Diversity and evolution of \textit{Bradyrhizobium} communities relating to Soybean cultivation: A review

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Abstract. Soybean is a nitrogen fixer. Also it is a model plant for the study of biological nitrogen fixation (BNF). Soybeans produce more protein and vegetable oil per acre than they do. Over 5000 years, China has been the centre of global soybean production. The Chinese Academy of Agriculture Sciences (CAAS) institute for crop germplasm resources has a national gene bank called the National Gene Bank (NGB) that is made up of nearly 24,000 soybean accessions, which include both wild and domesticated varieties. It started in the 18th century, but more intense cultivation started in the latter half of the 20th century. This has led to North America becoming the world's leading soybean producer. This present review is focused on the diversity and evolution of Bradyrhizobium communities relating to Soybean cultivation.

1. Introduction

Soybean has been studied as a model for Biological nitrogen fixation (BNF). Soybean genome sequencing is available at soybase.org (Glycine max and Glycine soja sequences are available at NCBI as well). Other legumes have seen significant progress on their nitrogen fixation abilities. Temperature and photoperiod affect BNF efficiency [1]. There are also several potentially antagonistic crop protection chemicals that may have an effect on the soybean cultivar's effectiveness in fixing atmospheric nitrogen. The critical selection criteria is the choice of a proper strain of Bradyrhizobium japonicum, which is highly strain-specific to soybean cultivar and susceptible to edaphic influences [2-4]. Soybean gets the majority of its nitrogen from a nutrient source known as Bio-N-Fertilizer (BNF), but in some conditions it can meet all of its nitrogen demand with this nutrient.
Rhizobium and Bradyrhizobium's positive impact on biological nitrogen fixation has been the focus in the recent past [5], as it is essential for sustainable and environmentally friendly food production and long-term crop productivity. Plant improvement aims to increase the percentage of seed production. B. japonicum strains form nitrogen-fixing root nodule symbiosis with soybean. For highly effective Bradyrhizobium japonicum inoculation, inoculated rhizobia need to survive and establish in the soil environment [6-8]. However, it is essential to obtain a good Bradyrhizobium japonicum strain to start cultivation in other areas where the soil is sandy or sandy loam with low nutrients.

It is estimated that between 60-80% of fixed nitrogen in nature is attributed to symbiotic nitrogen fixation. Interaction of the host plant (i.e., the substrate) results in nodules, which foster the formation of ammonium (NH4+) and decrease gaseous nitrogen (N2) to ammonium. The plant provides the carbon source for bacterial growth in exchange for fixed nitrogen. Bradyrhizobium japonicum establishes symbiotic nitrogen fixation only with soybean. These rod-shaped Gram-negative species produce abundant exopolysaccharides that show a range of functions during the initial colonization steps, increasing bacterial survival in the soil under adverse conditions. Additionally, Bradyrhizobium elkanii and Bradyrhizobium Liaoningense are capable of nodulating soybean. Bradyrhizobium japonicum, a slow-growing organism, has been extensively utilized to produce liquid and solid bio inoculants for seeds before planting.

2. Diversity and evolution of bacterial communities relating to Soybean cultivation

Cropping history and past inoculation can have a significant impact on Rhizobium diversity in soil. In a study of peanut nodulating Rhizobium in Cameroon, the highest diversity was found in sites with no history of peanut cultivation, suggesting that simply the introduction of a legume is capable of selecting for field presence of particular Rhizobium taxa [11]. However, in soils after 18 years of cropping where only 4 strains of bacteria had been introduced, genetic diversity of soybean Rhizobium (Bradyrhizobium japonicum) was found to be much greater than these 4 strains. As these soils had previously had no native Rhizobium capable of nodulating soybean, this suggests rapid evolution in and adaptation to the harsh [12]. Very little is known about native soil Rhizobium, especially about those nodulating soybeans. While evidence suggests that the Rhizobium community that typically nodulate promiscuous varieties are less efficient in terms of BNF than those found in commercial inoculants, it is still unknown whether this can be improved. A vast amount of mutation and potential horizontal gene transfer can happen when inoculants are introduced into harsh tropical soil environments [13]. Various studies have shown that prior to soybean expansion in the 1960’s soils were devoid of Rhizobium capable of nodulating soybean [14], and inoculants used by farmers were primarily from the slow growing species Bradyrhizobium japonicum and Bradyrhizobium elkanii. However, by the 2000’s, isolates from soybean nodules were shown to be both slow and fast growing and classified phylogenetically as Rhizobium tropici, Rhizobium sp., Agrobacterium sp., as well as fast-growing Bradyrhizobium japonicum and Bradyrhizobium elkanii., indicating that either inoculants strains underwent mutations, allowing them to speed up their lifecycle, or horizontal gene transfer allowed native strains that previously were incapable of nodulating soybean to become capable of both [15].

3. Bradyrhizobium japonicum

Bradyrhizobium japonicum is a Gram-negative, rod-shaped, nitrogen fixing symbiont of the Rhizobium family. Bradyrhizobium it has since been widely used for molecular genetics, physiology, and ecology because of its superior symbiotic nitrogen fixation activity. Bacterial genomes have a circular structure with a length of 9.11 million base pairs (or nucleotides) and approximately 8373 predicted genes, with an average GC content of 64.1%. At the root-hair tips of soybean plants, Rhizobium bacteria colonize in symbiosomes and are then located within the plant membrane. This symbiotic relationship provides a safe
niche for bacteria while also providing a constant carbon source for the plant. Soybean inoculation with Bradyrhizobium japonicum frequently boosts seed yield [17].

*The Bradyrhizobium japonicum* BNF symbiosis synthesizes a wide range of carbohydrates, including lipopolysaccharides, capsular polysaccharides, exopolysaccharides (EPS), nodule polysaccharides, lipochitin oligosaccharides, and cyclic glucans. Bacteria produce polysaccharide degrading enzymes, such as polygalacturonase and carboxymethylcellulose, which cleave glycosidic bonds in the epidermal layer of the roots, creating pits in the root's epidermis where bacteria can gain entry [18]. CO2 is the end product of the metabolism of the sugar trehalose by *Bradyrhizobium japonicum* [19]. On the other hand, UDP-glucose is a fast and efficient fuel, like sucrose and glucose, promoting plant growth causes more O2 to be released and more CO2 to be absorbed.

4. *Bradyrhizobium* evolutionary ecology

The understanding of *Rhizobium* evolutionary ecology has been, until recently, complicated by the confounding of classification based on phylogenetic descent, with classification based on symbiotic partners. Historically, six species of *Rhizobium*, in one genus, *Rhizobium*, were recognized, and classification was based primarily on the host plants on which *Rhizobium* was able to form nodules, known as the “cross inoculation” concept. Over time this was abandoned due to wide overlap in host range, and in 1982, the first proposed classification was made based on physiological properties, with the proposal of the genera *Bradyrhizobium* representing slow-growing acid intolerant bacteria [21].

However, Jordan [22] still suggests naming conventions within *Bradyrhizobium* to fall along host ranges with *Bradyrhizobium japonicum* representing soybean nodulating bacteria. However, DNA sequencing has made it possible to make distinctions based on gene structure and descent, allowing for more accurate speciation, and proposed phylogenies are continually being revised. For example, an early review in 1996 of phylogenies based on 16S sequences recognized seventeen species in 4 genera [23], while a more recent review by Graham [24] indicates more than 50 species of nodule forming bacteria in 12 genera including both α- and β-proteobacteria [25].

In recent years, speciation has become dependent on more than 16S sequences, with constitutive genes *atpD*, *glnII* and *recA* becoming increasingly important in understanding phylogeny [26]. Recent work by several researchers, has demonstrated how symbiotic ecotypes can exist across multiple *Rhizobium* species and genera, as symbiotic regions of *Rhizobium* genomes are mobile, conferring nodulation ability of the same host across multiple *Rhizobium* species.

5. Conclusion

There have been different attempts over the years to utilize Bradyrhizobium species in order to increase soybean yield due to the discovery of the soybean's very demanding need for nitrogen. Many scientists have investigated the positive effects of Bradyrhizobium inoculation on various legume crops. Glycine max gets an increase in nodulation when it forms a symbiotic relationship with Bradyrhizobium. Bradyrhizobium has had a large impact on the production of sustainable and environmentally friendly food in the recent past, as it has a major role in sustainable and environmentally friendly food production.

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