

Figure 1: Genomic diversity of the 121 fabaeae symbiont genomes selected for this study. Hierarchical clustering and heat map were based on the Average Nucleotide Identity (ANI) values between each couple of the 124 bacterial genomes. *Rlv* genospecies classification (gs) has been based on an ANI threshold of 95%. Star gathered Sm1021 and isolates phylogenetically distantly related to *Rlv* (ANI<90%). Reference bacteria *Sinorhizobium meliloti* Sm1021, *Rhizobium leguminosarum* symbiovar *trifoli* WSM1689, *Rhizobium leguminosarum* symbiovar *phaseoli* Rlp4292 were also included in the comparison. Additional informations are provided in the Table S1.

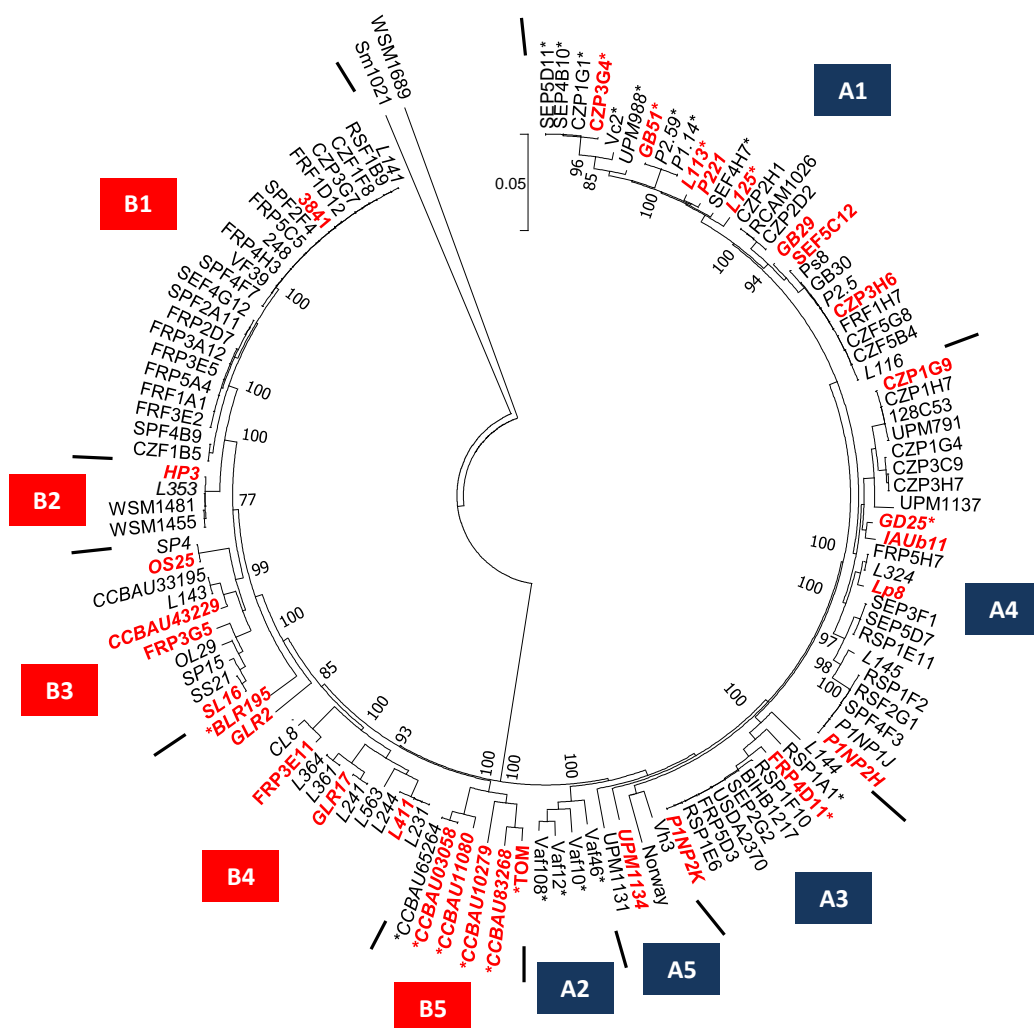


Figure 2: *Nod* gene cluster diversity of of the 121 fabaeae symbiont genomes selected for this study. Phylogenetic tree was based on the *nodABCDEFGHIJLMN* concatenated gene sequences of the 123 genomes. Boxes defined *Nod* groups. The 48 new fabaeae symbiont genomes are indicated in italic. The 32 bacteria of the core collection are indicated in red. Stars indicate bacteria carrying the *nodX* gene within the *nod* gene cluster. *Rhizobium leguminosarum* symbiovar *trifolii* WSM1689 and *Sinorhizobium meliloti* 1021 have been used as outgroups.

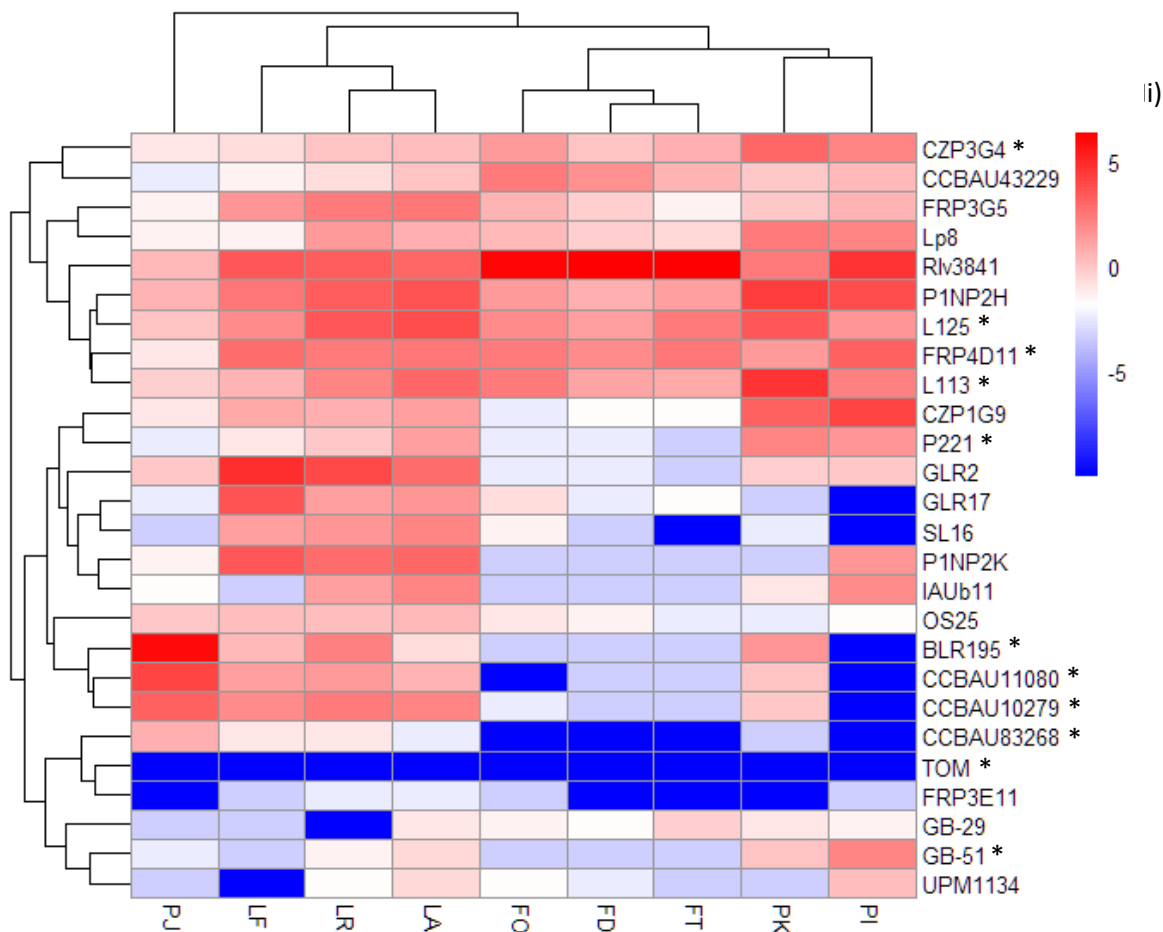


Figure 3: Competitiveness to Form root Nodule of rhizobia with Fabaeae plant species/genotypes. Hierarchical clustering and heat map based on the CFNi for each condition, including the 20 most competitive rhizobia within the core collection. Stars indicate bacteria carrying the *nodX* gene within the *nod* gene cluster. FO: *Vicia faba* cultivar 'Organdi'; FD: *Vicia faba* cultivar 'Diva'; FT: *Vicia faba* cultivar 'Tiffany'; PK: *Pisum sativum* cultivar 'Kayanne'; PI: *Pisum sativum* cultivar 'Isard'; PJ: *Pisum sativum* cultivar 'Afghanistan J11357'; LF: *Lens culinaris* cultivar 'Flora'; LR: *Lens culinaris* cultivar 'Rosana'; LA: *Lens culinaris* cultivar 'Anicia'.