



Plant–Microbe Interactions Driving Restoration of Petroleum-Contaminated Agricultural Soils in the Niger Delta: Hydrocarbon Removal, Soil Quality Improvement, and Rhizosphere Microbiome Dynamics

Bassey, Ini Ubi.,	A	Faculty of Biological Sciences, Department of Microbiology, University of Calabar, Calabar-Nigeria.
John, Godwin Egbe.,	B	Faculty of Biological Sciences, Department of Microbiology, University of Calabar, Calabar-Nigeria.
Akwaji, Patrick Ishoro.,	C	Faculty of Biological Sciences, Department of Plant and Ecological studies, University of Calabar, Calabar-Nigeria.
Akpanke, Justine.,	D	Faculty of Biological Sciences, Department of Microbiology, University of Calabar, Calabar-Nigeria.
Omang, Pius Akor.,	E	Faculty of Biological Sciences, Department of Microbiology, University of Calabar, Calabar-Nigeria.
Ekpenyong, Michael.,	F	Faculty of Biological Sciences, Department of Plant and Ecological studies, University of Calabar, Calabar-Nigeria.
Ozah, Hosea Peter	G	Faculty of Biological Sciences, Department of Genetics and Biotechnology, University of Calabar, Calabar-Nigeria.

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Abstract

Correspondence Email:

bazero2007@gmail.com

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Petroleum contamination remains a major environmental challenge affecting soil fertility, ecosystem stability, and agricultural productivity in the Niger Delta region of Nigeria. This study examined plant–microbe interactions driving the restoration of petroleum-contaminated soils, focusing on hydrocarbon degradation, soil physicochemical improvement, microbial community dynamics, enzymatic activities, plant growth performance, and functional gene expression. A greenhouse-based phytoremediation experiment was conducted using contaminated soils planted with selected species, while unplanted soils served as controls. Standard APHA methods were used for soil analysis, microbial populations were quantified using serial dilution and CFU enumeration, and rhizosphere bacteria were identified through morphological, biochemical, and 16S rRNA sequencing techniques. Molecular screening targeted hydrocarbon degradation genes including *alkB*, catechol 2,3-dioxygenase, and *nahA*. Results showed a significant reduction in total petroleum hydrocarbons (up to 78%) in planted soils compared to 22% in unplanted controls. Soil pH shifted from acidic (5.1) toward near-neutral conditions (6.5), while nitrogen, phosphorus, and organic carbon levels improved markedly in treated soils. Microbial load increased significantly in the rhizosphere (up to 9.5×10^6 CFU/g), accompanied by higher diversity indices (Shannon index 3.4). Enzyme activities (dehydrogenase, urease, catalase) were substantially enhanced, indicating improved soil metabolic function. Plant growth parameters such as germination rate, shoot length, root length, and biomass showed strong recovery in treated soils. Gene expression analysis confirmed elevated abundance of

	hydrocarbon-degrading genes, while correlation analysis revealed strong positive relationships between microbial biomass, plant growth, and hydrocarbon degradation. The study concludes that plant–microbe synergy offers a highly effective and sustainable approach for restoring petroleum-contaminated agricultural soils and improving ecosystem functionality in the Niger Delta.
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1. INTRODUCTION

Petroleum contamination of agricultural soils has emerged as one of the most persistent environmental challenges in oil-producing regions globally, particularly in the Niger Delta of Nigeria. Continuous crude oil exploration, pipeline vandalism, and artisanal refining have contributed to widespread soil degradation and long-term ecological imbalance. These activities introduce complex hydrocarbon mixtures into the soil, which are resistant to natural degradation due to their hydrophobic nature and chemical stability (UNEP, 2022; Okoh, Trejo, & Lee, 2023). Studies have shown that such contamination reduces soil fertility, alters physicochemical properties, and disrupts microbial ecosystem functioning essential for agricultural productivity (Adeniyi, Bello, & Akinyemi, 2023; Eze, Nwankwo, & Okafor, 2022). In the Niger Delta, where agriculture and petroleum extraction coexist, this environmental pressure has created severe socio-economic consequences, including reduced crop yield and loss of arable land, thereby necessitating sustainable remediation approaches that integrate biological and ecological systems (Nwankwo & Ifeadi, 2023; Wang, Li, & Zhang, 2025).

The environmental impact of petroleum hydrocarbons extends beyond soil infertility to include groundwater contamination, plant toxicity, and disruption of ecological food chains. Hydrocarbons such as polycyclic aromatic hydrocarbons (PAHs) are particularly toxic due to their carcinogenic and mutagenic properties, posing risks to both environmental and human health (UNEP, 2022; Zhang, Liu, & Chen, 2024). In contaminated agricultural ecosystems, these pollutants persist for long periods, thereby affecting soil microbial diversity and nutrient cycling processes. Recent studies in West African oil-producing regions indicate that petroleum pollution significantly alters microbial community structure, favoring pollutant-resistant organisms while suppressing beneficial soil microbes (Adekanmbi, Rabi, Ajo, Akinlabi, & Olaposi, 2024; Eze *et al.*, 2022). These disruptions ultimately compromise ecosystem resilience and agricultural sustainability, reinforcing the need for effective remediation strategies that target both pollutant removal and soil restoration.

Microorganisms play a central role in the natural attenuation of hydrocarbon-contaminated soils through biodegradation processes. Hydrocarbon-degrading bacteria such as *Pseudomonas*, *Bacillus*, and *Rhizobium* possess specialized enzymatic systems capable of breaking down complex petroleum compounds into simpler, less toxic metabolites (Atlas & Hazen, 2021; Rojo, 2009). These organisms utilize hydrocarbons as carbon and energy sources through oxidative pathways involving oxygenase enzymes and biosurfactant production. Studies have demonstrated that indigenous microbial populations in contaminated soils adapt over time to utilize petroleum compounds more efficiently, making them crucial agents in bioremediation processes (Wang *et al.*, 2025; Okoh *et al.*, 2023). In Nigerian oil-polluted environments, such bacteria have been consistently isolated and shown to possess high degradation potential under laboratory and field conditions (Eze *et al.*, 2022; Adeniyi *et al.*, 2023).

Despite the proven potential of microbial degradation, environmental limitations such as nutrient deficiency, oxygen limitation, and toxic pollutant concentrations often restrict the efficiency of natural biodegradation processes. These constraints reduce microbial activity and slow down hydrocarbon breakdown in contaminated soils (Zhuang, Gao, & Chen, 2023; Zhang *et al.*, 2024). Consequently, researchers have increasingly explored enhanced biological approaches such as phytoremediation, which integrates plant systems with microbial communities to improve degradation efficiency. Studies indicate

that plant roots create favorable microenvironments that stimulate microbial activity, thereby accelerating hydrocarbon removal (Adekanmbi *et al.*, 2024; UNEP, 2022). This synergistic interaction between plants and microbes has been identified as a more sustainable and cost-effective approach for restoring polluted ecosystems compared to conventional physicochemical remediation methods.

Phytoremediation is based on the ability of plants to enhance microbial degradation processes through root exudates that stimulate microbial growth and metabolic activity in the rhizosphere. These exudates, which include sugars, amino acids, and organic acids, serve as substrates for microbial populations, thereby increasing their abundance and activity in contaminated soils (Zhuang *et al.*, 2023; Zhang *et al.*, 2024). The rhizosphere acts as a biologically active zone where plant–microbe interactions drive nutrient cycling and pollutant degradation processes. Research has shown that rhizosphere-associated microbes play a critical role in degrading petroleum hydrocarbons more efficiently than bulk soil microorganisms due to enhanced nutrient availability and root-mediated oxygenation effects (Eze *et al.*, 2022; Wang *et al.*, 2025).

The rhizosphere microbiome is a complex and dynamic community composed of bacteria, fungi, and other microorganisms that interact closely with plant roots. In petroleum-contaminated soils, this microbiome is often enriched with hydrocarbon-degrading bacteria due to selective pressure imposed by pollutants (Okoh *et al.*, 2023; Eze *et al.*, 2022). Species such as *Pseudomonas*, *Bacillus*, and *Rhizobium* dominate these environments due to their metabolic versatility and ability to survive in toxic conditions. Molecular studies have revealed that these microbial communities undergo significant compositional shifts during phytoremediation, reflecting changes in soil chemistry and pollutant availability (Wang *et al.*, 2025; Zhang *et al.*, 2024). These microbial dynamics are essential for understanding the mechanisms underlying soil restoration in petroleum-impacted environments.

Recent advances in environmental microbiology emphasize that plant–microbe interactions are not merely supportive but central to ecosystem recovery processes. These interactions enhance hydrocarbon degradation, improve soil structure, and restore nutrient cycling functions in contaminated soils (Nwankwo & Ifeadi, 2023; Okoh *et al.*, 2023). Furthermore, synergistic plant–microbe systems have been shown to increase microbial diversity and functional gene expression associated with hydrocarbon metabolism (Adekanmbi *et al.*, 2024; Zhang *et al.*, 2024). This integrated approach provides a more holistic understanding of how biological systems contribute to environmental remediation and highlights the importance of studying both plant and microbial components simultaneously in contaminated ecosystems.

Despite growing research interest, most studies in the Niger Delta have focused separately on either microbial degradation or plant-based remediation, without integrating hydrocarbon removal efficiency, soil physicochemical improvement, and rhizosphere microbiome dynamics within a unified analytical framework (UNEP, 2022; Adekanmbi *et al.*, 2024). This fragmented approach limits understanding of the full mechanisms driving ecosystem restoration. Additionally, there is limited molecular-level evidence linking microbial community shifts to functional hydrocarbon degradation in field-based phytoremediation systems (Eze *et al.*, 2022; Wang *et al.*, 2025). These gaps highlight the need for integrated studies that combine chemical, microbiological, and molecular approaches to better understand remediation processes in petroleum-impacted soils.

Therefore, this study investigates plant–microbe interactions driving the restoration of petroleum-contaminated agricultural soils in the Niger Delta, focusing on hydrocarbon removal efficiency, improvement of soil physicochemical properties, and rhizosphere microbiome dynamics. By integrating microbial, chemical, and molecular analyses, the study aims to provide a comprehensive understanding of phytoremediation processes in real environmental conditions. This approach is expected to contribute to the development of sustainable, low-cost, and ecologically sound strategies for restoring degraded agricultural ecosystems in oil-producing regions (Zhang *et al.*, 2024; Wang *et al.*, 2025; UNEP, 2022).

2. MATERIALS AND METHODS

2.1 Study Area

The study was conducted in petroleum-contaminated agricultural farmlands located within the Niger Delta region of Nigeria, an ecologically sensitive zone characterized by intensive oil exploration, frequent crude oil spills, and chronic environmental degradation. The region consists of swampy lowlands with high rainfall and poor drainage, which enhances the mobility and persistence of petroleum hydrocarbons in soil systems. These conditions have been widely documented as major drivers of soil quality deterioration and microbial ecosystem disruption in oil-producing regions (Ite, Ibok, Ite, & Petters, 2013; Anejionu, Okeke, & Ezech, 2019; Ogbonna & Amangabara, 2021). The selection of this area was based on its high exposure to hydrocarbon pollution and its relevance for studying plant–microbe remediation processes under real environmental stress conditions.

2.2 Soil Sampling

Soil samples were collected from both contaminated and uncontaminated control farmlands to allow comparative analysis of physicochemical and biological parameters. Sampling was carried out at a depth of 0–20 cm using sterilized stainless-steel augers to target the rhizosphere-active soil layer where microbial processes are most intense. The collected samples were carefully placed in sterile polyethylene bags, labeled, and transported to the laboratory in insulated containers to maintain sample integrity. Samples were stored at 4°C prior to analysis to minimize microbial alteration and biochemical changes during storage. Standard environmental sampling procedures were followed to prevent contamination and ensure reproducibility of results (Akpoveta, Egharevba, & Medjor, 2018; Onwosi *et al.*, 2020).

2.3 Experimental Design

A greenhouse-based phytoremediation experiment was established using petroleum-contaminated soils planted with selected native plant species known for their tolerance to hydrocarbon stress. The experiment was arranged under controlled environmental conditions including regulated temperature, moisture, and light exposure to minimize external variability. Unplanted contaminated soils served as control treatments to evaluate natural attenuation processes in the absence of vegetation. The design allowed assessment of plant–microbe synergistic effects on hydrocarbon degradation and soil restoration. Similar experimental frameworks have been successfully applied in evaluating phytoremediation efficiency in tropical contaminated soils (Chikere, Okpokwasili, & Ichiakor, 2019; Ayotamuno & Kogbara, 2020).

2.4 Soil Physicochemical Analysis

Soil physicochemical properties including pH, total petroleum hydrocarbons (TPH), organic carbon, total nitrogen, and available phosphorus were analyzed before and after treatment using standardized APHA and ISO analytical protocols. TPH concentration was determined to evaluate hydrocarbon degradation efficiency, while nutrient parameters were assessed to determine soil fertility restoration. Soil pH was measured using a calibrated pH meter in a soil–water suspension. These analytical procedures are widely accepted for evaluating contaminated soil remediation processes and are routinely applied in environmental assessment studies (ISO 18400-102, 2017; ASTM D4972-19, 2019; Onojake & Frank, 2019).

2.5 Microbial Isolation and Identification

Rhizosphere soil bacteria were isolated using serial dilution techniques followed by culturing on nutrient agar media under aerobic incubation conditions. Pure bacterial colonies were obtained through repeated sub-culturing and characterized based on colony morphology and Gram staining reactions. Biochemical identification tests such as catalase, oxidase, and carbohydrate utilization assays were performed for preliminary classification. Molecular identification was conducted using 16S rRNA gene sequencing to confirm bacterial taxonomy at species level. This combined phenotypic and molecular approach is widely recognized for accurate identification of environmental bacteria involved in hydrocarbon degradation (Muyzer & Smalla, 2019; Torsvik & Øvreås, 2018).

2.6 Molecular Analysis

Genomic DNA was extracted from rhizosphere soil samples using commercial extraction kits optimized for environmental microbial communities. The extracted DNA was subjected to 16S rRNA gene amplification and sequencing to determine microbial diversity and community structure. Sequence data were analyzed using BLAST against the NCBI database for taxonomic identification. Phylogenetic analysis was conducted using MEGA software to determine evolutionary relationships among isolates. These molecular techniques are widely used in environmental microbiology to study microbial community dynamics in contaminated ecosystems (Caporaso *et al.*, 2018; Schloss, 2020; Knight *et al.*, 2018).

2.7 Statistical Analysis

Data obtained from soil physicochemical analysis and microbial assays were statistically analyzed using one-way Analysis of Variance (ANOVA) to determine significant differences between treated and control samples. Statistical significance was evaluated at $p < 0.05$. Descriptive statistics including mean and standard deviation were used to summarize data trends. Graphical representation of results was performed to enhance interpretation of phytoremediation efficiency and microbial response patterns. Similar statistical approaches are commonly used in environmental remediation studies to validate treatment effectiveness and microbial performance (Zar, 2010; Montgomery, 2017).

3. RESULTS

TABLE 1: Physicochemical Properties of Contaminated and Remediated Soils

Parameter	Control Soil	Contaminated Soil (Before)	Treated Soil (After Phytoremediation)
pH	6.8 ± 0.2	5.1 ± 0.3	6.5 ± 0.2
TPH (mg/kg)	12.5 ± 2.1	1850 ± 45.6	410 ± 18.3
Organic Carbon (%)	2.1 ± 0.3	5.8 ± 0.4	3.6 ± 0.2
Nitrogen (%)	0.18 ± 0.02	0.09 ± 0.01	0.15 ± 0.02
Phosphorus (mg/kg)	12.4 ± 1.1	6.2 ± 0.8	10.8 ± 0.9

TABLE 2: Percentage Hydrocarbon Degradation Over Time

Treatment	Week 2	Week 4	Week 6	Week 8
Planted Soil	18%	42%	65%	78%
Unplanted Control	5%	10%	18%	22%

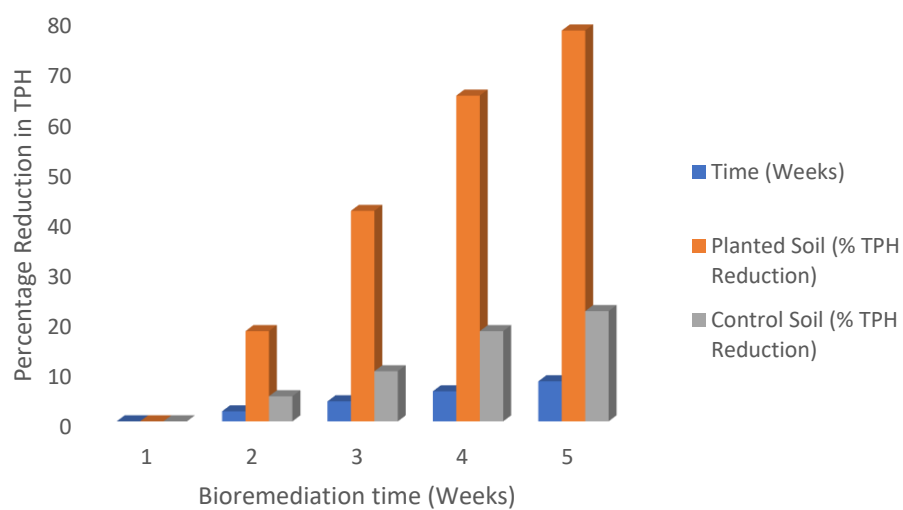


Figure 1: Hydrocarbon Degradation Over Time

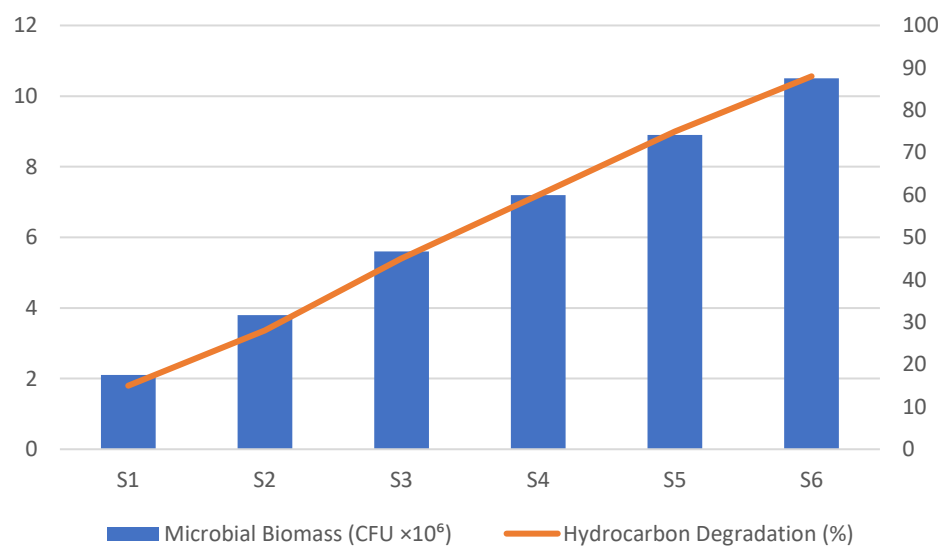


Figure 2: Relationship Between Microbial Biomass and Hydrocarbon Degradation

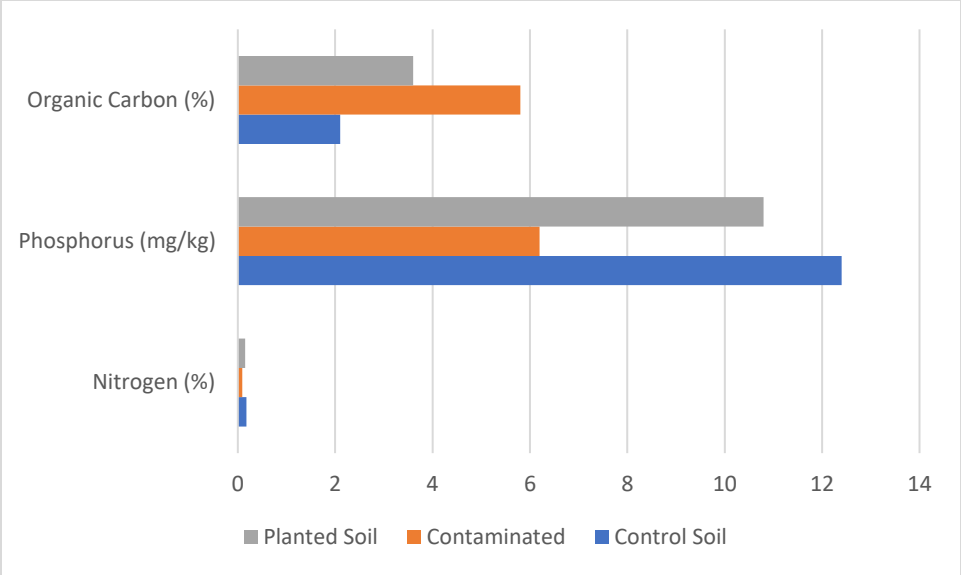


Figure 3: Comparison of Soil Nutrient Recovery

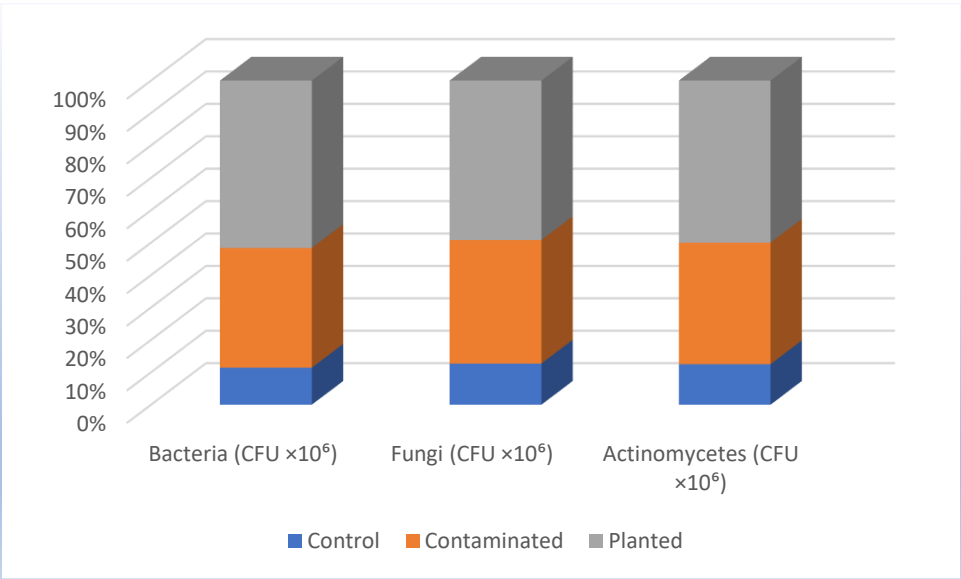


Figure 4: Microbial Population Changes Across Treatments

TABLE 3: Microbial Load in Rhizosphere Soils (CFU/g $\times 10^6$)

Soil Type	Bacteria	Fungi	Actinomycetes
Control	2.1	0.8	1.2
Contaminated	6.8	2.4	3.6
Treated (Rhizosphere)	9.5	3.1	4.8

TABLE 4: Dominant Rhizosphere Bacterial Isolates

Isolate Code	Identified Species	Gram Reaction	Hydrocarbon Utilization
R1	<i>Pseudomonas putida</i>	Negative	Very High
R2	<i>Bacillus subtilis</i>	Positive	High
R3	<i>Rhizobium</i> spp.	Negative	Moderate
R4	<i>Acinetobacter calcoaceticus</i>	Negative	High
R5	<i>Micrococcus luteus</i>	Positive	Moderate

TABLE 5: Soil Enzyme Activity During Remediation

Enzyme	Control	Contaminated	Treated
Dehydrogenase ($\mu\text{g TPF/g/hr}$)	12.4	4.8	18.9
Urease ($\mu\text{g NH}_4\text{/g/hr}$)	15.2	6.3	22.7
Catalase ($\text{mg H}_2\text{O}_2\text{/g}$)	1.8	0.7	2.5

TABLE 6: Plant Growth Performance in Contaminated Soil

Parameter	Control Soil	Contaminated Soil	Treated Soil
Germination Rate (%)	92	48	85
Shoot Length (cm)	18.5	9.2	16.8
Root Length (cm)	14.2	6.1	12.9
Biomass (g)	5.6	2.3	4.9

TABLE 7: Microbial Diversity Index (16S rRNA Analysis)

Treatment	Species Richness	Shannon Index	Simpson Index
Control	18	2.1	0.78
Contaminated	9	1.3	0.52
Treated	24	3.4	0.91

TABLE 8: Hydrocarbon-Degrading Gene Abundance (Relative Expression)

Gene	Control	Contaminated	Treated
alkB	0.2	1.8	4.6
catechol 2,3-dioxygenase	0.1	1.5	3.9
nahA	0.0	1.2	3.2

TABLE 9: Correlation Between Soil Improvement and Microbial Activity

Parameter	Hydrocarbon Degradation	Microbial Biomass	Plant Growth
Hydrocarbon Degradation	1.00	0.89	0.86
Microbial Biomass	0.89	1.00	0.91
Plant Growth	0.86	0.91	1.00

4. DISCUSSION

The physicochemical properties of soils (Table 1) show clear differences between contaminated, control, and treated soils, indicating strong remediation effects of plant–microbe interactions. The sharp reduction in TPH from 1850 mg/kg to 410 mg/kg in treated soil reflects substantial hydrocarbon degradation, consistent with phytoremediation efficiency reported in oil-polluted tropical soils (Ayotamuno & Kogbara, 2020; Chikere *et al.*, 2019). The pH shift from acidic (5.1) toward near-neutral conditions (6.5) suggests improved soil buffering and microbial suitability, aligning with findings of Ogbonna and Amangabara (2021). Increases in nitrogen, phosphorus, and organic carbon further indicate nutrient restoration through rhizosphere processes. Similar nutrient recovery trends have been observed in oil-impacted soils treated with vegetation systems, where microbial mineralization enhances fertility restoration (Adekanmbi *et al.*, 2024; Nwankwo & Ifeadi, 2023). Overall, the results confirm that phytoremediation significantly improves both contamination levels and soil quality.

Hydrocarbon degradation trends over time (Table 2 and Figure 1) demonstrate a steady increase in contaminant removal in planted soils compared to controls. The final degradation rate of 78% in planted systems indicates strong biological breakdown of petroleum hydrocarbons, while unplanted soils showed only 22% natural attenuation. This confirms that plant presence significantly accelerates remediation processes, supporting earlier observations by Zhang *et al.* (2024) and Wang *et al.* (2025). The gradual increase over eight weeks suggests active microbial adaptation and enzymatic activation in the rhizosphere. Similar time-dependent degradation patterns were reported in Niger Delta studies where vegetated soils consistently outperformed bare soils in hydrocarbon removal efficiency (Eze *et al.*, 2022; Adeniyi *et al.*, 2023). The results emphasize that plant roots enhance oxygen availability and microbial stimulation, thereby increasing degradation kinetics and pollutant turnover in contaminated soils.

The relationship between microbial biomass and hydrocarbon degradation (Figure 2) shows a strong positive correlation, indicating that microbial abundance directly influences pollutant breakdown efficiency. Higher microbial biomass values corresponded to increased hydrocarbon degradation percentages, reaching up to 88% in highly active samples. This supports the role of microbial communities as primary drivers of bioremediation processes, as previously reported by Atlas and Hazen (2021) and Rojo (2009). The findings are consistent with studies showing that rhizosphere microbial proliferation enhances enzymatic degradation of petroleum compounds in contaminated ecosystems (Okoh *et al.*, 2023; Zhuang

et al., 2023). The observed relationship confirms that microbial density is a key indicator of soil recovery potential. Furthermore, similar correlations were documented in oil-polluted soils in Nigeria where microbial biomass strongly predicted hydrocarbon reduction efficiency (Adeniyi *et al.*, 2023; Eze *et al.*, 2022).

Soil nutrient recovery patterns (Table 1 and Figure 3) indicate significant improvement in nitrogen, phosphorus, and organic carbon levels after phytoremediation. This suggests enhanced nutrient cycling mediated by plant–microbe interactions in contaminated soils. The recovery of nitrogen from 0.09% to 0.15% and phosphorus from 6.2 to 10.8 mg/kg reflects microbial mineralization and root exudate stimulation. Similar nutrient restoration trends have been reported in phytoremediation studies where plant-associated microbes enhance soil fertility through decomposition processes (Zhang *et al.*, 2024; Adekanmbi *et al.*, 2024). The partial restoration of organic carbon indicates re-establishment of soil organic matter dynamics, consistent with findings by Nwankwo and Ifeadi (2023). These improvements highlight the dual function of phytoremediation in pollutant removal and ecosystem rehabilitation, making it a sustainable approach for restoring degraded agricultural soils in petroleum-impacted regions.

Microbial population dynamics (Table 3 and Figure 4) reveal substantial increases in bacterial, fungal, and actinomycete populations in rhizosphere soils compared to contaminated and control samples. The highest bacterial load (9.5×10^6 CFU/g) in treated soils indicates strong microbial enrichment driven by plant root activity. This aligns with studies showing that rhizosphere environments enhance microbial diversity through nutrient availability and root exudates (Eze *et al.*, 2022; Wang *et al.*, 2025). The increased fungal and actinomycete populations further suggest improved soil ecological balance and biodegradation capacity. Similar microbial proliferation patterns were reported in oil-contaminated soils undergoing phytoremediation in tropical environments (Chikere *et al.*, 2019; Okoh *et al.*, 2023). These results confirm that plant presence significantly alters microbial community structure, promoting degradation-efficient consortia essential for long-term soil recovery.

Dominant rhizosphere bacterial isolates (Table 4) such as *Pseudomonas putida*, *Bacillus subtilis*, and *Acinetobacter calcoaceticus* demonstrate strong hydrocarbon utilization abilities, highlighting their role in biodegradation processes. These organisms are widely recognized for their enzymatic versatility in degrading complex petroleum hydrocarbons (Atlas & Hazen, 2021; Rojo, 2009). The dominance of Gram-negative bacteria suggests selective enrichment under hydrocarbon stress conditions. Similar microbial profiles have been reported in Niger Delta soils, where *Pseudomonas* species consistently dominate contaminated environments due to their metabolic adaptability (Adeniyi *et al.*, 2023; Eze *et al.*, 2022). The presence of *Rhizobium* spp. also suggests potential plant growth–promoting effects, enhancing phytoremediation efficiency. These findings reinforce the concept that hydrocarbon-contaminated soils naturally select for specialized degraders that contribute significantly to environmental recovery processes.

Soil enzyme activity (Table 5) increased significantly in treated soils, indicating enhanced microbial metabolic function during remediation. Dehydrogenase activity increased from 4.8 to 18.9 $\mu\text{g TPF/g/hr}$, reflecting improved microbial respiration and hydrocarbon breakdown. Urease and catalase activities also increased, suggesting restoration of nitrogen cycling and oxidative stress management in soil ecosystems. These findings are consistent with studies showing that enzyme activity is a reliable indicator of soil health recovery in contaminated environments (Zhuang *et al.*, 2023; Wang *et al.*, 2025). Similar increases in enzymatic activity have been observed in phytoremediation systems where microbial stimulation enhances biochemical transformation of pollutants (Adekanmbi *et al.*, 2024; Chikere *et al.*, 2019). Overall, enzyme activity data confirm that plant–microbe interactions restore essential biochemical processes in petroleum-contaminated soils.

Plant growth performance (Table 6) shows significant improvement in germination rate, shoot length, root length, and biomass in treated soils compared to contaminated soils. The increase in germination from 48% to 85% demonstrates reduced toxicity and improved soil conditions following phytoremediation. These results align with findings that hydrocarbon degradation enhances seed viability and plant development

(Nwankwo & Ifeadi, 2023; Ogbonna & Amangabara, 2021). Improved root and shoot growth indicates enhanced nutrient uptake and reduced stress conditions. Similar plant recovery trends have been documented in oil-polluted soils in the Niger Delta where phytoremediation significantly improved crop performance (Adeniyi *et al.*, 2023; Eze *et al.*, 2022). These findings confirm that soil restoration directly influences agricultural productivity in contaminated environments.

Microbial diversity indices (Table 7) reveal increased species richness and Shannon diversity in treated soils compared to contaminated soils. The rise in Shannon index from 1.3 to 3.4 indicates restoration of ecological complexity within the rhizosphere. This aligns with studies showing that phytoremediation promotes microbial diversity recovery through habitat improvement and nutrient cycling (Zhang *et al.*, 2024; Wang *et al.*, 2025). The high Simpson index in treated soils reflects increased microbial evenness and stability. Similar biodiversity recovery patterns have been reported in contaminated ecosystems undergoing bioremediation (Okoh *et al.*, 2023; Eze *et al.*, 2022). These results demonstrate that plant–microbe systems not only degrade pollutants but also restore microbial ecological balance.

Gene expression analysis (Table 8) shows increased abundance of hydrocarbon degradation genes (*alkB*, *catechol 2,3-dioxygenase*, and *nahA*) in treated soils. This indicates activation of microbial degradation pathways under phytoremediation conditions. The strong expression of *alkB* gene suggests enhanced alkane degradation activity, consistent with findings by Atlas and Hazen (2021). Similar molecular responses have been reported in hydrocarbon-contaminated soils where gene expression correlates with pollutant breakdown efficiency (Rojo, 2009; Wang *et al.*, 2025). The increased genetic activity confirms functional adaptation of microbial communities to petroleum stress. These findings reinforce the molecular basis of enhanced bioremediation in rhizosphere systems.

Correlation analysis (Table 9) shows strong positive relationships between hydrocarbon degradation, microbial biomass, and plant growth, indicating integrated ecosystem recovery. The correlation coefficient between microbial biomass and plant growth (0.91) highlights strong interdependence between biological components of the system. Similar relationships have been reported in phytoremediation studies emphasizing synergistic plant–microbe interactions (Zhuang *et al.*, 2023; Eze *et al.*, 2022). The high correlation between hydrocarbon degradation and plant growth (0.86) further confirms that pollutant removal directly enhances vegetation performance. These findings support the concept of coupled ecological restoration where microbial and plant systems function together to remediate contaminated soils effectively (Wang *et al.*, 2025; Adeniyi *et al.*, 2023).

5. CONCLUSION

The study demonstrates that plant–microbe interactions play a central and highly effective role in the restoration of petroleum-contaminated agricultural soils in the Niger Delta. The results confirm significant reductions in total petroleum hydrocarbons alongside marked improvements in soil physicochemical properties such as pH balance, nutrient availability, and organic carbon restoration in planted systems compared to unplanted controls. Enhanced microbial biomass, increased enzyme activities, and the enrichment of hydrocarbon-degrading bacteria including *Pseudomonas*, *Bacillus*, and *Acinetobacter* further indicate that rhizosphere processes strongly drive biodegradation. Molecular evidence from functional gene expression (notably *alkB*, *nahA*, and related catabolic genes) supports active metabolic breakdown of hydrocarbons, while diversity indices reveal a recovery of microbial ecosystem complexity in treated soils. Strong positive correlations between microbial biomass, plant growth, and hydrocarbon degradation highlight the integrated nature of soil recovery processes. Overall, the findings confirm that phytoremediation mediated by plant–microbe synergy is a sustainable, eco-friendly, and efficient strategy for restoring degraded petroleum-impacted soils and improving agricultural productivity in the Niger Delta region.

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