

plant demand; highly efficient symbioses can install endosphere and rhizosphere microbiomes that promote nutrient uptake beyond simple nutrient supply, including accumulation of beneficial Actinobacteria in roots (Lagunas et al., 2023). Over time, fixed nitrogen is transferred to soil through rhizodeposition, senescing roots, and residues, supporting non-legume crops and stimulating broader microbial activities in diversified systems (Qiao et al., 2024).

Excessive mineral N fertilization can suppress SNF by interfering with nodulation signaling, rhizobial chemotaxis to roots, and nitrogenase activity, thereby weakening the mutualism and altering rhizosphere microbial relationships (Abd-Alla et al., 2023). In contrast, organic inputs such as compost and vermicompost generally enhance nodulation, nodule biomass, plant growth, and yield, while improving soil biological quality and nitrogen availability (Mu et al., 2024). Free-living nitrogen-fixing bacteria in the legume rhizosphere, stimulated by legume-derived exudates (including flavonoids and coumarins), further contribute to N inputs and interact functionally with symbiotic rhizobia under intercropping or rotation schemes (Chen et al., 2022; Qiao et al., 2024).

3 Composition and Diversity of Rhizosphere Microbial Communities

3.1 Bacterial diversity in legume rhizospheres

Large-scale comparative analyses show that legume rhizospheres often exhibit lower bacterial α -diversity than non-legumes but are strongly enriched in nitrogen-cycling taxa and nitrogen-fixing genes, suggesting a specialized, function-driven bacterial assembly (Qin et al., 2025). Typical legume rhizospheres are dominated by Proteobacteria and Bacteroidetes, with notable representation of Bradyrhizobiaceae, Rhizobiaceae, and other diazotrophs, reflecting the central role of biological nitrogen fixation (Pivato et al., 2021; Yang et al., 2024). In intercropping systems, legume presence can shift bacterial communities in associated non-legume rhizospheres toward copiotrophic and nitrogen-transforming assemblages, often without major changes in overall diversity indices (Pang et al., 2022).

Cropping mode and fertilization regimes substantially modulate bacterial community richness, structure, and potential function in legume-involving systems. In hullless barley-pea mixed cropping, increasing nitrogen and phosphorus inputs caused a hump-shaped response in bacterial α -diversity, with mixed cropping supporting higher diversity than monocropping and enriching *Allorhizobium*-*Neorhizobium*-*Pararhizobium*-*Rhizobium* relative to cereal monoculture (Fu et al., 2023; Guo et al., 2024). Sugarcane-peanut and cereal-legume intercrops similarly increased bacterial richness and the diversity of nitrogen-fixing bacteria in rhizosphere and bulk soils compared with monocultures, aligning with improved crop performance and altered soil pH and phosphorus availability (Pang et al., 2022; Yang et al., 2023). These findings indicate that legume integration and moderate nutrient inputs can promote diverse, functionally advantageous bacterial consortia in the rhizosphere.

3.2 Fungal diversity and mycorrhizal associations

Arbuscular mycorrhizal fungi (AMF) are key fungal components of legume rhizospheres, enhancing phosphorus acquisition and stress tolerance while interacting with rhizobia-dependent nitrogen fixation (Alimi et al., 2021; Pires et al., 2021). Surveys of indigenous South African legumes revealed diverse AMF communities dominated by *Glomus* and *Acaulospora*, with species richness and spore density varying markedly among hosts and being strongly structured by soil properties such as texture and nutrient status (Alimi et al., 2025). Morphological assessments across leguminous and non-leguminous crops further identified *Acaulospora*, *Funneliformis*, *Gigaspora*, *Glomus*, and *Rhizophagus* as common AMF genera, with legume hosts often supporting higher spore counts and colonization frequencies, underlining their importance as AMF reservoirs (Pires et al., 2021).

Intercropping and integrated crop-livestock systems that include legumes can enhance AMF diversity, colonization, and inoculum potential in subsequent legume phases. In maize-soybean intercropping, AMF α -diversity in soybean rhizosphere soil increased relative to monoculture at comparable nitrogen levels, and *Glomus*-related taxa were dominant in both soil and roots, with their abundance responding to nitrogen inputs and crop identity (Figure 1) (Zhang et al., 2020; Alimi et al., 2021). In systems where grasses are intercropped with cowpea or pigeon pea, AMF spore density, colonization, and species richness in legume-associated rhizospheres