

7 Case Study: Rhizosphere Microbial Diversity in Soybean Cropping Systems

7.1 Overview of soybean rhizosphere microbiota

Soybean rhizospheres host complex, multi-kingdom microbial communities whose composition and function vary strongly across soils and regions. A metagenomic survey across 13 major soybean-producing regions in China identified over 43,000 microbial species (bacteria, archaea, fungi and viruses), with clear site-specific clustering and 556 hub taxa correlated with yield and involved in C, N, P and S cycling (Ren et al., 2025). Comparative work further shows that rhizosphere communities differ markedly from bulk soil, with enrichment of genera such as *Rhizobium*, *Novosphingobium*, *Phenylobacterium*, *Streptomyces* and *Nocardioides* and convergence in functional pathways linked to xenobiotic degradation, plant-microbe interactions and nutrient transport.

Soil background and plant genetics jointly modulate soybean rhizosphere assembly. Across contrasting soils and genotypes, soil type has the dominant effect, but soybean genotype subtly “tunes” recruitment and microbe-microbe networks, with wild *Glycine soja* maintaining higher rhizosphere diversity than domesticated lines (Figure 2). Other studies show that rhizocompartments (bulk soil, rhizosphere, roots, nodules) host distinct bacterial assemblages, and that rhizosphere networks include strong correlations between rhizobia and non-rhizobial taxa, which can in turn influence nodulation patterns and symbiotic efficiency (Han et al., 2020).

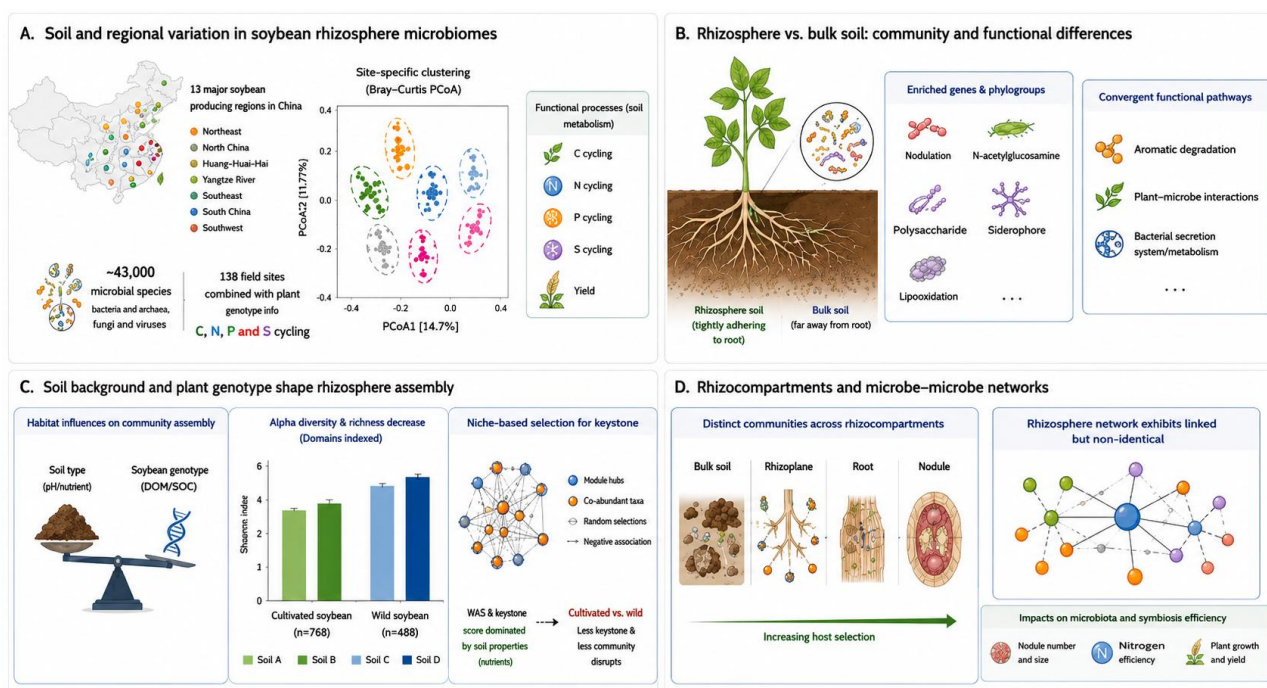


Figure 2 Multi-scale characterization of soybean rhizosphere microbiomes across contrasting soils, regions, and rhizocompartments

7.2 Effects of cropping patterns on microbial diversity

Cropping patterns substantially reshape soybean rhizosphere diversity, composition, and functional potential. In maize-soybean relay strip intercropping, soybean rhizosphere bacterial diversity increased compared with monoculture, with higher richness of *Pseudomonas*, *Bacillus* and other antagonists; several intercropping-derived strains suppressed *Fusarium* root rot and one *Pseudomonas chlororaphis* strain (IRHB3) promoted root growth and seedling survival under pathogen pressure (Chang et al., 2022). In coastal saline soils, soybean-corn intercropping altered soil C, N, P and salinity and significantly changed bacterial and fungal communities; intercropping increased Chao1 richness, shifted dominant phyla (Proteobacteria, Actinobacteria, Acidobacteria, Chloroflexi; Ascomycota, Mortierellomycota, Basidiomycota) and enriched taxa linked to nutrient cycling and bioremediation (Nyimbo et al., 2025).

At finer scales, belt/strip planting and intercropping layouts under field conditions also modulate multi-kingdom communities and link to yield traits. Metagenomic analysis of soybean-maize strip systems showed that bacteria