Functional and Structural Responses of Soil Fungi to Hydrocarbon Contamination in Gokana, Niger Delta region

Elizabeth Briggs

Lizzybriggs1@gmail.com

The Africa Centre of Excellence in Oilfield Chemicals Research (ACE-CEFOR), University of Port Harcourt, Rivers State

Chioma Blaise Chikere

University of Port Harcourt

Research Article

Keywords: Hydrocarbon, contamination, Fungi, diversity, Metagenomics

Posted Date: April 9th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-8860283/v1

Additional Declarations: No competing interests reported.

Abstract

Hydrocarbon contamination poses a major ecological challenge in the Niger Delta wetlands, disrupting soil health and microbial balance. This study investigated fungal community diversity and structure in hydrocarbon-polluted (PS-1) and unpolluted (UPS-3) wetland soils from Gokana, Niger Delta, using shotgun metagenomic sequencing. Total petroleum hydrocarbon (TPH) concentration was significantly higher in PS-1 (78.3 mg/kg) than in UPS-3 (10.8 mg/kg), exceeding the regulatory limit of 50 mg/kg. At the phylum level, *Ascomycota* dominated both soils (> 99% relative abundance) but exhibited reduced representation in PS-1, which showed a lower classification rate (18%) than UPS-3 (> 90%). The unpolluted soil was dominated by *Sordariomycetes* (~ 99%) and *Dothideomycetes* (~ 1%), whereas these classes were nearly absent in PS-1. At the family level, *Ophiocordycipitaceae* (~ 80%) predominated in UPS-3, indicating a stable decomposer community, while PS-1 lacked consistent family representation. Genus-level analysis revealed *Purpureocillium* (~ 85%) as dominant in UPS-3, while PS-1 contained poorly classified or hydrocarbon-tolerant genera such as *Aspergillus* and *Fusarium*. The unpolluted soil recorded higher diversity indices (Shannon = 8.4; Simpson = 0.97) compared to PS-1 (Shannon = 7.0; Simpson = 0.98), confirming reduced fungal richness and evenness under hydrocarbon stress. Overall, petroleum contamination suppressed sensitive saprotrophic fungi, favouring hydrocarbon-tolerant taxa, but the persistence of *Ascomycota* suggests adaptive resilience and potential for natural attenuation in contaminated wetland soils.

1.0 Introduction

Microbial degradation is one of the most promising natural pathways for the removal of petroleum hydrocarbons from contaminated soils (Mekonnen et al., 2024; Mohanta et al., 2024; Sui et al., 2021). According to Rani et al. (2024), fungi play key roles in hydrocarbon degradation due to their extensive networks of extracellular and intracellular enzymes, which allow them to transform a broad spectrum of hydrocarbon compounds. Fungi produce oxidative enzymes such as laccases (Roy et al., 2025), manganese peroxidases (Barros do Nascimento et al., 2025), and cytochrome P450 monooxygenases (Muhammed et al., 2025.), which convert hydrocarbons into less toxic intermediates and ultimately into carbon dioxide and water (Yadav et al., 2025). These enzymatic mechanisms enable fungi to degrade aliphatic hydrocarbons, aromatics, and complex PAHs, making them particularly valuable in bioremediation strategies (Al-Hawash et al., 2018; Alao and Adebayo, 2022; Dave and Das, 2021). Hydrocarbon pollutants, especially complex fractions like polycyclic aromatic hydrocarbons (PAHs), are persistent, toxic, and difficult to eradicate through physical or chemical means alone, making microbial remediation a critical natural process (Mekonnen et al., 2024; Singh et al., 2025). Fungi are integral components of soil microbial communities, contributing to organic matter decomposition, nutrient cycling, and symbiotic interactions with plants (Koshila et al., 2019; Zhu et al., 2024).

Previous studies on microbial responses to oil pollution in the Niger Delta have largely focused on bacteria, while fungal communities remain understudied, particularly at high taxonomic resolution (De Mello et al., 2023; Fenibo et al., 2024; Guarino et al., 2020; Sen et al., 2022). Wijayawardene et al (2021)

highlighted that investigations in the region in most cases have relied on culture-dependent approaches, which capture only a fraction of fungal diversity and often overlook rare or slow-growing taxa that may play significant roles in hydrocarbon degradation. These traditional methods also provide limited insights into community-level shifts, functional potential, and the interactions among taxa under pollution stress. Philippot et al (2024) and Rodriguez-Ramos et al (2021), further emphasized that understanding these shifts is essential because changes in fungal community composition can directly influence soil ecosystem functioning, including nutrient cycling, organic matter decomposition, and pollutant attenuation.

In this study, we investigated fungal diversity and community structure in hydrocarbon-polluted (PS-1) and unpolluted control (UPS-3) soils from Gokana, Rivers State, Nigeria. Using shotgun metagenomic sequencing, we aimed to characterize the taxonomic composition of fungal communities, quantify diversity shifts, and identify taxa enriched under hydrocarbon stress, thereby highlighting the potential of indigenous fungi for bioremediation of oil-polluted wetlands.

2.0 Materials and methods

2.1 Site description and sample collection

Samples were taken from crude oil polluted sites in K-Dere in Gokana Local Government area in the community of Ogoni land (Fig. 1). These sites have experienced prolonged pollution from oil industry facilities and exploration. Ogoni land covers over 1000 km^2 in Rivers State, South South, Niger Delta, Nigeria (Maina et al., 2024). Crude oil polluted and pristine soil samples were collected from various points at depths of 0–15 cm and 15–30cm in triplicates using sterilized soil auger (GPS coordinates is 4.64514826N, 7.23794585E). Samples were immediately kept at 4°C in a cooler box and transported to Production chemistry laboratory at Shell petroleum Development company (SPDC), Nigeria, for further analyses.

2.2 Determination of Total Petroleum Hydrocarbon (TPH) Concentrations

Total petroleum hydrocarbon (TPH) concentrations were quantified using Gas Chromatography–Flame Ionization Detection (GC-FID) following standard protocols (USEPA Method 8015B, 2020). Briefly, 10 g of air-dried soil was extracted with n-hexane and dichloromethane (1:1 v/v) by Soxhlet extraction for 16 h. The extracts were concentrated using a rotary evaporator and analysed using an Agilent 7890B GC-FID system equipped with a HP-5 capillary column (30 m × 0.32 mm × 0.25 µm). Calibration was performed using a series of n-alkane standards (C_{10}–C_{40}). TPH concentrations were expressed in mg/kg dry weight.

2.3 DNA Extraction and Quantification

Total genomic DNA was extracted from 0.5 g of soil using the DNeasy PowerSoil Pro Kit (Qiagen, Hilden, Germany) according to the manufacturer's protocol. DNA purity and concentration were verified using a

NanoDrop 2000 spectrophotometer (Thermo Fisher Scientific, USA) and agarose gel electrophoresis (1%). High-quality DNA with an A_{260}/A_{280} ratio between 1.8 and 2.0 was used for sequencing. All extractions were performed in triplicate to ensure reproducibility.

2.4 Shotgun Metagenomic Library Preparation and Sequencing

Sequencing libraries were prepared using the Nextera XT DNA Library Preparation Kit (Illumina, San Diego, USA). Libraries were quantified using the Qubit dsDNA HS Assay Kit and normalized to 4 nM. Paired-end sequencing (2 × 150 bp) was performed on the Illumina NovaSeq 6000 platform at Novogene (Singapore) to generate high-throughput metagenomic reads. Raw reads were quality filtered to remove adapters and low-quality bases (Phred score < 30) using Trimmomatic v0.39. Host and contaminant reads were filtered out using Bowtie2 v2.5.0, and clean reads were retained for downstream analyses.

2.5 Bioinformatics and Taxonomic Analysis

High-quality reads were taxonomically classified using the Kraken2 pipeline (Wood et al., 2019) with the NCBI RefSeq fungal genome database as reference. Unclassified reads were further analyzed using MEGAN6 for hierarchical taxonomic assignment. Functional annotation was performed with HUMAnN3 to identify genes associated with hydrocarbon degradation pathways, including cytochrome P450 monooxygenases, peroxidases, and hydrolases.

Alpha diversity metrics (Shannon and Simpson indices) and beta diversity analyses were computed in QIIME2 v2024.2. Statistical comparisons between polluted and unpolluted soils were performed using one-way ANOVA ($p < 0.05$) in R v4.3.1. Visualization of taxonomic distributions was done with GraphPad Prism v10.1 and R ggplot2 packages.

2.6 Data Quality Control and Validation

Negative extraction controls and sequencing blanks were included to monitor potential contamination. All sequencing data were checked for quality using FastQC v0.12.1. Rarefaction curves were plotted to assess sequencing depth sufficiency, ensuring even coverage across samples. The reproducibility of biological replicates was confirmed using principal coordinate analysis (PCoA) plots.

3. 0 Results

3.1 Total Petroleum Hydrocarbon (TPH) Concentrations

The concentration of total petroleum hydrocarbons (TPH) differed markedly between the two sampling sites. The hydrocarbon-polluted soil (PS-1) recorded a mean TPH concentration of 78.3 mg/kg, which exceeded the Department of Petroleum Resources (DPR, Nigeria) regulatory limit of 50 mg/kg, confirming petroleum contamination. In contrast, the unpolluted control soil (UPS-3) showed a considerably lower TPH concentration of 10.8 mg/kg, indicating minimal hydrocarbon influence.

3.2 Fungal Community Composition at the Phylum Level

At the phylum level in Fig. 3, Ascomycota dominated the fungal communities in both the polluted (PS-1) and unpolluted (UPS-3) soils. Its relative abundance reached nearly 100% in the unpolluted soil, indicating a healthy and diverse fungal assemblage, while in the polluted soil, Ascomycota remained prevalent but with a markedly lower classification rate (18%), reflecting reduced diversity and sequencing coverage.

3.3 Fungal Community Composition at the Class Level

At the class level in Fig. 4, Sordariomycetes dominated the unpolluted soil (UPS-3), accounting for nearly 99% of the classified reads, while Dothideomycetes contributed only about 1%. In contrast, the polluted soil (PS-1) showed no distinct abundance patterns, consistent with its low classification rate (18%) and reduced diversity.

3.4 Fungal Community Composition at the order Level

As shown in Fig. 5, the unpolluted soil (UPS-3) was dominated by Hypocreales, followed by Microascales and Botryosphaeriales, which together accounted for over 85% of the classified fungal reads. In contrast, the polluted soil (PS-1) showed no clear order-level structure and had a low classification rate (18%), indicating reduced diversity.

3.5 Fungal Community Composition at the Family Level

At the family level in Fig. 5, the unpolluted soil (UPS-3) was dominated by Ophiocordycipitaceae, which accounted for approximately 80% of the classified fungal reads. Minor families included Microascaceae and Botryosphaeriaceae, each representing less than 10%. In contrast, the polluted soil (PS-1) showed a low classification rate (18%) and lacked clear representation of these dominant families, indicating a strong reduction in taxonomic resolution and diversity

3.5 Fungal Community Composition at the Genus Level

At the genus level, the unpolluted soil (UPS-3) was overwhelmingly dominated by Purpureocillium (~ 85%), followed by Scedosporium, Lasiodiplodia, and Neoscytalidium, each representing less than 10% of the total fungal community. In contrast, the polluted soil (PS-1) showed no distinct genus-level structure and had a low classification rate (18%), reflecting reduced taxonomic resolution and loss of fungal diversity under hydrocarbon stress.

3.5 Fungal Community Composition at the Species Level

The unpolluted soil (UPS-3) revealed a diverse fungal community dominated by *Purpureocillium lilacinum* (~ 85%), followed by minor proportions of *Scedosporium apiospermum*, *Scedosporium boydii*,

Lasiodiplodia theobromae, and *Neoscytalidium dimidiatum*. While, the polluted soil (PS-1) had a lower classification rate (18%) and showed no detectable species-level abundance markedly, indicating strong suppression of fungal diversity under hydrocarbon stress. The Shannon (8.4) and Simpson (0.97) indices for UPS-3 were higher than those for PS-1 (Shannon = 7.0, Simpson = 0.98), confirming reduced species richness and evenness in the polluted soil.

4.0 Discussion

The elevated total petroleum hydrocarbon (TPH) concentration recorded in the polluted soil from K-Dere (78.3 mg/kg) confirms significant hydrocarbon contamination compared with the control soil (10.8 mg/kg) as illustrated in figure two (2) above. The TPH value in the polluted site exceeds the regulatory limit of 50 mg/kg, indicating active petroleum influence on soil quality and biological health. According to Kebede et al (2021), Mekonnen et al (2024) and Chikere et al (2019), hydrocarbon pollution is known to alter soil structure, reduce oxygen diffusion, and limit nutrient availability, thereby creating selective stress that affects microbial survival and activity. Such environmental conditions often suppress sensitive microorganisms while favouring the persistence of hydrocarbon-tolerant or metabolically adaptable taxa capable of utilizing hydrocarbons as carbon.

At the phylum level, Ascomycota dominated was more abundant and diverse in the unpolluted soil than in the polluted soil in Fig. 3. Its persistence in the polluted soil reflects the adaptive capacity of this phylum to environmental stress. Members of Ascomycota possess broad enzymatic systems that facilitate the breakdown of complex organic molecules, including hydrocarbons (Aranda et al., 2016; Shourie and Vijayalakshmi, 2022; Rani et al., 2024). These enzymes particularly laccases, manganese peroxidases, and cytochrome P450 monooxygenases oxidize aromatic and aliphatic hydrocarbons into less toxic intermediates (Dave and Das, 2021; Baker et al., 2019; Kumari et al., 2021). The dominance of Ascomycota in unpolluted soils (UPS-3) highlights its ecological importance in organic matter turnover, nutrient recycling, and maintenance of soil health, functions that are often compromised under hydrocarbon stress (Dou et al., 2025 Li et al., 2023; Zhan, 2024). However, despite this enzymatic resilience, the overall abundance of Ascomycota in PS-1 declined, with a lower classification rate of 18% under hydrocarbon stress, suggesting that only a subset of metabolically versatile species could withstand the toxic effects of petroleum hydrocarbons. Sui et al. (2021) and Ren et al. (2025) noted that hydrocarbon contamination likely alters soil pH, oxygen availability, and nutrient balance, further constraining fungal diversity and community stability.

At the class level, Sordariomycetes dominated the unpolluted soil (UPS-3), accounting for nearly 99% of the classified reads, while Dothideomycetes contributed only about 1%. Sordariomycetes are saprotrophic fungi that play critical roles in organic matter decomposition, lignocellulose degradation, and nutrient cycling in wetland ecosystems (Chen et al., 2023; Mirabile et al 2023). Their metabolic versatility allows them to thrive in healthy soils, supporting ecosystem productivity and stability. The near absence of Sordariomycetes and Dothideomycetes in hydrocarbon-polluted soil (PS-1) indicates that petroleum toxicity disrupts saprotrophic fungal communities, likely through reduced oxygen

availability and accumulation of toxic hydrocarbons. This decline highlights the vulnerability of key decomposer taxa under contamination and underscores the potential need for bioremediation strategies to restore functional fungal communities in impacted wetlands (Hu et al., 2020; Muwawa et al., 2024).

As stated in Fig. 5, the order level comprised of Hypocreales, Microascales, and Botryosphaeriales. These were predominant in the unpolluted soil, accounting for over 85% of classified reads. These group of fungi are associated with plant–soil symbioses and decomposition of cellulose-rich materials (Hou et al., 2023; Niu et al., 2024; Philips et al., 2019). Their dominance indicates a stable, functionally active ecosystem. Meanwhile, PS-1 showed no clear order-level structure, supporting the view that petroleum hydrocarbons disrupt community organization and reduce the ecological roles of decomposers. At the family level stated in Fig. 6, unpolluted soil (UPS-3) was dominated by Ophiocordycipitaceae (~ 80% relative abundance). These microbes are from a group within Hypocreales known for its saprotrophic and entomopathogenic members. They contribute to organic matter decomposition, nutrient cycling, and maintenance of microbial balance in healthy soils (Xiao et al., 2023; Sun et al., 2022; Tang et al., 2023). Their dominance reflects a stable and functional fungal community that supports ecosystem processes while polluted soil showed low taxonomic resolution and lacked consistent family representation.

As illustrated in Fig. 7, Purpureocillium was the most abundant genus in UPS-3 accounting for approximately ~ 85%, alongside minor genera such as Scedosporium, Lasiodiplodia, and Neoscytalidium. In PS-1, the community shifted toward poorly classified hydrocarbon-tolerant genera. According to Li (2020), petroleum hydrocarbons can be used by several fungal species as a carbon and energy source and assimilated into fungal biomass. Fungal taxa including Amorphoteca, Neosartorya, Talaromyces, Aspergillus, Fusarium, Paecilomyces, Sporobolomyces, Cephalosporium, Penicillium, and Graphium have all been reported to include potential degraders of petroleum hydrocarbons. These fungi secrete diverse oxidative and hydrolytic enzymes including peroxidases, esterases, and ligninolytic enzymes that enable them to metabolize petroleum hydrocarbons and survive in contaminated habitats (Chicca et al., 2022; Rani et al.,2024; Varjani 2017). The dominance of such genera illustrates a shift from nutrient-cycling fungi to hydrocarbon trophic consortia, representing an adaptive restructuring of the soil mycobiome (Ansari et al., 2025; D'Alessandro et al., 2023; Wang et al., 2025).

At the species level represented in Fig. 8, the unpolluted soil (UPS-3) exhibited a diverse fungal community dominated by *Purpureocillium lilacinum* (~ 85%), followed by minor proportions of *Scedosporium apiospermum*, *Scedosporium boydii*, *Lasiodiplodia theobromae*, and *Neoscytalidium dimidiatum*. *P. lilacinum* is a widely distributed saprotrophic and nematophagous fungus known for its ability to degrade complex organic matter and contribute to soil fertility in uncontaminated environments (Ali et al., 2024; Rigobelo et al., 2024). The coexistence of these taxa in UPS-3 reflects a balanced and functionally diverse community typical of healthy wetland soils. In contrast, the hydrocarbon-polluted soil (PS-1) showed no detectable species-level abundance estimates and had a markedly lower classification rate (18%), indicating strong suppression of fungal diversity under hydrocarbon stress. The Shannon (8.4) and Simpson (0.97) indices for UPS-3 were higher than those for PS-1 (Shannon = 7.0;

Simpson = 0.98), confirming that petroleum contamination substantially reduces fungal species richness and evenness, thereby altering community structure and ecological function.

In all, the observed decline in fungal diversity and the dominance of hydrocarbon-tolerant taxa in PS-1 suggest that petroleum contamination induces selective ecological pressure, favouring the survival of metabolically adaptable fungi at the expense of sensitive saprotrophs. Such community shifts can impair soil decomposition, nutrient recycling, and resilience. However, the persistence of Ascomycota and other tolerant taxa indicates a potential for natural attenuation and bioremediation, where surviving fungi may gradually degrade hydrocarbons and aid in the recovery of ecosystem balance in the Niger Delta wetlands.

5.0 Insights, challenges and recommendations

This study provides important insights into the ecological consequences of hydrocarbon contamination on fungal communities in the Niger Delta wetlands. The elevated total petroleum hydrocarbon concentration in the polluted soil (78.3 mg/kg) compared to the control (10.8 mg/kg) confirms significant petroleum influence and its impact on microbial balance. The dominance of *Ascomycota* in both soils highlights its adaptive resilience and enzymatic versatility, while the sharp decline of *Sordariomycetes*, *Dothideomycetes*, and *Ophiocordycipitaceae* in the polluted site reveals the sensitivity of key decomposer fungi to hydrocarbon toxicity. The replacement of these saprotrophic groups by hydrocarbon-tolerant genera such as *Aspergillus*, *Fusarium*, and *Talaromyces* demonstrates an ecological shift from nutrient recyclers to hydrocarbon-degrading communities. These adaptive changes underscore the ability of certain fungal taxa to survive and metabolize hydrocarbons, pointing to their potential use in natural attenuation and mycoremediation of contaminated soils.

However, this research encountered several challenges that reflect both environmental and methodological limitations. Field sampling in hydrocarbon-polluted wetlands was constrained by limited accessibility, unstable terrain, and safety risks associated with oil residues. Laboratory analyses were hindered by the complex soil matrix and the presence of inhibitory petroleum compounds, which reduced sequencing efficiency and taxonomic resolution (only 18% classification in PS-1). Differentiating between active degraders and dormant or dead fungal cells remains a major limitation of metagenomic approaches, while the absence of region-specific fungal genomic databases restricted detailed classification of indigenous Niger Delta species.

To address these challenges and strengthen future studies, it is recommended that metagenomic profiling be complemented with whole-cell biosensor systems capable of detecting hydrocarbons and heavy metals in situ. Integrating biosensor-based functional assays with molecular data will provide real-time insight into microbial activity and pollutant toxicity. Establishing a regional microbial genomic database will also enhance taxonomic accuracy and foster comparative ecological studies across oil-impacted ecosystems. In addition, future bioremediation programs should focus on enriching hydrocarbon-degrading fungi such as *Aspergillus*, *Trichoderma*, and *Purpureocillium lilacinum* to restore

soil function, organic matter turnover, and nutrient cycling. Long-term monitoring, coupled with interdisciplinary approaches that merge microbiology, environmental engineering, and biotechnology, will be vital for promoting sustainable restoration of wetland ecosystems affected by petroleum contamination in the Niger Delta.

6.0 Conclusion

This study provides new insights into the ecological impact of hydrocarbon contamination on fungal communities in Niger Delta wetland soils. Shotgun metagenomic analysis revealed that the polluted site (78.3 mg/kg TPH) exceeded the 50 mg/kg regulatory limit and exhibited markedly reduced fungal richness and evenness compared to the unpolluted control (10.8 mg/kg TPH). *Ascomycota* dominated both soils (> 99%), but diversity and classification depth declined sharply in the polluted soil (18%) in all levels, indicating hydrocarbon-induced stress. Taxonomic shifts from saprotrophic taxa such as *Sordariomycetes*, *Ophiocordycipitaceae*, and *Purpureocillium lilacinum* to hydrocarbon-tolerant genera including *Aspergillus* and *Fusarium* demonstrate a restructuring of the mycobiome toward pollutant-adapted consortia.

These findings highlight that petroleum hydrocarbons suppress sensitive decomposer fungi, impair nutrient cycling, and alter soil functionality. However, the persistence of metabolically versatile *Ascomycota* species suggests inherent resilience and potential for fungal-assisted bioremediation. This study contributes to the growing understanding of fungal ecological responses to oil pollution and emphasizes the need for integrated molecular and biosensor-based monitoring approaches to guide remediation efforts in hydrocarbon-impacted wetland ecosystems.

Declarations

7.0 Funding

This work was not funded

8.0 Data availability

All data generated or analysed during this study will be available upon request.

9.0 Ethics approval and consent participate

Not applicable. This study did not involve human participants or animals requiring ethical approval. We confirm that the manuscript has been read and approved by all named authors and that there are no other persons who satisfied the criteria authorship but are not listed. We further confirm that the order of authors listed in the manuscript has been approved by all of us.

10.0 Consent participation

yes

11.0 Declaration of Generative AI

During the preparation of this work, the author(s) utilized ChatGPT-4o to assist with enhancing language clarity and overall readability. All content generated was subsequently reviewed and edited by the author(s), who assumes full responsibility for the final version of the manuscript

12.0 Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper

References

1. Alao, M. B., & Adebayo, E. A. (2022). Fungi as veritable tool in bioremediation of polycyclic aromatic hydrocarbons-polluted wastewater. *Journal of Basic Microbiology*, *62*(3–4), 223–244. Al-Hawash, A. B., Alkooranee, J. T., Zhang, X., & Ma, F. (2018). Fungal degradation of polycyclic aromatic hydrocarbons. *Int. J. Pure Appl. Biosci*, *6*(2), 8–24.
2. Ali, A. A., Mahgoub, S. A., Ahmed, A. F., Mosa, W. F., El-Saadony, M. T., Mohamed, M. D., & El-Ashry, R. M. (2024). Utilizing endophytic plant growth-promoting bacteria and the nematophagous fungus Purpureocillium lilacinum as biocontrol agents against the root-knot nematode (Meloidogyne incognita) on tomato plants. *European Journal of Plant Pathology*, *170*(2), 417–436.
3. Al-Hawash, A. B., Alkooranee, J. T., Zhang, X., & Ma, F. (2018). Fungal degradation of polycyclic aromatic hydrocarbons. *Int. J. Pure Appl. Biosci*, *6*(2), 8–24.
4. Ansari, R. A., Egamberdievich, K. E., Raximovna, M. T., Sa'dinovna, Y. D., Enverovna, B. L., Abbasovich, A. S., … Kurbonovich, T. M. (2025). Phytomycobiomes and Ecosystem Services: Mechanisms, Evidence and Routes to Application. *Journal of Fungi*, *12*(1), 1.
5. Aranda, E. (2016). Promising approaches towards biotransformation of polycyclic aromatic hydrocarbons with Ascomycota fungi. *Current opinion in biotechnology*, *38*, 1–8.
6. Barros do Nascimento, A. C., Nhampossa, N. A., Félix, T. P., Itabaiana Jr, I., & Nascimento, R. P. D. (2025). Exploring fungal biodegradation pathways of 2, 4-D: Enzymatic mechanisms, synergistic actions, and environmental applications. *ACS omega*, *10*(35), 39398–39414.
7. Baker, P., Tiroumalechetty, A., & Mohan, R. (2019). Fungal enzymes for bioremediation of xenobiotic compounds. In *Recent advancement in white biotechnology through fungi: volume 3: perspective for sustainable environments* (pp. 463–489). Cham: Springer International Publishing.
8. Chen, Y. P., Su, P. W., Hyde, K. D., & Maharachchikumbura, S. S. N. (2023). Phylogenomics and diversification of Sordariomycetes. *Mycosphere (Online)*, *14*(1).
9. Chikere, C. B., Tekere, M., & Adeleke, R. (2019). Enhanced microbial hydrocarbon biodegradation as stimulated during field-scale landfarming of crude oil-impacted soil. *Sustainable Chemistry and*

Pharmacy, *14*, 100177.

10. Chicca, I., Becarelli, S., & Di Gregorio, S. (2022). Microbial involvement in the bioremediation of total petroleum hydrocarbon polluted soils: Challenges and perspectives. *Environments*, *9*(4), 52.
11. Dave, S., & Das, J. (2021). Role of microbial enzymes for biodegradation and bioremediation of environmental pollutants: challenges and future prospects. *Bioremediation for environmental sustainability*, 325–346.
12. D'Alessandro, A., Coletta, M., Cespi, M., Mozzicafreddo, M., Caprioli, G., & LA TERZA, A. (2023). Innovative Spent Coffee Ground-Based Biofertilizer: Effects on Soil Microbiome and Crop Health. In *3rd Global Soil Biodiversity Conference 2023-Book of Abstracts* (pp. 425–425). University College Dublin (UCD).
13. De Mello, K., Taniwaki, R. H., Macedo, D. R., Leal, C. G., & Randhir, T. O. (2023). Biomonitoring for watershed protection from a multiscale land-use perspective. *Diversity*, *15*(5), 636.
14. Dou, T., Zhang, K., Shi, X., Liu, W., Yu, F., & Liu, D. (2025). Crop–Mushroom Rotation: A Comprehensive Review of Its Multifaceted Impacts on Soil Quality, Agricultural Sustainability, and Ecosystem Health. *Agronomy*, *15*(3), 563.
15. Fenibo, E. O., Nkuna, R., & Matambo, T. (2024). Impact of artisanal refining activities on bacterial diversity in a Niger Delta fallow land. *Scientific Reports*, *14*(1), 3866.
16. Guarino, F., Improta, G., Triassi, M., Cicatelli, A., & Castiglione, S. (2020). Effects of zinc pollution and compost amendment on the root microbiome of a metal tolerant poplar clone. *Frontiers in microbiology*, *11*, 1677.
17. Hou, L. W., Giraldo, A., Groenewald, J. Z., Rämä, T., Summerbell, R. C., Huang, G. Z., … Crous, P. W. (2023). Redisposition of acremonium-like fungi in Hypocreales. *Studies in mycology*, *105*, 23.
18. Hu, W., Huang, L., He, Y., Liu, Y., Liu, Y., Kong, Z., … Ge, G. (2021). Soil bacterial and fungal communities and associated nutrient cycling in relation to rice cultivation history after reclamation of natural wetland. *Land Degradation & Development*, *32*(3), 1287–1300.
19. Ibanga, O. A., & Udoh, J. C. (2021). GIS-Based Oil Spill Incidents and Hazard Mapping in Gokana Local Government Area, Rivers State, Nigeria. *International Journal of Social Sciences*, *14*(1), 104–120.
20. Kebede, G., Tafese, T., Abda, E. M., Kamaraj, M., & Assefa, F. (2021). Factors influencing the bacterial bioremediation of hydrocarbon contaminants in the soil: mechanisms and impacts. *Journal of Chemistry*, *2021*(1), 9823362.
21. Koshila Ravi, R., Anusuya, S., Balachandar, M., & Muthukumar, T. (2019). Microbial interactions in soil formation and nutrient cycling. In *Mycorrhizosphere and pedogenesis* (pp. 363–382). Singapore: Springer Singapore.
22. Kumari, R., Singh, A., & Yadav, A. N. (2021). Fungal enzymes: Degradation and detoxification of organic and inorganic pollutants. In *Recent trends in mycological research: volume 2: environmental and industrial perspective* (pp. 99–125). Cham: Springer International Publishing.

23. Li, Q., Liu, J., & Gadd, G. M. (2020). Fungal bioremediation of soil co-contaminated with petroleum hydrocarbons and toxic metals. *Applied Microbiology and Biotechnology*, *104*(21), 8999–9008.
24. Li, W., Li, Z., Liu, Y., Nie, X., Zheng, H., Zhang, G., … Ma, Y. (2023). Soil nutrients shape the composition and function of fungal communities in abandoned ancient rice terraces. *Journal of Environmental Management*, *329*, 117064.
25. Maina, S., Donovan, N.J., Plett, K., Bogema, D., Rodoni, B.C., 2024. High-throughput sequencing for plant virology diagnostics and its potential in plant health certification. Front. Hortic. 3, 1388028.
26. Mekonnen, B. A., Aragaw, T. A., & Genet, M. B. (2024). Bioremediation of petroleum hydrocarbon contaminated soil: a review on principles, degradation mechanisms, and advancements. *Frontiers in Environmental Science*, *12*, 1354422.
27. Mirabile, G., Ferraro, V., Mancuso, F. P., Pecoraro, L., & Cirlincione, F. (2023). Biodiversity of fungi in freshwater ecosystems of Italy. *Journal of Fungi*, *9*(10), 993.
28. Mohanta, S., Pradhan, B., & Behera, I. D. (2024). Impact and remediation of petroleum hydrocarbon pollutants on agricultural land: a review. *Geomicrobiology Journal*, *41*(4), 345–359.
29. Muhammad, N., Liu, Y., Liu, Z., Wang, L., Yang, M., & Liu, M. (2025). Genome and transcriptome-based characterization of cytochrome P450 (CYP) monooxygenase superfamily gene and the key role of ZjCYP98A9a-89 in flavonoid biosynthesis during fruit development of jujube (Ziziphus jujuba Mill.). *Food Bioscience*, *64*, 105855.
30. Muwawa, E. M., Makonde, H. M., Obieze, C. C., de Oliveira, I. G., Jefwa, J. M., Kahindi, J. H., & Khasa, D. P. (2024). Diversity and assembly patterns of mangrove rhizosphere mycobiome along the Coast of Gazi Bay and Mida Creek in Kenya. *Plos one*, *19*(4), e0298237.
31. Niu, X., Al-Hatmi, A. M., Vitale, R. G., Lackner, M., Ahmed, S. A., Verweij, P. E., … de Hoog, S. (2024). Evolutionary trends in antifungal resistance: a meta-analysis. *Microbiology Spectrum*, *12*(4), e02127-23.
32. Phillips, A. J., Hyde, K. D., Alves, A., & Liu, J. K. (2019). Families in Botryosphaeriales: a phylogenetic, morphological and evolutionary perspective. *Fungal diversity*, *94*(1), 1–22.
33. Philippot, L., Chenu, C., Kappler, A., Rillig, M. C., & Fierer, N. (2024). The interplay between microbial communities and soil properties. *Nature Reviews Microbiology*, *22*(4), 226–239.
34. Rani, M. H. S., Nandana, R. K., Khatun, A., Brindha, V., Midhun, D., Gowtham, P., … Muthukumar, S. (2024). Three strategy rules of filamentous fungi in hydrocarbon remediation: an overview. *Biodegradation*, *35*(6), 833–861.
35. Ren, L., Zhang, J., Geng, B., Zhao, J., Jia, W., & Cheng, L. (2025). Ecological Shifts and Functional Adaptations of Soil Microbial Communities Under Petroleum Hydrocarbon Contamination. *Water*, *17*(8), 1216.
36. Rigobelo, E. C., Nicodemo, D., Babalola, O. O., & Desoignies, N. (2024). Purpureocillium lilacinum as an agent of nematode control and plant growth-promoting fungi. *Agronomy*, *14*(6), 1225.
37. Rodriguez-Ramos, J. C., Cale, J. A., Cahill Jr, J. F., Simard, S. W., Karst, J., & Erbilgin, N. (2021). Changes in soil fungal community composition depend on functional group and forest disturbance

type. *New Phytologist*, *229*(2), 1105–1117.

38. Roy, T., Paul, C., Pal, N., & Das, N. (2025). Fungal Oxidoreductases: Efficient Tool for Eco-Friendly and Sustainable Pesticide Bioremediation. In *Biotechnological Interventions in the Removal of Emerging Pollutants* (pp. 403–435). Singapore: Springer Nature Singapore.
39. Sen, K., Sen, B., & Wang, G. (2022). Diversity, abundance, and ecological roles of planktonic fungi in marine environments. *Journal of Fungi*, *8*(5), 491.
40. Shourie, A., & Vijayalakshmi, U. (2022). Fungal diversity and its role in mycoremediation. *Geomicrobiology Journal*, *39*(3–5), 426–444.
41. Singh, S. K., & Singh, R. K. (2025). An overview on remediation technologies for polycyclic aromatic hydrocarbons in contaminated lands: a critical approach. *Environment, Development and Sustainability*, *27*(2), 2753-2787Sui, X., Wang, X., Li, Y., & Ji, H. (2021). Remediation of petroleum-contaminated soils with microbial and microbial combined methods: Advances, mechanisms, and challenges. *Sustainability*, *13*(16), 9267.
42. Sun, T., Zou, W., Dong, Q., Huang, O., Tang, D., & Yu, H. (2022). Morphology, phylogeny, mitogenomics and metagenomics reveal a new entomopathogenic fungus Ophiocordycepsnujiangensis (Hypocreales, Ophiocordycipitaceae) from Southwestern China. *MycoKeys*, *94*, 91.
43. Tang, D., Zhao, J., Lu, Y., Wang, Z., Sun, T., Liu, Z., & Yu, H. (2023). Morphology, phylogeny and host specificity of two new Ophiocordyceps species belonging to the “zombie-ant fungi” clade (Ophiocordycipitaceae, Hypocreales). *MycoKeys*, *99*, 269.
44. Varjani SJ (2017) Microbial degradation of petroleum hydrocarbons. Bioresour Technol 223:277–286. https://doi.org/10.1016/j. biortech.2016.10.037
45. Wang, S., Wang, X., Xu, J., Na, R., Wang, Y., Wei, J., & Bao, Q. (2025). Soil fungal community structure and ecological functions in fairy rings of Leucocalocybe mongolica in Bayanbulak grassland. *Frontiers in Microbiology*, *16*, 1667514.
46. Wijayawardene, N. N., Bahram, M., Sanchez-Castro, I., Dai, D. Q., Ariyawansa, K. G., Jayalal, U., & Tedersoo, L. (2021). Current insight into culture-dependent and culture-independent methods in discovering Ascomycetous Taxa. *Journal of Fungi*, *7*(9), 703.
47. Wood, V., Lock, A., Harris, M. A., Rutherford, K., Bähler, J., & Oliver, S. G. (2019). Hidden in plain sight: what remains to be discovered in the eukaryotic proteome?. *Open biology*, *9*(2), 180241.
48. Xiao, Y. P., Wang, Y. B., Hyde, K. D., Eleni, G., Sun, J. Z., Yang, Y., … Wen, T. C. (2023). Polycephalomycetaceae, a new family of clavicipitoid fungi segregates from Ophiocordycipitaceae. *Fungal Diversity*, *120*(1), 1–76.
49. Yadav, U., & Anand, V. (2025). Endophytic Fungi-Derived Nanoparticles: A Sustainable Approach to Mitigating Biotic and Abiotic Stress in Plants. *Eco-Friendly Nanotechnology: Harnessing Small-Scale Technologies for a Cleaner and Healthier Planet*, 106–115.
50. Zhan, C. (2024). Microbial decomposition and soil health: mechanisms and ecological implications. *Molecular Soil Biology*, *15*.

51. Zhu, L., Wang, X., Liu, L., Le, B., Tan, C., Dong, C., … Hu, B. (2024). Fungi play a crucial role in sustaining microbial networks and accelerating organic matter mineralization and humification during thermophilic phase of composting. *Environmental Research*, *254*, 119155.

Figures

Figure 1

Map of Rivers state showing Gokana (adopted from Ibanga, & Udoh, 2021)

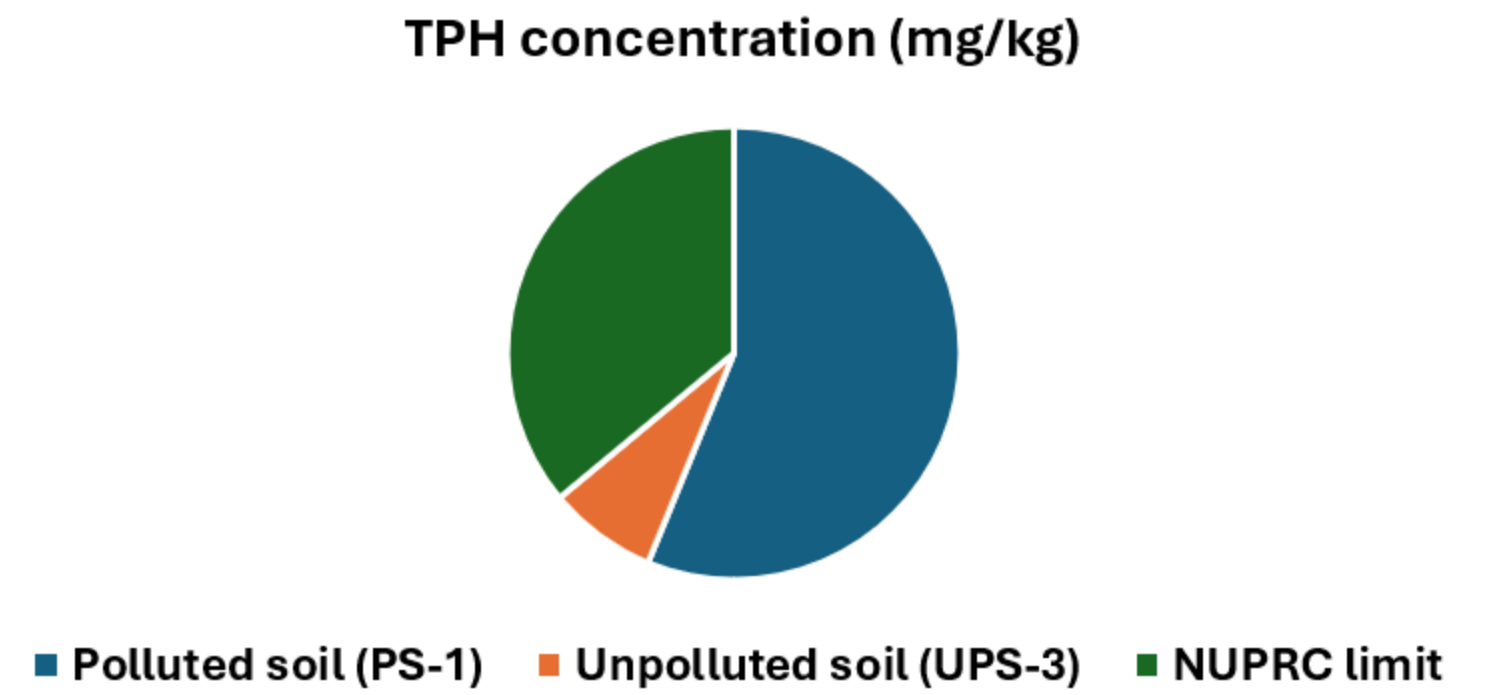

Figure 2

TPH (mg/kg) concentration in the different soil samples

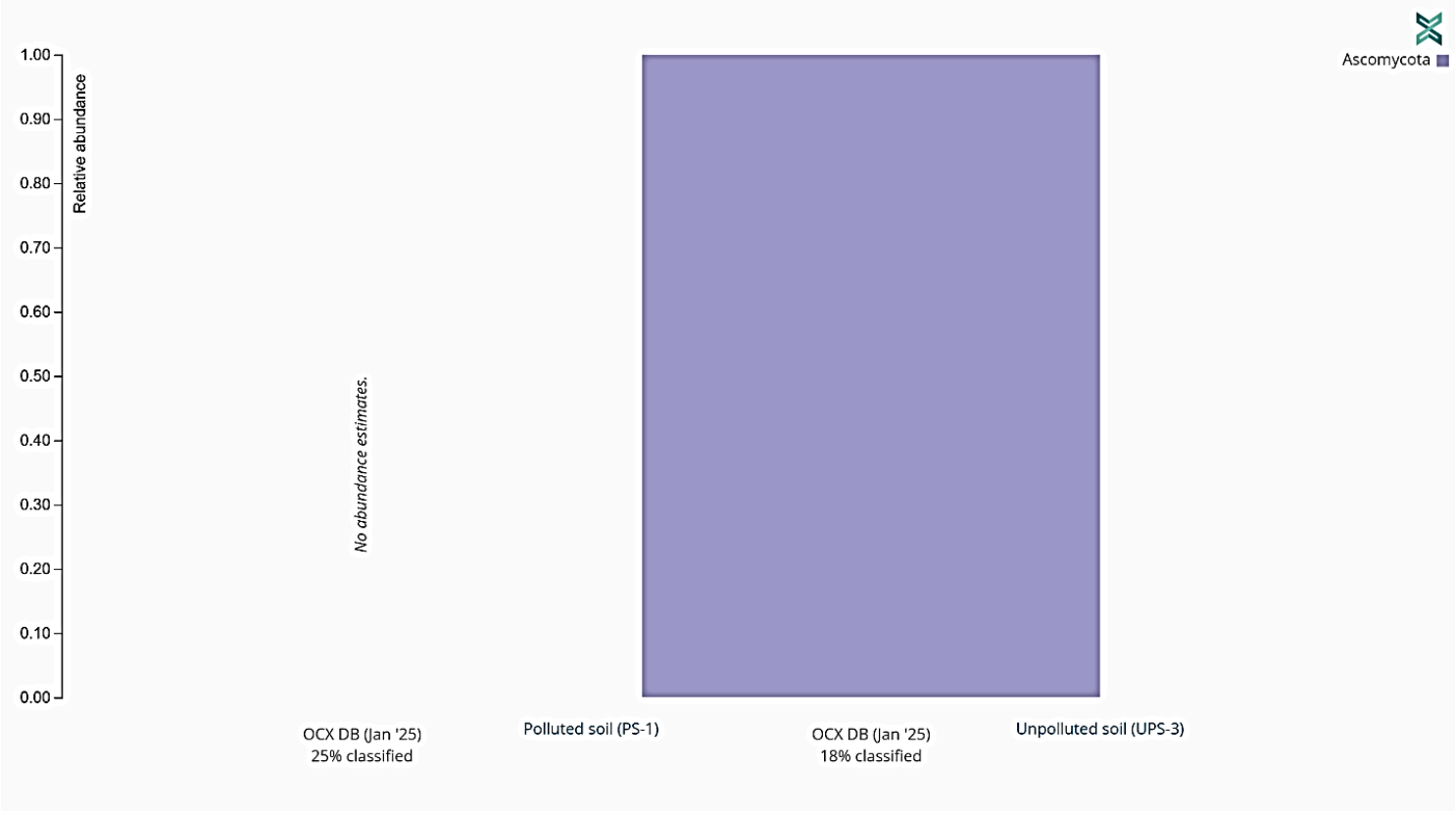

Figure 3

Fungal relative abundance and diversity at phylum level for polluted and unpolluted soil

Figure 4

Fungal relative abundance and diversity at class level for polluted and unpolluted soil

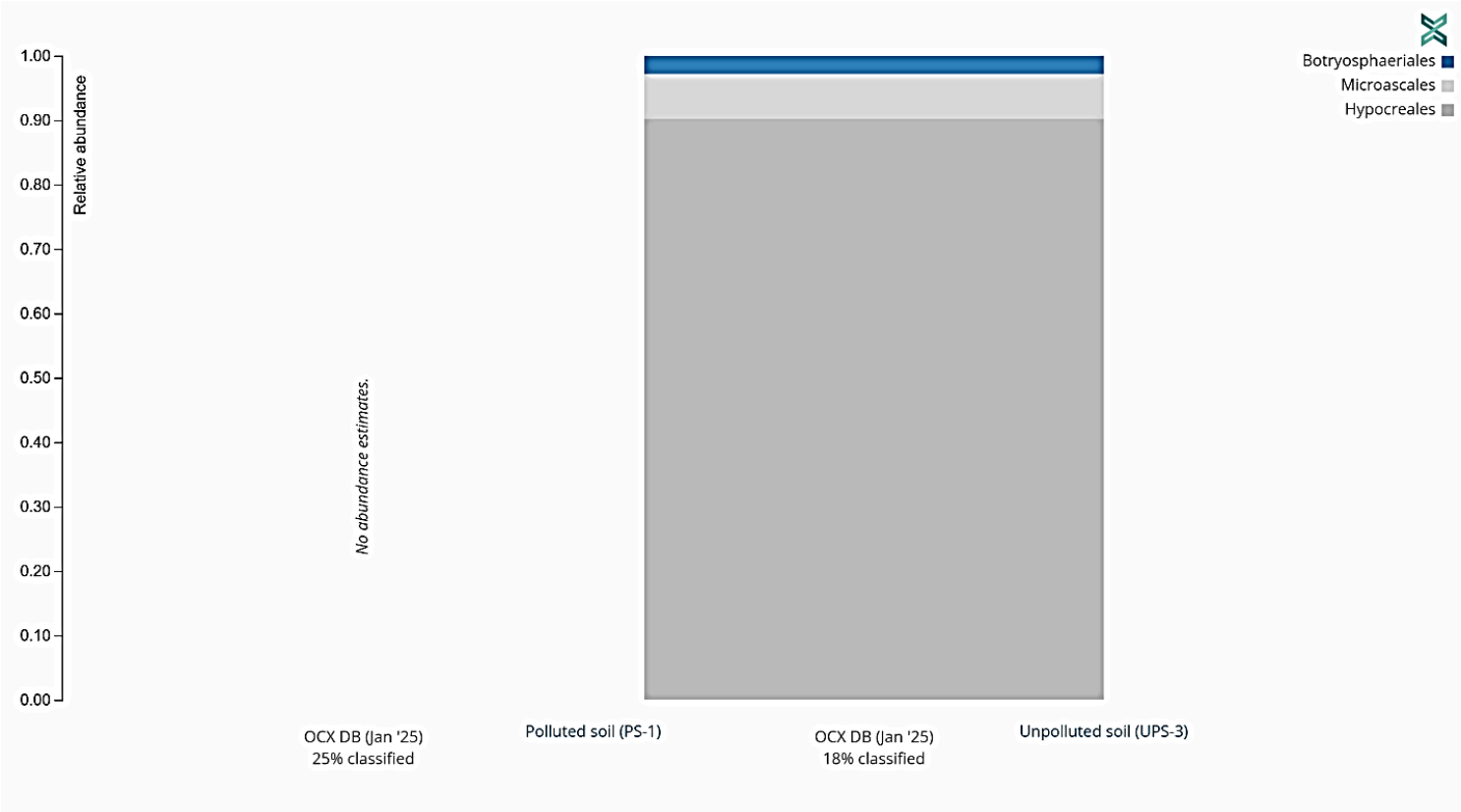

Figure 5

Fungal relative abundance and diversity at order level for polluted and unpolluted soil

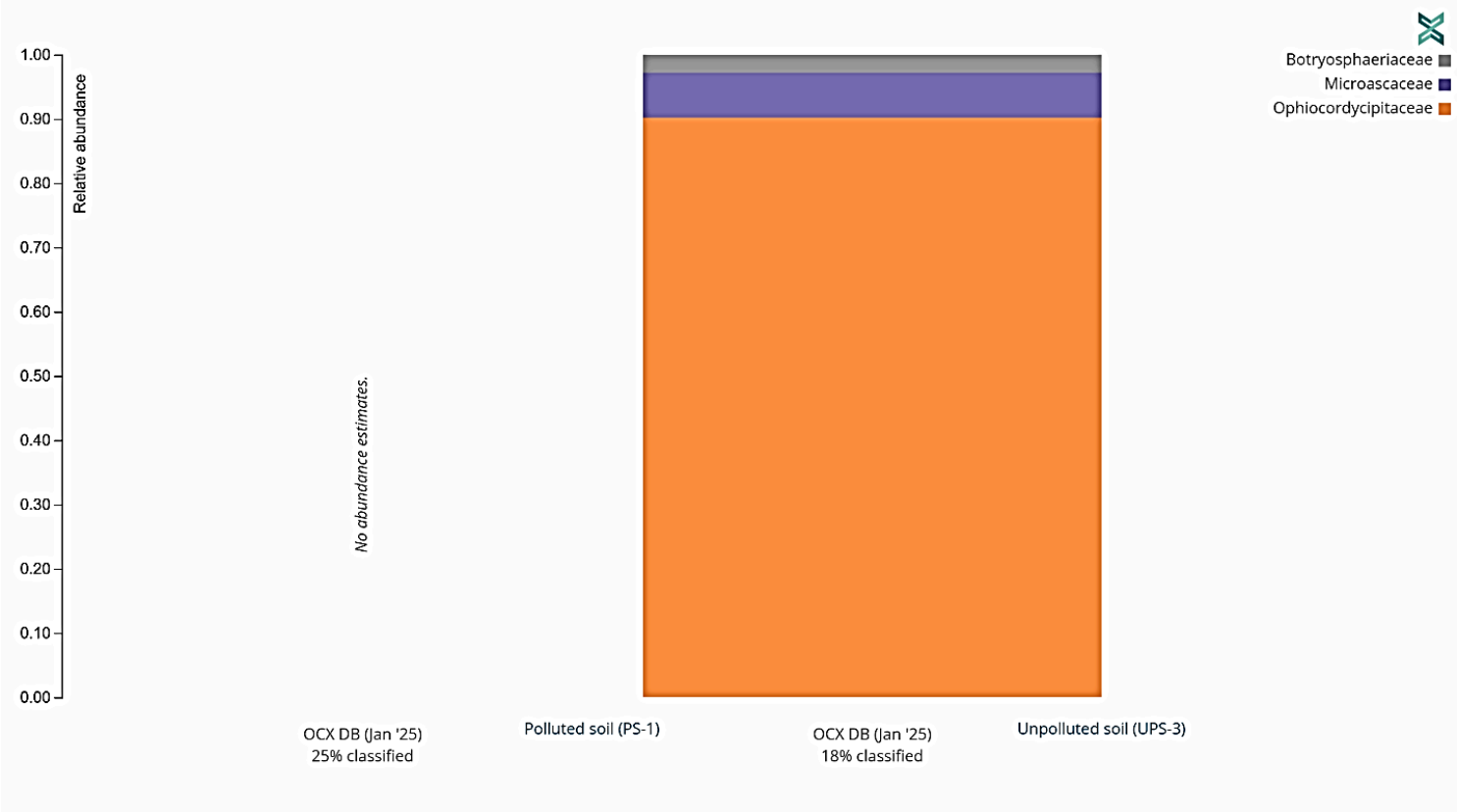

Figure 6

Fungal relative abundance and diversity at family level for polluted and unpolluted soil

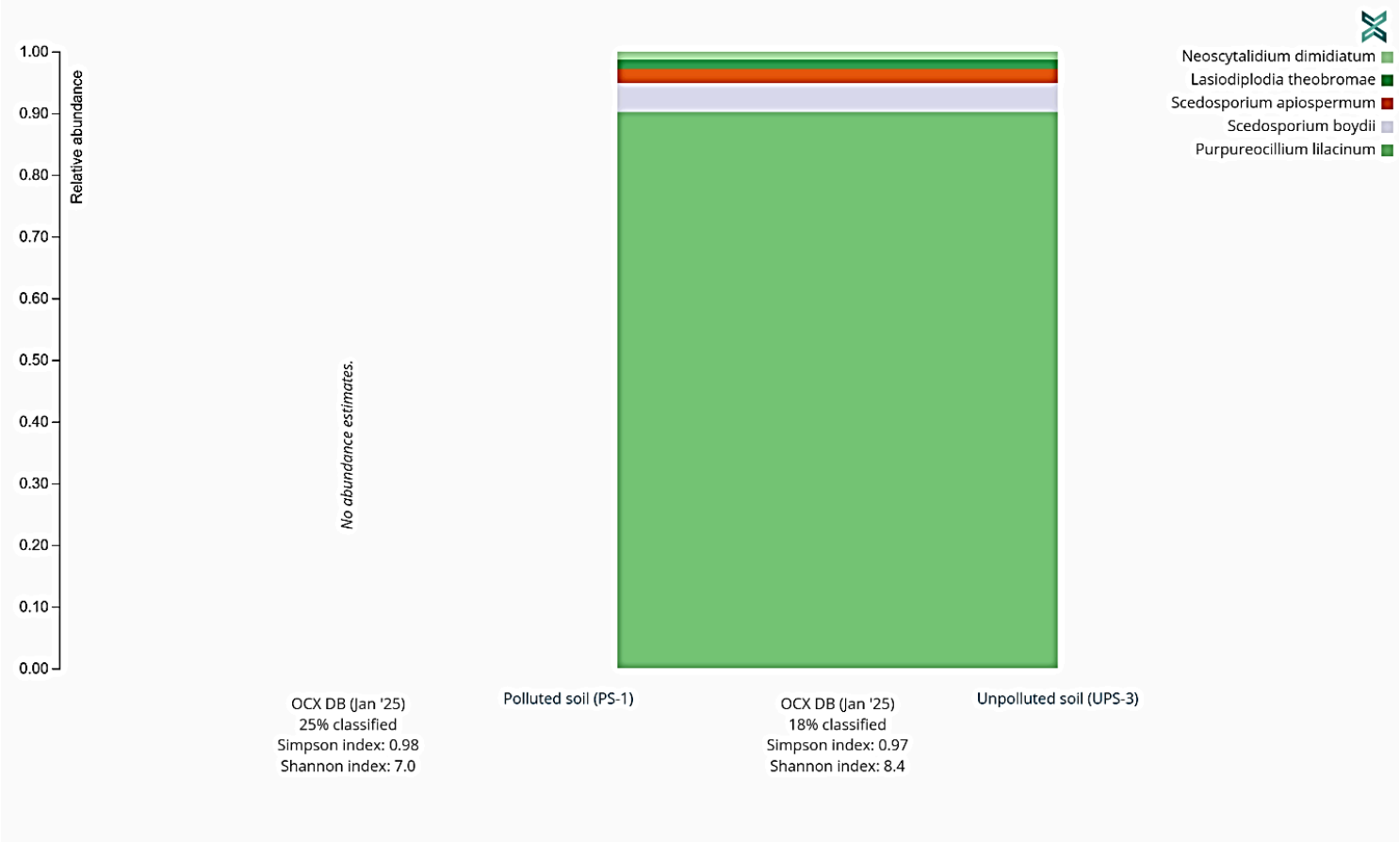

Figure 7

Fungal relative abundance and diversity at genus level for polluted and unpolluted soil

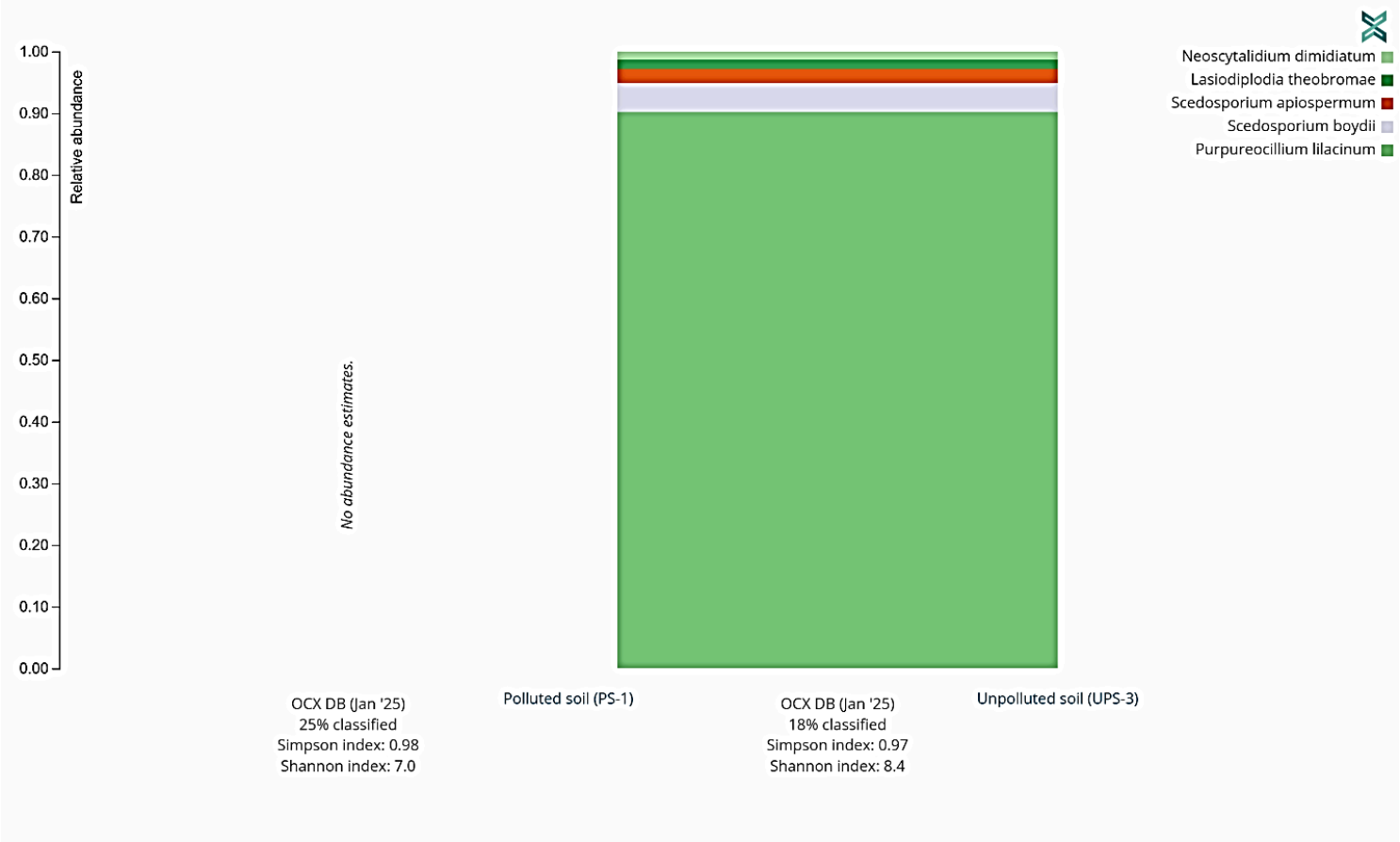

Figure 8

Fungal relative abundance and diversity at Specie level for polluted and unpolluted soil.