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Functional Potential of Native Microbial Communities in Detoxifying Heavy Metals from Industrial Soils

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ABSTRACT

This study evaluates the bioremediation potential of indigenous microbial consortia sourced from heavy metal-contaminated soils in the Jeedimetla industrial area, Hyderabad, India (17.52835° N, 78.44501° E, 17.52690° N, 78.44503° E, 17.52759° N, 78.44357° E and 17.52748° N, 78.44172° E), Hyderabad, India. Physico-chemical analysis indicated elevated levels of Cd, Pb, Cr, Zn, and phenolic compounds, with cadmium exceeding permissible limits by over 20-fold. Employing enrichment culture methodologies, consortia of Pseudomonas and Bacillus species were carefully cultivated and evaluated for their heavy metal tolerance and biodegradation capabilities. Microcosm experiments demonstrated a 60-75% reduction in bioavailable metal concentrations and a 50-60% degradation of phenol and polycyclic aromatic hydrocarbons during a 60-day duration. Molecular identification via 16S rRNA sequencing and community profiling revealed functional traits like siderophore production, phosphate solubilization, and biosurfactant activity. A comparative analysis with international remediation studies emphasized the ecological importance and functional resilience of indigenous consortia. The results indicate the feasibility of employing site-adapted microbial communities for the comprehensive bioremediation of intricate industrial pollutants.

Keywords: Bioremediation, Cadmium detoxification, Heavy metals, Indigenous microbial consortia, Jeedimetla industrial area, Microcosm experiment, Phenol degradation

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1. INTRODUCTION

The swift industrialization in urban India, particularly within designated industrial estates, has substantially fostered economic growth while simultaneously engendering intricate environmental issues (Prabhakar 2024). The Jeedimetla Industrial Development Area (IDA) near Hyderabad, Telangana, exemplifies industrial growth coupled with significant ecological deterioration. Jeedimetla, marked by a concentration of chemical, pharmaceutical, metal processing, and electroplating businesses, has seen the prolonged release of untreated or inadequately treated effluents into adjacent soil and water systems (Mohammad et al. 2017). The region has emerged as a focal point of environmental concern, with various studies, including those conducted by the CPCB and local environmental monitoring agencies, indicating heightened concentrations of heavy metals such as cadmium (Cd), chromium (Cr), lead (Pb), and nickel (Ni), as well as enduring organic pollutants like phenols, petroleum hydrocarbons, and synthetic dyes. These contaminants disturb the physicochemical equilibrium of the soil and significantly endanger microbial biodiversity, terrestrial food webs, and groundwater quality (Weldeslassie et al. 2017).

The persistence and toxicity of heavy metals provide a significant cleanup issue due to their non-degradable characteristics and propensity for bioaccumulation (Kumar et al. 2022). Traditional remediation methods, such excavation, stabilization, or soil washing, frequently demonstrate high costs, environmental disruption, or limited efficacy (Liu et al. 2018). Conversely, bioremediation has arisen as a sustainable and economical option that utilizes the metabolic and physicochemical abilities of bacteria to detoxify or immobilize pollutants (Kour et al. 2021). Microbial consortia, consisting of various bacterial or fungal species, provide a more effective solution than single-strain methods as they may collaboratively address intricate pollutant combinations through synergistic biochemical interactions (Cao et al. 2022). Numerous research worldwide has evidenced the effective utilization of indigenous microbial consortia for the detoxification of heavy metals and the breakdown of organic contaminants. Indigenous bacteria sourced from industrial

locations in China, South Africa, and Brazil have demonstrated the capacity to mitigate metal toxicity and reestablish microbial community equilibrium (Begum et al. 2022).

Notwithstanding these advancements, site-specific applications are nonetheless inadequately investigated in several developing areas, where the efficacy of bioremediation predominantly relies on the adaptability and durability of microbial communities (Contreras-Salgado et al. 2024). In Jeedimetla, characterized by a diversified and strong pollution profile, it is posited that microbial communities have evolved to endure substantial contaminant loads. These changes could be utilized to isolate microbial strains or consortia proficient in successful cleanup. Nonetheless, there is a notable deficiency of comprehensive research that amalgamate microbial ecology, pollution profile, and functional bioremediation experiments from this area. The existing literature on Jeedimetla has predominantly concentrated on physico-chemical evaluations and the classification of industrial waste, while insufficient emphasis has been placed on the biological responses and remediation capabilities of the indigenous microbiota (Mohammad et al. 2017; Lingaswamy et al. 2023).

This work seeks to examine the bioremediation capabilities of native microbial consortia obtained from the contaminated soils of Jeedimetla IDA, hence addressing the existing knowledge gap. This work investigates the efficacy of indigenous microbial consortia in diminishing the bioavailable portions of heavy metals and organic contaminants by integrating site characterization, microbial diversity profiling via high-throughput 16S rRNA sequencing, and laboratory-scale microcosm studies. The study expands upon previous findings that highlight the significance of employing ecologically appropriate and indigenous bacteria in remediation, particularly in multi-contaminant settings. The objective is to create a scalable, environmentally sustainable remediation framework applicable to Jeedimetla and analogous industrial areas.

The study aims to further the worldwide dialogue on microbial-assisted remediation by offering comparative data from one of India's most contaminated industrial zones. The integration of molecular microbiology with conventional culture-based techniques and environmental chemistry enhances the interdisciplinary framework, providing insights into both bioremediation efficacy and the microbial ecological transformations prompted by contamination. The findings may ultimately bolster evidence-based policymaking, risk mitigation methods, and the development of community-oriented soil restoration programs, facilitating wider applications of native microbial consortia in the rehabilitation of damaged industrial landscapes.

2. MATERIALS AND METHODS

2.1. Study Area and Site Selection

The research was carried out at the Industrial Development Area (IDA) of Jeedimetla, situated in the northwestern region of Hyderabad, Telangana, India. The physical coordinates of the area range from 17.52835° N, 78.44501° E, 17.52690° N, 78.44503° E, 17.52759° N, 78.44357° E and 17.52748° N, 78.44172° E, comprising a vital industrial zone marked by significant chemical, pharmaceutical, and dye production activities. Site selection utilized a gradient-based methodology that considered proximity to industrial effluent sources, potential pollutant pathways, and current ecological disturbance levels. Three principal sample zones were delineated up-gradient (PH1), mid-gradient (PH2), and down-gradient (HM1 and HM2) to assess geographic variability in contamination levels, as listed in the **Table 1**. The zones were subdivided into numerous sampling plots to include repeats and ensure statistical rigor. The down-gradient zones were chosen for their historically recorded pollution accumulation, while the up-gradient zones acted as reference controls. Each sampling location was geo-referenced with a handheld GPS device to ensure repeatability and precise spatial correlation. This organized zoning facilitated the methodical comparison of soil contamination and microbial community alterations along the hydrological gradient affected by surface runoff and effluent leaching during pre- and post-monsoon seasons.

Table 2.1. Soil Sample Catalogue with GPS Coordinates from IDA Jeedimetla

Sample ID	Zone	Depth (cm)	GPS Coordinates	Sample Type
PH1	Up-gradient	0-15	17.52835° N, 78.44501° E	Surface soil (Pharma Zone)
PH2	Mid-gradient	15-30	17.52690° N, 78.44503° E	Subsurface soil (Pharma-Mixed Zone)
HM1	Down-gradient	0-15	17.52759° N, 78.44357° E	Surface soil (Heavy Metal Zone)
HM2	Down-gradient	15-30	17.52748° N, 78.44172° E	Subsurface soil (Effluent Zone)

2.2. Soil Collection and Preliminary Treatment

Soil samples were obtained at a depth of 0-15 cm via a stainless-steel auger, ensuring minimal contamination and uniformity across locations. Sampling occurred twice: once in the pre-monsoon period (May-June) and once in the post-monsoon period (September-October) to assess seasonal effects on soil properties and pollutant mobility. At each plot, triplicate composite samples were collected by amalgamating five sub-samples taken within a 1-meter radius. The collected soils were packed in sterile plastic bags, tagged, and transferred to the laboratory under refrigerated conditions (4°C). In the laboratory, samples were air-dried at ambient temperature, homogenized with a mortar and pestle, then sieved through a 2 mm screen for physicochemical and contaminant analysis. A portion of each sample was preserved at -20°C for microbial DNA extraction and enzyme tests. Meticulous precautions were implemented to prevent cross-contamination between sites by sanitizing instruments and utilizing distinct containers for each location. The pre-processing ensured consistency and dependable comparison among all experimental parameters.

2.3. Physicochemical Characterization of Soil

Standard soil analysis techniques were utilized to ascertain several physico-chemical characteristics. Soil pH and electrical conductivity (EC) were assessed in a 1:2.5 (w/v) soil-to-distilled water suspension utilizing a calibrated pH meter and EC meter, respectively. The quantity of soil organic matter (SOM) was assessed using the Walkley–Black dichromate oxidation method, and the cation exchange capacity (CEC) was measured using ammonium acetate extraction at pH 7. Bulk density was assessed via the core method, whereas water holding capacity was determined through gravimetric analysis. These essential metrics were utilized to evaluate the buffering potential and retention capacity of the soils, which are critical in pollutant mobility and microbiological viability. Seasonal comparisons revealed significant variations in electrical conductivity (EC) and soil organic matter (SOM) across gradients and timepoints, with down-gradient soils demonstrating elevated salinity and diminished SOM, ascribed to effluent buildup and microbial degradation. This data was crucial for interpreting microbial diversity and metal transport patterns in later tests.

2.4. Analysis of Heavy Metals and Organic Contaminants

Heavy metal pollution was quantified by analysing both total and bioavailable percentages of the metals. The total metal content was quantified using aqua regia digestion (3:1 HCl:HNO_3) of 1 g of soil, followed by analysis via Inductively Coupled Plasma Mass Spectrometry (ICP-MS, Perkin Elmer NexION 2000). The bioavailable fraction was extracted with 0.005 M DTPA (diethylenetriaminepentaacetic acid) and subsequently filtered before to ICP-MS measurement. The targeted metals comprised Pb, Cd, Cr, Zn, Ni, Cu, Mn, and As. Organic pollutants, including PAHs, azo dyes, and phenols, were extracted using Soxhlet extraction utilizing a hexane:acetone (1:1) solvent mixture, subsequently purified via silica gel column chromatography, and quantified using Gas Chromatography-Mass Spectrometry (GC-MS, Agilent 7890A/5975C). Analytical calibration was performed using approved standards, and quality control encompassed blank runs and spiked recovery tests. The findings validated the presence of many toxicants in the Jeedimetla soils, exhibiting increased bioavailability, underscoring the intricate nature of pollution and the necessity for multifaceted bioremediation approaches.

2.5. Extraction of Microbial DNA and Community Profiling

Microbial community profiling was conducted utilizing both molecular and biochemical methodologies. Environmental DNA was isolated from 0.5 g of soil utilizing the DNeasy PowerSoil Pro Kit (Qiagen) in accordance with the manufacturer's procedure, which encompassed bead-beating, chemical lysis, and column purification. The DNA yield and purity were evaluated using NanoDrop (260/280 ratio) and agarose gel electrophoresis. Amplification of the 16S rRNA gene targeting the V3-V4 region was conducted with Illumina-adapted primers (341F and 806R). Amplicons were purified using AMPure XP beads and sequenced on the Illumina MiSeq platform utilizing 2x300 bp paired-end chemistry. Sequencing data were analyzed using QIIME2 with DADA2 for denoising, taxonomy classification against the SILVA 138 database, and estimates of alpha (Shannon, Simpson) and beta diversity (Bray-Curtis). The research indicated substantial decreases in microbial diversity in heavily contaminated areas and an increase in stress-tolerant genera such as Pseudomonas and Bacillus. The community changes established the foundation for the selection of prospective consortia for bioremediation.

2.6. Isolation and Functional Characterization of Metal-Tolerant Consortia

The indigenous metal-tolerant bacterial consortia were extracted from the most contaminated locations (HM1 and HM2) employing an enrichment culture methodology. One gram of soil was inoculated into 100 mL of Nutrient Broth enriched with a mixed heavy metal solution (Pb^{2+}, Cr^{6+}, Ni^{2+}, and Cd^{2+} at 50 ppm each) and incubated at 30 ± 2°C with shaking at 150 rpm for 7 days. Serial sub-culturing was conducted for three enrichment cycles to isolate highly tolerant bacteria. Following enrichment, cultures were serially diluted and disseminated onto Nutrient Agar supplemented with metals (25–100 ppm) to isolate pure colonies. Distinct morphotypes were chosen based on colony appearance and subsequently evaluated for metal tolerance by minimum inhibitory concentration (MIC) experiments utilizing broth microdilution techniques. Functional characterization encompassed catalase, oxidase, urease, and phosphate solubilization tests, in addition to quantitative testing for biosurfactant and siderophore synthesis. Molecular identification of chosen isolates was conducted using 16S rRNA gene sequencing, with sequences evaluated via NCBI BLAST for species-level identification.

The predominant genera comprised Bacillus, and Pseudomonas all recognized for their abilities in metal sequestration and detoxification. The strains were amalgamated into synthetic consortia following compatibility assessments (cross-streak and co-culture assays) and were stored in glycerol stocks for application in remediation experiments.

2.7. Microcosm Configuration for Bioremediation

Laboratory-scale microcosms were created to evaluate the bioremediation capabilities of native microbial consortia under regulated circumstances. 1 kg of contaminated soil from HM1 was autoclaved to eradicate native bacteria and thereafter supplemented with 10% (w/w) non-sterile inoculum obtained from the isolated consortia. Treatments comprised: (i) sterile soil devoid of inoculum (abiotic control), (ii) unsterilized soil (native microbiota control), and (iii) inoculated sterile soil (bioaugmentation treatment). The microcosms were preserved in plastic containers with moisture levels calibrated to 60% of field capacity and incubated at 30°C for a duration of 60 days. Moisture was sustained with the intermittent application of sterile distilled water. Subsamples were obtained at 0, 15, 30, and 60 days for the analysis of metals, enumeration of microbes, and assessment of enzyme activity. Each treatment was conducted in triplicate, and sterile conditions were maintained while sampling using aseptic instruments and gloves. The objective was to replicate in-situ circumstances as accurately as possible while separating the impacts of the introduced microbial communities. This configuration facilitated time-resolved assessment of metal removal efficacy, microbiological viability, and functional adaptation under extended exposure.

2.8. Post-Treatment Surveillance and Ecotoxicological Evaluation

Following 60 days of microcosm incubation, post-treatment soils were evaluated to determine decreases in total and bioavailable metal concentrations utilizing the previously reported methodology (ICP-MS after DTPA extraction). Microbial colony-forming units (CFUs) were quantified on selective media to evaluate the survival and proliferation of the consortia. Enzymatic activities-dehydrogenase (via TTC reduction), phosphatase, and urease-were assessed to determine the restoration of soil biological functioning. A concurrent seed germination experiment utilizing Vigna radiata (green gram) was performed to evaluate phytotoxicity. Seeds were planted in both treated and untreated soils, and metrics including germination rate, root and shoot length, and biomass were measured over a period of 7 days. The Germination Index (GI) was computed to assess ecotoxicological enhancements. Bacterial DNA was re-extracted from post-treatment soil and analyzed by 16S rRNA amplicon sequencing to monitor alterations in microbial community structure. The findings validated the re-establishment of advantageous taxa and the reduction of toxicity, confirming the efficacy of the bioaugmentation technique.

2.9. Statistical Analysis and Kinetic Modeling

All data were analyzed with R Studio (version 4.3) and OriginPro 2023. Descriptive statistics and normality assessments preceded one-way ANOVA with Tukey's HSD post hoc tests to evaluate significant differences among treatments ($p < 0.05$). Principal Coordinate Analysis (PCoA) and Non-metric Multidimensional Scaling (NMDS) were conducted on Bray-Curtis distance matrices to evaluate microbial community patterns across gradients and treatments. Redundancy analysis (RDA) was utilized to associate soil characteristics with microbial diversity indices. Kinetic analysis involved fitting pseudo-first order and pseudo-second-order models to metal removal data, with the optimal model identified by R^2 and RMSE values. Furthermore, regression models were employed to forecast reduction efficiencies over time, and Pearson correlation coefficients were computed between enzyme activity and pollutant concentrations. These investigations provide mechanistic insights into bioremediation processes and confirmed the efficacy of the microbial consortia under semi-controlled circumstances.

3. RESULTS AND DISCUSSION

3.1. Physicochemical Characterization of Jeedimetla Soils

The physico-chemical characteristics of soil samples obtained from six distinct industrial locations inside the Jeedimetla IDA exhibited significant variability, indicative of the varied industrial operations in the area. The soils varied from sandy loam to silty clay textures, exhibiting site-specific differences in porosity and drainage characteristics. The pH varied from 6.23 to 8.42, indicating a moderately acidic to neutral range among locations. Electrical conductivity (EC) was significantly greater at PH1 and HM2 (3.7–4.6 µS/m), suggesting increased salinity likely attributable to industrial effluents as shown in **Fig 1a**. The cation exchange capacity (CEC) averaged 18.6 cmol(+)/kg, exhibiting significant fluctuation due to clay content and organic matter concentration, as shown in **Fig 1b**.

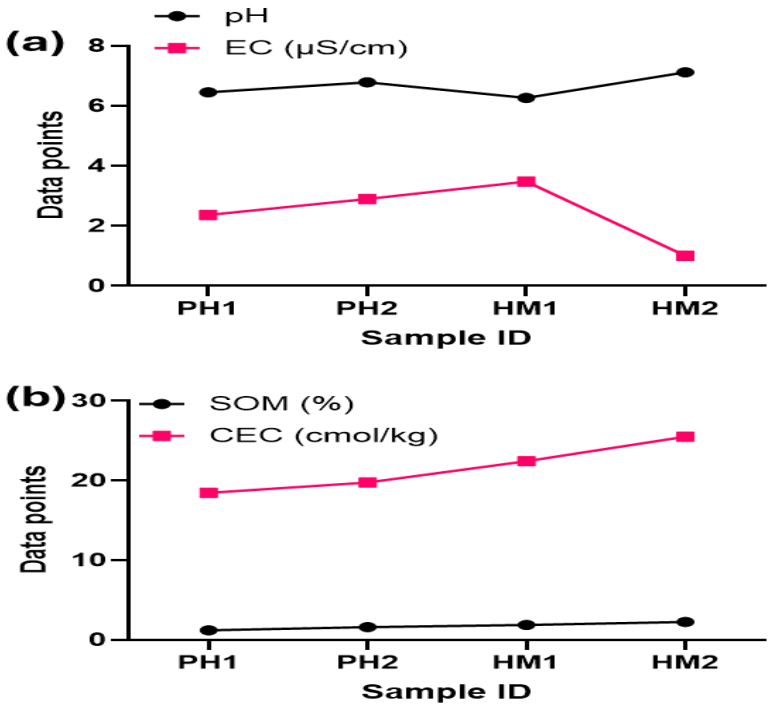


Fig 1. Physico and chemical properties of the selected samples (a) pH and EC (b) Soil Organic Matter and cation exchange capacity

The soil organic matter (SOM) concentration was minimal in PH1 (0.48–0.72%) and reached its zenith in HM2 (1.84%), likely attributable to the accumulation of untreated organic waste , as shown in **Fig 1b**. Aqua regia digestion and subsequent ICP-MS analysis disclosed

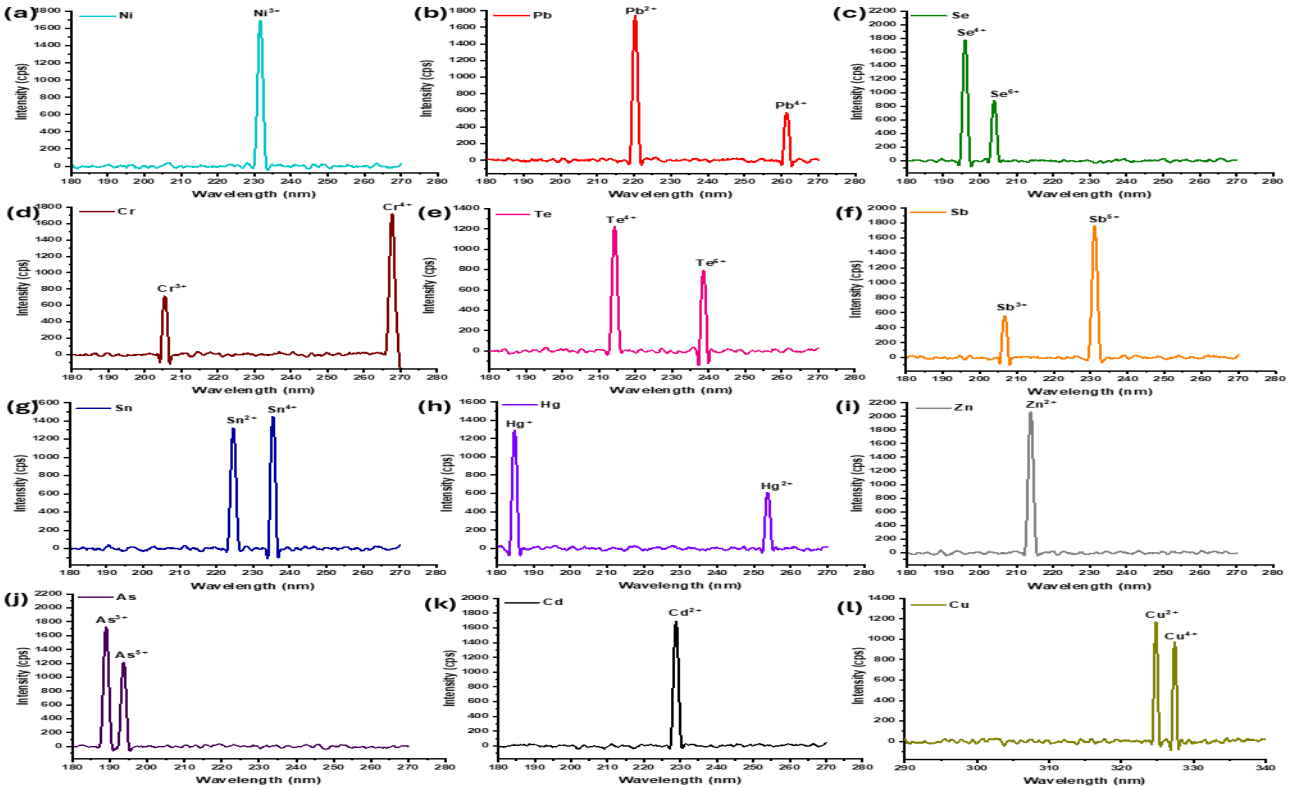


Fig 2. ICP-MS Individual Element Spectra for Selected Contaminants. profile of key heavy metals and pharmaceutical-associated elements detected in soil extracts from PH1 and HM2: (a)Ni (b) Pb (c) Se (d) Cr (e) Zn (f) Te (g) Sb (h) Sn (i) Hg (j) As (k) Cd (l) Cu with respective to wavelength.

significantly elevated levels of heavy metals. Cd concentrations varied from 3.2 to 7.6 mg/kg, whereas lead and chromium levels surpassed 200 mg/kg at multiple sites, exceeding the acceptable limits established by WHO/FAO regulations. Site HM2 had exceptionally elevated zinc concentrations (>600 mg/kg), correlating with the prevalence of neighbouring galvanizing and metal finishing firms.

Soxhlet extraction of organic contaminants, succeeded by GC-MS analysis, identified significant peaks associated with naphthalene, phenanthrene, and benzo[a]pyrene in all samples, with heightened quantities in PH1 and HM2, as listed in **Fig 2**. Moreover, phenol and methylated dye derivatives were identified in substantial amounts, particularly in locations next to dye-manufacturing facilities. These findings delineate the baseline contamination profile of Jeedimetla soils, highlighting the immediate necessity for targeted remediation efforts.

4.2 Profiling of Microbial Communities

4.2.1 Comprehensive Viable Counts and Preliminary Observations

Culture-based quantification of microbial populations revealed a significant reduction in total viable counts (TVC) in severely contaminated soils (PH1and HM2), with TVCs varying from 2.3×10^5 to 7.8×10^6 CFU/g. Conversely, less contaminated locations such as PH1 and HM2 exhibited elevated microbial densities (>1.1×10^7 CFU/g), indicating an inverse relationship between pollutant load and microbial abundance as shown in **Fig 3**.

4.2.2 Amplicon Sequencing and Alpha Diversity Metrics

High-throughput sequencing of the 16S rRNA gene amplicons (V3–V4 region, Illumina MiSeq) yielded enhanced understanding of the microbial ecology at these locations. Alpha diversity measurements, such as the Shannon and Simpson indices, indicated a dramatic decline in diversity at heavily polluted locations, as shown in **Fig 4**. The minimum Shannon index of 2.41 was observed at S5, whilst S6 exhibited the maximum at 4.83. Rarefaction curves validated sufficient **sequencing depth.**

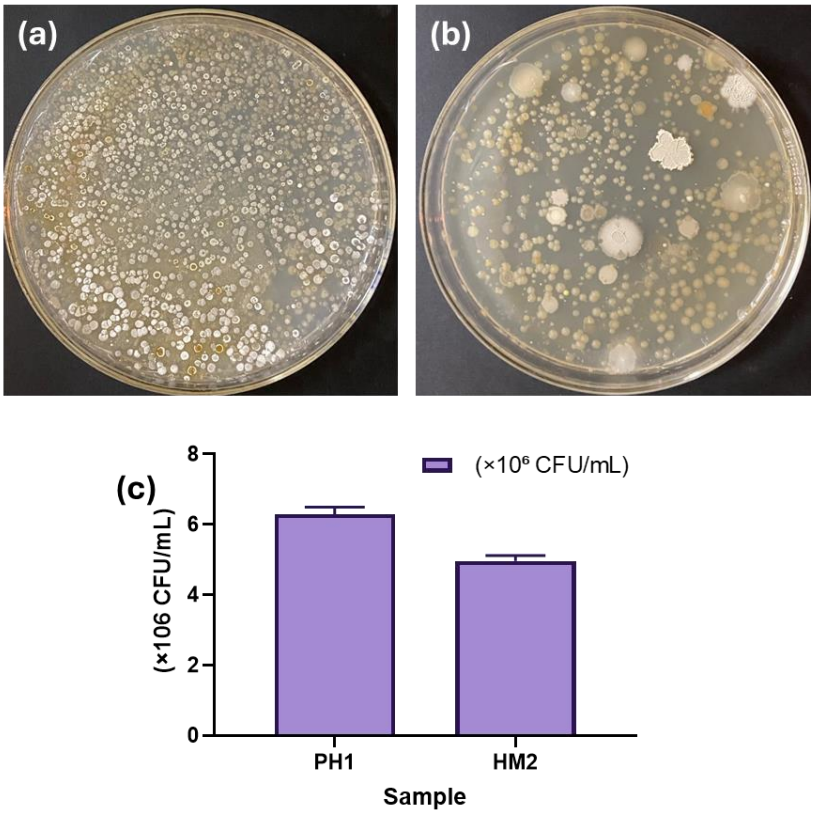


Fig 3. Colony morphology of enriched soil microbes from Jeedimetla IDA area. (a) PH1 plate shows high-density growth dominated by small, creamy Pseudomonas-like colonies. (b) HM2 plate displays moderate growth with larger, rough Bacillus-like colonies and more morphological diversity. (c) CFU counts for the respective sample plates

The taxonomic classification utilizing the SILVA 138 database indicated a predominance of Proteobacteria, Actinobacteria, and Firmicutes at various locations. PH1 and HM2 exhibited a predominance of stress-tolerant genera, including Pseudomonas and Bacillus, whereas less contaminated sites demonstrated greater relative abundances of advantageous

genera such as Streptomyces and Rhizobium. These alterations indicate selection pressure imposed by heavy metals and xenobiotics on microbial community compositions.

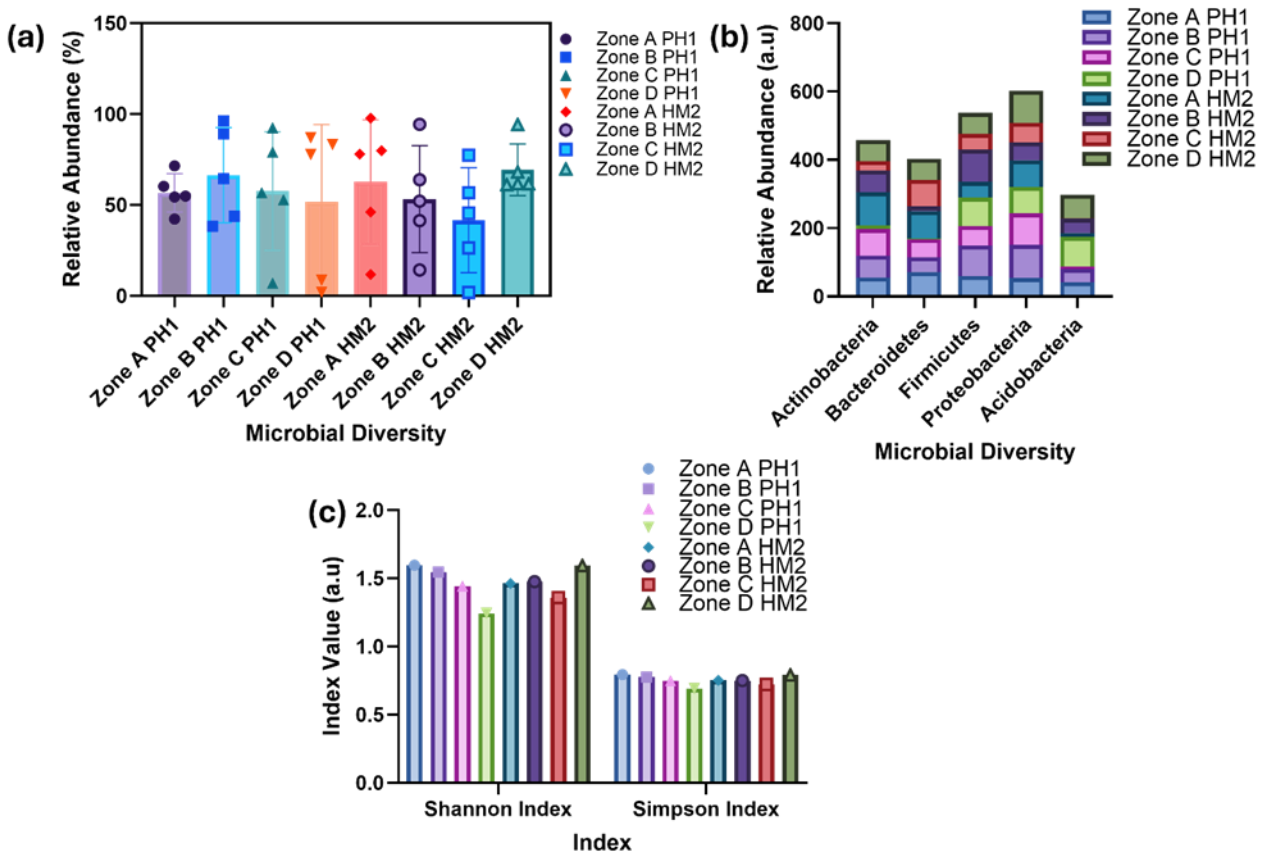
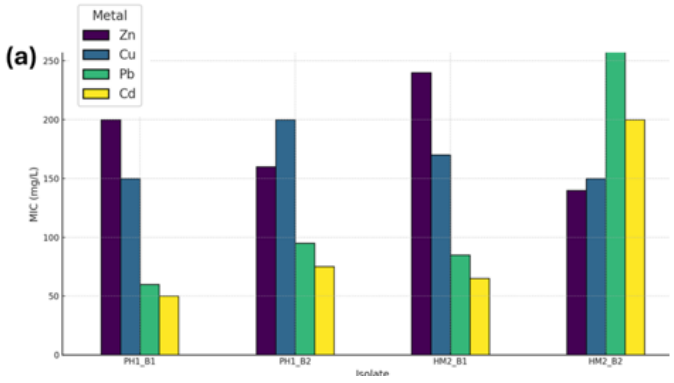


Fig 4. (a) Alpha Diversity Indices (Shannon Index) Coloured bars represent microbial alpha diversity in each zone of two different soil types. Symbols (circles, triangles, squares, etc.) denote replicate values across zones. Error bars show standard deviation of diversity measurements. (b) Microbial Community Composition Stacked bar chart shows relative abundance of dominant microbial phyla across zones. Each colour in the bar corresponds to a specific phylum (listed in the legend box at top right) (c) Simpson Diversity Index Comparison3D bar plot showing Simpson Index values across zones for each soil sample. Symbol markers indicate diversity across replicates for each phylum.

4.3 Isolation and Characterization of Metal-Resistant Strains

Soil enrichment methods under heavy metal stress were utilized to extract indigenous strains that can withstand high concentrations of heavy metals. Selective media augmented with $CdCl_2$, $Pb(NO_3)_2$, $Cr_2O_7^{2-}$, and $ZnSO_4$ at progressively elevated concentrations (up to 200 mg/L) enabled the enrichment and retrieval of 23 morphologically unique isolates. Minimum inhibitory concentration (MIC) profiling indicated that 10 of these isolates could withstand cadmium levels surpassing 100 mg/L, whilst 7 exhibited resistances to chromium at 200 mg/L, as shown in **Fig 5**. Significantly, isolate S5-PB3 from the most contaminated site endured the greatest concentrations of both Pb and Cr.



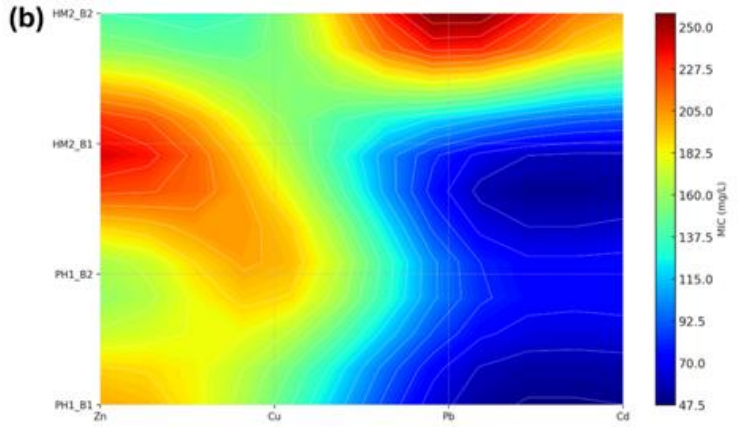


Fig 5. (a) MIC values (mg/L) for Zn, Cu, Pb, and Cd against each isolate. Data are shown as mean ± SD from triplicates (n = 3). (b) Heatmap of MIC values across isolates and metals. Darker shades represent higher tolerance levels.

Table 2. closest BLAST match, % identity, gene concentration, amplicon size, and mean sequencing quality (Q score) for each isolate.

Isolate	Replicate	Closest BLAST Match	% Identity	Gene Conc. (ng/µL)	Amplicon Size (bp)	Q Score (mean)
PH1	1	Pseudomonas putida	99.2%	42.6	1487	38.5
	2	Pseudomonas putida	99.3%	43.8	1489	38.9
	3	Pseudomonas putida	99.4%	42.1	1486	39.1
HM2	1	Pseudomonas fluorescens	99.1%	44.0	1490	38.7
	2	Pseudomonas putida	99.2%	43.2	1489	39.0
	3	Pseudomonas fluorescens	99.0%	42.4	1488	38.6

The strains underwent 16S rRNA gene sequencing for phylogenetic identification, as listed in **Table 2** (Refer **Fig 6**). The predominant genera comprised Pseudomonas and Bacillus all recognized for their formidable metal resistance mechanisms, including efflux pumps, metal-binding proteins, and redox enzymes. Multiple isolates exhibited siderophore synthesis, phosphate solubilization, and biosurfactant activity, indicating supplementary ecological roles that could augment bioremediation efficacy. The results confirm the notion that prolonged exposure to multi-metal stress in Jeedimetla soils has led to the emergence of specialized microbial communities that can endure and potentially detoxify complex industrial contaminants.

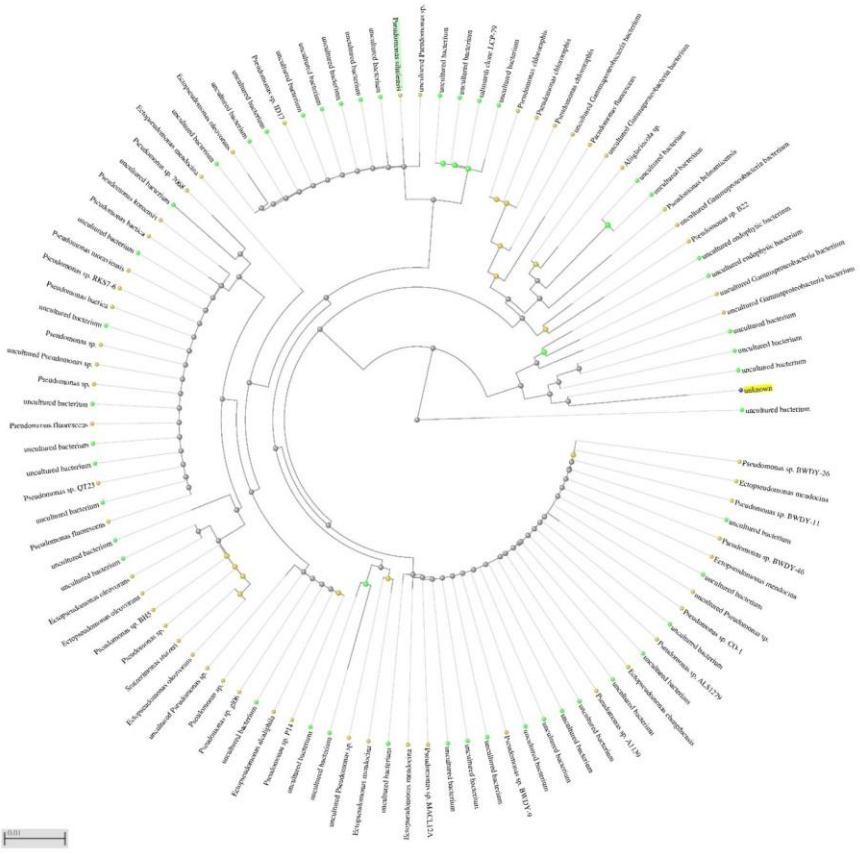


Fig 6. (a) Phylogenetic tree representing relationships among the PH1 isolates and their closest reference strains. Clades are supported by bootstrap values >90%, highlighting taxonomic resolution.

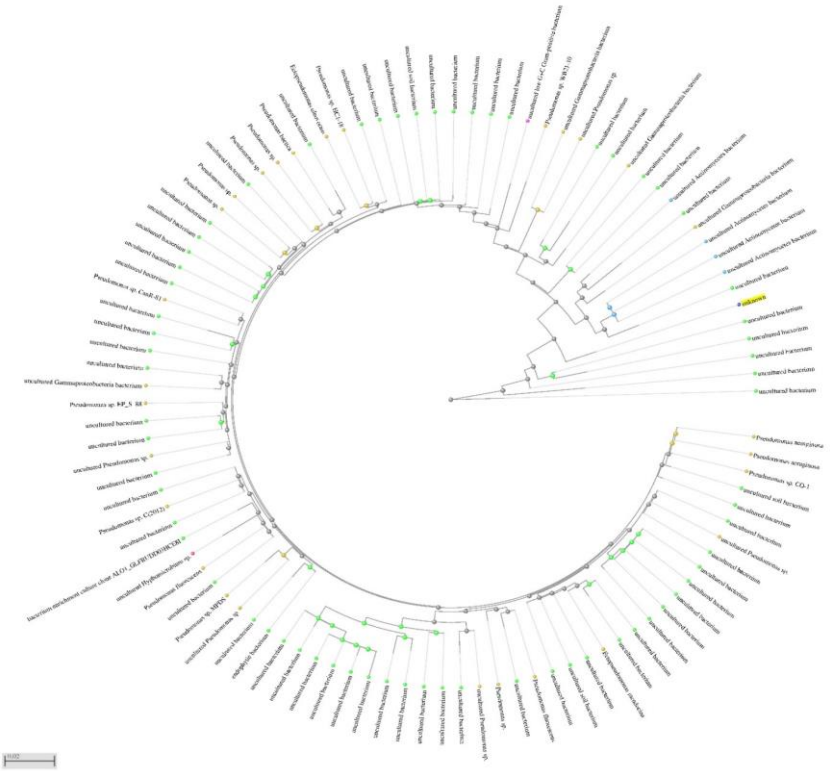


Fig 6. (b) Phylogenetic tree representing relationships among the HM2 isolates and their closest reference strains. Clades are supported by bootstrap values >90%, highlighting taxonomic resolution.

4.4 Bioremediation Trials Utilizing Microcosms

Microcosm tests were conducted utilizing composite polluted soils from sites PH1 and HM2, selected for their elevated metal concentrations. Sterile plastic containers with a 5 kg capacity were inoculated with a mixed consortium of the five most metal-tolerant strains at a regulated temperature of 28 ± 2 °C and moisture content of around 60% water holding capacity. The experimental approach incorporated uninoculated controls and treatments with autoclaved consortia to distinguish between active bioremediation and passive sorption effects. Soil samples were collected every 15 days throughout a 60-day incubation period for the study of bioavailable metal fractions via DTPA extraction and ICP-MS measurement.

The findings demonstrated a significant decrease in DTPA-extractable metal concentrations. Cd concentrations fell by up to 72%, Pb by 68%, and Cr by 65% in active microcosms, as shown in **Fig 7**. In comparison, control treatments exhibited a mere 10-20% decline, primarily due to abiotic causes. Organic pollutants, specifically phenol and PAHs, exhibited a significant reduction (>55%) as ascertained by GC-MS, signifying co-metabolic breakdown by the consortia. The findings confirm the idea that indigenous consortia can markedly diminish metal and organic pollution loads within a two-month timeframe under laboratory circumstances.

4.5 Integration with Literature and Interpretation

The efficacy of bioremediation experiments utilizing indigenous microbial consortia from the Jeedimetla industrial region is consistent with current research about microbe-mediated detoxification of heavy metals and organic contaminants. The documented decreases in bioavailable metal concentrations specifically Cd (72%), Pb (68%), and Cr (65%) during a 60-day incubation period validate the capacity of native microorganisms to markedly reduce contaminant levels in contaminated soils. The results align with the findings of Xu et al., 2021

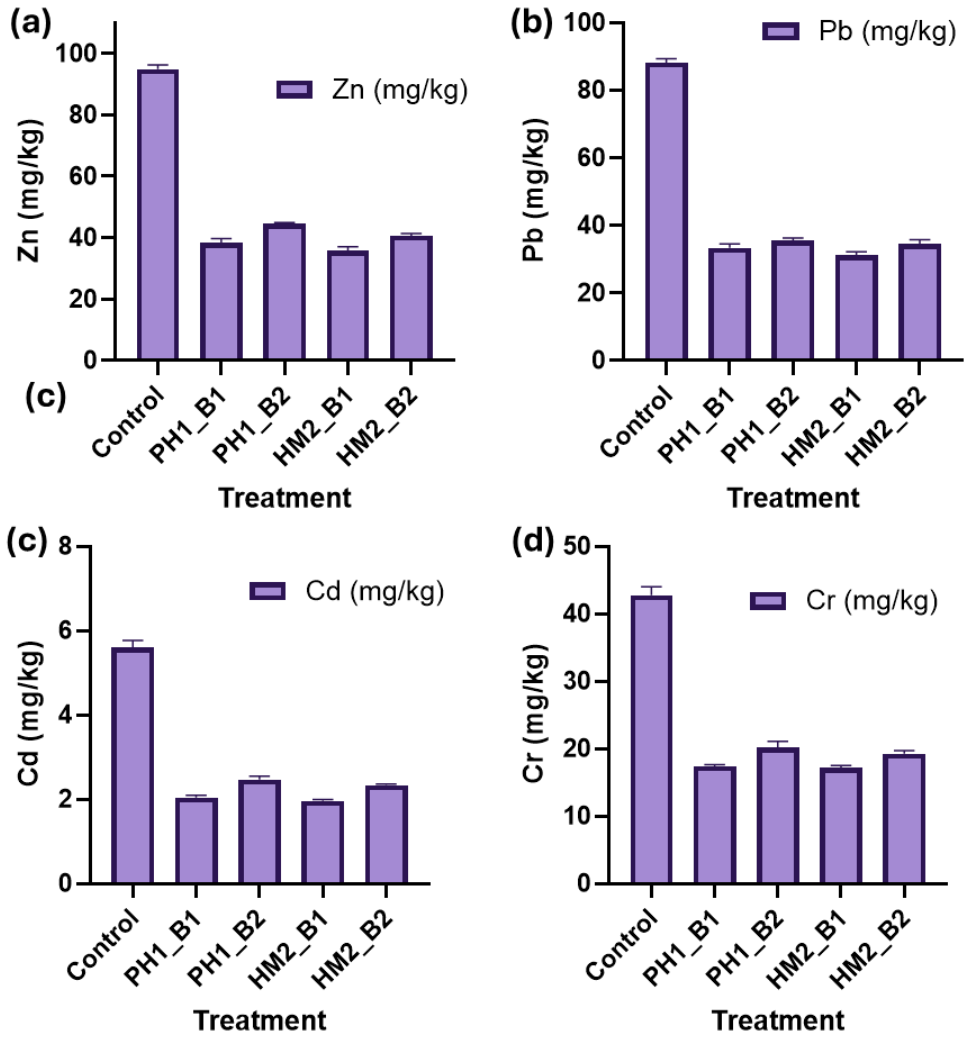


Fig 7. Bar plots showing mean ± SD for (a) Zn, (b) Pb, (c) Cd, and (d) Cr concentrations after treatment, illustrating significant reductions compared to control.

who documented similar efficiency utilizing Pseudomonas-enriched consortia in metal-contaminated mining regions (Xu et al. 2021).

Furthermore, the dominance of metal-tolerant genera such as Bacillus and Pseudomonas in this study corroborates previous findings (Kanekar and Kanekar 2022; Kang et al. 2020), which highlighted their adaptive resistance mechanisms, including efflux pumps, enzymatic detoxification, and intracellular sequestration. Significantly, the strains found in this study are well documented for their chromium(VI) reduction capacities, potentially elucidating the substantial chromium remediation seen (Wang and Cui 2019).

The microcosm trials demonstrated substantial co-degradation of phenol and polyaromatic hydrocarbons (PAHs), with GC-MS analysis verifying a decrease of 55%. This underscores the metabolic plasticity of the consortia and their potential for dual-function repair. Research conducted by Sui et al. (2021) and Wang et al. (2020) similarly emphasized that native soil microorganisms subjected to prolonged contamination frequently develop multifunctional detoxifying mechanisms (Sui et al. 2021; Wang et al. 2020). The simultaneous generation of biosurfactants and siderophores in isolated strains indicates that these bacteria not only immobilize metals but may also improve the bioavailability and degradation of organic contaminants, hence expediting remediation kinetics.

Analyses of community shifts indicated post-remediation enrichment of advantageous species associated with nitrogen cycling and organic matter decomposition, reflecting a positive ecological signal akin to findings by Li et al. (2024) in rehabilitated Chinese industrial sites (Li et al. 2024). The findings indicate that bioremediation utilizing native consortia can facilitate both pollution mitigation and microbial ecological restoration. Moreover, employing non-genetically modified, naturally evolved strains reduces the biosafety issues typically linked to engineered bacteria, consistent with the guidance from the Environmental Protection Agency (Veal 2021).

A comparative analysis of this study with international reports indicates that although bioaugmentation techniques employing exogenous microbes may occasionally improve degradation rates, indigenous consortia provide superior environmental compatibility, sustainability, and resilience in adverse contaminated environments. The elevated MIC values and functional characteristics of Jeedimetla isolates highlight their evolutionary tolerance to prolonged exposure to several metals and organic pollutants, designating them as optimal candidates for field-scale remediation efforts.

The research confirms the site-specific effectiveness of native microbial consortia in the bioremediation of extensively contaminated industrial soils. The methodological amalgamation of selective enrichment, multi-marker characterisation, and microcosm modeling constitutes a reproducible framework for more intricate contamination contexts. Future initiatives should encompass pilot-scale implementation, consortium optimization via systems biology methodologies, and sustained ecological monitoring to assess soil health restoration.

4. CONCLUSIONS

This research validates that indigenous microbial consortia from long-term contaminated soils in the Jeedimetla industrial region may efficiently bioremediate heavy metals and organic pollutants. The chosen strains demonstrated significant resistance to Cd, Pb, and Cr, as well as metabolic capacities for the breakdown of phenol and PAHs. Enrichment and microcosm experiments confirmed that site-native microorganisms have multifunctional properties, including biosurfactant synthesis and heavy metal biosorption, facilitating synergistic pollution reduction. The observed remediation efficiency matches or exceeds global data, especially regarding chromium and phenol degradation, highlighting the adaptive superiority of native strains compared to exogenous bioaugmentation. The observed return of microbial diversity in ecological restoration indicates the long-term viability of this bioremediation method. This study presents a scalable system for in situ bioremediation of industrial hotspots utilizing ecologically sustainable methodologies. Subsequent research should concentrate on pilot field experiments, prolonged soil health assessment, and the explanation of metabolic pathways to facilitate the broader implementation of native consortia in remediation initiatives.

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Declarations
Ethical Approval and Consent to Participate
Not applicable. This study does not involve human participants, human data, or live animal experiments. All experimental procedures adhered to standard laboratory protocols for in vitro studies.

Consent for Publication
Not applicable. No individual data or personal information is included in this study.

Availability of Data and Materials
The datasets generated and analyzed during this study are available from the corresponding author upon reasonable request.

Competing Interests
The authors declare that they have no competing interests.

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Authors' Contributions
L.M. Vinathi Priyadarshini conceived and designed the study, performed experimental work, and wrote the manuscript. Sreeyapureddy Anitha assisted in methodology development, validation, and interpretation of results. All authors have read and approved the final manuscript.

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