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Complete Genome Sequence of the Commensal *Streptococcus salivarius* Strain JIM8777[▽]

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The commensal bacterium *Streptococcus salivarius* is a prevalent species of the human oropharyngeal tract with an important role in oral ecology. Here, we report the complete 2.2-Mb genome sequence and annotation of strain JIM8777, which was recently isolated from the oral cavity of a healthy, dentate infant.

The commensal bacterium *Streptococcus salivarius* is one of the earliest colonizers of oral mucosal surfaces in infants (detectable a few hours after birth) and remains prevalent in the oropharyngeal tract throughout the human life span. *S. salivarius* often constitutes the majority of total cultivable flora on soft tissues of the mouth and in saliva and is a major component of biofilms colonizing the dorsal surface of the tongue and the buccal epithelium (3). It participates in the maintenance of the microbial equilibrium in the human oral cavity and is thought to contribute to oral health. For example, it exerts an antagonistic effect against pathogens involved in tooth decay, periodontitis, and sore throat (13, 14, 17–19). Moreover, *S. salivarius* influences the inflammatory responses triggered by periodontal and enteric pathogens *in vivo* (10, 15) and displays immunomodulatory and anti-inflammatory properties *in vitro* (7, 11, 12). Here, we provide the first complete genome sequence of a commensal strain isolated from the oral cavity of a healthy, dentate infant.

The complete genome sequence of *S. salivarius* strain JIM8777 was determined by using a conventional Sanger-based whole-shotgun strategy supplemented with next generation sequencing (NGS) short-read technology. Briefly, the ends of DNA inserts from two libraries were sequenced using dye terminator chemistry, and the reads were assembled into 299 contigs with Phred/Phrap software (8), providing 8-fold coverage. Contigs were ordered by using the PROJECTOR2 software (20) with the genome of the closely related *Streptococcus thermophilus* CNRZ1066 (2) as a reference. Gaps were closed by multiplex PCR followed by sequencing of the PCR product and primer walking (16). Finally, the use of the Life Technologies SOLiD sequencer with 446-fold coverage allowed for correction of 180 base substitution sequencing er-

rors, 25 single-nucleotide insertions, and 4 single-nucleotide deletions.

Annotation of coding sequences, ribosome-binding sites, transcriptional terminators, tRNA, and rRNA was performed using the AGMIAL annotation platform (4). Gene products were subjected to protein localization prediction using the software SurfG+ (1). The circular chromosome of *S. salivarius* JIM8777 is composed of 2,210,0574 bp with an overall G+C content of 40.9%. It includes 1,979 putative protein-coding genes, of which 1,580 (79.9%) could be annotated as encoding proteins with known biological functions and 399 (20.1%) could be annotated as encoding hypothetical proteins. The genome harbors 68 tRNA genes, 6 rRNA operons, 5 insertion sequence (IS) elements, and one putative prophage region.

Analysis of the genome of *S. salivarius* strain JIM8777 revealed the presence of genes shown to contribute to the stability of oral communities, such as genes involved in lactose uptake, urea catabolism, and bacteriocin production (5, 6, 9, 21). Comparative genomics with the closely related dairy bacterium *S. thermophilus* (also known as *S. salivarius* subsp. *thermophilus*) revealed that the commensal *S. salivarius* genome contains strikingly fewer pseudogenes and encodes a much higher number of predicted secreted/surface-exposed proteins. These features might reflect the specific adaptation of the two species to their respective ecological niches (oral cavity versus milk environment). The first complete genome sequence of this commensal *S. salivarius* strain will contribute to our understanding of the role of this species in oral ecology and human health.

Nucleotide sequence accession number. The complete genome sequence of *Streptococcus salivarius* strain JIM8777 has been deposited at DDBJ/EMBL/GenBank under accession number FR873482.

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