

PHYLOGENETIC ANALYSIS OF NODULATION AND NITROGEN FIXATION GENES OF A BRAZILIAN COLLECTION OF *Bradyrhizobium* STRAINS

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Abstract:

The genus *Bradyrhizobium* encompasses a variety of bacteria that can live in symbiotic and endophytic associations with legumes and non-legumes, and are characterized by physiological and symbiotic versatility and broad geographical distribution. In studies with *Bradyrhizobium* strains the comparison of phylogenies of nodulation and housekeeping genes has indicated a monophyletic origin of nodulation genes and diffusion by vertical and horizontal gene transfer, the last one probably influenced by the host plants. In previous studies with the strains analyzed in this study we have shown high diversity in the 16S rRNA, ITS rRNA, *atpD*, *glnII*, *dnaK* and *recA* housekeeping genes (Menna et al., 2006, 2009). However, despite indications of great genetic variability within the *Bradyrhizobium* genus, little is known about the phylogeny of the nodulation and nitrogen fixation genes. In this study the nodulation genes *nodY/K*, *nodA* and *nodZ* and the nitrogen fixation gene *nifH* of forty *Bradyrhizobium* strains were sequenced and analyzed. The great majority of the strains are from tropical regions and were isolated from members of the three subfamilies and nine tribes of the family Leguminosae (=Fabaceae). In all phylogenetic trees a high level of genetic diversity was observed and several clusters were correlated with the subfamilies of the host plants. One example was with the symbionts of *Glycine max* and *Acacia* sp., classified in the subfamilies Papilionoideae and Mimosoideae, respectively. In the phylogenetic trees built with *nodY/K* and *nodA* the symbionts of *Acacia* sp. were clustered in an isolated group, and no amplification was obtained for the *nodZ* gene. A successful amplification of *nifH* gene was obtained with all strains, and the resulting phylogenetic tree had similar clusters in comparison to the trees built with the nodulation genes (*nodY/K*, *nodA* and *nodZ*). The strains which failed in the amplification for some nodulation genes occupied an isolated position in the *nifH* tree. The comparison of all trees has shown no correlation between housekeeping and *nod* and *nifH* genes. The results pointed out the high diversity of nodulation and nitrogen fixation genes of tropical *Bradyrhizobium* strains and in several clusters high correlation between *nod* and *nifH* genes and the host plants was observed. Partially financed by: CNPq (577933/2008-6; 558455/2008-5; 470162/2009-0)

Key words: *Bradyrhizobium*, Phylogeny, Nodulation genes, Nitrogen fixation genes