

## Poster A-9

### Genomic coevolution of syntenic genes in Rhizobiales



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**Short Abstract:** Syntenic genes (with conserved chromosomal position) represent the ancestral gene set and we consider they are constrained to rearrangement. To assess the coevolution of syntenic (and non-syntenic) genes in Rhizobiales we evaluated the phylogeny of these genes and their relation with sequence conservation, functional role and prediction of network linkage.

#### Long Abstract:

Genomic coevolution of syntenic genes in Rhizobiales Humberto Peralta, Gabriela Guerrero, Alejandro Aguilar and Jaime Mora. Functional Genomics of Prokaryotes. Centro de Ciencias Genómicas, Universidad Nacional Autónoma de México. Cuernavaca, Morelos, México. Introduction. We reported recently that syntenic genes in Rhizobiales and Enterobacteriales (alpha and gamma proteobacteria, respectively) present special features regarding sequence identity, organization, essentiality and functional interrelationships. The syntenic genes, with relatively conserved position in the chromosomes, reflect not only the ancestral gene set but also restrictions for rearrangement due to their essential roles. Some Rhizobial species (alpha proteobacteria) are intensively studied for their nitrogen-fixing ability when in symbiosis with leguminous plants. The order Rhizobiales comprises both plant symbionts and plant and animal pathogens such as *Rhizobium*, *Agrobacterium* and *Brucella*, respectively. In rhizobia, genes responsible for the symbiotic interaction are commonly found on large plasmids or incorporated in a particular stretch of the chromosome called the symbiotic island. The physiological potential of the rhizobial chromosome allows cell survival under different conditions. There are similarities in the parasitic/symbiotic strategies employed by species of the Rhizobiales. Results. We analyzed the genomic sequences of four fast growing Rhizobiales (*Sinorhizobium meliloti*, *Agrobacterium tumefaciens*, *Mesorhizobium loti* and *Brucella melitensis*). We made a comprehensive gene classification to define chromosomal orthologs, genes with homologs in other replicons such as plasmids, and those species-specific. About two thousand genes were predicted to be orthologs in each chromosome and about 80% of these were syntenic. A high gene colinearity was found in pairs of organisms and a large fraction of the microsyntenic regions and operons were similar. Syntenic products showed higher identity levels than non-syntenic ones, suggesting a resistance to sequence variation due to functional constraints; also, an unusually high fraction of syntenic products contained membranal segments. Syntenic genes encode a high proportion of essential cell functions, presented a high level of functional relationships and a very low horizontal gene transfer rate. The sequence variability of the proteins can be considered the species signature in response to specific niche adaptation. Comparatively, an analysis with genomes of Enterobacteriales showed a different gene

organization but gave similar results in the synteny conservation, essential role of syntenic genes and higher functional linkage among the genes of the microsyntenic regions. Syntenic bacterial genes represent the core chromosomal segments present in the last common ancestor and determine the metabolic characteristics shared by related microorganisms, also show the resistance to sequence variation and rearrangement, possibly due to their essential character. In Rhizobiales and Enterobacteriales, syntenic genes encode a high proportion of essential cell functions and presented a high level of functional relationships. Our synteny analysis defined a multi-level gene organization in the bacterial chromosome. Restriction of sequence variation in these genes, with clear essential functional roles, appeared extended to the conservation of chromosomal arrangement. Perspectives. We consider that this group of genes share an evolutionary history, more than the non-syntenic genes do. How to evaluate it quantitatively? Are there more differences between these group of genes? Do they evolve in the same way that the rest of the genes in the chromosome? In order to answer these questions, we are analyzing the coevolution of common orthologs in Rhizobiales by comparing their phylogenetic trees (assessed by tol-mirror tree program) and conservation, functional role and network linkage. References. Guerrero, G., Peralta, H., Aguilar, A., Díaz, R., Villalobos, M.A., Medrano-Soto, A., Mora, J. 2005. Evolutionary, structural and functional relationships revealed by comparative analysis of syntenic genes in Rhizobiales. *BMC Evol. Biol.* 5:55. Pazos F, Ranea JA, Juan D, Sternberg MJ. 2005. Assessing protein co-evolution in the context of the tree of life assists in the prediction of the interactome. *J Mol Biol.* 352(4):1002-1015.