



## GENOMES AND TRANSCRIPTOMES OF BIOFERTILIZER BACTERIA

Martha G. López-Guerrero, Ernesto Ormeño-Orrillo, Julia Althabegoiti, Marco A. Rogel, Julio Martínez, Luis Lozano, Luis Servín, Víctor González, Esperanza Martínez-Romero  
Centro de Ciencias Genómicas, UNAM, Cuernavaca, CP 62210; emartine@ccg.unam.mx

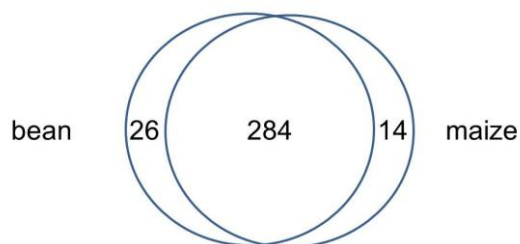
*Rhizobium*, symbiosis, nitrogen fixation

**Introduction.** Bacteria collectively known as rhizobia have been used in agriculture for over a hundred years. Rhizobia form nodules and fix nitrogen in the roots of legumes such as *Phaseolus vulgaris* (bean) and are plant growth promoters in cereals such as maize (1). As we get more knowledge of their biodiversity and modes of action, we have more tools to use them efficiently in agriculture.

**Methods.** Genome sequencing was with Illumina or Roche 454 platforms as described (2). RNA was isolated from bacteria maintained 3-5 days on roots in hydroponic conditions and sequenced from cDNA as described (3). Bioinformatic analyses were performed as described (2,3,4).

**Results.** We have reported the genomes of two *R. tropici* strains (CIAT899 and PRF81) strains that are successfully used in agriculture as inoculants of bean (4). In addition the genomes of *R. phaseoli* strains that have a high capacity to fix nitrogen in bean are available (3, 5). The transcriptome of *R. phaseoli* Ch24-10 on the roots of maize and bean has revealed a large number of genes with unknown functions, as well as genes involved in thiamine and gibberellin biosynthesis among many others. The role of gibberellins in symbiosis has not been explored.

**Fig.1** Venn diagram of *R. phaseoli* Ch24-10 genes expressed in maize or bean rhizoplane. Only extrachromosomal genes are considered.



**Conclusions.** Genomic analyses served to recognize diverse rhizobial lineages of closely related bacteria. Rhizobial genomes are revealing the genomic basis of broad host range nodulation and stress resistance in the *Rhizobium tropici* group.

In *R. phaseoli* that includes very efficient bean symbionts, there is an enormous task to determine the functions of some of the highly expressed genes at the maize and bean rhizospheres. The large overlap in genes expressed in bean and maize rhizoplane may reflect the thousand years these crops have been grown in association.

Gibberellin biosynthetic genes are found in genomes of all tropical rhizobia analyzed (6) and mutants in these genes are being constructed to determine their role in symbiosis with maize and bean. Additionally we are interested in sequencing the symbionts of some wild *Phaseolus* (bradyrhizobia) that will enlarge our knowledge of *Phaseolus* nodulating bacteria (2).

**Acknowledgements.** To PAPIIT IN205412.

### References.

1. Gutiérrez-Zamora ML, Martínez-Romero E. (2001) *J Biotechnol.* 4;91(2-3):117-126.
2. Servín-Garcidueñas LE, Rogel MA, Ormeño-Orrillo E, Delgado-Salinas A, Martínez-Romero J, Sánchez F, Martínez-Romero E. (2012) *J Bacteriol.* 194(22):6310-6311
3. López-Guerrero MG, Ormeño-Orrillo E, Acosta JL, Mendoza-Vargas A, Rogel MA, Ramírez MA, Rosenblueth M, Martínez-Romero J, Martínez-Romero E.. (2012) *Plasmid.* 68(3):149-158.
4. Ormeño-Orrillo E, Menna P, Almeida LG, Ollero FJ, Nicolás MF, Pains Rodrigues E, Shigeyoshi Nakatani A, Silva Batista JS, Oliveira Chueire LM, Souza RC, Ribeiro Vasconcelos AT, Megías M, Hungria M, Martínez-Romero E. (2012) *BMC Genomics* 13:735
5. González V, Acosta JL, Santamaría RI, Bustos P, Fernández JL, Hernández González IL, Díaz R, Flores M, Palacios R, Mora J, Dávila G.(2010), *Appl Environ Microbiol.*76(5):1604-1614.
6. Althabegoiti MJ, Lozano L, Torres-Tejerizo G, Ormeño-Orrillo E, Rogel MA, González V, Martínez-Romero E. (2012) *J Bacteriol* 194(23):6651-6652.