

4 Factors Influencing Rhizosphere Microbial Diversity

4.1 Plant genotype and species differences

Plant genetic variation shapes rhizosphere microbiome assembly by altering host filtering strength and the interface between rhizosphere and internal compartments. In *Medicago truncatula*, soil origin mainly structured rhizosphere communities, but plant genotype exerted strong effects in the root endosphere, indicating that different genotypes act as stronger or weaker microbial filters and influence which taxa progress inward (Brown et al., 2020). In soybean, soil type again dominated community composition, yet host genotype subtly “tuned” rhizosphere assembly and microbe-microbe interaction networks, demonstrating cooperative control by plant genetics and soil microbiome pool.

Species-level differences within legumes also generate distinct rhizosphere communities. Across five *Phaseolus* species, each recruited a characteristic bacterial assemblage, with notable contrasts in richness and dominant phyla; for example, *Phaseolus lunatus* showed the highest richness and an Acidobacteria-enriched rhizosphere, whereas Actinobacteria dominated several other species (Yang et al., 2023). More broadly, diversity in soil microbial community structure was greater among legume species than among grass species, and legumes generally supported higher bacterial diversity and enriched fungi, underscoring the strong niche differentiation imposed by legume species identity.

4.2 Agricultural management practices

Tillage and fertilization regimes alter soil structure, resources, and disturbance intensity, thereby reshaping rhizosphere-associated microbiomes in legume-based systems. In a long-term corn-soybean system, both tillage and fertility significantly shifted bacterial, fungal and oomycete communities, with no-till favoring ecological guilds such as arbuscular mycorrhizal fungi, mycoparasites, and nematophagous fungi, while conventional tillage promoted saprotrophs and plant pathogens. Fertilization further modified bacterial and fungal β -diversity and supported copiotrophic bacteria and *Fusarium* under conventional regimes, indicating that intensive inputs select for fast-growing competitors rather than mutualists (Srour et al., 2020).

Cropping sequences involving legumes also drive rhizosphere diversity and N-cycling potential. In sorghum systems, precropping with cowpea or soybean, compared with maize or no precrop, significantly altered rhizosphere bacterial α - and β -diversity and shifted key nitrogen-cycling genes (e.g., *amoC*, *narH*, *gltB*, *glnA*, *ureC*), with legume rotations enriching several N-transformation pathways (Enagbonma et al., 2025). In sugarcane rotations, soybean and peanut residues increased microbial biomass C, C mineralization, and nitrification capacity, although high-N soybean residues released more mineral N than low-N peanut residues, revealing crop- and residue-specific impacts on microbial functions linked to fertility (Paungfoo-Lonhienne et al., 2021).

4.3 Environmental and climatic factors

Environmental variables such as soil type, pH, and climate gradients strongly regulate rhizosphere microbial diversity and its functional consequences. Along an altitudinal and climatic gradient in mountain ecosystems, geographical and climatic factors directly and indirectly controlled rhizosphere bacterial and fungal diversity, with bacterial α -diversity and particular dominant taxa exerting strong positive or negative effects on soil multifunctionality. The balance of these effects determined net multifunctionality, and higher richness at the phylum level generally led to gains in multiple soil functions, highlighting the sensitivity of rhizosphere communities to long-term climatic contexts (Yang et al., 2023).

Among soil properties, pH is a particularly powerful predictor of rhizosphere bacterial diversity, structure, and function. In acidic crop soils, communities in pH < 5.5 versus > 5.5 clustered into distinct groups, with higher pH associated with greater bacterial abundance and diversity and more active nutrient-cycling functions (C, N, P, S) (Wan et al., 2020). In more acidic soils, bacterial interaction networks suggested reduced competition but downregulated functional genes, implying constrained ecosystem services and potentially lower crop yields when pH is not managed (Wan et al., 2020).