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Complete Genome Sequence of the Probiotic *Enterococcus faecalis* Symbioflor 1 Clone DSM 16431

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Here, we report the complete and annotated genome sequence of the probiotic *Enterococcus faecalis* Symbioflor 1 clone DSM 16431, included in a commercial probiotic product used for more than 50 years without any reports of infection. This sequence will provide new insights into the biology of this nonpathogenic and probiotic microorganism.

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Enterococci are facultative anaerobic Gram-positive cocci. They are regular commensals of the gastrointestinal tract, the oral cavity, and the vagina in humans (1). Enterococci can cause a wide variety of diseases in humans, including urinary tract infection, bacteremia, endocarditis, peritonitis, and wound infection (2, 3). Nevertheless, *Enterococcus faecalis* has potential benefits for human health and is currently used as food-starter cultures and probiotics. These organisms are used in traditional Mediterranean cheeses and other fermented foods such as sausages, olives, and vegetables. Furthermore, enterococci have been used as probiotics to improve the intestinal microbial balance (4, 5).

Here, we report the complete and annotated genome sequence of the nonpathogenic probiotic *E. faecalis* Symbioflor 1 clone DSM 16431. It was originally isolated in the 1950s from the stool specimen of a healthy human adult and has been in use as a probiotic for more than 50 years without any report or documentation of infection. Based on toxicological studies it has been shown that the strain is safe and can be used for direct human application (6, 7). The overall transcriptional responses of pathogenic *E. faecalis* strains and the Symbioflor 1 probiotic strain to growth in urine are highly conserved, suggesting that it is the presence or absence of virulence and adaptive traits rather than expression levels of these factors that determines pathogenic potential (8).

Three different kinds of libraries were prepared for sequencing. Initially, a genomic shotgun plasmid library (~2-kb inserts) was constructed and sequenced with Sanger sequencing technology. Subsequently, a standard library of sheared genomic DNA was sequenced on the GS FLX sequencer from Roche (Basel, Switzerland). A hybrid assembly with reads from both technologies (Sanger, 13,131 reads; 9.9 Mb; 454 pyrosequencing, 206,726 reads, 47.8 Mb) was created with the GS *de novo* assembler. Gaps between contigs were closed by PCR followed by Sanger sequencing. For larger gaps, a fosmid library (~40-kb inserts) (CopyControl fosmid library production kit, Epicenter, Madison, WI) was used as a template for genome closure. To further improve consensus quality, we also performed a sequencing run on the Illumina MiSeq system using a standard Nextera library, yielding 3,134,284 reads giving a total of 399.5 Mb (amounting to 164-fold coverage). The final assembly was conducted with MIRA version 3.9.4 (9), and DNASTAR SeqMan version 8.02 was employed to close remaining gaps. The genome comprises 2,810,675 bp and was annotated by using RAST (10) and GenDB (11). The circular genome contains 2,733 coding sequences and 63 tRNAs. The average GC content was determined to be 37.72%. Of note, Symbioflor 1 contains two major deletions in proximity to the *vanB*-associated island and the *efaB5* element, leading to the loss of *vanB* operon, bacteriocin, cytolysin L, enterococcal surface protein sp./*efaA*, gelatinase, and hyaluronidase genes (7, 12), thus providing important clues for its nonpathogenic nature. A unique region encoding a bacteriophage was detected at positions 1846700 through 1891973 by using PHAST (13).

Nucleotide sequence accession number. The genome sequence of *E. faecalis* Symbioflor 1 clone DSM 16431 has been deposited in the EMBL database under accession number HF558530.

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