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PROKARYOTES

Draft Genome Sequence of *Saccharomonospora* sp. Strain LRS4.154, a Moderately Halophilic Actinobacterium with the Biotechnologically Relevant Polyketide Synthase and Nonribosomal Peptide Synthetase Systems

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ABSTRACT The draft genome sequence of *Saccharomonospora* sp. strain LRS4.154, a moderately halophilic actinobacterium, has been determined. The genome has 4,860,108 bp, a G+C content of 71.0%, and 4,525 open reading frames (ORFs). The clusters of *PKS* and *NRPS* genes, responsible for the biosynthesis of a large number of biomolecules, were identified in the genome.

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Actinobacteria represent a group of microorganisms that are prolific in producing secondary metabolites (1). However, the biotechnological potential of its halophilic representatives remains unexplored (2). The ability to synthesize secondary metabolites is closely associated with the identification of the polyketide synthase (PKS) and nonribosomal peptide synthetase (NRPS) gene clusters in an actinobacterial genome sequence. These genes are responsible for the synthesis of antibiotics, biosurfactants, siderophores, immunosuppressants, antitumoral and antiviral agents, and biomolecules with important medical and biotechnological applications (3, 4).

The strain LRS4.154 is a moderately halophilic actinobacterium, isolated from a soil sample from Laguna del Rosario in Oaxaca, Mexico. Based on 16S rRNA gene sequence comparisons, the strain LRS4.154 could be affiliated with the genus *Saccharomonospora*, with *Saccharomonospora azurea* and *Saccharomonospora xinjiangensis* being the closest relatives, both sharing 98.4% 16S rRNA gene sequence similarity. The aim of this work was to sequence the draft genome of the strain LRS4.154 in order to unravel its potential for future applications in biomedical areas.

The draft genome sequence of *Saccharomonospora* sp. LRS4.154 was accomplished using a whole-genome shotgun strategy (5) on an Illumina HiSeq 2500 platform (2 × 100-bp paired-end) (STAB VIDA, Portugal), yielding 12,366,802 reads and 846.63 Mbp. The genome assembly was performed using the software Velvet version 1.2.10 (6) and resulted in 13 contigs (≥1,000 bp) with an N_{50} value of 731,563. The NCBI Prokaryotic Genome Annotation Pipeline (7) was used to identify open reading frames (ORFs) and provide a functional annotation of protein-coding genes, as well as other functional genome units.

The draft genome is estimated to contain 4,860,108 bp, with a G+C content of 71.0%. The reported coding density is 90.3%, with 0.916 genes per kbp. A total of 4,525 putative ORFs were predicted, with an average size of 985 bp, as well as two noncoding RNA (ncRNA), four rRNA (one 16S rRNA, one 23S, and two 5S rRNA), and 47 tRNA genes.

Analysis of the genome confirms the presence of six *PKS* and two *NRPS* gene clusters. These bioinformatic data suggest the potential of the halophilic actinobacterial strain LSR4.154 to produce secondary metabolites or unknown metabolites of PKS and NRPS origin. This is the first halophilic *Saccharomonospora* strain reported until now having those capabilities.

Accession number(s). This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession no. MWIH00000000. The version described in this paper is the first version, MWIH01000000.

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