

## Genome Sequence of a *Bradyrhizobium* Strain Isolated from Peanut Nodules

D. PAUDEL, F. LIU, L. WANG, S. MAYA, Z. PENG, **J. WANG\***, Agronomy Department, University of Florida, Gainesville, FL, 32611; M. CROOK, Department of Microbiology, Weber State University, Ogden, UT; and J. ANE, Departments of Bacteriology and Agronomy, University of Wisconsin–Madison, Madison, WI

In many legumes, the colonization of roots by rhizobia is via “root hair entry” and its molecular mechanisms have been extensively studied. However, the nodulation of peanuts (*Arachis hypogaea* L.) by *Bradyrhizobium* strains requires an intercellular colonization process called “crack entry,” which is understudied. To understand the intercellular crack entry process, it is critical to develop the tools and resources related to the rhizobium in addition to focus on investigating the mechanisms of the plant host. In this study, we isolated a *Bradyrhizobium* sp. strain, Lb8 from peanut root nodules and sequenced it using PacBio long reads. The complete genome sequence was a circular chromosome of 8,718,147 base-pair (bp) with an average GC content of 63.14%. No plasmid sequence was detected in the sequenced DNA sample. A total of 8,433 potential protein-encoding genes, one rRNA cluster, and 51 tRNA genes were annotated. Fifty-eight percent of the predicted genes showed similarity to genes of known functions and were classified into 27 subsystems representing various biological processes. The genome shared 92% of the gene families with *B. diazoefficiens* USDA 110 $\tau$ . A presumptive symbiosis island of 778 Kb was detected, which included two clusters of *nif* and *nod* genes. A total of 711 putative protein-encoding genes were in this region, among which 455 genes have potential functions related to symbiotic nitrogen fixation and DNA transmission. Of 21 genes annotated as transposase, 16 were located in the symbiosis island. Lb8 possessed both Type III and Type IV protein secretion systems, and our work elucidated the association of flagellar Type III secretion systems in bradyrhizobia. These observations suggested that complex rearrangement, such as horizontal transfer and insertion of different DNA elements, might be responsible for the plasticity of the *Bradyrhizobium* genome.