



Complete Genome Sequence of *Lactobacillus curvatus* NFH-Km12, Isolated from the Japanese Traditional Fish Fermented Food Kabura-zushi

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ABSTRACT Kabura-zushi is a traditional Japanese fermented food made from yellowtail, rice, salt, and *kōji*. In this study, the complete genomic sequence of *Lactobacillus curvatus* NFH-Km12, isolated from this unique food, is reported. NFH-Km12 has a 1.9-Mbp chromosome and contains 5 plasmids.

Lactobacillus curvatus is a lactic acid bacterium widely associated with food fermentation (1–3). *L. curvatus* has also been isolated from kabura-zushi, a traditional Japanese fermented food made from salted yellowtail, salted turnip, and *kōji* (malted rice) (4). Because of the unique environment produced through the combined fermentation of fish and vegetables, it was expected that *L. curvatus* from kabura-zushi would have a unique phenotype or genotype. To explore its genetic characteristics, *L. curvatus* NFH-Km12, isolated from kabura-zushi, was sequenced.

NFH-Km12 was cultured by *Lactobacillus de Man-Rogosa-Sharpe* (MRS) broth (Becton, Dickinson and Company, NJ, USA) under 30°C overnight and provided for DNA extraction by the phenol-chloroform method. Whole-genome sequencing of NFH-Km12 was carried out using Illumina MiSeq and Oxford Nanopore minION platforms. For sequencing, from almost 1 μg of extracted DNA, 2 × 300-bp paired-end libraries and around 10-kbp sheared libraries prepared using g-TUBE (Covaris, Inc., MA, USA) were used for MiSeq and minION sequencing, respectively. Hybrid *de novo* assembly of the 1.41 million reads from MiSeq sequencing and 82,421 reads from minION sequencing that were expected to have ~540× coverage was performed using Unicycler (5). Six circular contigs that were indicated as complete sequences by Unicycler were obtained from the assembly and were annotated using DFAST (6). The strain contained a 1,911,461-bp chromosome with a G+C content of 42.00% and 6 rRNA operons, 65 tRNAs, and 1,946 coding sequences (CDSs). The 5 remaining contigs were determined to be plasmids (pNFH-Km12A, 37,398 bp; pNFH-Km12B, 21,680 bp; pNFH-Km12C, 12,250 bp; pNFH-Km12D, 3,029 bp; pNFH-Km12E, 2,023 bp), with a total of 86 CDSs, making the isolate unlike previously reported *L. curvatus* strains.

Data availability. This whole-genome shotgun project has been deposited in ENA under BioProject number [PRJDB6985](https://www.ebi.ac.uk/bioproject/118885), and the assembly has been deposited in GenBank under the accession numbers [AP018699](https://www.ncbi.nlm.nih.gov/nuccore/118885) to [AP018704](https://www.ncbi.nlm.nih.gov/nuccore/118885).

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