

Research Article

Bacterial Diversity and Antimicrobial Resistance Profiles of Freshwater Fishes in Ganjam, Odisha

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Abstract

Bacteria are essential components of aquatic ecosystems, performing critical ecological functions and influencing the health of their hosts. With aquaculture recognized as the fastest-growing food production sector, ensuring the bacteriological safety of freshwater fish is vital for ecological sustainability and human health. This study aimed to isolate, characterize, and identify the bacterial diversity associated with the skin, fins, gills, and gastrointestinal tracts of eight freshwater fish species, including *Catla catla*, *Labeo rohita*, and selected catfishes, collected from various water bodies of the Ganjam district, Odisha. Bacteriological profiling was conducted for isolation, morphological characterization, selective media, and biochemical identification, using standard microbiological methods. 72 bacterial isolates were recovered and subjected to antibiotic susceptibility testing using the Kirby–Bauer disc diffusion method against ten antibiotics from different classes, including carbapenems, beta-lactams and polymyxins. Quantitative analysis demonstrated that the highest bacterial load in the gut of *Anabas testudineus* (2.8×10^7 CFU/ml), followed by *Labeo* species. Gram-positive bacteria were found to be more prevalent than Gram-negative bacteria species. The identified genera included Gram positive bacteria, such as *Bacillus*, *Lactobacillus*, *Staphylococcus*, *Streptococcus*, and *Micrococcus* as well as Gram negative bacteria, such as *Aeromonas*, *Pseudomonas*, and *Proteus*, while *Escherichia coli* and *Vibrio* species were not detected. The antibiogram revealed significant resistance to ampicillin, penicillin-G, and colistin, whereas chloramphenicol remained effective against most isolates. These findings indicate the occurrence of antimicrobial-resistant bacteria in commercially important freshwater fishes and highlight the importance of rational use of antibiotics, improved aquaculture management, and stringent food safety measures to mitigate potential public health risks.

Keywords

Aquaculture, Ganjam, Antimicrobial Resistance, Bacteriological Profiling, Food Safety, *Anabas testudineus*

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1. Introduction

The bacterial flora is the essential component of aquatic ecosystems, performing critical ecological functions with great diversity while influencing the health of their hosts [1]. Bacterial diversity in freshwater fishes is ecologically significant as these reflect the interaction between host, environment, diet, and pathogen exposure. Freshwater fish play an important role in the aquatic environment as well as in the human population. They are a great source of dietary protein, vitamins, minerals, and low-fat food, as well as a biological indicator of contaminated aquatic ecosystems [2].

India is one of the leading producers of freshwater fishes, with rapidly intensifying culture of carps, catfishes, and other species in different freshwater bodies [3, 4]. Freshwater fish may be susceptible to some infectious diseases temporarily in their lives. Bacteria are saprophytic in nature but become pathogenic under stress and unfavourable environmental conditions [5]. Bacterial diseases of fish cause huge economic loss as well as create a great concern for public health.

The antibiotics used in treating bacterial diseases are one of the common practice in the aquaculture sector; it plays a major role to control such bacterial infections and disease outbreaks in aquaculture. However the widespread and unlimited misuse of antibiotics in the fresh water aquatic systems for treating bacterial diseases induces antimicrobial resistance in various fish pathogens globally [6]. As a consequence, there is a possibility of transmission of antimicrobial resistance genes in bacteria from aquatic system to humans through fish by-products [7]. Multi-drug resistance (MDR) has escalated globally, causing significant concern in public health. The emergence of MDR bacteria from diverse sources emphasises the screening of MDR bacterial strains and judicious use of antibiotics [8].

Ganjam is a district of Odisha, located along south eastern coast of India, rich in fresh water bodies, such as rivers, riverine lakes, reservoirs, ponds, and tanks, contributing both in culture-based fisheries and inland capture fisheries [9]. The district is one of the major producers of freshwater fish in Odisha, with a diverse species, including Indian major carps and catfishes. However, the microbial ecology, specifically the bacterial flora associated with edible fresh water fish fauna, has not been meticulously explored. The present study provides the first systematic approach to identifying and documenting the common bacterial flora found in the primary edible fresh water fishes of Ganjam, along with their antibiotic susceptibility testing.

2. Materials & Methods

2.1. Study Area and Sample Collection

The present study was conducted in Ganjam district, Odisha (19°38'0" N, 85°07'0" E). A total of 65 freshwater fish samples representing eight species were collected from rivers, reservoirs, and ponds between July 2024 and December 2024.

Fish samples were transported under aseptic conditions in ice boxes to the laboratory for analysis.

2.2. Sample Preparation

Skin, gill, fin, and gut tissues were aseptically excised. One gram of tissue was homogenised in 9 mL sterile saline. Serial dilutions up to 10^{-8} were prepared for microbial enumeration.

2.3. CFU Enumeration and Isolation

Colony-forming units (CFU/ml) were determined using the Single Plate Serial Dilution Spotting (SPSDS) method [10]. Pure isolates of bacterial colonies were obtained by sub culturing on Luria-Bertani (LB) agar.

2.4. Identification of Bacteria

Isolates were subjected to Gram staining, morphological observation, and growth on selective media, including Mac-Conkey agar, Eosin Methylene Blue (EMB) agar, and Cetrimide agar. Biochemical tests, including catalase, oxidase, IMViC, urease, and Triple Sugar Iron (TSI) tests, were performed for identification [11-13].

2.5. Antibiotic Susceptibility Testing

The antibiotic susceptibility test was performed by Kirby-Bauer disc diffusion method using Mueller-Hinton agar following CLSI guidelines [14, 15]. Antibiotics tested included ampicillin (10 µg), penicillin-G (10 units), kanamycin (30 µg), meropenem (10 µg), trimethoprim (5 µg), chloramphenicol (30 µg), ciprofloxacin (5 µg), colistin (10 µg), tetracycline (30 µg), and nalidixic acid (30 µg).

3. Results

3.1. Fish Species and Sampling Sites

A total of 65 fish samples comprising 8 different species of freshwater fishes, including *Labeo rohita*, *Catla catla*, *Notopterus notopterus*, *Anabas testudineus*, *Chana punctata*, *Chana striata*, *Mugil cephalus*, and *Clarias batrachus*, were collected from distinct sampling sites, such as Rushikulya River, Baghua, and different ponds of Ganjam (Table 1). The total length of collected fish varied from 12 cm to 43 cm (Figure 1).

3.2. Bacterial Load

The highest bacterial load was recorded in the gut of *Anabas testudineus* (2.8×10^7 CFU/ml), followed by *Labeo rohita*. Generally, gut tissues showed higher bacterial counts than

skin, gill, and fin tissues (Table 2).

3.3. Isolation and Identification

Seventy-two bacterial isolates were obtained. Gram-positive bacteria accounted for 54%, while Gram-negative bacteria constituted 46%. Identified genera included *Bacillus*, *Staphylococcus*, *Streptococcus*, *Micrococcus*, *Lactobacillus*, *Aeromonas*, *Pseudomonas*, *Proteus*, and *Enterobacter* (Figure 3).

3.4. Antibiotic Resistance Pattern

Most isolates showed resistance to ampicillin and penicillin-G. Chloramphenicol and tetracycline exhibited higher effectiveness. Several isolates demonstrated multidrug resistance phenotypes (Figure 4).

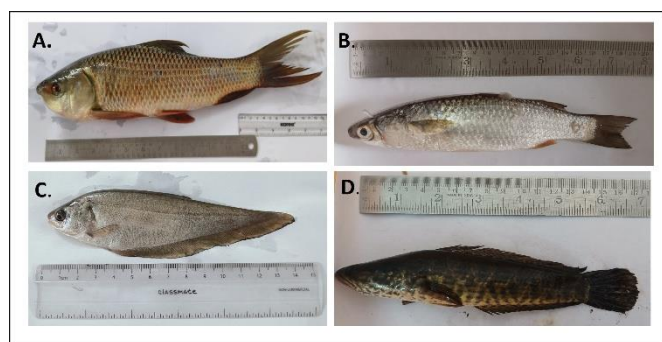


Figure 1. Fresh water fishes (A) *Labeo rohita*, (B) *Mugil cephalus*, (C) *Notopterus notopterus*, and (D) *Chana punctatus*.

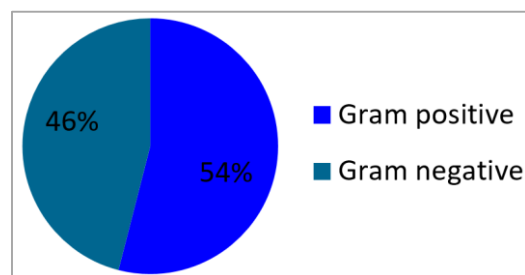


Figure 2. Percentage of Gram-positive and Gram-negative bacteria isolates.

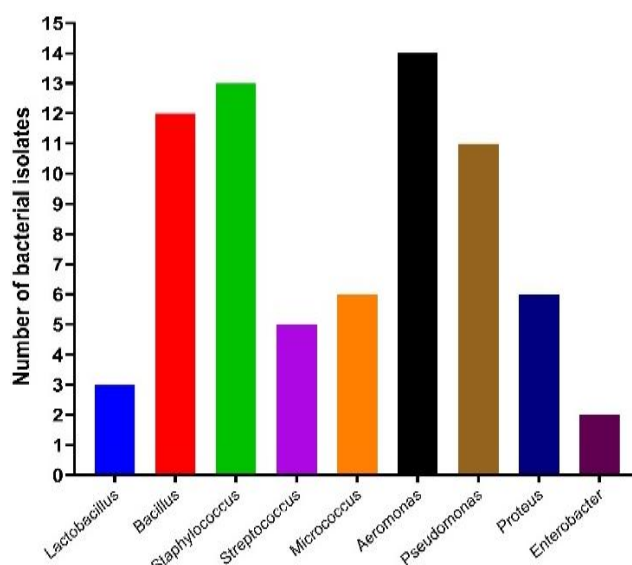


Figure 3. Occurrence of Bacterial Isolates from Freshwater Fishes.

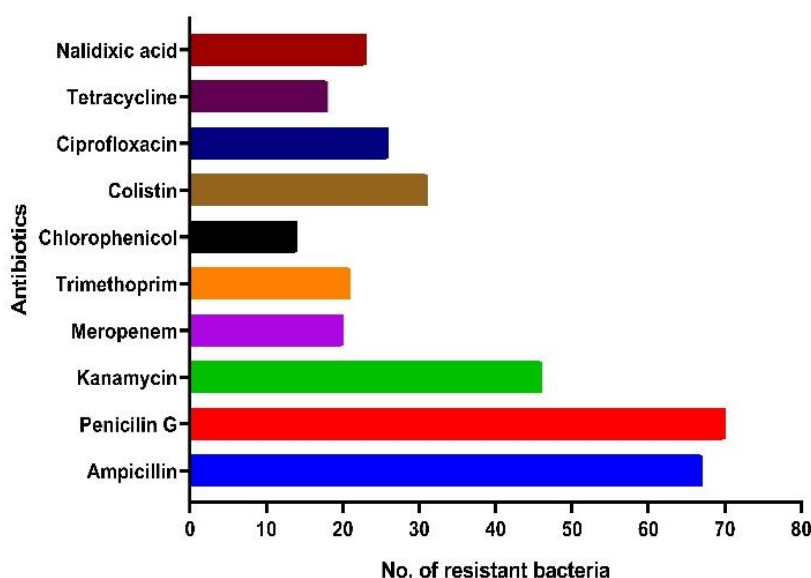


Figure 4. Antibiotic Resistance Pattern of Bacterial isolates.

Table 1. Collection Sites of Fish Samples.

Sampling Site	Name of fish	Common name	Length (cm)
Chhatrapur Pata, Chhatrapur	<i>Anabas testudineus</i>	Kau	12
	<i>Mugil cephalus</i>	Meji	19
Randha Bandha, Randha	<i>Labeo rohita</i>	Rohi	43
Baghua Nadi	<i>Notopterus notopterus</i>	Fali	14
Ganjam Pata, Ganjam	<i>Channa punctata</i>	Gadisha	17
	<i>Channa striata</i>	Seula	28
Rushikulya River, Ganjam	<i>Labeo rohita</i>	Rohu	30
	<i>Notopterus notopterus</i>	Fali	18
Rangeilunda Pond, Rangeilunda	<i>Clarias batrachus</i>	Magur	15
Lanjipali Bandha, Berhampur	<i>Catla catla</i>	Bhakur	30
	<i>Channa striata</i>	Seula	40
Ghodahada Dam	<i>Anabas testudineus</i>	Kau	14
Surada Pond, Surada	<i>Labeo rohita</i>	Rohu	35
Bada Bandha, Digapahandi	<i>Catla catla</i>	Bhakura	36

Table 2. Total Bacterial Load in Different Tissues of Fishes.

Sl. No.	Name of fish	Tissue sample	Bacterial load (cfu/ml)
01	<i>Anabas testudineus</i>	Gill	2.1×10^5
		Gut	2.8×10^7
		Fin	2.2×10^5
		Skin	2.2×10^6
02	<i>Clarias batrachus</i>	Gill	2.4×10^6
		Gut	1.7×10^5
		Fin	2.3×10^4
		Skin	3.1×10^5
03	<i>Labeo rohita</i>	Gill	1.9×10^6
		Gut	1.8×10^7
		Skin	4.1×10^5
		Fin	3.2×10^4
04	<i>Notopterus notopterus</i>	Gill	1.9×10^6
		Gut	3.1×10^6
		Skin	1.8×10^6
		Fin	2.5×10^5
05	<i>Catla catla</i>	Gill	1.5×10^5
		Gut	5.3×10^6
		Skin	1.5×10^5

Sl. No.	Name of fish	Tissue sample	Bacterial load (cfu/ml)
06	<i>Channa punctata</i>	Fin	4.1×10^4
		Gill	3.6×10^5
		Gut	1.5×10^5
		Skin	2.2×10^5
		Fin	3.1×10^5
07	<i>Mugil cephalus</i>	Gill	1.2×10^6
		Gut	2.5×10^6
		Skin	1.2×10^6
		Fin	2.2×10^4
		Gill	2.1×10^6
08	<i>Channa striata</i>	Gut	1.9×10^6
		Skin	1.6×10^5
		Fin	3.1×10^5

4. Discussion

The bacterial isolates recovered from the fish samples comprised both Gram-positive and Gram-negative bacteria, including *Bacillus* sp., *Lactobacillus* sp., *Micrococcus* sp., *Staphylococcus* sp., *Streptococcus* sp., *Aeromonas* sp., *Pseudomonas* sp., *Proteus* sp., and *Enterobacter* sp. These findings are consistent with earlier studies conducted by Austin and Austin [16], Ibrahim et al. [17], and Kyule et al. [18], who reported similar bacterial diversity in freshwater fish. The present investigation further indicates that inland freshwater bodies of the Ganjam district may serve as reservoirs of diverse bacterial communities. The highest bacterial load was observed in the gut of the fish, which is in agreement with reports from other aquatic ecosystems worldwide [19, 20]. In total, 72 bacterial isolates were obtained from the skin, fin, gill, and gut samples.

Among Gram-negative bacteria, *Aeromonas* spp. and *Pseudomonas* spp. were the most prevalent isolates recovered from the skin, gill, fin, and gut of apparently healthy fishes. These organisms are recognized as opportunistic pathogens associated with diseases such as hemorrhagic septicemia and epizootic ulcerative syndrome (EUS), leading to significant economic losses in the aquaculture sector. The isolation of *Aeromonas* spp. and *Pseudomonas* spp. from infected fish tissues has also been reported by various authors [21–24]. Additionally, *Proteus* sp. and *Enterobacter* sp. were identified in the present study, which aligns with the findings of Surendraraj et al. [25] and Rawash et al. [26].

Among Gram-positive bacteria, *Staphylococcus* spp. and

Bacillus spp. were the predominant isolates, while *Micrococcus* spp., *Streptococcus* spp., and *Lactobacillus* spp. were also recovered from the skin, fin, gill and gut of the fishes. Among these bacteria, some are natural inhabitants of aquatic environments. However, the presence of others may indicate contamination in aquatic environments or anthropogenic influence within the aquatic ecosystems [27–29].

The present study revealed that most bacterial isolates were resistant to ampicillin, penicillin-G, and kanamycin, while sensitive to chloramphenicol and tetracycline. The detection of multidrug-resistant (MDR) bacteria in freshwater fishes in this study corroborates the reported findings [30]. The emergence of antibiotic resistance may be due to the indiscriminate and misuse of antibiotics in aquaculture practices, which creates a selective pressure on bacterial populations and induces the development and dissemination of resistant bacterial strains.

5. Conclusions

This study explores significant bacterial diversity and also demonstrates the presence of antimicrobial-resistant isolates in freshwater fishes of Ganjam district. The detection of multidrug-resistant bacteria in aquaculture highlights the need for improved aquaculture management, prudent use of antibiotics, and regular microbial surveillance to safeguard food safety and public health.

Abbreviations

CFU Colony Forming Unit

SPSDS Single Plate Serial Dilution Spotting
 CLSI Clinical and Laboratory Standards Institute
 AMR Antimicrobial Resistance
 MDR Multidrug Resistance

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Author Contributions

Padmabati Nayak: Conceptualization, Investigation, Data curation, Writing – original draft

Sambit Kumar Dwibedy: Methodology, Formal analysis, Validation

Sushil K. Rathore: Conceptualization, Data curation, Supervision

Namita Panigrahy: Conceptualization, Supervision, Writing- review & editing

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Conflicts of Interest

The authors declare that they have no conflict of interest.

References

- [1] Vijayan, J., Nathan, V. K., Ammini, P., et al. Bacterial diversity in the aquatic system in India based on metagenome analysis-a critical review, *Env Sci and Pol Research*. 2023, 30: 28283-28406. <https://doi.org/10.1007/s11356-023-25195-2>
- [2] Schar, D., Zhao, C., Wang, Y., et al. Twenty-year trends in antimicrobial resistance from aquaculture and fisheries in Asia, *Nat Commun*. 2021, 12: 5384. <https://doi.org/10.1038/s41467-021-25655-8>
- [3] Ajayi, A. O., Odeyemi, A. T., Akinjogunla, O. J., et al. Review of antibiotic-resistant bacteria and antibiotic resistance genes within the one health framework, *Infect Ecol Epidemiol*. 2024, 14: 2312953. <https://doi.org/10.1080/20008686.2024.2312953>
- [4] Mohammed EAH, Kovács B, Kuunya R, et al. Antibiotic Resistance in Aquaculture: Challenges, Trends Analysis, and Alternative Approaches, *Antibiotics*. 2025, 14: 598. <https://doi.org/10.3390/antibiotics14060598>
- [5] Barde, R. D. Bacterial Diversity Associated with *Labeo rohita* Isolated from Cultured and Natural Water Bodies, *Euro J of Mol & Cli Med*. 2020, 7(11).
- [6] Watts, J. E., Schreier, H. J., Lanska, L., Hale, M. S. The rising tide of antimicrobial resistance in aquaculture: sources, sinks and solutions. *Mar Drugs*. 2017, 15(6): 158. <https://doi.org/10.3390/md15060158>
- [7] Pridgeon, J. W., Klesius, P. H. Molecular identification and virulence of three *Aeromonas hydrophila* isolates cultured from infected channel catfish during a disease outbreak in west Alabama (USA) IN 2009. *Dis Aquat Org*. 2011, 94(3): 249-53. <https://doi.org/10.3354/dao02332>
- [8] Adah, D. A., Saidu, L., Oniye, S. J., et al. Molecular characterization and antibiotics resistance of *Aeromonas* species isolated from farmed African catfish *Clarias gariepinus* Burchell, 1822. *BMC Vet Research*. 2024, 20: 16. <https://doi.org/10.1186/s12917-023-03860-5>
- [9] Bardhan, A., Murthy, S. H. Emerging Concerns: Prevalence of Antimicrobial Resistance in *Aeromonas* and *Escherichia coli* in Retail Fish from Ganges Delta's Diamond Harbour Region. *J Aquac*. 2024, 54–68. <https://doi.org/10.61885/joa.v33.2024.293>
- [10] Thomas, P., Sekhar, A. C., Upreti, R., et al. (2015) Optimization of single plate-serial dilution spotting (SP-SDS) with sample anchoring as an assured method for bacterial and yeast cfu enumeration and single colony isolation from diverse samples. *Biotechnol Rep*. 2015, 8: 45–55. <https://doi.org/10.1016/j.btre.2015.08.003>
- [11] Krieg, N. R., Holt, J. G., Bergy, S Manual of Systematic Bacteriology. Vol-1, Williams and Wilkins. 1984.
- [12] Collins, C. H., Lyne, P. M., Grange, G. M. Microbiological Methods. 6th Edn, 1989 Butterworths, London: 56-66.
- [13] Cheesburg, M. District Laboratory Practice in Tropical Countries. (Part II) Tropical Health Technology Publishers. 2002, Great Britain: 40-56.
- [14] Chandravansh, i P., Udgata, S. K., Kumari, J., et al. Isolation and Characterization of Multiple Antibiotic-Resistant *A. hydrophila* causing Mortality of Indian Major Carps in Ganjam District, Odisha. *Int J Curr Microbiol Appl Sci*. 2020, 9: 562–574. <https://doi.org/10.20546/ijcmas.2020.912.068>
- [15] CLSI. Performance Standards for Antimicrobial Susceptibility Testing. In: Wayne PA (ed) CLSI supplement M100, 30th edn. Clinical and Laboratory Standards Institute. 2020.
- [16] Austin, B., Austin, D. B. Bacterial fish pathogen Disease in farmed and wild fish. 2nd edn. 1993, Ellis Horwood, Chichester.
- [17] Ibrahim, B. U., Baba, J., Sheshi, M. S. Isolation and Identification of Bacteria Associated with Fresh and Smoked Fish (*Clarias gariepinus*) In Minna Metropolis, Niger State. Nigeria. *J of Appl & Env Microbio*. 2014, 2(3): 81-85. <https://doi.org/10.12691/jaem-2-3-4>
- [18] Kyule, D. N., Maingi, J. M., Njeru, E. M., et al. Molecular Characterization and Diversity of Bacteria Isolated from Fish and Fish Products Retailed in Kenyan Markets. *International Journal of Food Science*. 2022, 2022: 2379323. <https://doi.org/10.1155/2022/2379323>

- [19] Dayie, N. T. K. D., Nathan-Mensah, F. N. N., Kotey F. C. N., et al. Multidrug-Resistant Bacteria in Aquaculture Systems in Accra, Ghana. *Environ Health Insights*. 2024, 18: 11786302241299369.
<https://doi.org/10.1177/11786302241299369>
- [20] Rana, Md. L., Ullah. Md. A., Hoque, M. N., et al. Preliminary survey of biofilm forming, antibiotic resistant *Escherichia coli* in fishes from land-based aquaculture systems and open water bodies in Bangladesh. *Sci Rep*. 2025, 15: 7811.
<https://doi.org/10.1038/s41598-024-80536-6>
- [21] Rab, A., Afzal, N., Sarker, M., et al. Incidence of epizootic ulcerative syndrome of (EUS) in freshwater fishes in the endemic area of Punjab, Bangladesh *J Fish Res*. 2001, 5(1): 45-52.
- [22] Leung, T. L. F., Bates, A. E., Dulvy, N. More rapid and severe disease outbreaks for aquaculture at the tropics: implications for food security. *J of App Ecology*. 2013, 50(1): 215-222.
<https://doi.org/10.1111/1365-2644.2017>
- [23] Khatun, H., Hossain, M. D., Jahan, S. N., Khanom, D. A. Bacterial Infestation in Different Fish at Rajsahi. *J Sci Foundation*. 2011, 9(1&2): 77-84.
- [24] Surendraraj, A., Sabeena, F. K. H., Yathvamoorthi, R., Thamuran, N. Enteric bacteria associated with farmed freshwater fish and its culture environment in Kerala, India. *Research J of Microbio*. 2009, 4(9): 334-344.
<https://doi.org/10.17311/jm.2009.334.344>
- [25] Rawash, R., Saad, S. M., Hassanin, et al. Incidence of Enterobacteriaceae in some freshwater fishes. *Benha Vet Med Journal*. 2019, 37: 64-68.
<https://doi.org/10.21608/bvmj.2009.15658.1070>
- [26] Moshood, A. Y., TengkuHaziYamin, A. A. Isolation and Identification of Bacteria in Retailed Smoked Fish within Bauchi Metropolis. *Journal OF Pharm and Bio Sciences*. 2012, 3(1): 1-5.
- [27] Xie, F., Zhu, T., Zhang, F., et al. Using *Bacillus amyloliquefaciens* for remediation of aquaculture water, Springerplus. 2013, 2: 1.
<https://doi.org/10.1186/2193-1801-2-119>
- [28] Majumdar, B., Sarker, M. G. A., Khan, M. H., Choudhury, M. B. Incidence of ulcer type of disease in wild fishes of Bangladesh. *Bangladesh J Fish Res*. 2001, 5(2): 163-168.
- [29] Das, N., Dash, S., Khuntia, B. K. Assessment of Antimicrobial Resistance (AMR) in *Aeromonas hydrophila* Isolated from Freshwater Rohu (*Labeo rohita*) in Ganjam District, Odisha, *Biological Forum*. 2022, 14(1): 1847-1851.
- [30] Mengistu, T. S., Garcias, B., Castellanos, G., et al. Occurrence of multidrug resistant Gram-negative bacteria and resistance genes in semi-aquatic wildlife - *Trachemys scripta*, *Neovison vison* and *Lutra lutra* - as sentinels of environmental health, *Sci Total Environ*. 2022, 830: 154814.
<https://doi.org/10.1016/j.scitotenv.2022.154814>

Biography



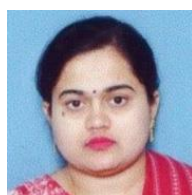
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Research Field

Padmabati Nayak: Aquaculture, Fish pathology, Environmental Microbiology.

Sambit Kumar Dwibedy: Biodiversity, Wildlife conservation, Molecular Microbiology

Sushil K. Rathore: Epidemiology, Virology, Population Genetics

Namita Panigrahy: Environmental Biotechnology, Industrial Microbiology, Microbial Remediation.