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Draft Genome Sequences of Two *Clostridium botulinum* Group II (Nonproteolytic) Type B Strains (DB-2 and KAPB-3)

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Clostridium botulinum **is important for food safety and studies of neurotoxins associated with human botulism. We present the draft genome sequences of two strains belonging to group II type B: one collected from Pacific Ocean sediments (DB-2) and another obtained during a botulism outbreak (KAPB-3).**

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Clostridium botulinum is a Gram-positive, anaerobic bacterium that is present naturally in soils and sediments around the world (1). *C. botulinum* produces a highly potent neurotoxin that may cause botulism when ingested (2). Botulism is characterized by a wide range of symptoms from vomiting and gastrointestinal distress to cranial nerve palsies that may progress to complete flaccid paralysis and death due to respiratory failure (3).

C. botulinum strains are organized into four metabolically and genetically distinct groups (I–IV) (4). Groups I and II are associated with human botulism (5). Group II is nonproteolytic and organized into three serotypes (A, B, or F) that are distinguished by the botulinum neurotoxin produced (5). Group II strains ferment a number of sugars, form spores with moderate heat resistance, are often linked with outbreaks of food-borne botulism involving fish and meat (6), and are a concern in the safe production of chilled ready meals (7).

Despite the importance of group II type B strains to food safety and studies of neurotoxin gene clusters (8), comprehensive sequencing of their genomes has only recently been performed. Here, we present the high-quality draft genome sequences of *C. botulinum* strain DB-2, obtained from sediments in 1968 from the Pacific Ocean, and strain KAPB-3, linked to a 1981 botulism outbreak caused by kapchunka (dried salted whitefish) in the United States.

Short-read sequence data were generated for these two genomes by preparing paired-end libraries with the Nextera XT DNA sample preparation kit (Illumina, San Diego, CA) and sequencing the libraries on an Illumina MiSeq benchtop sequencer for 500 cycles. The number of reads generated were 2,074,424 for DB-2 and 1,991,848 for KAPB-3. Error correction was performed with BayesHammer (9), and reads were assembled *de novo* into high-quality draft genomes with SPAdes version 3.1.1 (10), utilizing the MismatchCorrector tool. In total, the DB-2 assembly yielded 150 nonoverlapping contiguous sequences with 108-fold coverage, 27.18% GC content, and a combined length of 3,915,341 bases. The KAPB-3 assembly generated 128 nonoverlapping contiguous sequences with 112-fold coverage, 27.17% GC content, and a total length of 3,871,084 bp. Gene predictions and annotations were performed with the National Center for Biotechnology Information (NCBI) Prokaryotic Genome Annotation Pipeline (PGAP) (11). For DB-2 a total of 3,570 genes were identified, including 3,384 protein-coding regions, 54 pseudogenes, 50 rRNA sequences, and 81 transfer RNAs. For KAPB-3 a total of 3,509 genes were identified, including 3,325 protein-coding regions, 56 pseudogenes, 49 rRNA sequences, and 78 transfer RNAs.

Nucleotide sequence accession numbers. These whole-genome shotgun projects have been deposited at DDBJ/EMBL/GenBank under accession numbers JQOJ00000000 (DB-2) and JQOK00000000 (KAPB-3). The versions described in this paper are the first versions, JQOJ01000000 and JQQK01000000.

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