

BACTERIOLOGICAL QUALITY OF SOIL AND SURFACE WATER AROUND THE IKA-OGBOYAGA COAL MINING SITE, ANKPA, KOGI STATE, NIGERIA

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Abstract

Coal mining alters the physicochemical character of soils and water, and with it the microbial communities responsible for nutrient cycling and self purification, yet little is known about the bacteriology of Nigerian mining areas. This study determined the occurrence, diversity and habitat distribution of culturable bacteria in soils and stream water around the Ika-Ogboyaga coal mining area of Ankpa, Kogi State, comparing a mining impacted zone with an adjacent non mining reference zone over four months from August to November 2024. Water was sampled at three stations along the stream, upstream, midstream and downstream, and surface soil was sampled at a depth of 0 to 15 cm at three points in each zone, giving twelve samples per medium per zone. Bacteria were isolated by the serial dilution pour plate method on nutrient agar and identified presumptively by colonial and cellular morphology, Gram reaction and conventional biochemical tests, without serological or molecular confirmation. Occurrence was scored as presence or absence per sample, and richness and frequency of occurrence served as the measures of diversity. Thirteen bacterial taxa were recovered overall. Richness was consistently lower in the mining zone than in the reference zone in both media: four taxa against eight in stream water, a reduction of 50 percent, and eight against eleven in soil, a reduction of 27 percent. Mining zone assemblages were largely nested within reference zone assemblages, with Jaccard similarity of 0.333 for water and 0.727 for soil, and only *Shigella* spp. in water was exclusive to the mining zone. Occurrence in the mining zone was concentrated in a few resilient taxa: *Salmonella* spp. and *Shigella* spp. were recovered from every water sample, and *Bacillus* spp., *Enterococcus* spp. and *Salmonella* spp. from every soil sample. The persistence of enteric taxa alongside reduced overall richness indicates a community that is both biologically simplified and of public health concern. The study concludes that mining pressure at Ika-Ogboyaga has narrowed the culturable bacterial community to a stress tolerant subset while leaving enteric contamination undiminished, and recommends protection of the stream from both mine drainage and faecal input.

Keywords: coal mining; bacterial diversity; faecal indicator bacteria; soil and water quality; bioindicators; Ika-Ogboyaga; Kogi State

1. Introduction

The functioning of soil and water as living systems depends heavily on the microbial populations within them. Bacteria drive organic matter degradation, nitrogen transformation and the self purification processes by which contaminated water recovers. Where these communities are reduced or altered, the ecosystem services they underwrite are reduced with them, and the loss is not immediately visible because it registers in process rates rather than in anything that can be observed directly (Bhaduri et al., 2022).

Coal mining is among the most disruptive land uses for these systems. It exposes sulphidic overburden, generates acid mine drainage, raises the concentration of heavy metals in soil and water, and strips the soil of organic matter and structure (de Quadros et al., 2016; Munyai, Ogola and Modise, 2021). The resulting metallic stress acts as a powerful selective filter on microorganisms, reducing sensitive populations and favouring metal tolerant strains (Fashola, Ngole-Jeme and Babalola, 2016; Ibrahim et al., 2021). The outcome is not simply fewer bacteria but a different community, narrower in composition and dominated by organisms whose principal virtue is endurance rather than functional contribution.

Surface water near mining settlements faces a second and independent pressure. Faecal contamination from human and animal sources introduces enteric bacteria whose presence is used worldwide as the standard indicator of sanitary risk (Gruber, Ercumen and Colford, 2014; Nowicki et al., 2021). These two pressures, geochemical and sanitary, act on the same water body through different mechanisms, and there is no reason to expect them to move together. A stream may be simultaneously impoverished in its general bacterial community and heavily contaminated with enteric organisms, and that combination is the worst of both outcomes, since it pairs a reduced capacity for self purification with an undiminished pathogen load.

Coal is mined in Kogi, Enugu and neighbouring states, and local studies have documented acidification, metal contamination of drainage and degradation of soil near these operations (Ameh and Aina, 2020; Obiadi et al., 2016). What has not been examined is the bacteriological consequence. Physicochemical characterisation establishes that the environment has changed; it does not establish whether the biological community that processes that environment has survived the change.

This study addresses that gap for the Ika-Ogboyaga coal mining area of Ankpa, Kogi State. Its objectives are to determine the occurrence and richness of culturable bacteria in soil and surface water in a mining impacted zone and an adjacent non mining reference zone, to compare the composition of the two assemblages and identify shared and exclusive taxa, to quantify the frequency with which each taxon occurs, and to assess the implications for ecosystem function and public health.

2. Materials and Methods

2.1 Study Area

The study was carried out around the Mosra Energy Limited coal mine in the Ika-Ogboyaga environs of Ankpa Local Government Area, Kogi State, north central Nigeria. The area lies within the Anambra Basin coal belt, and mining activity has exposed overburden and altered surface drainage in the immediate vicinity of the pit. A stream flows through the area and was sampled at three stations along its course. The locations of the mining site and the sampling stations are shown in Figure 1.

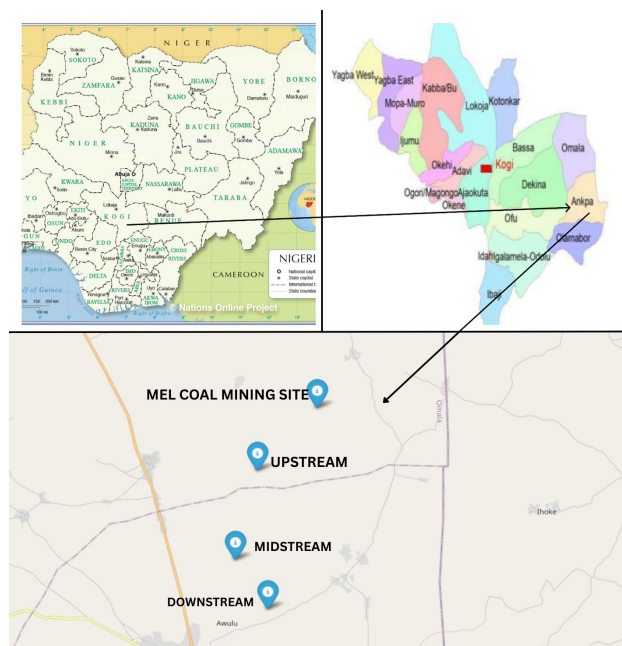


Figure 1: Map of the study area showing Nigeria, Kogi State, Ankpa Local Government Area, and the mining site with the upstream, midstream and downstream water sampling stations along the stream.

2.2 Study Design and Sampling

Sampling was conducted over four months, from August to November 2024, in two zones: a mining impacted zone and a non mining reference zone. Water was collected from the stream at three locations along its course, upstream, midstream and downstream, with the nearest mining zone station approximately 120 m from the mine and the reference station approximately 2.5 km away. Water samples were collected in sterile screw capped bottles, stored at 4 °C and processed within 24 hours of collection. Surface soils were collected from a depth of 0 to 15 cm using a sterile hand auger at three locations in each zone, packed in sterile polythene bags and transported in a cool box. Sampling equipment was sterilised between locations to prevent cross contamination.

The sampling structure therefore yielded three locations per zone across four months, giving twelve samples per medium per zone. Two features of the design should be stated at the outset because they constrain the inferences available. The four month window spans the late wet season and the onset of the dry season, which is a single wet to dry transition rather than a full annual cycle. The design comprises one mining zone and one adjacent reference zone, and the three sampling locations within each zone are treated as subsamples of that zone rather than as independent replicate sites.

2.3 Isolation and Identification of Bacteria

Enumeration and isolation were performed using the serial dilution pour plate method. Tenfold serial dilutions of soil suspensions, prepared as 10 g in 90 mL of sterile distilled water, and of water samples were prepared, and appropriate dilutions were plated on sterile nutrient agar and incubated at 30 °C for 24 to 48 hours. Colonies were characterised by form, elevation, margin, colour and surface, then purified by repeated subculture on fresh nutrient agar.

Pure cultures were identified by Gram staining and microscopic examination of cellular morphology, and assigned to genus and where possible to species using conventional biochemical tests including catalase, oxidase, coagulase, indole, methyl red, Voges-Proskauer, citrate utilisation, motility and sugar fermentation, interpreted against standard identification schemes. Isolates assigned to *Escherichia coli* were Gram negative, motile, catalase positive and oxidase negative rods that fermented lactose and glucose with gas production and gave the IMViC pattern indole positive, methyl red positive, Voges-Proskauer negative and citrate negative. Isolates assigned to *Salmonella* spp. were motile, lactose non fermenting, indole negative, methyl red positive, Voges-Proskauer negative and citrate positive.

All identifications reported here are presumptive. No serological or molecular confirmation was undertaken, and the taxonomic assignments should be read accordingly.

2.4 Data Analysis

Occurrence of each taxon was recorded as presence or absence in each sample, giving three locations by four months, or twelve samples, per medium per zone. Taxon richness was recorded as the number of distinct taxa recovered from each medium and zone combination,

$$S_{mz} = \text{number of distinct taxa recovered in medium } m, \text{ zone } z \quad (1)$$

and frequency of occurrence was computed as the percentage of samples in which a taxon was detected,

$$F_i = (n_i / N) \times 100 \quad (2)$$

where n_i is the number of samples positive for taxon i and $N = 12$ is the number of samples in that medium and zone combination. Taxa were classified as consistently present where occurrence reached 100 percent and as sporadic where occurrence was 33 percent or below. Compositional similarity between the mining and reference assemblages was quantified using the Jaccard index

$$J = a / (a + b + c) \quad (3)$$

in which a is the number of taxa shared by both zones, b the number exclusive to the mining zone and c the number exclusive to the reference zone. Values approach unity where the two assemblages are compositionally alike and zero where they share no taxa. The index is reported here because it distinguishes two patterns that a simple richness comparison cannot: the loss of taxa without replacement, and the substitution of one community by another.

No colony forming unit counts or most probable number estimates were made, so every measure reported here is based on detection frequency and not on bacterial density. The presence and absence matrices underlying all computations are given in Tables 2 to 5.

3. Results

3.1 Bacterial Richness and Community Composition

Thirteen bacterial taxa were presumptively identified across the study. Richness was lower in the mining zone than in the reference zone in both media. Surface water in the mining zone yielded four taxa against eight in the reference zone, a reduction of 50 percent, while soil yielded eight taxa against eleven, a reduction of 27 percent (Table 1, Figure 2). Soil supported richer assemblages than water in both zones.

Table 1: Bacterial richness and habitat distribution by medium and zone

Medium and zone	Number of taxa	Consistently present (100%)	Sporadic ($\leq 33\%$)
Surface water, mining	4	<i>Salmonella</i> , <i>Shigella</i>	<i>Enterobacter</i>
Surface water, non mining	8	none	<i>Proteus</i> , <i>Salmonella</i> , <i>Lactobacillus</i>
Soil, mining	8	<i>Enterococcus</i> , <i>Bacillus</i> , <i>Salmonella</i>	<i>Enterobacter</i> , <i>Pseudomonas</i>
Soil, non mining	11	<i>Enterobacter</i> , <i>Enterococcus</i> , <i>Bacillus</i> , <i>B. cereus</i> , <i>B. megaterium</i>	<i>Pseudomonas</i> , <i>Yersinia</i>

Note. Consistently present taxa occurred in all twelve samples; sporadic taxa occurred in 33 percent or fewer. Source: authors' computation from the presence and absence matrices in Tables 2 to 5.

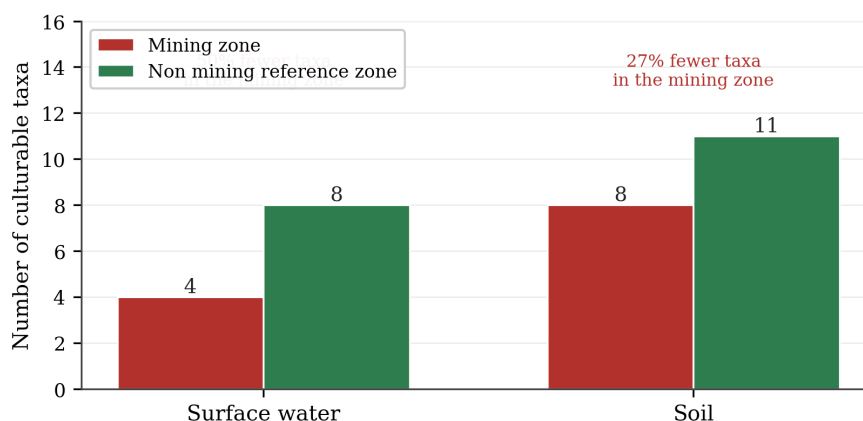


Figure 2: Culturable bacterial richness in surface water and soil in the mining and non mining zones. The reduction is proportionally larger in water than in soil.

Comparison of the two assemblages shows that mining zone communities were largely nested within reference zone communities rather than differing in kind. In surface water, three taxa were shared, five were exclusive to the reference zone and only one, *Shigella* spp., was exclusive to the mining zone, giving a Jaccard similarity of 0.333. In soil, eight taxa were shared, three were exclusive to the reference zone and none was exclusive to the mining zone, giving a Jaccard similarity of 0.727 (Figure 3). The pattern is one of subtraction rather than replacement: mining appears to have removed taxa without establishing a distinctive mining adapted community in their place.

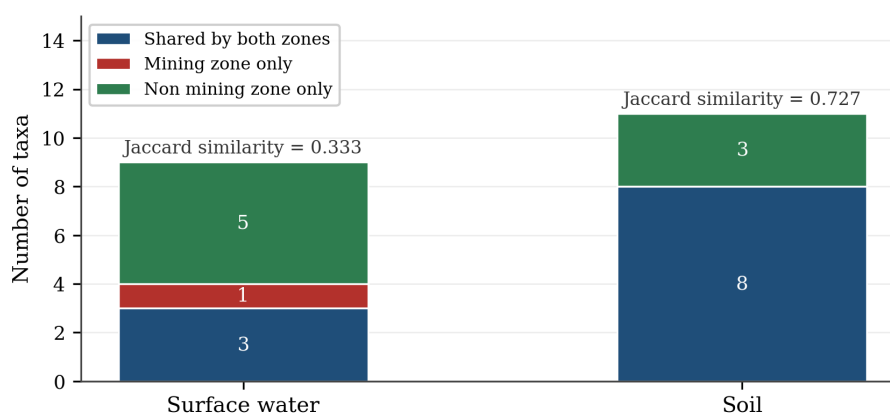


Figure 3: Shared and zone exclusive bacterial taxa for surface water and soil. The near absence of mining exclusive taxa indicates that the mining assemblage is a subset of the reference assemblage rather than a distinct community.

3.2 Bacterial Occurrence in Surface Water

Four taxa were recovered from surface water in the mining zone, namely *Enterobacter* spp., *Salmonella* spp., *Bacillus* spp. and *Shigella* spp., against eight in the reference zone. Within the mining zone, *Salmonella* spp. and *Shigella* spp. were recovered from every one of the twelve samples, while *Enterobacter* spp. was recovered from a single sample, an occurrence of 8.3 percent. The reference zone showed no taxon at 100 percent occurrence; its most frequent taxa, *Enterobacter* spp., *Pseudomonas* spp., *Bacillus* spp. and *Nocardia* spp., each occurred in 66.7 percent of samples.

3.3 Bacterial Occurrence in Soil

Soil supported richer assemblages than water in both zones, but the mining zone remained the poorer of the two, with eight taxa against eleven. In the mining zone, *Enterococcus* spp., *Bacillus* spp. and *Salmonella* spp. each occurred in all twelve samples, while *Enterobacter* spp. was reduced to a single occurrence at 8.3 percent and *Pseudomonas* spp. to 25.0 percent. In

the reference soil, five taxa occurred in all twelve samples, namely *Enterobacter* spp., *Enterococcus* spp., *Bacillus* spp., *Bacillus cereus* and *Bacillus megaterium*.

The contrast in *Enterobacter* occurrence is among the most striking single results in the dataset. In reference soil the taxon was recovered from every sample; in mining soil from one sample in twelve. The same collapse, from 66.7 percent to 8.3 percent, appears in water. Since *Enterobacter* includes plant growth promoting and metal tolerant strains (Abdullahi et al., 2021), its near disappearance under mining pressure is not readily attributed to metal sensitivity alone and warrants direct investigation.

3.4 Frequency of Occurrence of Bacterial Taxa

Figure 4 presents the frequency of occurrence of every taxon across the four medium and zone combinations. The pattern distinguishes the two zones clearly. In the mining zone occurrence is polarised: a small number of taxa are present in every sample while the remainder are sporadic or absent. In the reference zone occurrence is more evenly graded across a larger number of taxa. This is the signature of a community under selection, in which tolerant organisms occupy the space vacated by sensitive ones.

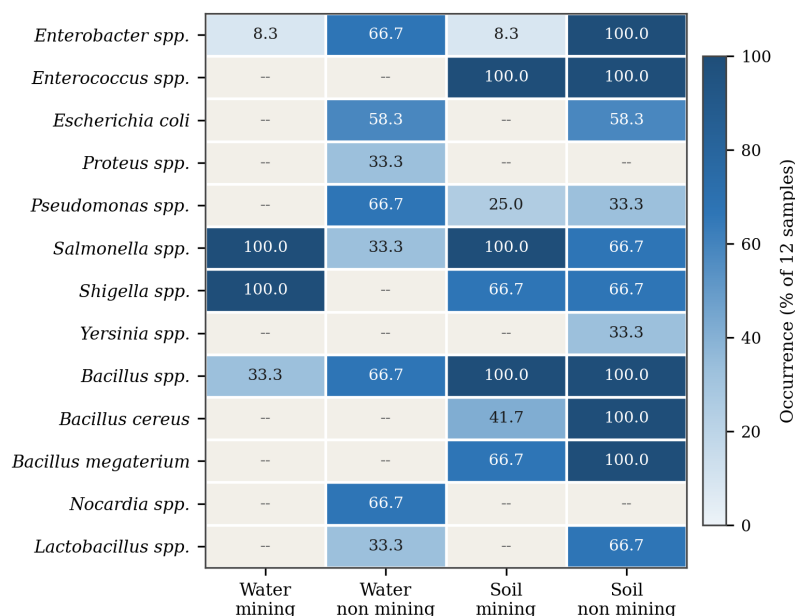


Figure 4: Frequency of occurrence of each bacterial taxon by medium and zone, as a percentage of the twelve samples per combination. Cells marked with a dash denote taxa not recovered from that medium and zone combination.

3.5 Enteric and Faecal Indicator Taxa

Figure 5 isolates the taxa of direct sanitary significance. *Salmonella* spp. and *Shigella* spp. were recovered from every water sample in the mining zone, and *Salmonella* spp. from every soil sample there. *Escherichia coli*, the conventional faecal indicator, was recovered from 58.3 percent of samples in both reference water and reference soil but was not recovered from the mining zone in either medium. *Enterococcus* spp. occurred in all soil samples in both zones but in no water sample.

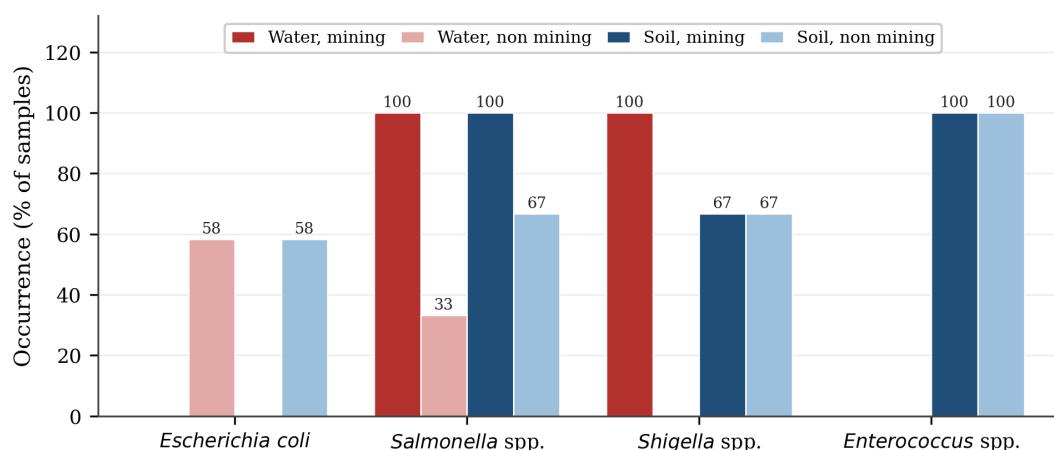


Figure 5: Occurrence of enteric and faecal indicator taxa across the four medium and zone combinations. The absence of *Escherichia coli* from the mining zone alongside universal occurrence of *Salmonella* and *Shigella* there is examined in Section 4.3.

3.6 Presence and Absence Matrices

Tables 2 to 5 present the underlying presence and absence records from which all richness and frequency values were computed. U, M and D denote the upstream, midstream and downstream water stations; P1, P2 and P3 denote the three soil sampling points within each zone.

Table 2: Presence and absence of bacterial taxa in surface water, mining zone

Taxon	Aug U	Aug M	Aug D	Sep U	Sep M	Sep D	Oct U	Oct M	Oct D	Nov U	Nov M	Nov D
<i>Enterobacter</i> spp.	+	–	–	–	–	–	–	–	–	–	–	–
<i>Salmonella</i> spp.	+	+	+	+	+	+	+	+	+	+	+	+
<i>Bacillus</i> spp.	+	–	–	+	–	–	+	–	–	+	–	–
<i>Shigella</i> spp.	+	+	+	+	+	+	+	+	+	+	+	+

Note. U, M and D denote upstream, midstream and downstream stations. The plus sign denotes detection and the minus sign non detection.

Table 3: Presence and absence of bacterial taxa in surface water, non mining reference zone

Taxon	Aug U	Aug M	Aug D	Sep U	Sep M	Sep D	Oct U	Oct M	Oct D	Nov U	Nov M	Nov D
<i>Enterobacter</i> spp.	+	+	–	+	+	–	+	+	–	+	+	–
<i>Escherichia coli</i>	+	–	+	+	–	+	–	–	+	+	–	+
<i>Proteus</i> spp.	–	+	–	–	+	–	–	+	–	–	+	–
<i>Pseudomonas</i> spp.	+	–	+	+	–	+	+	–	+	+	–	+
<i>Salmonella</i> spp.	–	–	+	–	–	+	–	–	+	–	–	+
<i>Bacillus</i> spp.	+	–	+	+	–	+	+	–	+	+	–	+
<i>Nocardia</i> spp.	+	–	+	+	–	+	+	–	+	+	–	+
<i>Lactobacillus</i> spp.	+	–	–	+	–	–	+	–	–	+	–	–

Note. U, M and D denote upstream, midstream and downstream stations.

Table 4: Presence and absence of bacterial taxa in soil, mining zone

Taxon	Aug P1	Aug P2	Aug P3	Sep P1	Sep P2	Sep P3	Oct P1	Oct P2	Oct P3	Nov P1	Nov P2	Nov P3
<i>Enterobacter</i> spp.	+	–	–	–	–	–	–	–	–	–	–	–
<i>Enterococcus</i> spp.	+	+	+	+	+	+	+	+	+	+	+	+
<i>Pseudomonas</i> spp.	+	–	+	–	–	+	–	–	–	–	–	–
<i>Bacillus</i> spp.	+	+	+	+	+	+	+	+	+	+	+	+
<i>Shigella</i> spp.	+	+	–	+	+	–	+	+	–	+	+	–
<i>Salmonella</i> spp.	+	+	+	+	+	+	+	+	+	+	+	+
<i>Bacillus cereus</i>	–	+	+	–	+	+	–	+	–	–	–	–
<i>Bacillus megaterium</i>	+	+	–	+	+	–	+	+	–	+	+	–

Note. P1, P2 and P3 denote the three soil sampling points within the zone.

Table 5: Presence and absence of bacterial taxa in soil, non mining reference zone

Taxon	Aug P1	Aug P2	Aug P3	Sep P1	Sep P2	Sep P3	Oct P1	Oct P2	Oct P3	Nov P1	Nov P2	Nov P3
<i>Enterobacter</i> spp.	+	+	+	+	+	+	+	+	+	+	+	+
<i>Enterococcus</i> spp.	+	+	+	+	+	+	+	+	+	+	+	+
<i>Pseudomonas</i> spp.	–	+	–	+	–	–	+	–	–	+	–	–
<i>Escherichia coli</i>	+	–	+	–	–	+	+	–	+	+	–	+
<i>Bacillus</i> spp.	+	+	+	+	+	+	+	+	+	+	+	+
<i>Shigella</i> spp.	+	+	–	+	+	–	+	+	–	+	+	–
<i>Lactobacillus</i> spp.	+	–	+	+	–	+	+	–	+	+	–	+
<i>Yersinia</i> spp.	+	–	–	+	–	–	+	–	–	+	–	–
<i>Salmonella</i> spp.	–	+	+	–	+	+	–	+	+	–	+	+
<i>Bacillus cereus</i>	+	+	+	+	+	+	+	+	+	+	+	+
<i>Bacillus megaterium</i>	+	+	+	+	+	+	+	+	+	+	+	+

Note. P1, P2 and P3 denote the three soil sampling points within the zone.

4. Discussion

4.1 Reduced Richness Under Mining Pressure

The central finding is that the mining zone supported consistently fewer culturable bacterial taxa than the adjacent reference zone, in both media and across all four months. The reduction was proportionally larger in water, at 50 percent, than in soil, at 27 percent. This direction of effect is consistent with the international literature on mining impacted microbiomes, in which acidification, metal loading and loss of organic matter reduce microbial richness and biomass (de Quadros et al., 2016; Liu et al., 2023; Munyai, Ogola and Modise, 2021).

The greater sensitivity of the water column is worth dwelling on, because it is the opposite of what a simple exposure argument would predict. Soil, being nearer the source and retaining contaminants, might be expected to show the larger effect. That water shows the larger reduction suggests that the soil matrix buffers its community, offering microhabitat heterogeneity, sorption sites and organic matter that moderate exposure, while the water column offers no such refuge. An organism in a stream is exposed to whatever the stream carries; an organism in soil may occupy a pore in which conditions differ markedly from the bulk. The practical implication is that surface water is the more sensitive medium for monitoring, and the one in which impact will register earliest.

4.2 Subtraction Rather Than Substitution

The Jaccard values quantify something a richness comparison alone would miss. In soil the index of 0.727 indicates that the mining assemblage is largely a subset of the reference assemblage, and no taxon at all was exclusive to mining soil. In water the index of 0.333 reflects a larger compositional difference, but even there the single mining exclusive taxon was *Shigella* spp., an enteric organism rather than a mining specialist.

This nested structure carries an interpretive weight that deserves emphasis. Had mining selected for a distinctive community of metal tolerant specialists, one would expect taxa present in the mining zone and absent from the reference, and the Jaccard index would fall while mining exclusive richness rose. That is not the pattern observed. What the data show is loss without compensation: sensitive taxa disappear and nothing takes their place. From the standpoint of ecosystem function this is the less favourable of the two possibilities, because a substituted community may still perform the processes the original one performed, whereas a depleted community has simply lost capacity.

The taxa that persisted are those one would expect to persist. *Bacillus* species are among the most resilient soil bacteria, form endospores that survive desiccation and chemical stress, and are widely used as bioindicators and as plant growth promoting inoculants (Bhaduri et al., 2022). *Enterococcus* species are notable for environmental adaptability across a wide range of conditions (Byappanahalli et al., 2012; García-Solache and Rice, 2019; He et al., 2025). Their dominance in the mining zone is therefore a measure of stress rather than of health.

4.3 Enteric Contamination Alongside Impoverishment

The sanitary findings run on an axis independent of the ecological ones, and the combination is the more concerning for that. *Salmonella* spp. and *Shigella* spp. were recovered from every water sample in the mining zone. Both are frank enteric pathogens rather than mere indicators, and their universal occurrence in a stream used by surrounding communities is a public health finding in its own right (Adesakin et al., 2020; Dimpor et al., 2025).

One result requires careful handling rather than the obvious reading. *Escherichia coli*, the conventional faecal indicator, was recovered from 58.3 percent of reference samples in both media but from none in the mining zone, while frank pathogens were universal there. It would be a serious error to read the absence of *E. coli* as evidence that the mining zone is free of faecal contamination. The more plausible interpretation is that the stressors acting in the mining zone suppress *E. coli* more effectively than they suppress *Salmonella* and *Shigella*, so that the indicator fails while the hazard it is meant to indicate persists. The reliability of *E. coli* as a contamination indicator is known to vary with environmental conditions (Ishii and Sadowsky, 2008; Nowicki et al., 2021), and these data furnish a pointed illustration. Any monitoring programme for this stream that relied on *E. coli* alone would return a reassuring result from the most contaminated location.

This observation should be qualified by the method. Identifications were presumptive, based on colonial morphology, Gram reaction and biochemical profile without serological or molecular confirmation. Differential recovery on nutrient agar under stress conditions is itself a possible contributor to the pattern. The finding is nonetheless robust enough to warrant confirmation work, and the direction of the risk it implies is clear.

4.4 Implications for Ecosystem Function and Resilience

Reduced bacterial richness translates into reduced functional redundancy, which is the property that allows a community to maintain process rates when individual populations are lost. A soil or stream supporting eleven taxa can lose several and continue to cycle nutrients; one supporting four has little margin. The mining zone communities are therefore not only smaller but more brittle, and less able to absorb further disturbance, whether from continued mining, seasonal extremes or additional contamination.

The same logic applies to self purification in the stream. The capacity of flowing water to degrade organic load depends on a diverse heterotrophic community. Where that community has been narrowed to a few stress tolerant taxa, the stream processes waste more slowly, which in turn prolongs the survival of the enteric organisms documented in Section 3.5. The

ecological and sanitary findings are thus connected rather than merely coincident: impoverishment plausibly extends the persistence of pathogens downstream.

4.5 Limitations

Five limitations qualify these findings. First, the study relied on culturable bacteria identified by morphological and biochemical tests; culture dependent methods recover only a small fraction of environmental bacteria, and the richness values reported here are therefore minima rather than inventories. Molecular approaches would be expected to recover substantially more taxa in both zones, though there is no reason to expect the direction of the mining effect to reverse. Second, identifications were presumptive and were not confirmed serologically or molecularly, so taxonomic assignments carry corresponding uncertainty. Third, no colony forming unit or most probable number counts were made, so the analysis addresses occurrence and not abundance; a taxon detected in every sample may nonetheless be present at low density. Fourth, the design comprised one mining zone and one reference zone with three subsample locations each, which means that zone level differences cannot be statistically separated from other differences between the two areas, and formal inferential testing was accordingly not attempted. Fifth, sampling spanned four months across a single wet to dry transition rather than a full annual cycle, so seasonal variation is only partly captured.

No physicochemical measurements, of pH, heavy metal concentration or organic carbon, were taken alongside the bacteriology. This is the most consequential of the gaps, because it means that the mechanism linking mining to reduced richness is inferred from the literature rather than demonstrated in this system. Paired physicochemical and microbiological sampling is the single most valuable extension of this work.

5. Conclusion and Recommendations

This study found that the culturable bacterial diversity of the Ika-Ogboyaga coal mining zone was lower than that of an adjacent non mining reference zone in both surface water and soil, across four months of sampling. Thirteen taxa were recovered overall, with four in mining water against eight in reference water and eight in mining soil against eleven in reference soil. Mining assemblages were largely nested within reference assemblages, indicating loss of taxa without replacement. Occurrence in the mining zone concentrated in a few stress tolerant taxa, notably *Bacillus*, *Enterococcus*, *Salmonella* and *Shigella*.

Two conclusions follow. Ecologically, the mining zone supports a simplified community with reduced functional redundancy and therefore reduced resilience to further disturbance. In terms of public health, the stream carries frank enteric pathogens in every sample taken from the mining zone, and the conventional faecal indicator organism failed to register that contamination. The two findings compound one another, since a community less able to self purify will retain pathogens longer.

The following recommendations are made.

1. **Pair bacteriological and physicochemical monitoring.** Future sampling should measure pH, heavy metal concentrations and organic carbon alongside bacterial occurrence, so that the mechanism of community change can be demonstrated rather than inferred.
2. **Do not rely on *Escherichia coli* alone for this stream.** Monitoring should include direct assay for *Salmonella* and *Shigella*, since the indicator organism was absent precisely where the pathogens were universal.
3. **Protect the stream from faecal input as a separate priority from mine drainage.** The two pressures are independent, and controlling mine discharge alone would leave the sanitary risk untouched.
4. **Advise against untreated use of the stream in the mining reach.** Given detection of enteric pathogens in all twelve water samples, communities drawing on this reach should be advised to treat water before domestic use.
5. **Extend sampling to a full annual cycle and add replicate zones.** This would capture seasonal variation and permit the zone effect to be separated statistically from other differences between areas.
6. **Apply culture independent methods.** Molecular characterisation would establish how much of the community the culture based approach missed and whether the mining effect holds across the uncultured fraction.

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Ethical Statement

This study did not involve human or animal subjects, and ethical approval was therefore not required.

Conflict of Interest

The authors disclose no competing interests.

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Data Availability

The datasets generated and analysed during this study are available from the corresponding author on reasonable request. The complete presence and absence matrices are reproduced as Tables 2 to 5 of this article.

Authors Contributions

Monday Abuh: conceptualisation, study design, field sampling, laboratory analyses, data analysis and drafting of the manuscript. **Dauda Tanko:** conceptualisation, study design, interpretation of results, review and editing. **Onas Somdare Peace:** study design, interpretation of results, review and editing. All authors read and approved the final manuscript.

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