

and viruses dominate inter-root communities and are more sensitive to planting mode than fungi or archaea, with shifts in *Pseudomonas*, rhizobia and other genera across modes that favored either soybean or maize yields (Wang et al., 2024). In maize-soybean systems compared over three years, conversion from monocropping to intercropping increased microbiome network modularity and functional diversity and enriched genes for nitrate assimilation, nitrification and dissimilatory nitrate reduction, changes that were closely related to higher yields in intercropped soybean (Shu et al., 2024).

### 7.3 Implications for sustainable agriculture

Evidence from soybean systems indicates that managing rhizosphere microbiota offers powerful levers for sustainable intensification. Long-term comparisons of soybean continuous monocropping versus maize-soybean rotation show that both long-term continuous soybean (13 years) and rotation can elevate soil pH and available N, P, K, and increase network complexity, while enriching beneficial *Bradyrhizobium*, *Gemmatimonas* and *Mortierella* and reducing pathogenic *Fusarium* compared with short-term continuous soybean (Liu et al., 2020). Similarly, in wheat-soybean double-cropping, introducing wheat/soybean-wheat/maize rotations improved soybean yield and a soil fertility index and shifted rhizosphere fungi toward plant growth-promoting, nematophagous and biocontrol groups, while continuous wheat/soybean favored lignocellulose degraders and pathogens (Sun et al., 2022).

Conceptual and review work suggests that such cropping-based microbiome effects can be deliberately exploited. One framework proposes dividing rhizosphere microbiota into environment-dominated and plant genetic-dominated components, with agronomic practices (e.g., rotations, intercropping, reduced tillage) used to steer the former and breeding used to enhance the latter, thereby stabilizing beneficial consortia in crops like soybean (Xun et al., 2024). More broadly, rhizosphere microbiome engineering-using indigenous consortia and designed inoculants-has been highlighted as a route to reduce synthetic inputs, enhance yield and resilience, and align soybean production with long-term soil health and environmental sustainability goals (Mahmud et al., 2021).

## 8 Challenges, Future Perspectives, and Conclusions

Despite rapid methodological advances, major knowledge gaps limit the application of rhizosphere microbiomes in legume-based systems. A key challenge is the complex assembly mechanisms of rhizosphere communities, where environment-dominated and plant genetic-dominated components interact in ways that are still poorly quantified, especially under realistic field conditions. This complexity hampers prediction of microbiome responses to agronomic practices or legume genotypes, and constrains efforts to design stable microbial consortia for enhanced nitrogen fixation and stress resilience.

Translating microbiome insights into reliable bioinoculants also remains difficult. Many beneficial strains perform well in controlled experiments but fail under variable soils, climates, and management, in part because interactions with native microbiota and environmental heterogeneity are insufficiently understood. Challenges specific to nitrogen-fixing systems include the ecological competitiveness of inoculant strains, context-dependent performance of symbiotic and free-living diazotrophs, and the need to match microbial partners with host genetics and local microbiomes to achieve consistent field-level benefits.

Future rhizosphere research in legumes will likely focus on predictive and integrative frameworks that connect soil factors, plant genetics, and management to microbiome structure and function. Building data-driven, high-throughput models that quantify how soil properties and agronomic practices shape environment-dominated microbiome components is a priority for precise rhizosphere regulation in real cropping systems. At the same time, identifying genes and loci controlling plant genetic-dominated microbiome fractions will support breeding of “microbiome-assisted” legumes and potentially N-self-fertilizing crops.

There is also strong momentum toward microbiome engineering and synthetic communities tailored to legume growth stages and stresses. Multi-omics meta-analyses already reveal developmental stage-specific growth-promoting marker bacteria in legumes that could guide design of multi-species inoculants. Conceptual frameworks such as microbiome-mediated smart agriculture systems emphasize combining reduced tillage,