Phenotypic and molecular diversity of Lupinus mariae-josephi endosymbiotic Bacteria

Durán D.1,2, Sánchez C.1, Imperial J.1, Ruiz-Argüeso T.1 and Rey L.1
1. Departamento de Biotecnología, Universidad Politécnica de Madrid and Centro de Biotecnología y Genómica de Plantas (CBGP), Pozuelo de Alarcón, Madrid. 2. CSIC. daviddurandwendt@alumnos.upm.es

Abstract

Lupinus mariae-josephi is a new lupin species recently described in a Southeastern area of Spain (Valencia) it is capable of tightly (high pH) and wide time periods. Bacteria from L. mariae-josephi have been isolated and correspond to endo-growing bacteria symbiotically and phylogenetically distinct to endosymbionts isolated from other lupins of the Iberian Peninsula and adapted to growth in acid soils. Cross inoculation experiments revealed that the L. mariae-josephi endosymbionts bacteria are unable to nodulate with well-known Lupinus spp. Their species affiliation was examined by a multilocus sequence analysis of four housekeeping genes (16S rDNA, glnII, recA, and ppp III) and the symbiotic nod fix genes. Single- and concatenated phylogenetic analyses of these genes consistently revealed that L. mariae-josephi endosymbiotic bacteria belong to a clade within the Bradyrhizobium genus, highly different from the Bradyrhizobium clades that includes currently named Bradyrhizobium species as well as the endosymbiotic bacteria from lupinus species tested in this study. Within this clade the L. mariae-josephi bacteria belong to several subgroups that may correspond to novel sister species. The phylogenetic analysis based on the nod fix genes showed that L. mariae-josephi endosymbiotic bacteria define a novel branch in the nod-fix-lineage and likely fit a common ancestor for the symbiotic genes with nodulating isolates from Retama spp.

At this moment two draft genome sequences belonging to a lupinus strain (79,317 proteins) B. canariense USDA110 US110 was sequenced to date, and one genome sequenced to date, B. canariense USDA110, presents a single cluster with nod genes from diverse origins. USDA110 fix genes are found in a single cluster homologous to that of USDA110, B. japonicum poses a complete copy of its gene homologous to that from USDA110 and an incomplete one similar to that of USDA110, LmjC strains show a parental origin in the lupinus species that infects. Preliminary data indicate that USDA110 contains a potential second replication (<100 genes) with high homology to Bradyrhizobium BTai1 ploidal sequence.

Results

Genome properties of B. canariense USDA110 and B. sp LmjC genomes have a very large chromosome with a high number of unique proteins, like the rest of Bradyrhizobium genomes sequenced to date. At this moment two draft genome sequences belonging to a lupinus strain (79,317 proteins) B. canariense USDA110 US110 was sequenced to date, and one genome sequenced to date, B. canariense USDA110, presents a single cluster with nod genes from diverse origins. USDA110 fix genes are found in a single cluster homologous to that of USDA110, B. japonicum poses a complete copy of its gene homologous to that from USDA110 and an incomplete one similar to that of USDA110, LmjC strains show a parental origin in the lupinus species that infects. Preliminary data indicate that USDA110 contains a potential second replication (<100 genes) with high homology to Bradyrhizobium BTai1 ploidal sequence.

Conclusions

Endosymbiotic bacteria isolated from Lupinus mariae-josephi group together in a new clade within the Bradyrhizobium genus, and they are well differentiated from the currently named species and, singularly, from the nodulating isolates from other lupins of the Iberian Peninsula.

- B. canariense USDA110 and B. sp. LmjC genomes have a very large chromosomes with a high number of unique proteins, like the rest of Bradyrhizobium genomes sequenced to date.
- nod and fix genes are highly conserved among USDA110, LmjC and USDA110. LmjC presents in ploidal cluster with genes from diverse origins.
- LSLU101, fix genes are in a single cluster homologous to the one of the USDA110. LmjC possesses a complete set of genes homologous to those from USDA110 and an incomplete cluster similar to B. medici.
- LUSL15, together with Type III and Type IV secretion system. USDA110 has a Type II homologues to those from USDA110, and three copies of TOX, two copies of one of USDA110 and other FIP1 homologues.
- Preliminary data indicate that USDA110 contains a potential second replication (<100 genes) with high similarity to Bradyrhizobium BTai1 ploidal sequence.

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