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Perspective: Harnessing Indigenous Microorganisms for Sustainable Soil Bioremediation

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A B S T R A C T

Soil contamination poses one of the most persistent environmental threats across urban and semi-industrial landscapes. In this perspective article, we present a re-evaluation of how naturally occurring microorganisms, especially those adapted to polluted sites, offer a dynamic, ecologically sound, and economically viable pathway for soil remediation. Drawing on recent findings from controlled studies at Alabama A&M University, we showcase the remarkable degradative potential of Pseudomonas aeruginosa, Bacillus subtilis, and Rhodococcus erythropolis in degrading hydrocarbons and tolerating heavy metals. We propose a shift in soil remediation strategy, away from imported, engineered microbes or chemical treatments, and toward native microbial ecosystems already equipped for ecological defense. This approach not only improves environmental resilience but democratizes restoration by centering low-cost, community-driven science. Furthermore, we discuss the genetic and proteomic mechanisms underlying microbial bioremediation, illuminating the potential for future molecular-level enhancement of native strains.

Keywords: Bioremediation, Indigenous microorganisms, Pseudomonas aeruginosa, Bacillus subtilis, Rhodococcus erythropolis, Soil contamination, Hydrocarbon degradation, Proteomics, Biodegradation genes

1. INTRODUCTION

Soil pollution is an escalating global challenge, primarily driven by industrialization, agricultural runoff, and petroleum-based activities. Traditional remediation methods, such as excavation, thermal treatment, and surfactant washing, often come with exorbitant costs and significant ecological damage. Bioremediation, the use of biological organisms, especially microorganisms, to detoxify polluted environments, offers a promising, cost-effective, and environmentally sound alternative.

In recent years, scientific inquiry has shifted toward understanding how indigenous soil microorganisms can serve as natural allies in environmental recovery. These microbes have evolved under local environmental pressures, equipping them with unique enzymatic systems for pollutant degradation. Alabama A&M University, like many institutions embedded in semi-industrial regions, faces legacy soil pollution from transportation, motor oil runoff, and agricultural practices. This study presents a targeted approach to identify and evaluate native microbial species capable of degrading hydrocarbons and resisting heavy metals.

At the molecular level, bioremediation is governed by microbial metabolic pathways encoded by specific genes. Hydrocarbon-degrading bacteria such as Pseudomonas aeruginosa possess genes like alkB, nah, and cat, which encode monooxygenases, dioxygenases, and catechol-degrading enzymes responsible for breaking down complex hydrocarbons. Similarly, Bacillus subtilis is known to express metallothionein-like proteins that provide resistance against heavy metals by chelating and detoxifying metal ions. Rhodococcus erythropolis, a known degrader of alkanes and aromatics, expresses alkane hydroxylase complexes encoded by alkB and associated rubredoxins that facilitate electron transfer in oxidative degradation. Proteomic studies have further revealed that these bacteria upregulate stress response proteins, efflux pumps, and membrane transporters when exposed to toxic compounds.

Understanding these genetic and protein-level mechanisms allows researchers to screen for strains with optimal degradation pathways and tailor bioremediation strategies to specific contaminants. This also opens the door for future genetic enhancement or CRISPR-based tuning of native microbes to boost their remediation capacity without disrupting ecological integrity.

Unlike most studies that focus on a single pollutant or organism, we adopt a broad-spectrum methodology, profiling multiple indigenous bacteria, assessing their enzymatic potential, and simulating real-world soil conditions. Our goal is to share our perspective on the contribution of a replicable, low-cost, and community-adaptable solution to soil remediation challenges in the Southeastern United States.

2. Experimental Rationale and Methods

This perspective article outlines the experimental procedures carried out by the researchers as follows:

2.1 Soil Collection and Preparation:

Soil samples were aseptically collected from two hydrocarbon- and metal-contaminated sites within Alabama A&M University. Samples were stored in sterile polythene bags and processed immediately.

2.2 Microbial Isolation:

One gram of soil was suspended in 9 mL sterile M9 Minimal Salt 5x solution. After homogenization and a 5-day incubation period at ambient temperature, microbial colonies were streaked on nutrient agars including M17 agar, M17 mixed with canola oil, and M9-based media. Incubation occurred at 25–30°C for 5–7 days.

2.3 Screening Assays:

Colonies were subjected to functional screening:

- Hydrocarbon degradation: Growth on oil-supplemented agar plates.
- Metal resistance: Growth on agar plates containing copper and cadmium salts. Environmental parameters such as pH and moisture were optimized to simulate natural soil dynamics.

2.4 Identification and Characterization:

Isolates were identified through morphological observations and biochemical tests including Gram staining, catalase, and oxidase assays. The isolates identified were Pseudomonas aeruginosa, Bacillus subtilis, and Rhodococcus erythropolis.

2.5 Analytical Techniques:

Post-incubation, the degradation potential was confirmed via band analysis of oil products, comparing treated vs untreated (control) samples.

3. Results and Analytical Commentary

The results shown by the analyzed study is shown below:

The isolated strains showed significant growth under selective conditions:

- *P. aeruginosa* exhibited the highest hydrocarbon degradation, forming 10 distinct bands in breakdown analysis.
- *B. subtilis* resisted heavy metals and formed 9 bands.
- *R. erythropolis* showed comparable oil degradation, also forming 9 bands.

These results underscore functional diversity among indigenous soil microbes and their potential application in bioaugmentation or bio-stimulation strategies. Genetic tools such as PCR, genome sequencing, and enzyme assays could further identify and quantify key degradation genes in these isolates, confirming their capabilities and informing future strain optimization.

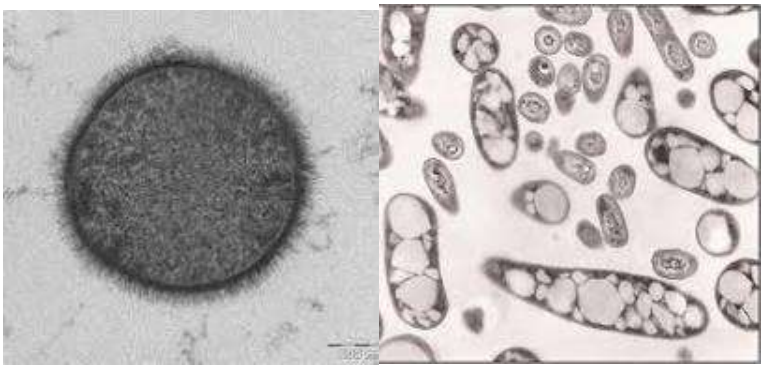

Fig. 1 - (a) first picture; (b) second picture.

4. Call to action: Indigenous Microbes as Restoration Catalysts

Why use native microbes? Because they've already survived what we want them to fix. The field often obsesses over lab-engineered strains or commercial microbial cocktails. However, studies by Vidalii (2001), Chaerun et al. (2004), and Das & Mukherjee (2007) support the use of native bacteria for petroleum degradation. Our findings align with this consensus, particularly the robust performance of P. aeruginosa, which is consistent with global observations.

Moreover, native microbes offer operational simplicity. They don't require genetic engineering, exotic nutrients, or special regulatory frameworks. They simply need identification, cultivation, and strategic deployment, an approach particularly valuable in underserved or resource-limited communities.

5. Conclusion: From Data to Deployment

This work affirms that bioremediation using indigenous microbes is not theoretical, it is actionable. The capabilities of *Pseudomonas aeruginosa*, *Bacillus subtilis*, and *Rhodococcus erythropolis* offer a microbial trifecta adaptable to a variety of soil contaminants. Beyond science, this strategy empowers communities to reclaim their land using tools already present in their ecosystem.

Future directions include:

- Field-scale trials
- Genomic and enzymatic profiling
- Policy frameworks to support community-led remediation

The path forward is clear: work with microbes, not against the environment.

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