Draft Genome Sequence of *Gillisia* sp. Strain CBA3202, a Novel Member of the Genus *Gillisia*, Which Belongs to the Family *Flavobacteriaceae*

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*Gillisia* sp. strain CBA3202, which belongs to the family *Flavobacteriaceae*, was isolated from sand of the seashore on Jeju Island, Republic of Korea. The draft genome of *Gillisia* sp. CBA3202 contains 2,981,404 bp with a G+C content of 34.9%. This is the second genome sequence of the *Gillisia* strains.

The genus *Gillisia*, which belongs to the family *Flavobacteriaceae*, is known to consist of Gram-negative, aerobic, chemo- heterotrophic, and rod-shaped bacteria (8) and is phylogenetically located in the marine clade of the family *Flavobacteriaceae* that includes many marine species (2). The genus currently includes 6 species: *Gillisia hiemivivida* (2), *G. illustrata* (2), *G. limnaea* (8), *G. mitskevichiae* (6), *G. myxillae* (4), and *G. sandarakina* (2). The strains belonging to the genus *Gillisia* were isolated from microbial mats in Antarctica (8), sea-ice algae in Antarctica (2), seawater in Japan (6), and the marine sponge *Myxilla incrustans* in the United States (4). A new isolate, *Gillisia* sp. strain CBA3202, was isolated from sand of the seashore on Jeju Island, Republic of Korea; this isolate has 99.1% 16S rRNA gene sequence similarity with *Gillisia mitskevichiae* KMM 6034T. The present article is an announcement of the second genome-sequencing project of the *Gillisia* strains.

Genomic DNA for *Gillisia* sp. CBA3202 was extracted by using the G-spin genomic DNA extraction kit (INTRON Biotechnology, Republic of Korea), and the draft genomic DNA sequence was determined using the Ion Torrent PGM sequencer (100-bp library) (7) with the 316D sequencing chip according to the manufacturer’s instructions. A total of 1,695,985 reads spanning 153 Mb were generated (51.3-fold coverage of the genome). The genome sequences were assembled using CLC genomics workbench 4.7.2 (CLC Bio, Denmark) into 116 contigs (>200 b in size) with an N50 contig size of approximately 77 kb. The draft genome of *Gillisia* sp. CBA3202 is 2,981,404 bp in length, with a G+C content of 34.9%. The gene prediction and annotation for the assembled contigs were determined by combining results from the RAST Server: rapid annotations using subsystems technology pipeline (1). The 16S and 23S rRNA genes and tRNA genes are predicted to number 1, 1, and 35, respectively. Based on the RAST results, the draft genome includes 3,075 CDSs (coding sequences). Among the predicted CDSs, 12 genes are annotated to metabolize aromatic compounds. More detailed analysis for the genome of *Gillisia* sp. CBA3202 and comparative analysis with other *Gillisia* strains can give further information about the metabolism and genonomic differences of the *Gillisia* species.

**Nucleotide sequence accession numbers.** This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AJLT00000000. The version described in this paper is the first version, AJLT01000000.

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**REFERENCES**