



# Draft Genome Sequence of *Enterococcus dispar* CoE-457-22, Isolated from Traditionally Produced Montenegrin Dry Sausage

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**ABSTRACT** *Enterococcus dispar* was isolated for the first time from synovial fluid and stool cultures and described as a new species in 1991. Here, we report the genome of *E. dispar* CoE-457-22, which was obtained from traditionally produced Montenegrin dry sausage (sudzuk).

Limited information is available about *Enterococcus dispar*. Similar to other enterococci, *E. dispar* has been isolated from the environment (1, 2), animals (3), food (4), and clinical samples (5–8). Genomic analysis of strain CoE-457-22, which was isolated from Montenegrin dry sausage, may provide useful information on environmental adaptation, safety aspects (9), and contributions to the typicity of traditional food products (10).

Sample enrichment and isolation of bacterial strains from traditional Montenegrin dry sausage (sudzuk) were performed using de Man, Rogosa, and Sharpe (MRS) agar (Thermo Fisher Scientific, Oxoid Deutschland) according to the ISO 15214:1998 method (11). Colonies that were morphologically suspected to be lactic acid bacteria (LAB) were subcultured on MRS agar for species identification by matrix-assisted laser desorption/ionization–time of flight mass spectrometry (MALDI-TOF MS) (Microflex LT/SH system with the MBT Compass IVD 4.1.100 module; Bruker, Billerica, MA, USA) and whole-genome sequencing (WGS).

Genomic DNA was isolated from overnight cultures grown on blood agar at 37°C using the MagAttract high-molecular-weight (HMW) DNA kit (Qiagen, Hilden, Germany). Libraries were prepared using a DNA preparation (M) kit (Illumina, Inc., San Diego, CA, USA), and 2 × 150-bp sequencing was performed on a NextSeq 2000 instrument (Illumina, Inc.) as described previously (12). A long-read sequencing library was prepared using the rapid barcoding sequencing kit (SQK-RBK004; Oxford Nanopore Technologies, Oxford, UK) and sequenced with a FLO-MIN106D R9.4.1 SpotON flow cell on a MinION Mk1C device, according to the manufacturer's instructions. A total of 6,841 Nanopore reads, with an  $N_{50}$  value of 5,883 bp, were obtained using guppy v6.1.5 in fast base-calling mode and filtered using Filtlong v0.2.1 with the following parameters: min\_length, 1000; keep\_percent, 90; target\_bases, 50000000. A total of 5,349,760 Illumina reads were quality controlled using FastQC v0.11.9 and used untrimmed in the final hybrid assembly using Unicycler v0.5.0, which resulted in 6 contigs with a mean coverage of 287-fold, an  $N_{50}$  value of 2,293,182 bp, a genome size of 2.7 Mb, and a GC content of 37.2% (Table 1).

The Comprehensive Antibiotic Resistance Database (CARD) and tools from the Center for Genomic Epidemiology (<http://www.genomicepidemiology.org>) were used for detection of antimicrobial resistance genes (ARGs), virulence genes (VGs), plasmids, and pathogen families. BAGEL4 (13) and antiSMASH v6.0 (14) were used to detect genes for the synthesis of secondary metabolites and aromatic compounds. Default parameters were used for all software

**Editor** Irene L. G. Newton, Indiana University, Bloomington

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The authors declare no conflict of interest.

**Received** 3 October 2022

**Accepted** 11 November 2022

**TABLE 1** Characteristics of *Enterococcus dispar* CoE-457-22

Attribute	Finding
Assembly size (bp)	2,662,631
Avg contig length (bp)	443,771
No. of contigs	6
$N_{50}$ (bp)	2,293,182
GC content (%)	37.2
Genome coverage (×)	287
Total no. of genes	2,604
Total no. of coding sequences	2,537
No. of RNA genes	67
No. of noncoding RNA genes	4
No. of tRNAs	60
No. of CRISPR/Cas elements	1
Pathogenic families	Hypothetical protein (GenBank accession no. <a href="#">BAF77294</a> , <a href="#">BAF77275</a> , and <a href="#">BAF77283</a> ), transmembrane amino acid transporter protein (GenBank accession no. <a href="#">CBJ22574</a> ), conserved hypothetical protein (GenBank accession no. <a href="#">CBJ22562</a> , <a href="#">CBJ22569</a> , <a href="#">CBJ22565</a> , and <a href="#">CBJ22571</a> ), small subunit ribosomal protein S19P (GenBank accession no. <a href="#">ABP89047</a> ), 30S ribosomal protein S21 (GenBank accession no. <a href="#">ABP90399</a> ), polyribonucleotide nucleotidyltransferase (GenBank accession no. <a href="#">CBJ22582</a> ), and ribosomal protein L29 (GenBank accession no. <a href="#">AA080083</a> )

unless otherwise specified. Vancomycin and tetracycline susceptibility testing was performed using Etest strips (bioMérieux, Vienna, Austria).

The NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (15) identified 2,604 genes, 2,537 coding sequences, 19 pseudogenes, and 67 RNA genes (Table 1). Basic Local Alignment Search Tool (BLAST) (16) analysis revealed 99.56% similarity of the 16S rRNA genes between CoE-457-22 and *E. dispar* ATCC 21566. Digital DNA-DNA hybridization (dDDH) (formula d4) (<https://tygs.dsmz.de>) and average nucleotide identity (ANI) (17) analyses revealed values of 94.8% and 98.99%, respectively, for similarity between CoE-457-22 and *E. dispar* ATCC 51266.

CoE-457-22 carried the ARGs *tetM*, *vanY*, and *vanT* and was sensitive to vancomycin and resistant to tetracycline. Plasmids, VGs, bacteriocin genes, and secondary metabolite biosynthetic gene clusters were not detected. PathogenFinder identified 12 pathogenic families (18) (Table 1).

**Data availability.** This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under BioProject accession number [PRJNA882413](#) and BioSample accession number [SAMN30933858](#). This is the first version of this genome. The raw sequence reads have been deposited in the Sequence Read Archive (SRA) under the accession numbers [SRR21656176](#) and [SRR22245459](#).

## ACKNOWLEDGMENT

The research was funded through a grant from the Ministry of Science and Technological Development of Montenegro, Centre of Excellence for Digitalization of Microbial Food Safety Risk Assessment and Quality Parameters for Accurate Food Authenticity Certification (FoodHub) (grant 013660/2 from 2019).

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