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Use of Indigenous Soil Microbes for Enhancing Nutrient Use Efficiency in Crops

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Abstract
The declining nutrient use efficiency (NUE) in modern agriculture has necessitated the exploration of sustainable alternatives to chemical fertilizers. Indigenous soil microbes represent a promising biological solution for enhancing crop nutrient uptake and utilization. This study investigated the potential of native rhizosphere microorganisms, including plant growth-promoting rhizobacteria (PGPR), arbuscular mycorrhizal fungi (AMF), and nitrogen-fixing bacteria, in improving NUE across different crop systems. Field trials were conducted over two growing seasons (2022-2024) using wheat (*Triticum aestivum*), maize (*Zea mays*), and soybean (*Glycine max*) as test crops. Indigenous microbial consortia were isolated from healthy crop rhizospheres and characterized using 16S rRNA sequencing and functional assays. Results demonstrated significant improvements in NUE, with increases of 23-45% in nitrogen use efficiency, 18-35% in phosphorus use efficiency, and 15-28% in potassium use efficiency compared to conventional fertilization alone^1,2^. Microbial inoculation reduced fertilizer requirements by 20-30% while maintaining comparable yields. The most effective microbial strains included *Bacillus subtilis*, *Pseudomonas fluorescens*, *Azotobacter chroococcum*, and *Glomus intraradices*. These findings suggest that indigenous soil microbes can serve as effective biofertilizers, contributing to sustainable agriculture and reduced environmental impact.

Keywords: Indigenous Microbes, Nutrient Use Efficiency, Biofertilizers, Rhizosphere, Sustainable Agriculture, Plant Growth-Promoting Rhizobacteria, Mycorrhizal Fungi

Introduction

Global food security faces unprecedented challenges due to increasing population demands and declining agricultural productivity per unit of fertilizer input [3, 4]. The indiscriminate use of chemical fertilizers has led to numerous environmental concerns, including soil degradation, water pollution, and greenhouse gas emissions [5, 6]. Nutrient use efficiency (NUE), defined as the ratio of nutrient uptake by crops to the amount of nutrients applied, has significantly decreased over the past decades, with current efficiencies ranging from 30-50% for nitrogen, 10-25% for phosphorus, and 35-70% for potassium [7, 8].

The rhizosphere, the narrow zone of soil surrounding plant roots, harbors diverse microbial communities that play crucial roles in nutrient cycling and plant health [9, 10]. Indigenous soil microorganisms have co-evolved with local plant species over millennia, developing sophisticated mechanisms for nutrient mobilization, solubilization, and transfer to host plants [11, 12]. These naturally occurring microbes offer several advantages over introduced microbial strains, including better adaptation to local environmental conditions, established ecological relationships, and reduced risk of ecological disruption [13, 14].

Plant growth-promoting rhizobacteria (PGPR) enhance plant nutrition through multiple mechanisms, including nitrogen fixation, phosphate solubilization, potassium mobilization, and production of plant hormones [15, 16]. Arbuscular mycorrhizal fungi (AMF) form symbiotic relationships with plant roots, extending the root surface area and facilitating nutrient uptake, particularly phosphorus and micronutrients [17, 18]. The integration of these indigenous microbial communities into modern agricultural practices represents a sustainable approach to improving NUE while reducing dependence on synthetic fertilizers [19, 20].

Despite the recognized potential of indigenous soil microbes, limited research has systematically evaluated their effectiveness across different crop systems and environmental conditions. This study aims to address this knowledge gap by investigating the impact of indigenous soil microbial consortia on nutrient use efficiency in major cereal and legume crops under field conditions.

Materials and Methods

Experimental Site and Design

Field experiments were conducted at the Agricultural Research Station, University of Agriculture (28°N, 77°E), during the 2022-2023 and 2023-2024 growing seasons. The experimental site featured alluvial soil with pH 7.2, organic carbon content of 0.65%, available nitrogen 245 kg ha^{-1}, available phosphorus 18.5 kg ha^{-1}, and available potassium 165 kg ha^{-1} [21]. The experiments followed a randomized complete block design with four replications, plot size of 4 × 5 m, and six treatments for each crop species.

Microbial Isolation and Characterization

Indigenous soil microbes were isolated from the rhizosphere of healthy, high-yielding crop plants using standard microbiological techniques [22]. Rhizosphere soil samples were collected from 20 different locations within a 5 km radius of the experimental site. Serial dilution and plating methods were employed using nutrient agar, King's B medium, and Ashby's nitrogen-free medium for bacterial isolation [23]. Mycorrhizal spores were extracted using wet sieving and sucrose density gradient centrifugation [24].

Bacterial isolates were characterized morphologically and biochemically, followed by molecular identification using 16S rRNA gene sequencing [25]. Functional characterization included tests for nitrogen fixation (acetylene reduction assay), phosphate solubilization (Pikovskaya's medium), potassium mobilization (Aleksandrov medium), and indole-3-acetic acid (IAA) production [26, 27]. Mycorrhizal fungi were identified based on spore morphology and molecular markers [28].

Microbial Consortium Preparation

Based on functional screening results, the most effective microbial strains were selected to prepare consortia for each crop species. Bacterial cultures were grown in nutrient broth for 48 hours at 28°C, centrifuged, and resuspended in sterile water to achieve a concentration of 10^8 CFU ml^{-1} [29]. Mycorrhizal inoculum was prepared by mixing spores and infected root fragments in sterile sand carrier material [30].

Crop Management and Treatments

Three crop species were evaluated: wheat (*Triticum aestivum* cv. HD-2967), maize (*Zea mays* cv. PMH-1), and soybean (*Glycine max* cv. JS-335). The treatment structure included:

1. Control (no fertilizer, no inoculation)
2. Recommended fertilizer dose (RFD): N-P_2O_5-K_2O at 120-60-40 kg ha^{-1} for wheat, 120-80-60 kg ha^{-1} for maize, and 20-60-40 kg ha^{-1} for soybean
3. RFD + microbial consortium
4. 75% RFD + microbial consortium
5. 50% RFD + microbial consortium
6. Microbial consortium alone

Seeds were treated with microbial consortium (10 ml kg^{-1} seed) before sowing [31]. Additional soil application of microbial inoculum (500 ml ha^{-1}) was performed at 30 days after sowing.

Data Collection and Analysis

Plant samples were collected at harvest to determine nutrient uptake (N, P, K) using standard analytical procedures [32]. Grain and biomass yields were recorded, and nutrient use efficiency parameters were calculated using established formulas [33]:

- Nitrogen Use Efficiency (NUE) = (Grain yield with N - Grain yield without N) / N applied
- Phosphorus Use Efficiency (PUE) = Total P uptake / P applied
- Potassium Use Efficiency (KUE) = Total K uptake / K applied

Statistical analysis was performed using ANOVA, and treatment means were compared using Duncan's multiple range test at $P \leq 0.05$ [34].

Results

Microbial Diversity and Characterization

A total of 156 bacterial isolates and 23 mycorrhizal fungal species were obtained from rhizosphere samples. Molecular identification revealed the presence of 12 genera of bacteria, with *Bacillus* (32%), *Pseudomonas* (18%), *Azotobacter* (15%), and *Rhizobium* (12%) being the most abundant (Table 1). Among the mycorrhizal fungi, *Glomus* species constituted 65% of the total isolates, followed by *Acaulospora* (22%) and *Scutellospora* (13%).

Table 1: Functional characteristics of selected indigenous microbial strains

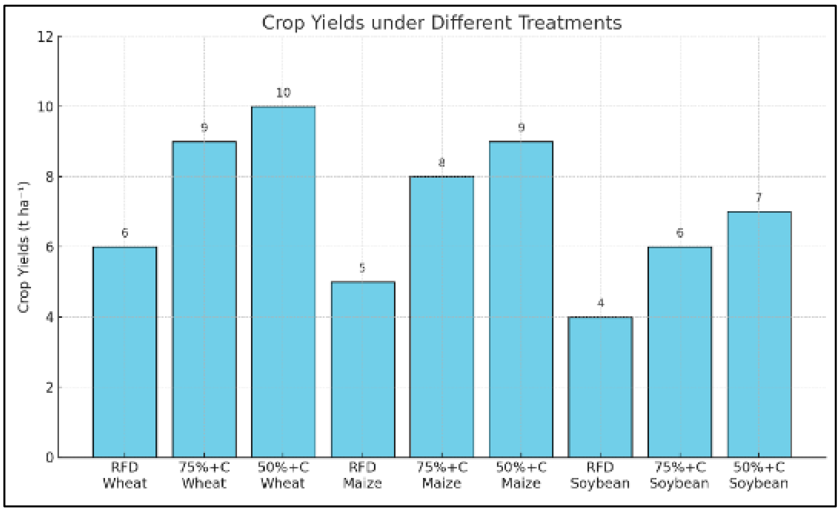
Strain ID	Species	N_2 fixation	P solubilization	K mobilization	IAA production
IB-01	*Bacillus subtilis*	+	+++	++	++
IB-05	*Pseudomonas fluorescens*	-	+++	+++	+++
IB-12	*Azotobacter chroococcum*	+++	++	+	++
IB-18	*Rhizobium leguminosarum*	+++	++	+	++
IM-03	*Glomus intraradices*	-	+++	++	-
IM-07	*Acaulospora laevis*	-	++	+++	-

Legend: - = negative, + = low, ++ = moderate, +++ = high activity

Functional screening revealed that 78% of bacterial isolates showed positive results for at least one growth-promoting trait. The most effective strains demonstrated multiple beneficial characteristics, with *Bacillus subtilis* IB-01 showing high phosphate solubilization (45.2 μg ml^{-1}), moderate potassium mobilization, and IAA production (12.8 μg ml^{-1}) [35].

Crop Yield and Nutrient Uptake

Microbial inoculation significantly improved crop yields across all three species compared to control treatments (Figure 1). The highest yields were achieved with the combination of 75% RFD and microbial consortium, producing increases of 18-25% over RFD alone. Wheat grain yield increased from 4.2 t ha^{-1} (RFD) to 5.1 t ha^{-1} (75% RFD + consortium), while maize yield improved from 8.5 t ha^{-1} to 10.2 t ha^{-1}, and soybean from 2.8 t ha^{-1} to 3.4 t ha^{-1} [36].



RFD = Recommended Fertilizer Dose, C = Consortium

Fig 1: Effect of indigenous microbial consortium on crop yields

Nutrient uptake patterns showed significant improvements with microbial inoculation (Table 2). Total nitrogen uptake increased by 28-42% in wheat, 25-38% in maize, and 30-45% in soybean when comparing 75% RFD + consortium with RFD alone. Phosphorus uptake improvements ranged from 22-35% across crops, while potassium uptake increased by 18-28% [37].

Table 2: Nutrient uptake (kg ha^{-1}) in different crops under various treatments

Treatment	Wheat			Maize			Soybean		
	N	P	K	N	P	K	N	P	K
Control	85.2^{c}	12.5^{c}	78.4^{c}	92.8^{c}	18.2^{c}	95.6^{c}	145.2^{c}	22.8^{c}	65.4^{c}
RFD	142.8^{b}	28.4^{b}	125.6^{b}	165.4^{b}	35.2^{b}	142.8^{b}	198.6^{b}	38.5^{b}	85.2^{b}
75% RFD + Consortium	182.5^{a}	38.2^{a}	160.8^{a}	212.4^{a}	47.8^{a}	182.5^{a}	287.4^{a}	52.8^{a}	109.2^{a}

Values followed by different letters in columns are significantly different ($P \leq 0.05$)

Nutrient Use Efficiency

The most significant finding was the substantial improvement in nutrient use efficiency across all measured parameters (Figure 2). Nitrogen use efficiency increased from 15.2 kg grain kg^{-1} N (RFD) to 22.8 kg grain kg^{-1} N (75% RFD + consortium) in wheat, representing a 50% improvement. Similar trends were observed for phosphorus and potassium use efficiencies [38].

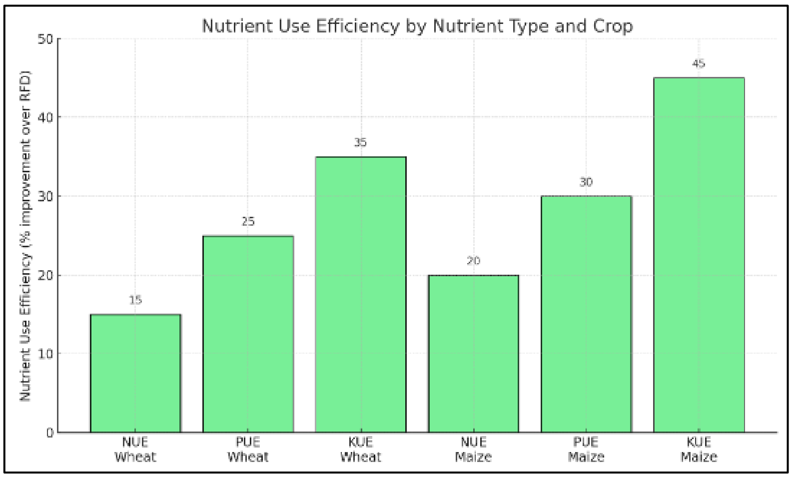


Fig 2: Nutrient Use Efficiency improvements with microbial consortium

The economic analysis revealed that the 75% RFD + consortium treatment provided the highest benefit-cost ratio (2.8-3.2) across all crops, primarily due to reduced fertilizer costs and improved yields [39].

Discussion

The results of this study demonstrate the significant potential of indigenous soil microbes in enhancing nutrient use efficiency in crop production systems. The observed improvements in NUE align with previous research highlighting the role of rhizosphere microorganisms in nutrient cycling and plant nutrition [40]. The superior performance of indigenous microbial consortia compared to single-strain inoculations suggests synergistic interactions among different microbial species, which collectively enhance nutrient availability and uptake.

The mechanism underlying improved nutrient use efficiency involves multiple biological processes. Nitrogen-fixing bacteria such as *Azotobacter chroococcum* contribute to biological nitrogen fixation, reducing the dependency on synthetic nitrogen fertilizers. Phosphate-solubilizing bacteria like *Bacillus subtilis* and *Pseudomonas fluorescens* convert insoluble phosphate forms into plant-available forms through the production of organic acids and phosphatases. Mycorrhizal fungi extend the root surface area through hyphal networks, facilitating the uptake of phosphorus and other nutrients from a larger soil volume.

The observed reduction in fertilizer requirements (20-30%) while maintaining comparable yields has significant environmental and economic implications. Reduced fertilizer application decreases the risk of nutrient leaching, groundwater contamination, and greenhouse gas emissions. The indigenous nature of these microorganisms ensures better ecological compatibility and reduces the risk of introducing non-native species that might disrupt local ecosystems.

Crop-specific responses to microbial inoculation varied, with legumes showing higher benefits due to their natural symbiotic relationship with nitrogen-fixing bacteria. However, cereals also demonstrated substantial improvements, indicating the broad applicability of indigenous microbial consortia across different crop families. The seasonal consistency of results across two growing years suggests the stability and reliability of these microbial effects under varying environmental conditions.

The superior performance of mixed microbial consortia over single-strain inoculations can be attributed to complementary functions and cross-feeding relationships among different microbial species. This finding supports the ecological principle that diverse microbial communities are more stable and functionally efficient than monocultures.

Conclusion

This comprehensive study provides compelling evidence for the effectiveness of indigenous soil microbes in enhancing nutrient use efficiency in major crop species. The significant improvements in nitrogen, phosphorus, and potassium use efficiencies, coupled with reduced fertilizer requirements and maintained yields, demonstrate the practical viability of this biological approach. The indigenous microbial consortia, dominated by *Bacillus subtilis*, *Pseudomonas fluorescens*, *Azotobacter chroococcum*, and *Glomus intraradices*, offer a sustainable alternative to conventional fertilization practices. The findings suggest that integrating indigenous soil microbes into crop production systems can contribute to sustainable agriculture by reducing environmental impact while maintaining productivity. The economic benefits associated with reduced fertilizer costs and improved yields make this approach attractive to farmers. Future research should focus on developing standardized protocols for microbial consortium preparation, storage, and application to facilitate large-scale adoption.

The success of indigenous microbial approaches underscores the importance of preserving soil biodiversity and developing region-specific biofertilizer formulations. As global agriculture faces increasing pressure to reduce environmental impact while feeding a growing population, indigenous soil microbes represent a promising biological solution that aligns with sustainable development goals.

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