The scale **Journal Website:** https://thescalejournal.com.ng/
An Interdisciplinary Journal of **https://doi.org/10.5281/zenodo.20283478**
The ACADEMIC STAFF UNION OF POLYTECHNICS - ZONE D
ISSN: 2992-3727 Published 30th May, 2026

ASSESSMENT OF FUNGAL CONTAMINATION, OF RIVER AVU, AMAOKWA ITEM, BENDE LOCAL GOVERNMENT AREA ABIA STATE NIGERIA

Ndukwe, Okorie K. [1]; Okike- Osisiogu, Florence U. [2]
[1,2] Biology/Microbiology Department Ogbonnaya Onu Polytechnic, Aba.
Corresponding Author: okoriendukwe1@gmail.com , 08163338293

ABSTRACT
This study assessed the total fungal count, prevalence, and morphological characteristics of fungal isolates from surface water samples collected at upstream, midstream, and downstream sections of River Avu in Amaokwa Item, Bende Local Government Area, Abia State, Nigeria. Water samples were systematically obtained and analyzed for fungal load, while identification of isolates was based on cultural features, microscopic examination, and morphological traits. Results showed that downstream samples recorded the highest total fungal count, reaching 4.2×10^3 cfu/mL, indicating increased contamination likely due to surface runoff and anthropogenic activities. Midstream and upstream samples exhibited comparatively lower counts, ranging between **1.1×10^3** and **3.0×10^3 cfu/mL**. The most prevalent fungal genera included *Penicillium*, *Aspergillus*, *Rhizopus*, and *Geotrichum*, with *Penicillium* and *Aspergillus* species consistently detected in midstream and downstream zones. Morphological analysis revealed distinct colony structures and conidiophore arrangements that aided accurate identification of isolates. These findings emphasize the importance of routine microbial monitoring of surface water sources, especially those used for domestic purposes, due to potential health risks posed by mycotoxigenic and opportunistic fungal pathogens.

Keywords: Morphological characteristics, Fungal isolates, Upstream · Midstream · Downstream ·

INTRODUCTION

Rivers have been a vital source of water for human civilization since ancient times. They provide water for various domestic uses, including drinking, cooking, bathing, and sanitation. The importance of rivers as a source of water for domestic use cannot be overstated, as they support the basic needs of millions of people worldwide (Shafiq *et al*., 2013). Access to clean water is essential for public health, yet many communities in tropical regions face challenges due to microbial contamination of surface and stored water sources. In Amaokwe Item, Bende Local Government Area of Abia State, Nigeria, river Avu, serves as primary sources for drinking, cooking, bathing, and irrigation. However, microbial contamination particularly by fungi remains a significant challenge to water quality and public health. in many developing regions. Fungi are ubiquitous in nature and can colonize aquatic environments and can proliferate under favorable conditions, including the presence of organic matter and stagnant water. Their presence in drinking and domestic water sources has been linked to allergic reactions, respiratory issues, and opportunistic infections, particularly in immunocompromised individuals (Mhlongo *et al*., 2019). Recent studies have revealed alarming levels of fungal contamination in rural water sources, including hand-dug wells and surface water bodies, where antifungal-resistant and aflatoxigenic species have been detected (Iwaloye, 2022). These findings raise serious concerns about the safety of water used for drinking, cooking, and hygiene in underserved communities. Despite the growing evidence, fungal contaminants are often overlooked in water quality regulations and monitoring

programs (Hageskal *et al*., 2009). This study aims to assess the fungal load and species diversity in surface water samples collected from upstream, midstream, and downstream locations of Iyi Avu river. Using morphological and microscopic techniques, to identify key fungal genera and evaluate their prevalence across sampling points. The results contribute to the understanding of aquatic fungal ecology and support the development of targeted interventions to improve water safety in line with WHO and USEPA standards.

METHODS

Sample Collection

Water samples were collected from three surface water locations upstream, midstream, and downstream Each location was sampled in triplicate (labeled A, B, and C) to ensure representativeness and reproducibility. Bottles were submerged approximately 30 cm below the surface, facing upstream. Samples were stored in cold condition and transported to the laboratory within 6 hours. Analysis was conducted within 24 hours to ensure microbial viability. Each sample was labeled with date, time, location, and environmental observations. Sampling was conducted during the dry season to minimize dilution effects from rainfall, which can influence microbial load (Adefisoye & Okoh, 2016).

Total Fungal Count (TFC)

Total Fungal Count was determined using the standard pour plate method. Samples were serially diluted and inoculated on Sabouraud Dextrose Agar (SDA) supplemented with chloramphenicol to inhibit bacterial growth. Plates were incubated at 25°C for 5–7 days, and colony-forming units (cfu) were counted and expressed as cfu/mL.

Isolation and Identification

Distinct fungal colonies were sub cultured for purification. Morphological identification was based on colony texture, pigmentation, and growth pattern. Microscopic examination involved lactophenol cotton blue staining to observe hyphal structure, conidiophores, and spore arrangement. Identification was guided by fungal taxonomy keys (de Hoog *et al*., 2000)

Prevalence Analysis

The presence or absence of each fungal isolate was recorded across the three surface water zones. Prevalence percentages were calculated based on etection frequency across the sampling points

RESULTS

The total fungal count (TFC) from the various sampling points is presented in Table 1. The fungal population ranged from 1.1×10^3 to 4.2×10^3 cfu/mL across the sampling stations. The downstream section recorded the highest counts, ranging from 2.2×10^3 to 4.2×10^3 cfu/mL, averaging **3**.47 $\times 10^3$ cfu/mL indicating greater fungal contamination in that zone. The midstream samples showed moderate counts (1.1×10^3–1.5×10^3 cfu/m), averaging 1.27 $\times 10^3$ while the upstream had comparatively lower counts (1.1×10^3–3.0×10^3 cfu/mL). averaging 2.07 $\times 10^3$ cfu/ **ml.** These variations suggest increasing fungal load along the water flow, possibly due to accumulation of organic matter and anthropogenic activities downstream.

The distribution, Morphological and microscopic analyses of fungal isolates from different sampling points along the river is shown in Tables 2. Four fungal genera were identified from the water samples:

Penicillium sp., *Aspergillus* sp., *Geotrichum* sp., and *Rhizopus* sp. Four fungal genera were isolated from surface water samples across upstream, midstream, and downstream sites Table 3. The occurrence of these isolates varied across the sampling points *Penicillium* sp., *Aspergillus* sp., and *Rhizopus* sp. were the most prevalent, each detected in two out of the three sampling locations (66.6 %). *Geotrichum* sp. was the least prevalent, occurring only at the midstream section (33.3 %). *Rhizopus* sp. was present at both upstream and downstream, while *Penicillium* sp. and *Aspergillus* sp. were isolated from midstream and downstream samples. **%**).. course.

Table 1: Total fungal count (TFC) from surface water

Source	Sample A	Sample B	Sample C	Average TFC (×10³ CFU/mL)
		2.1	3.0	2.07
Upstream	1.1			
Midstream	1.2	1.1	1.5	1.27
Downstream	4.0	4.2	2.2	3.47

Table 2: Prevalence of each isolate in surface Water

Isolates	Upstream	Midstream	Downstream	%
Penicillium sp.	-	+	+	66.6
Aspergillus sp	-	+	+	66.6
Geotrichum sp.	-	+	-	33.3
Rhizopus sp.	+	-	+	66.6

Table 3: Morphological and microscopic characteristics of fungi isolate from surface water

S/N	Cultural Morphological	Microscopy	Probable fungal isolate
1	Large fluffy white colonies almost covering the whole surface	Non – septate branched hyphal enlarge at the apex to form cornidophorex they produce brownish black *ceridia* in chains.	*Penicillium* sp.
2	Black powdery conidiophores	Conidiophores arising from long branched foot calls, irregularly roughened.	*Aspergillus niger*
3	Fast growing colonies forming hyaline ariel hyphae, rhizoids are pigmented with brownish sporangiophores	Differentiated into stolons and nodes with rhizoids and sporangiophores, sporangiophores are short ellipsoidal with almost pointed ends.	*Rhizopus* sp.
4	Darkly pigmented colonies with white aerial mycelium, consisting of numerous black sclerotia and light brown-coloured conidial masses, reverse is dark brown.	Straight conidia with, fusiform and attenuated at the ends	*Geotrichum s*p.

Discussion

Analysis of Total Fungal Count (TFC) across different sampling locations showed notable increase in fungal contamination downstream. The observed fungal load also varied across the sampling points, with downstream samples exhibiting the highest concentration. This finding suggests that contaminants accumulate along the flow path, enriching the water with organic substrates that support fungal growth. Similar observations have been reported by Novak Babič *et al*. (2017), who reported that environmental pollutants and nutrient availability downstream enhance microbial diversity and abundance. The result of this study suggests that reduced water flow and increased pollutant input such as agricultural runoff and sewage discharge may contribute to elevated fungal presence downstream. This observation is in agreement with Iwaloye (2022), who reported high fungal concentrations in untreated rural water sources in Nigeria.

The data presented in Tables 2 and 3 provide valuable insight into the extent of fungal contamination in surface water across three sampling locations, upstream, midstream, and downstream. Four fungal isolates, were identified across the sampling locations, *Penicillium sp.*, *Aspergillus sp.*, and *Rhizopus sp.* The study revealed that fungal diversity increased downstream, with *Penicillium*, *Aspergillus*, and *Rhizopus* persisting across multiple sites, while *Geotrichum* was restricted to the midstream. This pattern supports earlier findings that surface waters act as reservoirs for filamentous fungi, many of which are opportunistic pathogens (Góralska *et al,* 2020). The consistent downstream presence of *Penicillium* and *Aspergillus* suggests that anthropogenic inputs and nutrient enrichment may favor their growth. The irregular distribution of *Rhizopus* aligns with reports of patchy fungal contamination in aquatic systems (Al-Gabr *et al*, 2013).

Morphological and microscopic analyses identified: *Penicillium sp.*, *Aspergillus niger*, *Rhizopus sp.*, and *Geotrichum sp.* often linked to moist environments and decaying organic matter. These fungi are known for their ubiquity in moist environments These fungi pose potential health risks, particularly to immunocompromised individuals due to their ability to produce mycotoxins or act as opportunistic pathogens (Kadaifciler & Demirel, 2018; Al-Meshal, 2022). Microscopic examination, especially of conidiophores and hyphal structures, was pivotal for accurate taxonomy and ecological interpretation (de Hoog *et al*., 2000). While *Rhizopus* and *Geotrichum* are generally saprophytic, they may cause infections under favorable conditions (Almiman, 2024; Kadaifciler & Demirel, 2018). These fungi have been linked to allergic reactions, respiratory infections, and invasive diseases, especially among immunocompromised individuals (Hageskal *et al*., 2009; Mhlongo *et al*., 2019**).** The presence of *Rhizopus* and *Geotrichum* species further underscores the potential risk of waterborne fungal exposure in contaminated environments**.** The detection of diverse fungal species in surface samples raises significant public health concerns. The dominance of *Penicillium* and *Aspergillus* species, particularly in midstream and downstream sites, is of concern due to their potential to produce mycotoxins and act as opportunistic pathogens These fungi have been linked to allergic reactions, respiratory infections, and invasive diseases, especially among immunocompromised individuals (Hageskal *et al*., 2009; Mhlongo *et al*., 2019). The absence of defined fungal thresholds highlights a gap in water safety frameworks, calling for their integration into monitoring protocols (Novak Babič *et al.,*). Regular fungal surveillance is crucial in regions relying on untreated or stored water to prevent potential outbreaks and safeguard vulnerable populations (WHO, 2016; USEPA, 2015).

CONCLUSION

This study confirmed the presence of *Penicillium*, *Aspergillus niger*, *Rhizopus*, and *Geotrichum* in surface water samples. The observed distribution patterns revealed greater fungal diversity downstream, indicating that anthropogenic activities and nutrient enrichment contribute significantly to contamination. The persistence of these fungi underscores potential public health risks and highlights the need for routine monitoring of surface waters for fungal contaminants. Such surveillance is vital not only for protecting community health but also for preserving water quality in ecosystems increasingly impacted by human activities. Accordingly, the study recommends integrating fungal assessments into community water safety plans and promoting public education on safe water storage practices.

REFERENCES

Adefisoye, M. A., & Okoh, A. I. (2016). Identification and antimicrobial resistance prevalence of pathogenic Escherichia coli strains from treated wastewater effluents in Eastern Cape, South Africa. *MicrobiologyOpen*, *5*(1), 143–151. https://doi.org/10.1002/mbo3.317

Al-Meshal, A. S. (2022). Detection of fungi in irrigation water sources using different isolation methods. *Journal of Pure and Applied Microbiology*, 16(2), 1330–1336. https://doi.org/10.22207/JPAM.16.2.61

Almiman, B. (2024). Identifying the optimal temperature and water activity conditions of phytopathogenic fungi recovered from Al-Baha province. *Journal of Umm Al-Qura University for Applied Sciences*, 10, 640–651. https://doi.org/10.1007/s43994-024-00131-3

de Hoog, G. S., Guarro, J., Gené, J., & Figueras, M. J. (2000). *Atlas of Clinical Fungi* (2nd ed.). Centraalbureau voor Schimmelcultures.

Hageskal, G., Lima, N., & Skaar, I. (2009). The study of fungal contamination of drinking water. *Mycological Research*, 113(2), 165–172. https://doi.org/10.1016/j.mycres.2008.10.002

Iwaloye, O. F. (2022, October 3). Study reveals alarming fungal contamination in rural Nigeria's drinking water. *The GuardianNigeria*. https://guardian.ng/features/study-reveals alarming-fungal contamination-in-rural-nigerias-drinking-water/

Kadaifciler, D. G., & Demirel, R. (2018). Fungal contaminants in man-made water systems connected to municipal water. *Journal of Water and Health*, 16(2), 244–252. https://doi.org/10.2166/wh.2018.272

Mhlongo, N. T., Tekere, M., & Sibanda, T. (2019). Prevalence and public health implications of mycotoxigenic fungi in treated drinking water systems. *Journal of Water and Health*, 17(4), 517–531. https://doi.org/10.2166/wh.2019.122 Novak Babič, M., Gunde-

Shafiq, M., Iqbal, Z., & Ahmad, M. (2013). *Fungal contamination in drinking water: neglected issue*. Journal of Environmental Biology, 34(2), 197 202.

United States Environmental Protection Agency (USEPA], 2015). *Water Quality Standards Handbook.* https://www.epa.gov/wqs-tech/water quality-standards-handbook

World Health Organization. (2016). *Protecting surface water for health: Identifying, assessing and managing drinking-water quality risks in surface-wate catchments*.https://www.who.int/publications/i/item/9789241510554