteria in the water of Dalvayi Lake, Mysore, Int. J. LifeSc. Bt & Pharm. Res. 1(2): 334-339.

Sharma, V.K. & Hobson, P.N. (1985). A sporulation medium for strict anaerobes, Applied Microbiology International, 1(2): 31-32.

Sinha, D.K., Choudhary, S.P. & Narayan, K.G. (1991). Microbiological characteristics of marketed rohu (*Labeo rohita*). Indian J. Fish., 38: 69-71.

Sridhar, K.R. (2009). Fungi in tree conopy – An appraisal. In: Applied Mycology (eds. Rai M., Bridge P.), CAB International, UK: 73-91.

Sudheep, N.M. & Sridhar, K.R. (2011). Diversity of lignicolous and Ingoldian fungi on woody litter in River Kali (Western Ghats, India). Mycology, 2: 98-108.

Sugita, H., Tokuyama, K. & Deguchi, Y. (1985). The Intestinal microflora of carp, *Cyprinus carpio*, grass carp, *Ctenopharyngodon idella* and Tilapia, Sarotheradon niloticus. Bull. Japan Soci. Sci. Fish, 51: 325-329.

Surendran, P.K., Joseph, J., Shenoy, A.V., Perigreen, P.A., Iyer, K.M. & Gopakumar, K. (1989). Studies on spoilage of commercially important tropical fishes under iced

storage. Fish. Res., 7: 1-9.

Surendraraj, A., Sabeena Farvin, K.H., Yathavamoorthi, R. & Thampuran, N. (2009). Enteric bacteria associated with farmed freshwater and its culture environment in Kerala, India. Res. J. Microbiol., 4: 334-344.

Suseela, M.R. (2009). Conservation and diversity of fresh water algae. In: Anand, N. (ed). Biology and biodiversity of microalgae. Centre for advanced studies in botany. University of Madras, Chennai, India, pp. 41.

Turner, J.W. Good, B. (2009). Plankton composition and environmental factors contribute to Vibrio seasonality. 3(9): 1082-1092.

Usha, C., Nandini, N., Jumbe, A.S., Anupama, B.S. & Goud, S. (2008). Intestinal pathogens and microbial pollution of urban lakes – A case study on Yellamallappa Chetty Lake, Bangalore, India, In: Proceedings of Taal 2007, World Lake Conference. (Eds. Sengupta, M. and Dalwani, R.). pp 1742-1752.

Werren, J.H. and O'Neill, S.L. (1997). The evolution of heritable symbionts. In: O'Neill, S.L., Hoffmann, A.A. and Werren, J.H., Eds., Influential Passengers: Inherited Microorganisms and Arthropod Reproduction, Oxford University Press, Oxford, 1-41.

WHO. (1984). Updated its definition of health and launched a program to promote health, pp. 42.