HAL
open science

Complete Genome Sequence of the Commensal Streptococcus salivarius Strain JIM8777

Eric Guédon, Christine Delorme, Nicolas Pons, Corinne Cruaud, Valentin Loux, Arnaud Couloux, Céline Gautier, Nicolas Sanchez, Séverine Layec, Nathalie Galleron, et al.

To cite this version:

Eric Guédon, Christine Delorme, Nicolas Pons, Corinne Cruaud, Valentin Loux, et al.. Complete Genome Sequence of the Commensal Streptococcus salivarius Strain JIM8777. Journal of Bacteriology, 2011, 193 (18), pp.5024-5025. 10.1128/JB.05390-11 . hal-03649194

HAL Id: hal-03649194

https://hal.science/hal-03649194v1

Submitted on 22 Apr 2022

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

JOURNAL OF BACTERIOLOGY, Sept. 2011, p. 5024–5025 Vol. 193, No. 18
0021-9193/11/$12.00 doi:10.1128/JB.05390-11
Copyright © 2011, American Society for Microbiology. All Rights Reserved.

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

Eric Guédon,[1,2]* Christine Delorme,[1,2] Nicolas Pons,[1,2] Corinne Cruaud,[4] Valentin Loux,[3] Arnaud Couloux,[4] Céline Gautier,[1,2] Nicolas Sanchez,[1,2] Séverine Layec,[1,2] Nathalie Galleron,[1,2] Mathieu Almeida,[1,2] Maarten van de Guchte,[1,2] Sean P. Kennedy,[1,2] S. Dusko Ehrlich,[1,2] Jean-François Gibrat,[3] Patrick Wincker,[4] and Pierre Renault[1,2]*

INRA, UMR1319 Micalis, F-78350 Jouy-en-Josas, France[1]; INRA, AgroParisTech, UMR Micalis, F-78350 Jouy-en-Josas, France[2]; INRA, UR1077 Mathématique, Informatique et Génome, F-78350 Jouy-en-Josas, France[3]; and Génoscope (CEA), UMR8030, CNRS and Université d'Evry, Evry, France[4]

Received 17 June 2011/Accepted 29 June 2011

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 errors, 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.

* Corresponding author. Mailing address: Institut Micalis (Microbiologie de l'Alimentation au service de la Santé), INRA (UMR1319) et AgroParisTech, Domaine de Vilvert, F-78350 Jouy-en-Josas cedex, France. Phone: 33 1 34 65 25 25. Fax: 33 1 34 65 25 21. E-mail: eric.guedon@jouy.inra.fr.

▽ Published ahead of print on 8 July 2011.

This research was funded by the INRA and by the grant "Séquençage d'organismes pathogènes ou commensaux" from Genoscope.

REFERENCES

1. **Barinov, A., et al.** 2009. Prediction of surface exposed proteins in Streptococcus pyogenes, with a potential application to other Gram-positive bacteria. Proteomics **9:**61–73.
2. **Bolotin, A., et al.** 2004. Complete sequence and comparative genome analysis of the dairy bacterium Streptococcus thermophilus. Nat. Biotechnol. **22:** 1554–1558.
3. **Bowden, G. H., D. C. Ellwood, and I. R. Hamilton.** 1979. Microbial ecology of the oral cavity. Adv. Microb. Ecol. **3:**135–217.
4. **Bryson, K., et al.** 2006. AGMIAL: implementing an annotation strategy for prokaryote genomes as a distributed system. Nucleic Acids Res. **34:**3533–3545.
5. **Chen, Y. Y., M. J. Betzenhauser, J. A. Snyder, and R. A. Burne.** 2002. Pathways for lactose/galactose catabolism by Streptococcus salivarius. FEMS Microbiol. Lett. **209:**75–79.
6. **Chen, Y. Y., K. A. Clancy, and R. A. Burne.** 1996. Streptococcus salivarius urease: genetic and biochemical characterization and expression in a dental plaque streptococcus. Infect. Immun. **64:**585–592.
7. **Cosseau, C., et al.** 2008. The commensal Streptococcus salivarius K12 downregulates the innate immune responses of human epithelial cells and promotes host-microbe homeostasis. Infect. Immun. **76:**4163–4175.
8. **Ewing, B., L. Hillier, M. C. Wendl, and P. Green.** 1998. Base-calling of automated sequencer traces using phred. I. Accuracy assessment. Genome Res. **8:**175–185.
9. **Fontaine, L., et al.** 2007. Quorum-sensing regulation of the production of Blp bacteriocins in Streptococcus thermophilus. J. Bacteriol. **189:**7195–7205.
10. **Frick, J. S., et al.** 2007. Identification of commensal bacterial strains that modulate Yersinia enterocolitica and dextran sodium sulfate-induced inflammatory responses: implications for the development of probiotics. Infect. Immun. **75:**3490–3497.
11. **Guglielmetti, S., et al.** 2010. Oral bacteria as potential probiotics for the pharyngeal mucosa. Appl. Environ. Microbiol. **76:**3948–3958.
12. **Kaci, G., et al.** 2011. Inhibition of the NF-κB pathway in human intestinal epithelial cells by commensal Streptococcus salivarius. Appl. Environ. Microbiol. **77:**4681–4684.
13. **Levesque, C., J. Lamothe, and M. Frenette.** 2003. Coaggregation of Streptococcus salivarius with periodontopathogens: evidence for involvement of fimbriae in the interaction with Prevotella intermedia. Oral Microbiol. Immunol. **18:**333–337.
14. **Sanders, C. C., and W. E. Sanders, Jr.** 1982. Enocin: an antibiotic produced by Streptococcus salivarius that may contribute to protection against infections due to group A streptococci. J. Infect. Dis. **146:**683–690.
15. **Sliepen, I., et al.** 2009. Microbial interactions influence inflammatory host cell responses. J. Dent. Res. **88:**1026–1030.
16. **Sorokin, A., et al.** 1996. A new approach using multiplex long accurate PCR and yeast artificial chromosomes for bacterial chromosome mapping and sequencing. Genome Res. **6:**448–453.
17. **Tamura, S., et al.** 2009. Inhibiting effects of Streptococcus salivarius on competence-stimulating peptide-dependent biofilm formation by Streptococcus mutans. Oral Microbiol. Immunol. **24:**152–161.
18. **Tanzer, J. M., A. B. Kurasz, and J. Clive.** 1985. Competitive displacement of mutans streptococci and inhibition of tooth decay by Streptococcus salivarius TOVE-R. Infect. Immun. **48:**44–50.
19. **Teughels, W., et al.** 2007. Bacteria interfere with A. actinomycetemcomitans colonization. J. Dent. Res. **86:**611–617.
20. **van Hijum, S. A., A. L. Zomer, O. P. Kuipers, and J. Kok.** 2003. Projector: automatic contig mapping for gap closure purposes. Nucleic Acids Res. **31:**e144.
21. **Wescombe, P. A., N. C. Heng, J. P. Burton, C. N. Chilcott, and J. R. Tagg.** 2009. Streptococcal bacteriocins and the case for Streptococcus salivarius as model oral probiotics. Future Microbiol. **4:**819–835.