



Genomics of prokaryotes, handling the data analysis bottleneck.

Glimpses at Pan-Genomes.

Population genomics of host specificity in *Rhizobium leguminosarum* bv. *viciae*

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Legumes establish a root-nodule symbiosis with soil bacteria collectively known as rhizobia. This symbiosis allows legumes to benefit from the nitrogen fixation capabilities of rhizobia and thus to grow in the absence of any fixed nitrogen source. This is especially relevant for Agriculture, where intensive plant growth depletes soils of useable, fixed nitrogen sources. One of the main features of the root nodule symbiosis is its specificity. Different rhizobia are able to nodulate different legumes. *Rhizobium leguminosarum* bv. *viciae* is able to establish an effective symbiosis with four different plant genera (*Pisum*, *Lens*, *Vicia*, *Lathyrus*), and any given isolate will nodulate any of the four plant genera. A population genomics study with rhizobia isolated from *P. sativum*, *L. culinaris*, *V. sativa* or *V. faba*, all originating in the same soil, showed that plants select specific genotypes from those available in that soil. This was demonstrated at the genome-wide level, but also for specific genes. Accelerated mesocosm studies with successive plant cultures provided additional evidence on this plant selection and on the nature of the genotypes selected. Finally, representatives from the major rhizobial genotypes isolated from these plants allowed characterization of the size and nature of the respective pangenome and specific genome compartments. These were compared to the different genotypes –symbiotic and non-symbiotic—present in rhizobial populations isolated directly from the soil without plant intervention.

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