



Draft Genome Sequence of *Oenococcus kitaharae* CRBO2176, Isolated from Homemade Water Kefir

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ABSTRACT Here, we announce the draft genome sequence of an *Oenococcus kitaharae* strain isolated from homemade water kefir in Bordeaux, France. *O. kitaharae* CRBO2176 is deposited at the Biological Resources Center Oenology (CRBO) of the Institute of Vine and Wine Science (ISVV; Villenave d'Ornon, France).

Lactic acid bacteria are important in various fermentation processes, for which some species are described as highly versatile, while others are adapted to specific niches (1). This is especially true in fermented beverages, which harbor distinct members of the genus *Oenococcus* (2). Wine and apple ciders are undoubtedly the favorite habitats of *Oenococcus oeni* species, and strains have progressively been domesticated to this complex environment (2, 3). A few strains of *O. oeni* (4), as well as members of the three sister species, namely, *Oenococcus sicerae* (5), *O. alcoholitolerans* (6), and *O. kitaharae* (7), have also been isolated from overripe fruits and beverages with low alcohol content, such as water kefir (8). Here, we report the draft genome sequence of an *O. kitaharae* isolate from water kefir to enrich the limited genomic resources of *Oenococcus* species and better understand the processes of adaptation to kefir.

A homemade kefir prepared from figs (Bordeaux, France) was plated onto red grape juice agar (9), and the plates were incubated at 25°C for 5 days under anaerobic conditions. Slow-growing isolates were purified three times by single-colony isolation. Among these, an isolate (CRBO2176) was selected, and colony PCR was performed using the universal 16S primers fD1 and rD1 (10). Sequence analysis of the amplicon showed 99.9% similarity to *O. kitaharae* DSM 17330 (GenBank accession number [CM001398](#)) based on the Ribosomal Database Project (RDP) Classifier algorithm (RDP trainset 18/release 11.5) (11). For whole-genome sequencing, the strain was statically cultivated for 72 h at 25°C in MRS broth (pH 6). Genomic DNA was extracted using the Promega DNA Wizard kit (2) and submitted to the Genome-Transcriptome Facility of Bordeaux for library preparation (QIAseq FX DNA; Qiagen, Courtaboeuf, France) and whole-genome sequencing (Illumina MiSeq v3), producing 2 × 254-bp paired-end reads.

Default parameters were used for all software unless otherwise specified. A total of 445,075 raw read pairs were obtained, trimmed using Trimmomatic v0.39 (12), and

TABLE 1 Characteristics of the kefir isolate and genome assembly in this study

Parameter	Finding
No. of contigs	7
Largest contig (bp)	647,507
Total length (bp)	1,754,187
N_{50} (bp)	578,835
N_{75} (bp)	411,412
L_{50}	2
L_{75}	3
GC content (%)	42.77

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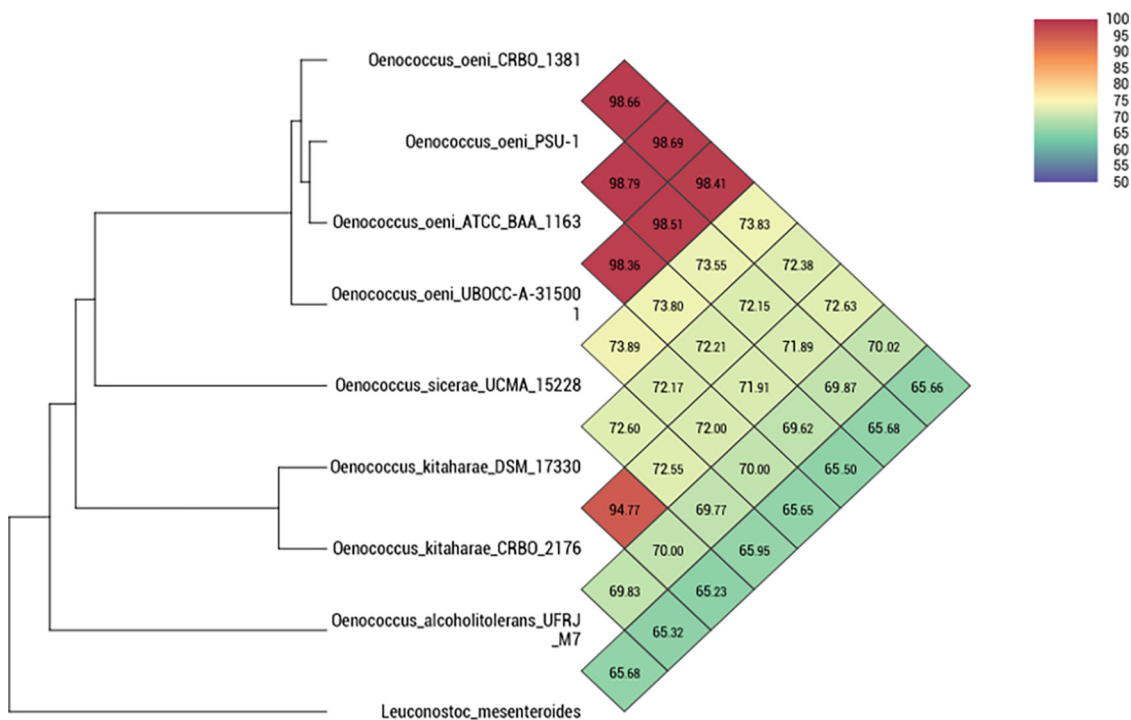


FIG 1 Heatmap showing the average nucleotide identity by orthology (OrthoANI) between strain CRBO2176 and all the type strains of the genus *Oenococcus*, calculated using OAT software, with *Leuconostoc mesenteroides* ATCC 8293 (GenBank accession number [GCA_000014445.1](https://www.ncbi.nlm.nih.gov/GenBank/ accession/GCA_000014445.1)) used as the outgroup.

assembled using SKESA v2.4.0 (13), generating 7 contigs with a genome length of 1,754,187 bp and 66-fold coverage (Table 1). Plasmids and prophages were absent from CRBO2176 according to PlasmidFinder v2.1.1 (14) and PHASTER (Web service; accessed August 2022) (15). The NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v6.2 (16) was used to predict 1,771 genes, with 1,721 coding DNA sequences, 44 tRNA genes, and 3 rRNA genes.

Like other members of the genus *Oenococcus*, strain CRBO2176 can reliably be distinguished from all other *Leuconostocaceae* and *Lactobacillaceae* species by the presence of conserved signature indels (CSIs) in 13 proteins: DNA-directed RNA polymerase subunit beta, two different CSIs in translocase subunit SecY, 50S ribosomal protein L13, molecular chaperone DnaK, riboflavin kinase, Sua5/YciO/YrdC/YwIC family protein, RluA family pseudouridine synthase, amino acid permease, TatD family hydrolase, YidC/Oxal family membrane protein insertase, class I S-adenosylmethionine (SAM)-dependent RNA methyltransferase, and GTPase HflX (17).

The draft genome showed a Mash (18) (MinHash v1.1) distance of 0.0333 and an average nucleotide identity of 94.77% (calculated using OrthoANI v1.40 [19]) with the type strain DSM 17330 (GenBank accession number [NZ_CM001398](https://www.ncbi.nlm.nih.gov/GenBank/ accession/NZ_CM001398)), isolated from shochu (Fig. 1).

Data availability. The 16S rRNA gene sequence, genome sequence, and raw sequencing reads for CRBO2176 have been deposited at GenBank under accession numbers [OP985037](https://www.ncbi.nlm.nih.gov/GenBank/ accession/OP985037) and [JANJQP000000000](https://www.ncbi.nlm.nih.gov/GenBank/ accession/JANJQP000000000), BioProject accession number [PRJNA865506](https://www.ncbi.nlm.nih.gov/BioProject/ accession/PRJNA865506), BioSample accession number [SAMN30114423](https://www.ncbi.nlm.nih.gov/BioSample/ accession/SAMN30114423), and SRA accession number [SRR21928607](https://www.ncbi.nlm.nih.gov/SRA/ accession/SRR21928607).

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