

Complete Genome Sequence of the Clinical *Streptococcus salivarius* Strain CCHSS3[∇]

Christine Delorme,^{1,2*} Eric Guédon,^{1,2} Nicolas Pons,^{1,2} Corinne Cruaud,³ Arnaud Couloux,³ Valentin Loux,⁴ Hélène Chiapello,⁴ Claire Poyart,⁵ Céline Gautier,^{1,2} Nicolas Sanchez,^{1,2} Mathieu Almeida,^{1,2} Sean P. Kennedy,^{1,2} S. Dusko Ehrlich,^{1,2} Jean-François Gibrat,⁴ Patrick Wincker,³ and Pierre Renault^{1,2}

INRA, UMR1319 Micalis, F-78350 Jouy-en-Josas, France¹; INRA, AgroParisTech, UMR Micalis, F-78350 Jouy-en-Josas, France²; Génoscope (CEA), UMR8030, CNRS and Université d'Evry, Evry, France³; INRA, UR1077 Mathématique, Informatique et Génome (MIG), F-78350 Jouy-en-Josas, France⁴; and INSERM U1016, Institut Cochin; CNRS (UMR 8104); Faculté de médecine, Université Paris Descartes, Paris, France—APHP, Service de bactériologie, Centre national de référence des streptocoques, Hôpital Cochin, France⁵

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***Streptococcus salivarius* is a commensal species commonly found in the human oral cavity and digestive tract, although it is also associated with human infections such as meningitis, endocarditis, and bacteremia. Here, we report the complete sequence of *S. salivarius* strain CCHSS3, isolated from human blood.**

Streptococcus salivarius belongs to the salivarius group of the viridans streptococci (7). This commensal species, a prevalent inhabitant of the oral mucosa, has also been associated with human infections and is one of the most common viridans streptococci causing bacteremia independently of neutropenia state (4, 9). *S. salivarius* meningitis has often been described as being related to fistulas and to cranial and intestinal trauma (3). Nevertheless, the majority of meningitis cases due to *S. salivarius* were recognized as being iatrogenic consequent upon invasive spinal procedures (1). The complete genome from a *S. salivarius* buccal commensal strain was determined previously (8), while an incomplete sequence is available for a strain isolated from skin (GenBank accession no. N2ACLO00000000). We report here the complete genome sequence of *S. salivarius* CCHSS3, a strain isolated from human blood, which was chosen from eight clinical strains characterized by multilocus sequence typing analysis (5).

The genome sequence of *S. salivarius* CCHSS3 was determined by using (i) a conventional whole-shotgun strategy with the Sanger technology to produce a circular draft of the genome, and (ii) NGS sequencing technology to correct potential sequencing errors. The initial genome draft was assembled into 374 contigs with Phred/Phrap software (6) with 15-fold coverage from sequences provided by a small-insert and a long-insert genome library. The contigs were ordered by using Projector2 software (11) using the complete genome sequence of *S. salivarius* JIM8777 (8) as a template. Gap closures were carried out by testing combinatory pools of primers to amplify junction fragments (10) and followed by Sanger sequencing by primer walking. IS boundaries were systematically sequenced to perform correct assembly. Fi-

nally, mismatch and small insertion-deletion correction were carried out by SOLiD sequencing technology with 110-fold coverage. Genome annotation was performed using the AGMIAL annotation platform (2).

The circular chromosome of *S. salivarius* CCHSS3 is composed of 2,217,184 bp with an overall G+C content of 40%. It comprises 2,032 genes, including 2,027 protein-coding genes; 74% of them (1,468) were annotatable with known proteins with biological function, and 534 (26%) were annotated as corresponding to hypothetical protein. The genome also harbors 68 tRNA genes covering all amino acids and 6 rRNA operons.

Comparison of the commensal JIM8777 and clinical CCHSS3 genomes revealed a chromosomal inversion symmetrical to the origin of replication switching about two-thirds of the CCHSS3 genome compared to strain JIM8777 and the closely related species *Streptococcus thermophilus*. Orthologous genes had an average of 95% identity at the nucleotide level. Remarkably, the two strains differ by more than 400 specific genes and their numbers of IS elements, which are, respectively, 5 and 56. No known virulence factor, antibiotic resistance determinant, or putative genomic island representative of the accessory genomes of pathogenic species was found. The complete genome sequence of clinical *S. salivarius* strain will promote studies to understand host interaction and opportunistic pathogenicity within salivarius group.

Nucleotide sequence accession number. The complete genome sequence of *S. salivarius* strain CCHSS3 is accessible at GenBank under the accession number FR873481.

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* Corresponding author. Mailing address: Institut Micalis (Microbiologie de l’Alimentation au service de la Santé), INRA (UMR1319) et AgroParisTech, Domaine de Vilvert, F-78352 Jouy-en-Josas, cedex, France. Phone: 33 1 34 65 25 26. Fax: 33 1 34 65 25 21. E-mail: christine.delorme@jouy.inra.fr.

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