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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Streptococcus salivarius* PS4, a Strain Isolated from Human Milk

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***Streptococcus salivarius* is a commensal species commonly found in the human oropharyngeal tract. Some strains of this species have been developed for use as oral probiotics, while others have been associated with a variety of opportunistic human infections. Here, we report the complete sequence of strain PS4, which was isolated from breast milk of a healthy woman.**

The commensal bacterium *Streptococcus salivarius* belongs to the viridans streptococci, being the prototype species of the *S. salivarius* group. This group also includes *Streptococcus thermophilus*, one of the most industrially relevant lactic acid bacteria species. *S. salivarius* is among the earliest colonizers of the infant oral mucosal surfaces and remains prevalent in the human oropharyngeal tract throughout the life span (12), where it contributes to oral health (8, 10, 11). In fact, some strains have found commercial applications as oral probiotics (12).

This species has also been isolated from human colostrum and milk (5, 9), which may explain why it may be detectable in the mouth a few hours after birth (3). While the complete genomes of commensal and clinical *S. salivarius* strains have been determined previously (1–4), here we provide the first genome sequence of a commensal streptococcal strain isolated from breast milk of a healthy woman. *S. salivarius* PS4 (formerly strain VM18) was selected for genome sequencing because of its safety in animal models and its ability to produce exopolysaccharides and antimicrobial compounds (including a bacteriocin), to form biofilms, and to inhibit the infectivity of the type 1 human immunodeficiency virus (HIV-1) *in vitro*, with distinct inhibitory effects against R5- and X4-tropic HIV-1 (9).

The entire genome of *S. salivarius* PS4 was sequenced by 454 pyrosequencing on a GS-FLX sequencer to 13-fold coverage (454 Life Sciences, Branford, CT). The initial draft assembly provided 96 contigs when we used the Newbler program v. 2.3 (Roche Applied Science). The draft genome includes 2.05 Mb with a GC content of 39.8%, a total of 1,742 genes, and 44 RNA-encoding sequences. Coding regions were predicted using the BG7 prediction system (Era7 Technologies, Granada, Spain), which proceeds from protein similarity detection to open reading frame prediction. The BG7 system avoids the loss of genes with frameshifts or alterations in the start or stop codons and is tolerant to fragmentation of genes in different contigs (which is frequent in next-generation sequencing [NGS] genome projects). The semiautomatic annotation of the sequences resulted in 56 final contigs, 1,553 protein-coding genes, 38 tRNA-encoding genes, and 3 rRNA operons. No known virulence factor, antibiotic resistance determinant, or putative genomic island representative of the accessory genomes of pathogenic species was found. A cluster related to exopolysaccharide synthesis was found in contigs 00064 and 00016. This *eps* cluster is composed of genes encoding proteins involved in regulation of exopolysaccharide synthesis, chain length determination, and membrane translocation. These genes are followed by genes encoding several glycosyltransferases required for assembly of the basic repeating unit and enzymes involved in repeat unit polymerization. The 3′ end of the cluster contains genes encoding proteins related to membrane translocation of the polymer subunits and enzymes needed for the production of nucleotide precursors. The *S. salivarius* PS4 genome sequence will be useful for comparative genomics and for obtaining better knowledge of the genetic basis of its potentially probiotic traits, particularly of its potential interactions with HIV-1 and dendritic cells. Recently, such an approach was successfully applied to a *Lactobacillus* strain isolated from breast milk (6, 7).

Nucleotide sequence accession numbers. The results from this whole-genome shotgun project have been deposited at DDBJ/EMBL/GenBank under the accession number AJFW00000000. The version described in this paper is the first version, AJFW01000000.

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