Review Article Open Access

Rhizosphere Microbial Diversity in Legume Cropping Systems

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Computational Molecular Biology, 2026, Vol.16, No.3 doi: 10.5376/cmb.2026.16.0014

Received: 23 Apr., 2026

Accepted: 28 May, 2026

Published: 12 Jun, 2026

Preferred citation for this article:

Shen W.L., Luo D., and Zhou X.H., 2026, Rhizosphere microbial diversity in legume cropping systems, Computational Molecular Biology, 16(3): 194-204 (doi: 10.5376/cmb.2026.16.0014)

Abstract Rhizospheric microorganisms associated with leguminous crops constitute a vital component in maintaining the stability of agroecosystems and promoting healthy plant growth; their diversity and functions directly influence soil nutrient cycling, nitrogen fixation efficiency, and crop stress tolerance. This study presents a comprehensive review of rhizospheric microbial diversity in leguminous crops, systematically analyzing the characteristics of the rhizosphere microenvironment, the composition of microbial communities, and their ecological functions. Particular emphasis is placed on exploring the roles of various microorganisms-including bacteria, fungi, and archaea-in plant nutrient uptake, disease suppression, and the maintenance of soil health. Furthermore, the article summarizes the primary factors influencing rhizospheric microbial diversity-such as plant genotype, tillage systems, fertilization methods, and environmental conditions-and introduces the application of modern research technologies, including high-throughput sequencing, metagenomics, and bioinformatics, in the study of rhizosphere microecology. Additionally, using soybean cropping systems as a case study, the paper analyzes variations in microbial community structure under different cultivation patterns and discusses their significance for sustainable agricultural development. Finally, this study outlines the challenges currently facing this field of research and identifies future directions-such as synthetic microbiomes, precision agriculture, and microbial engineering-with the aim of providing a theoretical foundation for the green and efficient production of leguminous crops and the effective management of agroecosystems.

Keywords Leguminous crops; Rhizospheric microorganisms; Microbial diversity; Symbiotic nitrogen fixation; Sustainable agriculture

1 Introduction

The rhizosphere, the narrow soil zone influenced by plant roots, harbors an immense and still largely unexplored diversity of microorganisms that shape plant nutrition, health, and soil functioning (Chukwuneme and Babalola, 2025). In legume-based systems, this belowground biodiversity underpins key agroecosystem services, particularly biological nitrogen fixation and improved soil fertility, making legumes central to sustainable agriculture and food security (Schaedel et al., 2021). Understanding how legumes assemble and interact with their rhizosphere microbiomes is therefore critical for designing low-input, high-efficiency cropping systems.

Research has established that the rhizosphere microbiome is a central driver of nutrient cycling, carbon sequestration, and ecosystem functioning in terrestrial systems. Microbial communities associated with plant roots form a “second genome” whose collective genes far exceed those of the host plant and are crucial for growth promotion, stress tolerance, and disease suppression. For legumes, the best-known interaction is the symbiosis with rhizobia, but it is now clear that non-rhizobial members of the rhizosphere and nodule microbiome also contribute to nodule formation, plant fitness, and broader agroecosystem benefits (Yang et al., 2024). Given the pressures of climate change and the need to reduce synthetic fertilizer inputs, harnessing this microbial diversity has major significance for sustainable intensification of legume cropping systems.

Recent advances in high-throughput sequencing and multi-omics approaches have transformed understanding of rhizosphere microbiomes by enabling cultivation-independent analysis of taxonomic and functional diversity (Chukwuneme and Babalola, 2025). Large-scale comparative studies show that legumes assemble rhizosphere communities with lower overall diversity but with strong enrichment of nitrogen-cycling taxa and nitrogen-fixing genes relative to non-legumes, revealing a pronounced functional specialization for nitrogen acquisition. At the