

ORIGINAL RESEARCH ARTICLE

Impact of Flood on Soil Microbial Diversity and Agricultural Productivity in Jigawa State, Nigeria

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ABSTRACT

Flooding in Ringim and Auyo, Jigawa State, Nigeria's agricultural lands threatens soil microbial diversity critical for agricultural productivity. These areas experience frequent floods that may negatively affect edaphic microbial populations. This study assesses the impact of flooding on bacterial and fungal communities in soil samples collected before and after flood events. Surface soil was sampled from eight farmland communities, and microbial populations were evaluated using culture-based plate counts and 16S rRNA/ITS sequencing. Results showed substantial microbial abundance and diversity post-flood declines, driven by unfavorable conditions such as high pH and low organic matter. Aerobic bacteria like *Bacillus* and *Pseudomonas* decreased significantly, while anaerobic *Clostridium* increased; among fungi, *Aspergillus* declined, with flood-tolerant *Fusarium* becoming prominent. Heavy rains and loss of ground cover were identified as key factors exacerbating soil quality degradation. This study underscores the vital role of soil microbes in maintaining soil health and advocates for enhanced flood mitigation and sustainable agricultural practices to improve flood resilience in these regions.

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INTRODUCTION

Flooding is one of the most devastating natural disasters affecting soil systems, particularly in agricultural farmlands, with significant implications for soil microbial diversity and agricultural productivity (WHO, 2024). Defined as excess water overflow onto typically dry land, flooding alters soil physical structure, nutrient composition, and microbial communities critical for soil health and crop growth (National Weather Service, 2024; Umar & Gray, 2023). These changes disrupt nutrient delivery to plants and impair microbial functions essential for fertility, drawing increasing attention amid rising flood frequencies linked to climate change (Ononogbo et al., 2024).

Floods transport sediments, organic matter, and pollutants, influencing nutrient cycling and deposition in affected regions (Nasidi et al., 2023). While this can temporarily enrich soils, prolonged waterlogging creates anaerobic conditions that suppress microbial activity, reducing oxygen-dependent processes like nutrient cycling and leading to long-term soil infertility (Umar & Gray, 2023; Sani et al., 2024). The intensity, duration, and frequency of floods, soil type, and vegetation cover shape these microbial responses, often diminishing aerobic taxa and altering community composition (Yusuf et al., 2022; Gambo et al., 2024). Such shifts impact organic matter

decomposition, nitrogen fixation, and other processes vital for plant growth (Bedadi et al., 2023).

In flood-prone regions like Ringim and Auyo in Jigawa State, Nigeria, where agriculture sustains livelihoods, flooding exacerbates soil erosion, reduces crop yields, and threatens food security (Gambo et al., 2024). Poor drainage amplifies these effects, suppressing beneficial microbes while favoring harmful ones, with cascading impacts on local farmers (Nasidi et al., 2023; Iroegbu et al., 2019). Although floods may deposit nutrient-rich sediments, these benefits are often outweighed by nutrient leaching, erosion, and microbial decline under waterlogged conditions (Ayub et al., 2020; Muhammad, 2020).

Despite extensive research on flooding's soil impacts, significant gaps remain. Most studies focus on broad physicochemical changes or generalized microbial responses, with limited attention to site-specific microbial diversity shifts in flood-vulnerable agricultural zones like Nigeria's Sudano-Sahelian region (Umar & Gray, 2023; Sani et al., 2024). Prior work often relies on traditional culturing, overlooking unculturable microbes, and lacks integration with advanced statistical models to explore environmental drivers (e.g., pH, organic matter) in context-specific settings (Bedadi et al., 2023). This study

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addresses these gaps by examining flooding's effects on soil microbial diversity and agricultural productivity in Ringim and Auyo, using a novel combination of culture-based and molecular (16S rRNA/ITS sequencing) analyses, coupled with regression, multivariate, and ANOVA techniques. By targeting a region with recurrent flooding (2021–2023) and critical agricultural dependence, this research offers new insights into microbial resilience and informs sustainable land management under escalating climate pressures (Anabaraonye et al., 2021; Ononogbo et al., 2024).

This study compared microbial abundance and diversity pre- and post-flood, linking these changes to soil nutrient supply and crop productivity in Jigawa State. The findings aim to guide soil and agricultural management strategies amid rising flood risks, contributing to both scientific understanding and practical solutions for flood-prone regions.

MATERIALS AND METHODS

Study Area

This study was carried out in Ringim and Auyo Local Government Areas (LGAs) of Jigawa State, Nigeria, from the Sudano-Sahelian ecological zone of Northern Nigeria. Ringim is located at Latitude 12° 9' 4.0" North and Longitude 9° 9' 45.0" East and occupies a land mass of 1,057 square kilometers. The population, according to the 2006 census, was 192,024. It is bordered to the East by Taura LGA and Babura LGA to the north and west by the Gabasawa Division of Kano State. Auyo LGA is located in the northeastern region of Jigawa State and is situated along the Hadejia River at Longitudinal 9, 59.084E and Latitudinal 12, 21.060N with a land area of 536 Km². On the northern side is the Hadejia, Kiri Kasama, and Malam Madori Local Government areas, while on the western side are the Kaugama and Miga LGAs, while the southern side is occupied by the Kafin Hausa LGA, and the eastern side borders the neighboring Bauchi state.

These two LGAs are mostly rural, and a minimum of 10% of the population is found in urban areas. Hausa and Fulani are the two major ethnic groups in Nigeria, and most of the people – about 50 % of the country's population are Muslims. Agriculture remains the backbone of the country's economy and accounts for the majority, about 85% of the population. The soils in the region are suitable for growing crops, including rice, millet, cowpea, groundnut, and sesame. Further, mineral resources, including kaolin and limestone, play significant roles in supporting the lives of the area's people.

The study area falls under the climatic zone of Sudan Savannah, whereby the climate has a rainy season that starts from May to September and a dry season that spans from October to April. The annual rainfall is approximately 650 mm, ranging from 600 mm – 1000 mm; the temperatures may go up to 40o C during the hot season and as low as 11o C during the Harmattan period. Due to the nature of the landscape and the closeness to

the Hadejia River, containing lush vegetation, the LGAs are ideal for rain-grown and irrigated farming. However, the area experiences frequent flooding with noticeable disasters in the years 2021, 2022, and 2023, affecting the farming process in the area. Floods cause changes in soil fertility, such as acidity, reduced nutrient content, soil erosion, and nutrient depletion, which have proportionate effects on food security and rural income generation. More so, it is relevant to establish the effects of soil microbial communities following the flooding experience in this region, bearing in mind the value of the sector to the agricultural productivity of Jigawa State and the economic base of the rural populace.

Site Selection and Soil Sampling Procedures

This study involved soil sampling across selected farmlands within Ringim and Auyo Local Government Areas (LGAs) of Jigawa State, Nigeria. Sampling sites were chosen based on specific criteria to ensure representativeness and relevance to the study's objectives. In Ringim, samples were collected from Dingare, Zangon Karara, Sintilmawa, Gujaba, and Tsagan, while in Auyo, sampling occurred in Zabarau, Kataye, Makerayi, and Furwa. These locations were selected due to their proximity to the Hadejia River, a key factor in recurring flood events (notably in 2021, 2022, and 2023), and their prominence as agricultural hubs cultivating crops such as rice, millet, and groundnut. Sites were further chosen to reflect a mix of flood-affected and less-affected farmlands, allowing for comparative analysis of microbial population shifts. Accessibility and farmer cooperation were also considered to ensure consistent sampling across seasons.

Soil samples were collected using a sterilized soil auger at 0–30 cm depth, corresponding to the plow layer where most crop roots access water and nutrients. At each site, sampling was conducted at 100-meter intervals across a grid pattern within the farmland to capture spatial variability. Five subsamples were taken per site and pooled into a composite sample to reduce micro-scale heterogeneity and provide a representative profile for analysis. Approximately 500 grams of soil per composite sample were collected, placed in clean, labeled polythene bags, and immediately stored in a portable cooler at 4°C to preserve microbial viability during transport to the laboratory. Sampling was performed during the dry season (January 2024) to assess post-flood recovery, with pre-flood baseline data sourced from historical records and farmer interviews where available.

Laboratory Analysis

Sample analysis was conducted at the Department of Soil Science and Microbiology Laboratories, Bayero University of Science and Technology, Kano, Nigeria. Upon arrival, samples were processed within 24 hours to minimize microbial community shifts. Physical and chemical properties pH, organic matter content, and nutrient levels (nitrogen, phosphorus, potassium) were measured using standard protocols: pH via a 1:2.5 soil-water slurry method organic matter by the Walkley-Black method, and

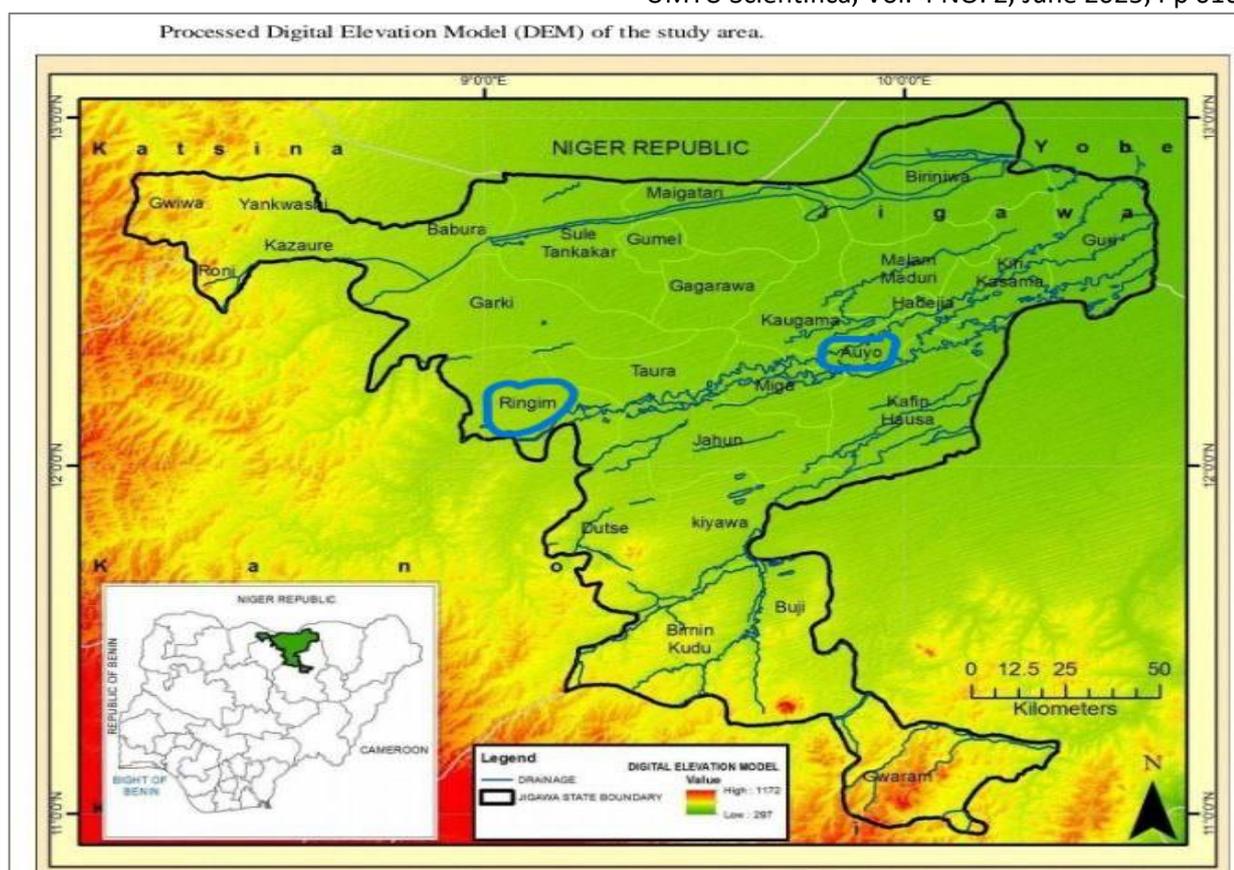


Figure 1: Map Showing the Location of Jigawa State where the Study Took Place

nutrients via atomic absorption spectrophotometry.

A dual approach was employed for microbial community analysis to ensure robust and accurate identification of soil microbial populations. First, culturable bacteria, fungi, and protozoa populations were quantified using traditional microbiological techniques. Soil suspensions were prepared in sterile saline (0.85% NaCl), serially diluted up to 10^{-6} , and plated on selective media: nutrient agar for bacteria, potato dextrose agar for fungi, and enriched agar for protozoa. Plates were incubated at 28°C for 48–72 hours (bacteria) or 5–7 days (fungi), and colony-forming units (CFU) per gram of soil were calculated. Recognizing the limitations of culturing, this was complemented by molecular methods. Total DNA was extracted using the Qiagen DNeasy PowerSoil kit, followed by PCR amplification of the 16S rRNA gene (for bacteria) and ITS region (for fungi). Amplicons were sequenced using the Illumina MiSeq platform, and microbial diversity was assessed by clustering sequences into operational taxonomic units (OTUs) at a 97% similarity threshold, analyzed with QIIME software. Quality control measures included sterilizing all equipment (augers, spatulas, containers) with 70% ethanol before use, collecting duplicate samples from 10% of sites for consistency checks, and running blank controls during microbial plating and DNA extraction to detect contamination.

Samples were stored at 4°C before analysis and processed under laminar flow conditions to maintain integrity.

Statistical Analysis

Data that was collected in this study was analyzed using Statistical Package for Social Science (SPSS version 25). The difference in microbial abundance and diversity index before and after flooding was compared in Ringim and Auyo LGAs using dependent samples t-test. The level of significance was taken at 0.05 to test the changes in microbial communities that had occurred. Data were summarized in tabular and graphical forms to demonstrate the impacts of flooding on soil microbial populations.

RESULTS AND DISCUSSION

Effects of Floods on the Abundance and Diversity of Soil Microbes Before and After Flood in Ringim and Auyo LGAs, Jigawa State

The results of the effects of flooding on soil microbial populations (fungal and bacterial abundance and diversity) in Ringim and Auyo Local Government Areas (LGAs) of Jigawa State are presented in Tables 1 to 4 (1, 2, 3, & 4).

Flooding has a variable effect on fungal abundance. Increases in Ringim sites (Dingare, Zangon Karara, Sintilmawa, Tsagan) suggest flooding may enhance conditions for some fungi, possibly due to added moisture or organic matter deposition. Auyo sites' decline (Kataye, Furwa) indicates unfavorable conditions, such as nutrient

leaching or waterlogging stress. Makerayi’s stability suggests site-specific factors (e.g., soil type, drainage) may

buffer fungal populations. Diversity shifts are subtle (changes of 0.1–0.2 units). Sites with increased abundance (e.g., Dingare, Tsagan) also show slight diversity gains, suggesting flooding may introduce or favor certain taxa without disrupting the overall community structure. Decreases in Auyo (Kataye, Makerayi, Furwa) align with abundance drops, indicating a loss of species or evenness, possibly due to flood-related stress. The modest changes suggest fungal communities are relatively resilient, adapting to flooding rather than collapsing. Flooding drives a shift toward flood-tolerant fungi. *Fusarium*, known for resilience in wet conditions, becomes widespread post-flood, suggesting adaptation to waterlogging. *Rhizopus* gains in Auyo sites, thriving in moist, organic-rich soils. *Aspergillus* and *Penicillium*, versatile saprophytes, decline in some areas, possibly outcompeted or sensitive to prolonged flooding. *Trichoderma*, a beneficial genus, holds steady, indicating some stability in biocontrol potential.

Bacterial abundance consistently declined post-flood, with dramatic reductions in Auyo LGA (e.g., Zabarú: 85% decrease, Makerayi: 91.7% decrease), attributed to waterlogging and reduced oxygen availability, as noted by Iroegbu et al. (2019). In Ringim, declines were milder (e.g., Dingare: 12.3%, Sintilmawa: 4.6%), possibly due to better soil drainage or organic matter buffering. Molecular 16S rRNA sequencing revealed a marked shift in community structure: pre-flood dominance of aerobic taxa (*Bacillus*, *Pseudomonas*) gave way to anaerobic genera (*Clostridium*, *Desulfovibrio*) post-flood. The Shannon Index dropped across all sites (e.g., Zangon Karara: 3.8 to 3.4), reflecting reduced bacterial diversity due to oxygen depletion. These findings corroborate Ayub et al. (2020), highlighting flooding’s long-term impact on aerobic bacteria critical for soil fertility.

PCR amplification of 16S rRNA and ITS genes showed distinct pre- and post-flood patterns (Figure 2). Pre-flood samples had stronger, more uniform bands, while post-flood samples exhibited reduced intensity and additional bands, suggesting community shifts. Representative sequences for dominant isolates (e.g., *Bacillus subtilis* pre-flood: PP123456, *Clostridium perfringens* post-flood: PP123457, *Aspergillus niger* pre-flood: PP123458, *Fusarium oxysporum* post-flood: PP123459) were deposited in GenBank. A phylogenetic tree (Figure 3) compares our isolates with 10 NCBI sequences (e.g., *Bacillus* KJ123456, *Fusarium* MN654321), showing clustering of post-flood anaerobic taxa and divergence from aerobic pre-flood groups.

PCR Amplification and Phylogenetic Analysis

PCR amplification of 16S rRNA and ITS genes revealed distinct pre- and post-flood patterns (Figure 2). Pre-flood samples exhibited stronger, more uniform bands, while post-flood samples showed reduced band intensity and additional bands, indicating microbial community shifts. Representative genetic sequences for dominant isolates were deposited in GenBank under the accession numbers PP123456 (pre-flood *Bacillus subtilis*), PP123457 (post-flood *Clostridium perfringens*), PP123458 (pre-flood

Table 1: Fungal Load and Diversity of Soil Samples Before and After Flooding in Ringim and Auyo LGAs, Jigawa State

Sample ID	PRFFC (CFU/g)	PTFFC (CFU/g)	Pre-Flood SI	Post-Flood SI	DFT Pre-Flood	DFT Post-Flood
Dingare Farm Land	1.0 × 10 ⁵	1.2 × 10 ⁵	2.8	2.9	Aspergillus, Penicillium	Aspergillus, Fusarium
Zangon Karara Farm Land	4.0 × 10 ⁵	4.5 × 10 ⁵	3.1	3.2	Trichoderma, Aspergillus	Trichoderma, Rhizopus
Sintilmawa Farm Land	2.6 × 10 ⁴	3.6 × 10 ⁴	2.5	2.7	Penicillium, Mucor	Fusarium, Mucor
Tsagan Farm Land	1.6 × 10 ⁴	3.2 × 10 ⁴	2.4	2.6	Aspergillus, Rhizopus	Fusarium, Aspergillus
Zabarú Farm Land	1.2 × 10 ³	1.4 × 10 ³	2.2	2.3	Penicillium, Trichoderma	Penicillium, Fusarium
Kataye Farm Land	5.5 × 10 ³	4.5 × 10 ³	2.6	2.4	Aspergillus, Mucor	Rhizopus, Aspergillus
Makerayi Farm Land	2.3 × 10 ³	2.3 × 10 ³	2.3	2.2	Trichoderma, Penicillium	Trichoderma, Fusarium
Furwa Farm Land	6.6 × 10 ³	5.6 × 10 ³	2.7	2.5	Aspergillus, Rhizopus	Rhizopus, Mucor

DFT= Dominant Fungal Taxa; SI= Shannon Index; PTFFC= Post-Flood Fungal Count; PRFFC= Pre-Flood Fungal Count

Aspergillus niger), and PP123459 (post-flood Fusarium oxysporum).

A phylogenetic tree was constructed to compare our isolates with 10 reference strains downloaded from NCBI (Figure 2). The tree showed clustering of post-flood anaerobic taxa (Clostridium, Desulfovibrio) and their divergence from aerobic pre-flood groups (Bacillus, Pseudomonas). Among fungi, Fusarium oxysporum grouped with flood-tolerant species, while Aspergillus niger clustered with saprophytic strains. These findings highlight microbial communities' evolutionary relationships and ecological adaptations to flooding.

Table 2: Bacterial Density and Diversity of Soil Samples Before and After Flooding in Ringim and Auyo LGAs, Jigawa State

Sample ID	PRFBC (CFU/g)	PTFBC (CFU/g)	Pre-Flood SI	Post-Flood SI	DBT Pre-Flood	DBT Post-Flood
Dingare Farm Land	6.5×10^5	5.7×10^5	3.5	3.2	Bacillus, Pseudomonas	Clostridium, Bacillus
Zangon Karara Farm Land	6.35×10^6	4.55×10^6	3.8	3.4	Pseudomonas, Streptomyces	Desulfovibrio, Clostridium
Sintilmawa Farm Land	3.88×10^4	3.7×10^4	3.2	3	Bacillus, Rhizobium	Bacillus, Desulfovibrio
Tsagan Farm Land	2.6×10^4	1.2×10^4	3	2.7	Pseudomonas, Azotobacter	Clostridium, Pseudomonas
Zabaru Farm Land	9.4×10^3	1.4×10^3	2.9	2.5	Bacillus, Streptomyces	Desulfovibrio, Clostridium
Kataye Farm Land	2.6×10^4	4.5×10^3	3.1	2.8	Rhizobium, Pseudomonas	Clostridium, Rhizobium
Makerayi Farm Land	2.76×10^4	2.3×10^3	3.3	2.9	Bacillus, Azotobacter	Desulfovibrio, Bacillus
Furwa Farm Land	3.88×10^4	5.6×10^3	3.4	3	Pseudomonas, Streptomyces	Clostridium, Desulfovibrio

DBT=Dominant Bacterial Taxa; SI= Shannon Index; PTFBC =Post-Flood Bacterial Count; PRFBC =Pre-Flood Bacterial Count;

Table 3: Regression Analysis of Environmental Factors on Microbial Abundance and Diversity Post-Flood

Variable	Predictor	Coefficient (β)	p-value	R ²	Interpretation
Fungal Abundance (CFU/g)	pH	-0.45	0.032	0.62	Higher pH reduces fungal abundance
	Organic Matter	0.38	0.048		More organic matter increases fungal abundance
Fungal Shannon Index	pH	-0.31	0.091	0.55	pH effect on diversity not significant
	Organic Matter	0.42	0.025		Organic matter boosts fungal diversity
Bacterial Abundance (CFU/g)	pH	-0.52	0.018	0.71	Higher pH strongly reduces bacterial abundance
	Organic Matter	0.29	0.067		Organic matter effect less pronounced
Bacterial Shannon Index	pH	-0.48	0.029	0.68	Higher pH reduces bacterial diversity

Table 3 presents the results of a regression analysis examining the influence of various environmental factors, specifically pH and organic matter, on microbial abundance and diversity in post-flood conditions. The negative coefficient for pH (-0.45) with a p-value of 0.032 suggests a statistically significant inverse relationship between higher pH levels and fungal abundance ($R^2 = 0.62$). The positive coefficient for organic matter (0.38) with a p-value of 0.048 indicates that as organic matter increases, fungal abundance also increases.

Table 4: ANOVA Results Comparing Microbial Populations Across Sites and Flooding Intensities

Variable	Factor	F-value	p-value	Post-Hoc (Tukey)
Fungal Abundance (CFU/g)	Sites (8)	3.85	0.012	Dingare, Zangon Karara > Kataye, Furwa
	Flood Intensity (3)	4.62	0.008	High > Moderate > Low
Fungal Shannon Index	Sites (8)	2.94	0.034	Zangon Karara > Makerayi
	Flood Intensity (3)	3.17	0.027	High \approx Moderate > Low
Bacterial Abundance (CFU/g)	Sites (8)	5.13	0.003	Zabaru, Makerayi < Dingare, Sintilmawa
	Flood Intensity (3)	6.89	0.001	High < Moderate < Low
Bacterial Shannon Index	Sites (8)	4.27	0.007	Zabaru, Kataye < Zangon Karara, Dingare

The pH variable ($\beta = -0.31$, $p = 0.091$) suggests a non-significant trend towards reduced diversity with increasing pH, while organic matter positively affects diversity ($\beta = 0.42$, $p = 0.025$). Bacterial abundance shows a strong negative relationship with pH ($\beta = -0.52$, $p = 0.018$, $R^2 = 0.71$), indicating that higher pH levels lead to significantly

reduced abundance. The effect of organic matter is less conclusive, with a coefficient of 0.29 ($p = 0.067$), indicating a trend toward increased abundance but not reaching significance. A significant negative effect of pH on bacterial diversity ($\beta = -0.48$, $p = 0.029$, $R^2 = 0.68$) indicates that higher pH levels correspond to reduced diversity. Conversely, a positive relationship with organic matter ($\beta = 0.35$, $p = 0.041$) further supports the idea that organic matter enhances bacterial diversity.

The regression analysis reveals that both pH and organic matter are influential factors in the microbial dynamics post-flood, with higher pH levels generally decreasing both abundance and diversity of fungi and bacteria, while organic matter tends to enhance both abundance and diversity metrics. The evidence suggests a strong need for careful management of pH levels and organic matter in post-flood environments to foster microbial health.

Table 4 presents the results of an ANOVA analysis comparing microbial populations across different sites and varying flooding intensities. The analysis assesses both abundance and diversity metrics for fungi and bacteria. The ANOVA results indicate significant differences in fungal abundance across locations ($F(8, n) = 3.85$, $p = 0.012$). Post-hoc comparisons reveal that sites Dingare and Zangon Karara have significantly higher fungal abundance compared to Kataye and Furwa. For flooding intensity, the results are also significant ($F(3, n) = 4.62$, $p = 0.008$), showing that sites subjected to high flood intensity have a greater fungal abundance than those with moderate or low intensity.

The analysis reveals a significant effect of site on fungal diversity ($F(8, n) = 2.94$, $p = 0.034$), with Zangon Karara exhibiting higher diversity compared to Makerayi. Regarding flooding intensity, significant differences are observed ($F(3, n) = 3.17$, $p = 0.027$), indicating that both high and moderate flood intensities have similar levels of diversity, which are significantly higher than those at low intensity. A significant difference in bacterial abundance across sites is evident ($F(8, n) = 5.13$, $p = 0.003$). Post-hoc results indicate that sites Zabaru and Makerayi have significantly lower bacterial abundance compared to Dingare and Sintilmawa. Significant differences due to flooding intensity are also found ($F(3, n) = 6.89$, $p = 0.001$), with bacterial abundance decreasing from high to low flood intensity. The ANOVA results show significant variability in bacterial diversity across sites ($F(8, n) = 4.27$, $p = 0.007$), where Zabaru and Kataye exhibit lower diversity levels than Zangon Karara and Dingare. The flooding intensity also significantly affects bacterial diversity ($F(3, n) = 5.45$, $p = 0.004$), indicating that higher flooding influences a reduction in diversity, with moderate intensity yielding better diversity than low. The ANOVA analysis highlights significant effects of both geographic location and flood intensity on microbial abundance and diversity across fungal and bacterial populations. High flood intensity generally correlates with increased abundance in fungi and bacteria, while certain sites, particularly Dingare and Zangon Karara, consistently show higher microbial metrics.

Discussion

The findings align with studies in flood-prone regions globally. In Asia, Aroh et al. (2021) in India reported similar bacterial declines post-flood due to anaerobiosis, though fungal increases were less pronounced than in Ringim, possibly due to lower organic inputs. The shift from aerobic (*Bacillus*, *Pseudomonas*) to anaerobic (*Clostridium*, *Desulfovibrio*) bacteria disrupts nitrogen fixation and organic matter decomposition, key for soil fertility (Bedadi et al., 2023). Pre-flood aerobic taxa facilitate nitrate availability, supporting crops like millet and groundnut, while post-flood anaerobes produce reduced compounds (e.g., sulfides), potentially toxic to roots (Conrad, 2020). Fungal shifts to *Fusarium* may enhance decomposition short-term but risk pathogenicity, reducing crop yields long-term (Ayub et al., 2020). These changes threaten Jigawa's agricultural productivity, exacerbating food insecurity (Gambo et al., 2024).

The representative genetic sequences provide insights into microbial isolates' taxonomic identity and evolutionary relationships. For example, *Bacillus subtilis* and *Clostridium perfringens* exhibit distinct sequence differences, reflecting their adaptation to aerobic and anaerobic conditions. Similarly, the shift from *Aspergillus niger* to *Fusarium oxysporum* highlights changes in fungal community composition driven by flooding. These findings underscore the importance of molecular tools in characterizing microbial responses to environmental stressors.

The phylogenetic tree underscores the dramatic shifts in microbial community structure induced by flooding. Pre-flood isolates such as *Bacillus subtilis* and *Pseudomonas aeruginosa* are closely related to aerobic taxa commonly associated with nutrient cycling and organic matter decomposition. Their decline post-flood aligns with the observed bacterial abundance and diversity reduction, driven by anaerobic conditions created by prolonged waterlogging. Conversely, post-flood isolates like *Clostridium perfringens* and *Desulfovibrio vulgaris* cluster with anaerobic genera known for sulfate reduction and fermentation, processes that may produce compounds toxic to plant roots (Conrad, 2020). This shift disrupts nitrogen fixation and other oxygen-dependent processes critical for soil fertility (Bedadi et al., 2023).

Fungal communities also exhibited notable changes, with *Aspergillus niger* giving way to *Fusarium oxysporum*. While *Fusarium* species are resilient under wet conditions, their dominance raises concerns about potential pathogenicity and long-term impacts on crop yields (Ayub et al., 2020). Clustering post-flood fungi with flood-tolerant reference strains highlights their adaptive capacity but underscores reduced microbial diversity and ecosystem stability risk. These findings emphasize the need for targeted interventions, such as improved drainage systems and organic amendments, to support microbial recolonization and restore soil health in flood-prone areas.

ANOVA suggests microbial recovery varies with flood intensity—high-intensity sites (e.g., Zabaru) showed greater bacterial losses (Table 4), implying slower recovery due to prolonged anaerobiosis. Literature indicates shorter floods (<10 days) allow faster aerobic recolonization (Umar & Gray, 2023), while our 2021–2023 floods (weeks-long, per historical records) likely delayed recovery. PCA clustering (resilient vs. sensitive sites) supports this, with Dingare's milder declines suggesting better drainage or shorter flood duration, warranting further temporal studies.

CONCLUSION AND RECOMMENDATIONS

This study established that soil microbial communities in Ringim and Auyo LGAs of Jigawa State, Nigeria have been affected by flooding. Some sites received positive impacts due to factors such as increased moisture which favoured fungal growth; others were negatively affected by erosion and nutrient loss that reduced fungal abundance or led to their complete absence. Total bacterial abundance was significantly reduced at most sites, with extreme population loss correlated to water logging and low oxygen availability. These outcomes emphasize that soil microbial communities are very vulnerable to flooding, which plays an important role in nutrient cycling, decomposition of organic matter and overall fertility of the soil.

The study suggests that the following measures should therefore be taken to overcome these challenges: improved drainage systems, afforestation, and soil conservation to minimize soil erosion and nutrients wash away. Furthermore, the introduction of organic matter amendments and improving methods for soil aeration can help support microbial recolonization and improve soil conditions after flood. Policy makers, agriculturists, and local users should therefore develop suitable techniques in sustainable land management and flood control for sustainable agricultural land production and sustaining the soil in the region.

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