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). The unannotated genes may be assigned upon closure of our sequencing project began.

The genome sequence of *Brachybacterium squillarum* M-6-3T, 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-6-3T (3,191,479 bp), a Gram-positive bacterium with high (72.8%) G+C content. whereas ribosomal RNA identities were confirmed using RfAMmer software (9).

The unclosed draft genome of *B. squillarum* M-6-3T 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-6-3T* 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 sever (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.

This work was supported by a grant from the Next-Generation BioGreen 21 Program (grant PJ008208), Rural Development Administration, Republic of Korea.