Permanent Draft Genome Sequences for *Mesorhizobium* sp. Strains LCM 4576, LCM 4577, and ORS3428, Salt-Tolerant, Nitrogen-Fixing Bacteria Isolated from Senegalese Soils

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**ABSTRACT** The genus *Mesorhizobium* contains many species that are able to form nitrogen-fixing nodules on plants of the legume family. Here, we report the draft genome sequences for three *Mesorhizobium* strains. The genome sizes of strains LCM 4576, LCM 4577, and ORS3428 were 7.24, 7.02, and 6.55 Mbp, respectively.
TABLE 1  Genome statistics

| Mesorhizobium strain | No. of reads | N50 contig size (kb) | Assembly size (Mb) | No. of contigs | Sequencing depth (×) | No. of CDSs<sup>a</sup> | G+C content (%) | Accession no. |
|----------------------|--------------|----------------------|-------------------|---------------|---------------------|---------------------|----------------|---------------|
| LCM 4576             | 19,900,494   | 236                  | 7.24              | 89            | 509.8               | 6,665               | 63.54          | MDDT000000000  |
| LCM 4577             | 8,750,732    | 305.7                | 7.02              | 56            | 220.3               | 6,464               | 63.74          | MDDU000000000  |
| ORS3428              | 16,898,886   | 144.6                | 6.55              | 191           | 477.7               | 5,145               | 63.12          | MDFL000000000  |

<sup>a</sup>CDSs, coding sequences.

limited to 200 mM. Because of these properties, these strains could potentially be used in association with leguminous plants for the reforestation of saline lands. The genomes of *Mesorhizobium* sp. strains LCM 4576, LCM 4577, and ORS3428 were sequenced to provide information on their physiology and ecology and to identify molecular markers that are involved in its tolerance to salinity. Comparative genomics of the highly salt-tolerant strain LCM 4577 with the two moderately salt-tolerant strains LCM 4576 and ORS3428 may provide insight on the molecular mechanisms involved in their tolerance to salinity.

Sequencing of the draft genomes of *Mesorhizobium* sp. strains LCM 4577, LCM 4576, and ORS3428 was performed at the Hubbard Center for Genome Studies (University of New Hampshire, Durham, NH) using Illumina technology (11). A standard Illumina shotgun library was constructed and sequenced using the Illumina HiSeq 2500 platform with paired-end reads (2 × 250 bp), which generated 8,750,732 to 19,900,494 reads (Table 1). The Illumina sequence data were trimmed by Trimmomatic version 0.32 (12) and assembled using Spades version 3.5 (13) and ALLPaths-LG version r52488 (14). Data on the final draft assemblies for *Mesorhizobium* sp. strains LCM 4576, LCM 4577, and ORS3428 are presented in Table 1. The final assembled genomes of *Mesorhizobium* sp. strains LCM 4576, LCM 4577, and ORS3428 were 7,241,525, 7,019,804, and 6,552,800 bp, respectively, with an average G+C content of 64% (Table 1). These genomes were annotated via the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) and resulted in 6,665, 6,464, and 5,145 candidate protein-encoding genes, respectively.

**Accession number(s).** The draft genome sequences have been deposited in GenBank under the accession numbers listed in Table 1.

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