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**Draft Whole-Genome Sequence of *Bacillus sonorensis* Strain L12, a Source of Nonribosomal Lipopeptides**

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The *Bacillus sonorensis* L12 draft genome sequence is approximately 4,647,754 bp in size with a G+C content of 45.2%. Over 86% of the genome contains protein-encoding genes, including several gene clusters for *de novo* biosynthesis of the nonribosomal lipopeptides iturin, bacitracin, and fengycin, which could mean that the strain exhibits antifungal effects. The assembled draft genome sequence of strain L12 contains 34 contigs, a genome size of 4,647,754 bp, and a G+C content of 45.2%. The genome was 425,108 bp larger than the *B. licheniformis* DSM13T genome. Strain L12 has 78 tRNA genes and 4,236 protein-coding genes representing 86.8% of the draft genome sequence.

Preliminary genome analysis revealed that strain L12 carries gene clusters for *de novo* biosyntheses of the nonribosomal lipopeptides fengycin, iturin, and bacitracin, which have potential biotechnological applications (9, 10). It therefore represents a potential strain which can be used as a cloning tool for genetic engineering and production of improved and novel antimicrobial agents and also as a bioprotective agent for controlling plant fungal pathogens in crop farming. Further comparative genomic analyses will also provide valuable insight into the evolutionary and phylogenetic status of this species and contribute to a deeper understanding of its ecology and evolution.

**Nucleotide sequence accession numbers.** This whole genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AOFM00000000. The version described in this paper is the first version, AOFM01000000.

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**REFERENCES**

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