

Genetic variation in host-specific competitiveness of the symbiont *Rhizobium leguminosarum* symbiovar *viciae*

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Abstract

Legumes in the tribe Fabeae form nitrogen-fixing root nodules resulting from symbiotic interaction with the soil bacteria *Rhizobium leguminosarum* symbiovar *viciae* (Rlv). These bacteria are all potential symbionts of the Fabeae hosts but display variable competitiveness to form root nodules (CFN) when co-inoculated in mixture. Because CFN and nitrogen-fixation capacity behave generally as genetically independent traits, the efficiency of symbiosis is often suboptimal when Fabeae legumes are exposed to natural bacterial populations present in soil. A core collection of 32 bacteria was constituted based on the genomic comparison of a collection of 121 genome sequences representative of known worldwide diversity of the rhizobium symbiovar. A variable part of the *nodD* gene sequence was used as a DNA barcode to discriminate and quantify each of the 32 bacteria in a mixture. This core collection was co-inoculated on a panel of 9 genetically diverse *Pisum sativum*, *Vicia faba* and *Lens culinaris* cultivars. We estimated the relative CFN of the bacteria with the diverse hosts by DNA metabarcoding on the nodulated root systems. Comparative genomic analyses within the bacterial core collection allowed us to identify genes associated with host-dependent CFN. These results highlight the emergent properties of rhizobial populations and present a new strategy to identify genetic markers related to important symbiotic traits operating at this level.

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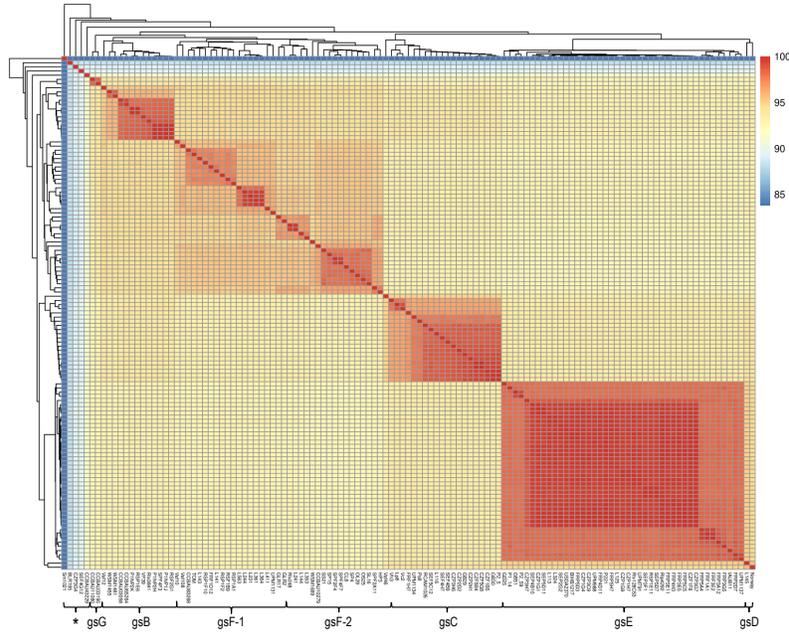


Figure 1: Genomic diversity of the 121 fabae symbiont genomes selected for this study. Hierarchical clustering and heat map were based on the Average Nucleotide Identity (ANI) values between each couple of the 124 bacterial genomes. *Rlv* genospecies classification (gs) has been based on an ANI threshold 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.

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