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Draft Genome Sequence of *Enterococcus faecalis* Strain UCD-PD3

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Here, we present the draft genome sequence of *Enterococcus faecalis* strain UCD-PD3. The assembly contains 2,861,314 bp in 73 contigs. This strain was isolated from a feral domestic cat (*Felis catus*) anal sac secretion sample, as part of a project on isolating and characterizing the microbes present in feline anal sacs.

*Enterococcus faecalis* is commonly found in the gut of mammals and is known to be a symbiotic bacterium (1). *E. faecalis* UCD-PD3 was isolated from feline anal sac secretions collected as a part of a larger study of the microbiology of cats (kittybiome). Here, the goal was to isolate and characterize bacterial isolates from anal sacs from the domestic cat *Felis catus*. Anal sacs were expressed as a part of a spay and neuter clinic on feral cats. The anal sac is considered an anaerobic environment, capable of supporting the growth of *E. faecalis*, an aerotolerant anaerobe (2). Swab samples of the secretions were collected and placed in 1× phosphate-buffered saline (PBS). We inoculated 50 μl of diluted anal sac secretion onto Colombia blood agar and incubated at 37°C for 5 days under low-oxygen conditions (BD GasPak EZ container system). One colony was selected and subcultured onto Colombia blood agar and streaked for isolation. A fresh colony was subcultured three times and incubated under the same conditions for 5 days each time. DNA was then extracted directly from an isolated colony using a Promega Wizard genomic DNA purification kit. PCR was performed to amplify the 16S rRNA gene using 27F and 1391R primers. A paired-end library was created using a Nextera XT library preparation kit (Illumina) in preparation for whole-genome sequencing. Using a PippinPrep (Sage Science), we selected 600- to 900-bp fragments. The size-selected library was sequenced on a MiSeq sequencing. Using a PippinPrep (Sage Science), we selected 600- to 900-bp fragments. The size-selected library was sequenced on a MiSeq

A paired-end library was created using a Nextera XT library preparation kit (Illumina) in preparation for whole-genome sequencing. Using a PippinPrep (Sage Science), we selected 600- to 900-bp fragments. The size-selected library was sequenced on a paired-end 300-bp run of an Illumina MiSeq. Following the completion of quality trimming and error correction by the A5-miseq assembly pipeline, 807,883 high-quality reads were assembled into 73 contigs, with 36× coverage and a G+C content of 37.6% (7, 8). Genome completeness was estimated using PhyloSift software, which searched for 37 highly conserved single-copy marker genes, and one copy of each was found in this assembly (9).

Annotation was performed using RAST (10). *E. faecalis* strain UCD-PD3 contains 2,686 predicted coding sequences and 59 noncoding RNAs. The full-length 16S rRNA sequence (1,552 bp) was analyzed using BLAST and matched with 100% identity with other *E. faecalis* strains.

**Accession number(s).** This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession no. LYBN00000000. The version described in this paper is version LYBN01000000.

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**REFERENCES**

