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Complete Genome Sequence of *Micromonospora* Strain L5, a Potential Plant-Growth-Regulating Actinomycete, Originally Isolated from *Casuarina equisetifolia* Root Nodules

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***Micromonospora* species live in diverse environments and exhibit a broad range of functions, including antibiotic production, biocontrol, and degradation of complex polysaccharides. To learn more about these versatile actinomycetes, we sequenced the genome of strain L5, originally isolated from root nodules of an actinorhizal plant growing in Mexico.**

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Micromonospora species live in varied environments, including within legume and actinorhizal root nodules (1–4). Very few *Micromonospora* genomes have been fully sequenced, even though many species enhance plant growth (5). Here, we contribute to this effort with the complete genome sequence of *Micromonospora* strain L5, which was isolated from nodules of *Casuarina equisetifolia* trees growing in Mexico (1, 2).

The *Micromonospora* strain L5 genome was sequenced at the Joint Genome Institute (JGI) using a combination of Illumina (6) and 454 technologies (7). An Illumina GAii shotgun library with reads of 868 Mb, a 454 Titanium draft library with an average read length of 510 to 525 bp, and paired-end 454 libraries with average insert sizes of 10 kb and 14 kb were generated for this genome. All general aspects of library construction and sequencing performed at the JGI can be found at http://www.jgi.doe.gov/. Illumina sequencing data were assembled with Velvet (8), and the consensus sequences were shredded into 1.5-kb overlapped fake reads and assembled with the 454 data. Draft assemblies were based on 793.7 Mb of the 454 draft data and all of the 454 paired-end data. The Newbler parameters were -consed, -a 50, -l 350, -g, -m, -ml 20. The initial Newbler assembly contained 181 contigs in 8 scaffolds.

We converted the initial 454 assembly into a Phrap assembly by making fake reads from the consensus, collecting the read pairs in the 454 paired-end library. The Phred/Phrap/Consed software package (High Performance Software, LLC) was used for sequence assembly and quality assessment (9–11) in the following finishing process. Illumina data were used to correct potential base errors and increase consensus quality by using the software Polisher developed at JGI (A. Lapidus, unpublished data). After the shotgun stage, reads were assembled with parallel Phrap (High Performance Software, LLC). Possible misassemblies were corrected with gapResolution (C. Han, unpublished data) or Dupfinisher (12), or by sequencing cloned bridging PCR fragments with subcloning. Gaps between contigs were closed by editing in Consed, by PCR, and by bubble PCR primer walks. A total of 732 additional reactions and 4 shatter libraries were necessary to close gaps and to raise the quality of the finished sequence.

The genome has a size of 6,907,073 bp, 6,332 predicted open reading frames (ORFs), and a GC content of 72.86%. It most likely has a circular chromosome, based on its close relationship to *M. aurantiaca* (13). We found 4,248 known protein and 1,984 hypothetical ORFs, 52 tRNAs, and 2 rRNAs. The largest number of orthologs was shared with *M. aurantiaca* ATCC 27029 (NCBI accession number NC_014391). Although strain L5 was reported to fix nitrogen via numerous physiological tests (14), we could not find bona fide *nif* gene sequences in the L5 genome even with the use of different sets of *nif* primers. Genes were found for synthesis of a broad range of cell-wall-degrading enzymes, a Sec-independent system, the Tat (twin arginine translocation) export pathway, and type II and VII secretion systems.

Nucleotide sequence accession number. The complete sequence of *Micromonospora* L5 has been deposited at NCBI GenBank under accession no. CP002399.

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