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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Enterococcus mundtii* CRL1656

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We report the draft genome sequence of *Enterococcus mundtii* CRL1656, which was isolated from the stripping milk of a clinically healthy adult Holstein dairy cow from a dairy farm of the northwestern region of Tucumán (Argentina). The 3.10-Mb genome sequence consists of 450 large contigs and contains 2,741 predicted protein-coding genes.

Enterococcus mundtii is a coccoid, Gram-positive, pigmented lactic acid bacterium (LAB) that belongs to the family *Enterococcaceae* (2). The strain *E. mundtii* CRL1656 was isolated from the stripping milk of a cow from the region of Trancas, province of Tucumán, Argentina. This bacteriocinogenic LAB strain has been proposed as a probiotic microorganism to prevent mastitis in cows (3). The genomic DNA was extracted from the cultured bacterium according to Pospiech and Newman (6).

In this report, the draft genome sequence of *E. mundtii* CRL1656 consisting of 450 contigs is presented. The genome sequence was obtained using a whole-genome shotgun (WGS) strategy (231,679 reads totaling ~89 Mb; ~28.71-fold coverage of the genome) with a 454 GS Titanium pyrosequencer at the Instituto de Agrobiotecnología Rosario (INDEAR, Rosario), Argentina.

Quality filtered reads were *in silico* assembled using the 454 Newbler 2.3 assembler, giving 450 large contigs. The draft genome includes 3,102,251 bases with a G+C content of 38.31%. Genome annotation was done using the standard operating procedures (SOPs) for prokaryotic annotation from ISGA (4) and from the Rapid Annotation Using Subsystem Technology (RAST) server (1). A total of 2,764 coding sequences (CDS) and 65 structural RNAs (49 tRNAs) were predicted. Annotation covered 297 RAST subsystems (43%) with 1,176 CDS, with 64 CDS being labeled as hypothetical proteins. On the other hand, 1,588 CDS (57%) did not belong to any subsystems, and 871 of those corresponded to hypothetical proteins. A comparison between *E. mundtii* CRL1656 and the related microorganism *Enterococcus faecium* DO (GenBank accession number NZ_ACIY00000000) indicated that these two bacteria share 1,363 CDS with known functions. Furthermore, the same comparative analysis performed against the *Enterococcus faecalis* V583 genome (GenBank accession number NC_004668), which has been extensively annotated, indicated that 1,328 CDS with known function are also present in the *E. mundtii* genome.

As this strain is adapted to dairy and plant environments, a large set of genes (406) related to sugar metabolism (lactose and galacto-oligosaccharide as well as raffinose and stachyose utilization, etc.) was detected. In addition, the obtained genome contains putative genes for 11 histidine kinases and 15 response regulators. Genes related to the prokaryotic immune system CRISPR (5), frequently found in other LAB, were not detected. Twenty-two genes that might be related to the resistance to antibiotics and toxic compounds were also found. Of note, 3 of them encode putative β-lactamases, 4 are involved in resistance to fluoroquinolones, and 2 encode multidrug efflux pumps. Moreover, 12 genes coding for transposases (4 of them corresponding to insertion sequences not related to any known family) were detected. A cluster of 3 genes involved in bacteriocin synthesis was found in contig 00009. Further *in silico* comparative and experimental work will be needed to determine the beneficial or potentially probiotic characteristics of this microorganism.

Nucleotide sequence accession number. The draft genome sequence of *E. mundtii* CRL1656 is available in the GenBank database under the accession number AFWZ00000000.1.

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