

Genome Sequence of *Brachybacterium squillarum* M-6-3^T, Isolated from Salt-Fermented Seafood

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***Brachybacterium squillarum* M-6-3^T was isolated from salt-fermented seafood in Korea and belongs to the Dermabacteraceae, a rather isolated family within the actinobacterial suborder Micrococccineae. Here, we present the draft genome sequence of the type strain *Brachybacterium squillarum* M-6-3^T (3,191,479 bp), a Gram-positive bacterium with high (72.8%) G+C content.**

The genus *Brachybacterium* belongs to the family Dermabacteraceae (class Actinobacteria). Organisms belonging to that genus are Gram-positive bacteria containing genomic DNA with high guanine and cytosine content (4, 18). Since the genus was first identified in 1988, 14 species (*Brachybacterium alimentarium*, *B. conglomeratum*, *B. faecium*, *B. fresconis*, *B. muris*, *B. nesterenkovi*, *B. paraconglomeratum*, *B. phenoliresistens*, *B. rhamnosum*, *B. sacelli*, *B. saurashtrense*, *B. squillarum*, *B. tyrofermentans*, and *B. zhongshanense*) have been isolated from various sources (2–4, 6–8, 13, 15, 16, 20). We isolated type strain *B. squillarum* M-6-3^T, a Gram-positive, nonmotile, coccoid-shaped bacterium with high G+C content, while studying the microbial diversity of salt-fermented foods made of tiny shrimp (13). The genus *Brachybacterium* has been characterized previously (4), and the strain possesses a type A4 γ peptidoglycan with meso-diaminopimelic acid as the diagnostic cell-wall di-amino acid (13). In the present report, we describe the genome sequence of *B. squillarum* M-6-3^T; only a complete genome sequence of *B. faecium*, the type species, had been reported (10) when our sequencing project began.

The genome sequence was determined using the Roche/454 GS (FLX Titanium) and Illumina paired-end sequencing platforms (8-kb library and 100-bp library, respectively). A total of 163,759 reads were obtained using the Roche/454 GS platform, providing approximately 13-fold genome coverage. The Illumina platform yielded 10,407,717 reads, corresponding to 245-fold coverage. The Roche/454 GS and Illumina reads were assembled using GS Assembler 2.5.1 software (Roche Diagnostics, Branford, CT) and CLC genomics workbench 4.7.2 software (CLCbio, Denmark), respectively.

The sequences were assembled into 8 large contigs, which were then assembled into a scaffold with an N50 contig size of approximately 80.2 kb (where N50 is the contig length such that at least 50% of the bases of the assembly are contained within contigs of the same size or larger). Gene prediction (5, 11) and annotation data were archived using in-house annotation systems and several open-access databases (12, 14, 17, 19),

whereas ribosomal RNA identities were confirmed using RNAmmer software (9).

The unclosed draft genome of *B. squillarum* M-6-3^T is 3,191,479 bp long, with 72.8% G+C content. There are 2,935 putative coding sequences (CDSs), and the genome sequence contains 50 predicted tRNA genes and two predicted copies of the 5S, 16S, and 23S rRNA genes. Of the 2,935 genes identified, 2,145 CDSs were classified into 18 (J, K, L, D, O, M, N, P, T, C, G, E, F, H, I, Q, R, and S) functional COG categories. The unannotated genes may be assigned upon closure of the genome.

In comparison with the *B. faecium* genome, the genome of M-6-3^T contains a higher percentage of genes associated with carbohydrate transport and metabolism (G), whereas there are no annotated genes associated with defense mechanisms (V), intracellular trafficking and secretion (U), and RNA processing and modification (A). Comparative tools available on the RAST server (1) identified 2,060 genes shared between *B. squillarum* and *B. faecium* (the only publicly available genome corresponding to the genus *Brachybacterium*).

Nucleotide sequence accession numbers. The sequence determined in this whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. AGBX00000000. The version described in this paper is the first version, available under accession no. AGBX01000000.

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