Draft Genome Sequence of the Sponge-Associated Strain *Bacillus atrophaeus* C89, a Potential Producer of Marine Drugs

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***Bacillus atrophaeus* C89, isolated from the marine sponge *Dysidea avara*, is a potential producer of bioactive compounds, such as neobacillamide A and bacillamide C. Here, we present a 4.2-Mb assembly of its genome. The nonribosomal peptide synthetases (NRPSs) make it possible to produce the bioactive compounds.**

The development of sponge drugs is limited by sponge collection and the low concentration of natural products (8). Some sponge-associated bacteria are involved in the synthesis of sponge-derived natural products. Hence, bacterial cultivation could potentially solve the problem of the production bottleneck (8). *Bacillus atrophaeus* C89 was isolated from the marine sponge *Dysidea avara* in the South China Sea, which can produce bacillamide C and a new compound of neobacillamide A (9). (The identification of C89 was revised as *B. atrophaeus* after the *de novo* sequencing.)

The sequencing was finished using the Illumina IIx genome analyzer system. Consequently, 1,011.27 Mb of raw data were generated with 245-fold coverage and assembled into 21 scaffolds by SOAPdenovo (4). The sequence was annotated using Glimmer 3.0 (1), and functional descriptions were obtained using the Clusters of Orthologous Genes (COG) (7) and KEGG (5) databases. Genes encoding rRNA were identified by RNAmmer (3).

The draft genome sequence of *B. atrophaeus* C89 comprises 4,211,832 bases with a G+C content of 43.1%. The number of contigs is 84. There are 4,348 coding sequence (CDSs), among which 3,268 CDSs are assigned putative biological functions. The functions of approximately 300 CDSs are currently unknown. *B. atrophaeus* C89 contains genes related to cell wall and cell recognition (232 CDSs), signal transduction (192 CDSs), and cell motility and intracellular traffic (40 CDSs). The observed type III secretion system can modulate host cellular functions, thereby promoting mutualistic symbioses (6). Besides this, the whole genome contains 558 rRNA genes, 45 tRNA genes, and 93 transposase genes. There are 270 genes related to carbohydrate metabolites and 293 genes coding for amino acid transport and metabolism. The genome contains 104 secondary metabolite genes and 63 defense-related genes; in particular, the NRPS gene cluster (7,011 bp) (GenBank no. JQ687535) is inferred to be involved in the synthesis of bacillamide C and neobacillamide A (2). Meanwhile, the synthetic pathways of streptomycin, novobiocin, and vancomycin were identified.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AJRJ000000000](https://www.ncbi.nlm.nih.gov/nuclseq/AJRJ000000000). The version described in this paper is the first version, AJRJ01000000.

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