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# GENOME ANNOUNCEMENTS

## Genome Sequence of *Bacillus subtilis* subsp. *spizizenii* gtP20b, Isolated from the Indian Ocean▽

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***Bacillus subtilis*** **is an aerobic spore-forming Gram-positive bacterium that is a model organism and of great industrial significance as the source of diverse novel functional molecules. Here we present, to our knowledge, the first genome sequence of *Bacillus subtilis* strain gtP20b isolated from the marine environment. A subset of candidate genes and gene clusters were identified, which are potentially involved in production of diverse functional molecules, like novel ribosomal and nonribosomal antimicrobial peptides. The genome sequence described in this paper is due to its high strain specificity of great importance for basic as well as applied researches on marine organisms.**

*Bacillus subtilis* is a member of the Gram-positive bacteria of the genus *Bacillus* and has been used as a model organism to investigate differentiation, gene/protein regulation, and cell cycle events in bacteria for more than a century (1, 2). *B. subtilis* has industrial importance, e.g., as a source for diverse novel functional molecules like antimicrobial peptides (2, 6). Members of the genus are ubiquitous in nature. Various strains of *B. subtilis* have been isolated from diverse habitats, including seawater (4). The first *B. subtilis* genome was sequenced a decade ago (6) and updated recently (2, 9). Although draft genomes of four further strains were also released (8, 9), no genome of a *B. subtilis* strain from a marine habitat has been decoded.

*B. subtilis* subsp. *spizizenii* strain gtP20b was isolated from the sediment at a 608-m depth in the Indian Ocean and from the layer close to the bottom surface of the ocean. The sampling was taken through a multicorer during the cruise of the research ship *Sonne* on expedition 130 in 1998 and stored at −20°C. Raw reads of the strain genome were generated by using Illumina GA (Solexa) and assembled with the Velvet program (14). Based on the reference genome of *B. subtilis* strain 168 (6, 7), a draft genome of gtP20b was completed. By subsequent PCR and resequencing, 100 genome gaps were closed, but four gaps and 23 unmatched short contigs (>200 bp) remained, with the contigs having an accumulative length of 151.5 kb and believed to be genome specific and distributed in the remaining gaps.

The genome sequence of gtP20b comprises 4,247,908 bases with a G+C content of 44.8% and covers more than 99% of the whole genome (2, 8). It contains 4.331 open reading frames (ORFs), 77 tRNAs, including one pseudogene, and 30 rRNAs (3). Phylogenetic analysis revealed that gtP20b is closely clustered with *B. subtilis* strain 168 and *B. subtilis* subsp. *natto* but phylogenetically apart from *Bacillus amyloliquefaciens* and *Bacillus licheniformis* (10). Furthermore, 81.7% of the ORFs have orthologs in strain 168 (BLASTP < 1e−5), but 444 ORFs were not found in the released genomes of the *Bacillus* genus; of these, 392 ORFs did not give hits in current public databases.

At least 59 genes were found to be potentially involved in secondary metabolism. They form diverse gene clusters with varied degrees of synteny to other *B. subtilis* strains. A set of hits was retrieved from antimicrobial peptide (AMP) databases (5, 11, 12, 13), including subtilisin A (*sboA*), surfactin (*sfp*), beta-lactamase precursor (*penP*), and replicative DNA helicase (*dnaC*). However, they showed strong variations at both DNA and amino acid levels compared with those of other *B. subtilis* strains, suggesting the potential of strain gtP20b as a unique source for novel AMPs. This genome sequence is due to its high strain specificity of great importance for both basic and applied researches.

**Nucleotide sequence accession numbers.** This whole genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession number AEHM00000000. The version described here is the first version under the accession number AEHM01000000.

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