Genome Sequence of the Pattern-Forming Social Bacterium *Paenibacillus dendritiformis* C454 Chiral Morphotype

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***Paenibacillus dendritiformis* is a Gram-positive, soil-dwelling, spore-forming social microorganism. An intriguing collective faculty of this strain is manifested by its ability to switch between different morphotypes, such as the branching (T) and the chiral (C) morphotypes. Here we report the 6.3-Mb draft genome sequence of the *P. dendritiformis* C454 chiral morphotype.**

Paenibacillus dendritiformis is a bacterial species discovered in the early 1990s (6). The genus *Paenibacillus*, including *P. dendritiformis* (15), was originally included within the genus *Bacillus* and then reclassified as a separate genus in 1993 (1). Bacteria belonging to this genus have been detected in a variety of heterogeneous environments, such as soil, rhizosphere, insect larvae, and clinical samples (9, 11–13). In recent years, there has been an increasing interest in studies of *Paenibacillus* spp. since many were found to be important for industrial, agricultural, and medical applications.

P. dendritiformis is marked by its complex spatial organization of the colony, which can form different patterns, presumably enabling the strain to cope more efficiently within the environment (2, 3, 5). When grown on solid medium, *P. dendritiformis* exhibits the remarkable ability to adopt at least two colonial morphologies: the branching morphotype (T), marked by tip splitting, and the chiral morphotype (C), marked by curly branches with well-defined handedness (2, 4, 5, 7). The transition between the two morphotypes is possible in both directions but not necessarily by the same pathway. Development of such complex colonies requires self-organization and cooperative behavior of individual cells while employing sophisticated chemical communication. Therefore, sequencing of the *P. dendritiformis* C454 genome paves the way for elucidating some of the regulatory processes involved in cell-cell communication, colonial patterning, and more generally, the cooperative bacterial response to various environmental conditions that involves epigenetic and genome-wide changes.

DNA preparation, genome sequencing, and draft assembly. Genomic DNA was isolated using Qiagen's DNeasy blood and tissue kit (catalog no. 69504). The whole genome was sequenced by Illumina GA II (8) and 454 Life Sciences (10) on a GS-20 sequencer. The Illumina data set contained 18,671,143 high-quality filtered reads, each 80 bp long, and coverage equivalent to 221×. The 454 data set resulted in 1,334,919 high-quality filtered reads with an average read length of 97 bp and coverage equivalent to 19×. Initial assembly of quality filtered reads from both technologies was performed using the Newbler 2.5.3 assembler and refined with Minimus (Amos 2.0.5) (14). The assembled sequence resulted in 199 scaffolds larger than 500 bp, with a total length of 6,375,964 bp (GC content, 54%). Automated annotation was per-

formed using the NCBI prokaryotic genomes automatic annotation pipeline (PGAAP). The draft genome harbors 5,660 protein-coding sequences, 31 tRNAs, 45 phage-related genes, and a high number of signal transduction genes. The *P. dendritiformis* C454 genome carries genes required for competition over resources (e.g., iron, amino acids, and sugar transporters) and for producing offensive (antibiotics and lytic enzymes) and defensive (resistance to antibiotics and other toxins) compounds. These genes can support traits needed to thrive in the heterogeneous and highly competitive environments.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AHKH00000000](#). The version described in this paper is the first version, AHKH00000000.

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