

Draft Genome Sequences of the Biocontrol Bacterium *Mitsuaria* sp. Strain H24L5A

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***Mitsuaria* sp. strain H24L5A is a plant-associated bacterium with proven capacities to suppress plant pathogens. Here, we report the draft genome sequences and automatic annotation of H24L5A. Comparative genomic analysis indicates H24L5A's similarity to the *Leptothrix* and *Methylibium* species, as well as several genes potentially contributing to its biocontrol activities.**

Mitsuaria sp. strain H24L5A was isolated from the rhizosphere of a mixed-species hay shown to contribute to the suppressiveness of soilborne plant pathogens (3). The strain was identified through profiling of terminal restriction fragments (TRF) of bacterial 16S rRNA genes statistically associated with damping-off disease suppression (5). Representative strains were subsequently recovered using marker-assisted selection, and once isolated, strain H24L5A demonstrated the capability to suppress fungal and oomycete plant pathogens *in vitro* and to reduce lesion severity in tomato and soybean infected with damping-off pathogens (4). Phylogenetic analysis based on 16S rRNA genes indicated that strain H24L5A belonged to the genus *Mitsuaria* (4). This genus had been previously studied for degradation of specific substrates, such as chitosan and gallic acid (1, 8). H24L5A was the first strains of this genus to be indentified from soil and associated with suppression of plant diseases (4).

The genomic DNA of *Mitsuaria* sp. strain H24L5A was isolated, and the library was prepared from a sheared DNA fraction of ~300 bp using Illumina paired-end sample preparation kits according to the manufacturer's instructions. This library was sequenced on an Illumina Genome Analyzer II (Illumina, San Diego, CA) for 76 cycles, generating ~2.6 million paired-end reads amounting to ~192 million nucleotides. The short-read sequences were assembled using Velvet version 0.7.55 (10, 11) into assemblies with hash lengths of 31 nucleotides (nt) and a minimum contig length of 900 nt. The assembly was uploaded to the Rapid Annotation using Subsystems Technology (RAST) server (2) and visualized with the SEED viewer (9).

The H24L5A assembly has a total of 6,655,047 nt spread across 607 contigs, and it harbors 5,225 protein-encoding genes (PEGs) with an average sequence coverage of ~10.4-fold. Additionally, 3,781 (72.4%) of the annotated PEGs were greater than 450 nt in length. rRNA genes were not fully assembled. However, 30 tRNA sequences were identified. Using the public SEED database, bacterial genomes most closely related to H24L5A turned out to be *Leptothrix cholodnii* SP-6 (genome identifier [ID] 395495.3) and *Methylibium petroleiphilum* PM1 (genome ID 420662.8). Some 3,290 (63.0%) and 3,270 (62.6%) of the annotated PEGs of H24L5A were mapped to the genomes of *L. cholodnii* SP-6 and *M. petroleiphilum* PM1, respectively, with an average DNA sequence identity of 53.0% and 53.7%, respectively.

Of the approximately 2,000 PEGs predicted to be unique to H24L5A in comparison with *L. cholodnii* SP-6 and *M. petroleiphilum* PM1, 816 (39.7%) and 826 (39.8%), respectively, were iden-

tified (i.e., not assigned as hypothetical proteins). Among these were genes encoding chitinase, chitosanase, and cellulases, as well as numerous transporters. The existence of chitinolytic enzymes in the H24L5A genome is consistent with the observation of its chitinolytic activity *in vitro* against fungal and oomycete pathogens (4). Additionally, hydrolytic products of pathogen and/or plant cell wall components may enhance such activities, because they can act as elicitors of plant defense responses (6, 7).

Nucleotide sequence accession numbers. The assembled short-read genome sequences of *Mitsuaria* sp. H24L5A were deposited in the European Nucleotide Archive (<http://www.ebi.ac.uk/genomes/wgs.html>) under the accession numbers CAFG01000001 to CAFG01000607.

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