

Nitrogen is crucial for grain production as crops rely on inorganic soil nitrogen. Fertilizers are used but are costly, making them a major expense. Crop rotation with legumes can reduce fertilizer needs and boost productivity, as decomposing legumes release nitrogen for future crops. Legumes, like soybeans and peanuts, also have their own economic value as sources of oil. One of the most notable characteristics of legumes is their ability to form symbiotic relationships with rhizobia enabling them to fix atmospheric nitrogen and provide an inorganic nitrogen source usable by the plants. This symbiosis allows legumes to be self-sufficient in nitrogen, supporting effective growth even in nitrogen-deficient soils. Successful nitrogen fixation by legumes requires well-formed root nodules, and studies have demonstrated that efficient nodule formation positively correlates with higher productivity in legumes.

Nitrogen fixation in legumes requires significant energy, which is partially supplied by the plant through photosynthesis. Rhizobia have genes for energy use and nitrogen fixation. Different rhizobia genera form specific partnerships with certain legumes; for example, soybeans pair with some *Bradyrhizobium* and *Ensifer* species. This compatibility relies on signals between legume roots and rhizobia, where root-secreted flavonoids trigger rhizobia to produce Nod-factors. These factors are recognized by the plant, facilitating symbiosis. Rhizobia genes allow them to detect flavonoids and biosynthesize Nod-factors.

Horizontal gene transfer (HGT) promotes bacterial diversity by transferring genetic material between species through vectors like bacteriophages and plasmids. This leads to mosaic genomes with DNA from different sources. In rhizobia, essential symbiotic genes, including those for nitrogen fixation and Nod-factor synthesis, are often acquired through HGT, enabling soil bacteria to evolve and form plant symbioses. In some rhizobia, like *Sinorhizobium meliloti*, symbiosis-related genes are on plasmids, while in *Bradyrhizobium diazoefficiens* strain USDA 110, these genes are in the chromosome, forming a symbiosis island. This region, 7.5% of the USDA110 genome, is a putative mobile genetic element. Genome comparisons show that while general sequences vary, the symbiosis island remains highly conserved, indicating horizontal transfer.

We are conducting research on the genomes and symbiosis of rhizobia. Ongoing research focuses on understanding the genomes and symbiosis mechanisms of rhizobia to identify unknown factors influencing these interactions. By examining external genetic elements that are not well understood, we aim to uncover alternative regulatory systems. Comprehensive genome-based studies are crucial for elucidating these complex systems, which could lead to improved nitrogen fixation and greater efficiency in agricultural practices.

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