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GENOME ANNOUNCEMENT

Genome Sequence of *Micromonospora lupini* Lupac 08, Isolated from Root Nodules of *Lupinus angustifolius*

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***Micromonospora* strains have been isolated from diverse niches, including soil, water, and marine sediments and root nodules of diverse symbiotic plants. In this work, we report the genome sequence of *Micromonospora lupini* Lupac 08 isolated from root nodules of the wild legume *Lupinus angustifolious*.**

The genus *Micromonospora* is the type genus of the family *Micromonosporaceae* and includes microorganisms with potential biotechnological applications such as antibiotic producers, xylanolytic and cellulolytic strains, and degraders of natural rubber (2, 9). These bacteria are Gram positive, filamentous, and aerobic. Colonies are typically light orange, becoming red, brown, or purple with the production of single-spore sporangiophores. Micromonosporae have been isolated from soil, water, and marine sediments, and these microorganisms have recently been reported as natural inhabitants of root nodule tissues of legumes where this bacterium has been isolated from at least 20 different legume plant species, both wild and cultivated (1, 5) as well as from actinorhizal plants (7).

Strain Lupac 08 was isolated from the root nodules of *Lupinus angustifolius* and identified using a combination of phylogenetic, chemotaxonomic, and morphological analyses that led to the description of *Micromonospora lupini* sp. nov. (6). Given the large number of *Micromonospora* strains recovered from symbiotic tissues, the genome of strain Lupac 08 was sequenced to obtain information about the potential ecological role of *Micromonospora* in interaction with legumes and actinorhizal plants.

The genome sequence of *M. lupini* Lupac 08 was determined using the 454 FLX system and Titanium platform (454 Life Sciences). Highly pure genomic DNA samples from strain Lupac 08 were prepared and used to construct a GS FLX shotgun and a GS FLX long paired-end library. Sequences were assembled in 50 contigs and four scaffolds ranging from 583 to 7,083,659 bp using the GS De Novo Assembler (Newbler).

The draft genome of *M. lupini* Lupac 08 has 7,327,024 bp with a GC content of 71.96%. Manual validation of the automatic annotation was performed using the MaGe (Magnifying Genomes) interface (8) and 7,054 protein-coding genes, 10 rRNA genes (3 genes for 5S rRNA, 4 genes for 16S rRNA, and 3 genes for 23S rRNA), and 77 tRNA genes were predicted.

Preliminary information derived from the genomic data indicates that *M. lupini* Lupac 08 contains several genes encoding hydrolytic enzymes such as cellulases, amylases, xylanases, and pectinases that may have a role in the colonization process.

Studies of bacterial secondary metabolism have largely targeted the discovery of new compounds and the mechanisms for their biosynthesis, but little is known about the ecological functions of secondary metabolites. These molecules may act as signals, pigments, lectins, and siderophores. As with most actinobacteria, *M. lupini* Lupac 08 is capable of producing bioactive molecules, and we recently confirmed the production of previously unknown molecules (3, 4). Preliminary data obtained from the genome sequence of *M. lupini* Lupac 08 indicate that it contains a significant number of genes involved in secondary metabolism.

Nucleotide sequence accession number. This Whole Genome Shotgun project has been deposited at EMBL/GenBank under accession no. CAIE01000001.

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