

# Genome Sequence of *Paenibacillus* sp. Strain Aloe-11, an Endophytic Bacterium with Broad Antimicrobial Activity and Intestinal Colonization Ability

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***Paenibacillus* sp. strain Aloe-11, a Gram-positive, spore-forming, facultatively anaerobic bacterium isolated from the root of *Aloe chinensis* in the southwest region of China, has excellent antibiotic activity and intestine colonization ability. Here, we present the 5.8-Mb draft genome sequence of *Paenibacillus* sp. strain Aloe-11.**

*Paenibacillus*, whose members once belonged to the genus *Bacillus*, was reclassified as a separate genus in 1993 (1). More than 120 *Paenibacillus* species have been isolated from a variety of habitats and widely used in areas such as agriculture, industry, medicine, and environmental remediation (11–14). *Paenibacillus* sp. strain Aloe-11, an endophytic bacterium isolated from the root of *Aloe chinensis*, has many biological functions, such as antibiotic activity against many pathogenic bacteria and fungi and the ability to enhance the immune function of animals with its polysaccharide. According to our studies with mice and chickens, *Paenibacillus* sp. strain Aloe-11 can colonize the intestine over 15 days after feeding of the bacteria is stopped and can significantly promote forage fiber degradation and reduce the cellulose content in feces.

Whole-genome shotgun sequencing of *Paenibacillus* sp. strain Aloe-11 was completed at Beijing Genomics Institute by using Solexa paired-end sequencing technology (2). A total of 10,147,096 filtered paired-end reads (~913.2 Mb) were obtained, representing an average of 160-fold coverage of the genome. All reads were assembled into 334 contigs (>200 bp) and 52 scaffolds using SOAPdenovo version 1.04 (9). The unclosed draft genome sequence of strain Aloe-11 shows that it has a genome size of 5,812,362 bp with a GC content of 46.62% and an  $N_{50}$  of 230,166 bp. Based on the genomic data, 5,275 protein-coding sequences (CDS) were predicted by GeneMark.hmm (3) and annotated by BLAST sequence similarity searches against the COG, KEGG, UniProt, and nr databases, and 73 tRNA genes were also identified by using tRNAScan-SE (10).

According to comparative genome analysis with other 18 sequenced *Paenibacillus* strains, *Paenibacillus* sp. strain Aloe-11 is closest to *Paenibacillus polymyxa* SC2, but polymyxin-synthetic genes were not detected in strain Aloe-11. Several giant nonribosomal peptide synthetase (NRPS) genes were identified in the genome of *Paenibacillus* sp. strain Aloe-11, which are involved in the biosynthesis of antibiotics such as fusaricidin (5) and bacitracin (8) and of other unknown products. In the genome, there is one NRPS gene cluster, a 30-kb DNA fragment, containing four genes (*lchAA*, *lchAB*, *lchAC*, and *lchAD*) involved in the biosynthesis of surface-active lipopeptides, e.g., lichenysin (7). We also found in the genome a rich set of genes encoding secreted enzymes involved in the degradation of various plant-derived polysaccharides, including cellulases, xylanases, and pectinase. The siderophore involved in Fe<sup>3+</sup> ion uptake has two synthesis pathways in *Paenibacillus* sp. strain Aloe-11 that are dependent on NRPSs (6) and

siderophore synthetases (4). Given its high strain specificity and potential applications in multiple areas, the genome sequence of *Paenibacillus* sp. strain Aloe-11 is important to basic and applied research, and it will also facilitate the understanding of evolutionary relationships among *Paenibacillus* organisms.

**Nucleotide sequence accession numbers.** This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [AGFI00000000](https://www.ncbi.nlm.nih.gov/nuccore/AGFI00000000). The version described in this paper is the first version, AGFI01000000.

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