



THE PANGENOME OF PLANT-SELECTED *Rhizobium leguminosarum* bv *viciae* SUB-POPULATIONS

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Rhizobium leguminosarum bv *viciae* (Rlv) is a bacterium able to establish effective symbioses with four different legume genera: *Pisum*, *Lens*, *Lathyrus* and *Vicia*. Classic studies using trap plants have previously shown that, given a choice, different plants prefer specific genotypes of rhizobia, which are adapted to the host (1, 2).

In previous work we have performed a Pool-Seq analysis based on pooled DNA samples from Rlv nodule isolates obtained from *Pisum sativum*, *Lens culinaris*, *Vicia faba* and *V. sativa* plants, used as rhizobial traps. This experiment allowed us to test the host preference hypothesis: different plant hosts select specific sub-populations of rhizobia from the available population present in a given soil. We have observed that plant-selected sub-populations are different at the single nucleotide polymorphism (SNP) level.

We have selected individual isolates from each sub-population (9 fava-bean isolates, 14 pea isolates, 9 vetch isolates and 9 lentil isolates) and sequenced their genomes at draft level (ca. 30x, 90 contigs). Genomic analyses have been carried out using J-species and CMG-Biotools. All the isolates had similar genome size (7.5 Mb) and number of genes (7,300). The resulting Average Nucleotide Identity (ANI_m) tree showed that *Rhizobium leguminosarum* bv *viciae* is a highly diverse group. Each plant-selected subpopulation showed a closed pangenome and core genomes of similar size (11,500 and 4,800 genes, respectively). The addition of all four sub-population results in a larger, closed pangenome of 19,040 genes and a core genome of similar size (4,392 genes). Each sub-population contains a characteristic set of genes but no universal, plant-specific genes were found. The core genome obtained from all four sub-populations is probably a representative core genome for *Rhizobium leguminosarum*, given that the reference genome (*Rhizobium leguminosarum* bv. *viciae* strain 3841) contains most of the core genome. We have also analyzed the symbiotic cluster (*nod*), and different *nod* cluster genotypes were found in each sub-population.

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