

Available online at www.sciencedirect.com

ScienceDirect

journal homepage: www.e-jmii.com

Correspondence

Identification of *Streptococcus sinensis* from a patient with endocarditis using MALDI-TOF mass spectrometry, 16S rDNA- and *sodA*-based phylogeny



Dear Editor,

A 37-year-old man was admitted to a French University hospital for an impaired general state with weight loss and intermittent fever for three months. He had a mitral regurgitation. Examination showed an oral temperature of 38.7 °C, purpura of the lower extremities, hepatosplenomegaly and a grade 3 systolic murmur. Trans-thoracic echocardiography revealed a massive mitral regurgitation, a voluminous mitral vegetation and another one on the atrial side of the mitroaortic trigone, supporting the diagnosis of infective endocarditis (IE). A dental examination revealed six teeth in need of extraction. Empirical intravenous antibiotherapy with amoxicillin (6 g/d), amoxicillin + clavulanate (6 g/d) and gentamicin (6 mg/kg) was started. Three sets of blood cultures were positive for Gram-positive cocci arranged in chains. The strain was identified as *Streptococcus sinensis* by matrix-associated laser desorption ionization-time of flight (MALDI-TOF) mass spectrometry (Biotyper, Bruker) (score value: 2.2). As the Bruker database only contains the *S. sinensis* HKU4 reference strain profile, profile, a phylogenetic molecular identification was performed. The Bioinformatics Bacterial Identification tool positioned the 1479 bp primer-less 16S rDNA sequence (GenBank accession number: KU598921) close to *S. sinensis* type strain HKU4 (GenBank accession no. AF432856), the sequence presenting 99% identity in a 1479 nucleotide overlap using the NCBI Blast program.¹ The phylogeny based on the *sodA* gene analysis confirmed this position (Fig. 1). The strain was susceptible to penicillin G (0.013 mg/L), ceftriaxone (0.047 mg/L), levofloxacin

(0.38 mg/L), rifampicin (0.023 mg/L), linezolid (0.38 mg/L) and vancomycin (0.38 mg/L). Treatment was modified according to the antimicrobial susceptibility: gentamicin (6 mg/kg) and amoxicillin (12 g/d) for 6 days, then amoxicillin (12 g/d) for 3 weeks. The patient also underwent an aortic valve replacement with a bioprosthetic valve six days after the first antibiotic treatment. Gram stain and culture of the excised valve were negative (probably due to prior antibiotherapy) but 16S rDNA and *sodA* molecular analysis of the excised valve confirmed the presence of *S. sinensis*.

S. sinensis together with *Streptococcus cristatus* belongs to the revised phylogenetic “cristatus clade” of the Mitis group of the genus *streptococci*.² *S. sinensis* is a prevalent organism in the oral microbiome and was detected in 22% of saliva samples from healthy volunteers in Hong Kong.³

Few cases of *S. sinensis*-associated IE were reported. This species was documented as a causative agent of IE in six patients throughout the world.^{4,5} No other infections besides IE caused by *S. sinensis* have been described thus far in humans, suggesting that bacteria may possess virulence factors to adhere to and colonize heart valves and to cause endocardial damage. However, as other viridans streptococci, it could cause many types of infections. The number of IE cases or other type of infections due to *S. sinensis* is probably underestimated because commercial kits often misidentify *S. sinensis* as *Streptococcus intermedius* or *Streptococcus anginosus* and identification of viridians streptococci at the species level is not performed routinely. Therefore *S. sinensis* could be considered as an emerging pathogen whose identification at the species level is of obvious interest in this case of severe infection.

<https://doi.org/10.1016/j.jmii.2018.04.004>

1684-1182/Copyright © 2018, Taiwan Society of Microbiology. Published by Elsevier Taiwan LLC. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

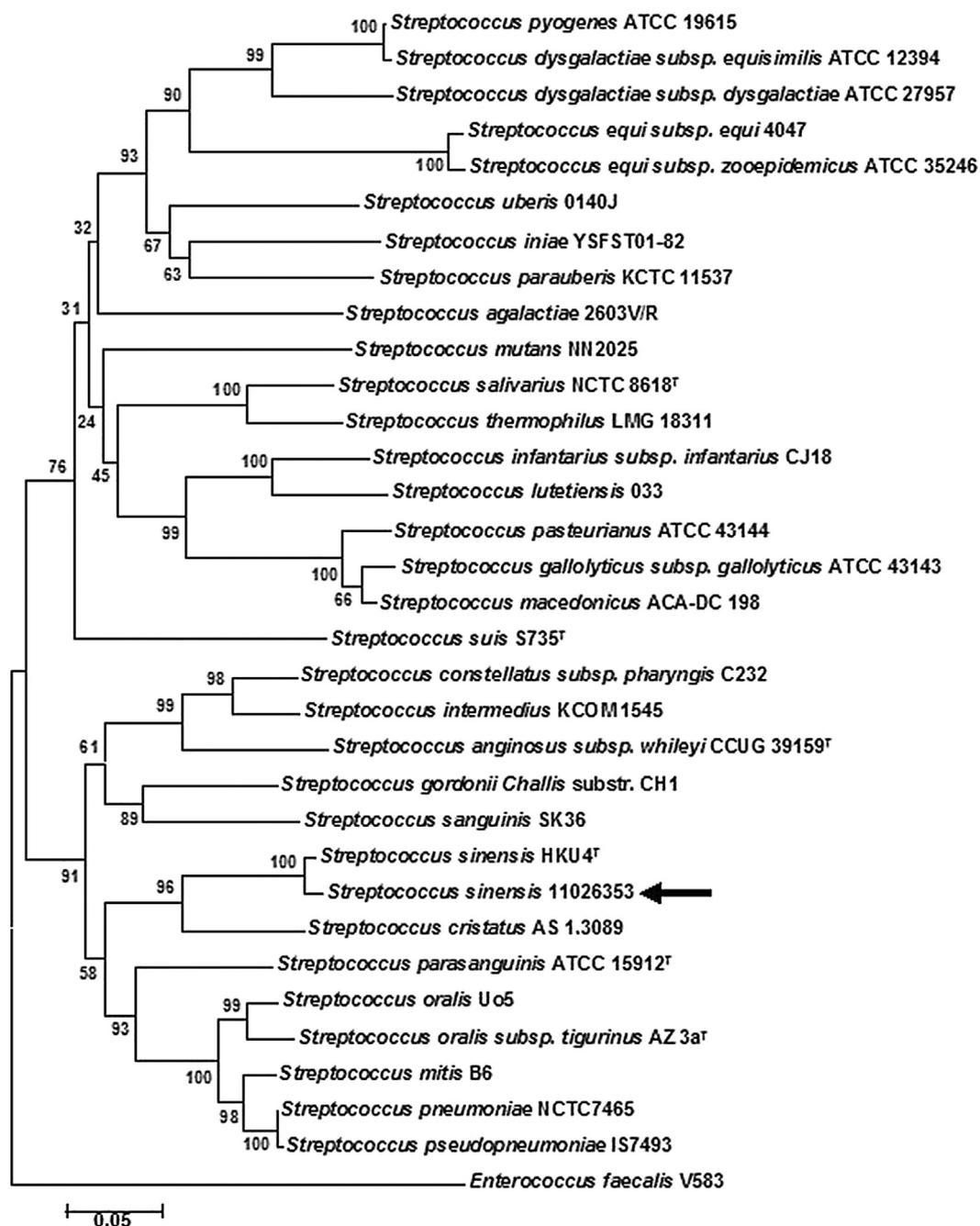


Figure 1. Evolutionary relationships of *Streptococcus* taxa based on the *sodA* gene. The phylogeny is based on the alignment of approximately 606 nucleotides of the *sodA* gene. The phylogenetic analysis was generated with the MEGA software version 6.06 and the neighbor-joining method. The optimal tree with the sum of branch lengths = 2.73452332 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches. The tree is not rooted and drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Kimura 2-parameter and are represented in the units of the number of base substitutions per site. All ambiguous positions were removed for each sequence pair. There were a total of 508 positions in the final dataset. The *sodA* gene of *Enterococcus faecalis* was used as an unrelated outgroup sequence. Only the cluster presenting the *S. sinensis* strain 11026353 (arrow) is shown. All sequences are labeled by species, strain name and/or collection number. ^T, type strain.

Conflicts of interest

All authors have no conflicts of interest to declare.

Acknowledgments

We are grateful to Alexis Groppi (Centre de Bioinformatique de Bordeaux (CBiB) – Centre de Génomique Fonctionnelle Bordeaux – Université de Bordeaux, France) for confirming the phylogenetic analysis of *sodA* and 16S rDNA genes using a PhyML-based phylogeny.

References

1. Devulder G, Perriere G, Baty F, Flandrois JP. BIBI, a bioinformatics bacterial identification tool. *J Clin Microbiol* 2003;41: 1785–7.
2. Jensen A, Scholz CF, Kilian M. Re-evaluation of the taxonomy of the Mitis group of the genus *Streptococcus* based on whole genome phylogenetic analyses, and proposed reclassification of *Streptococcus dentisani* as *Streptococcus oralis* subsp. *dentisani* comb. nov., *Streptococcus tigurinus* as *Streptococcus oralis* subsp. *tigurinus* comb. nov., and *Streptococcus oligofermentans* as a later synonym of *Streptococcus cristatus*. *Int J Syst Evol Microbiol* 2016;66: 4803–20.
3. Woo PC, Teng JL, Tsang SN, Tse CW, Lau SK, Yuen KY. The oral cavity as a natural reservoir for *Streptococcus sinensis*. *Clin Microbiol Infect* 2008;14:1075–9.
4. Uckay I, Rohner P, Bolivar I, Ninet B, Djordjevic M, Nobre V, et al. *Streptococcus sinensis* endocarditis outside Hong Kong. *Emerg Infect Dis* 2007;13:1250–2.
5. Seta V, Teicher E, Fortineau N, Ladouceur M, Lambotte O. Infective endocarditis caused by *Streptococcus sinensis*. *Med Mal Infect* 2015;45:56–7.

Julien Goret

Univ. Bordeaux, INRA, USC EA 3671, *Mycoplasma and Chlamydia Infections in Humans*, F-33000 Bordeaux, France

CHU Bordeaux, Hôpital Pellegrin, Laboratoire de Bactériologie, F-33000 Bordeaux, France

Thomas Baudinet

CHU Bordeaux, Hôpital Saint-André, Service de Cardiologie, F-33000 Bordeaux, France

Fabrice Camou

Nahéma Issa

CHU Bordeaux, Hôpital Saint-André, Service de Réanimation Médicale, F-33000 Bordeaux, France

Prune Gaillard

CHU Bordeaux, Hôpital Saint-André, Service de Cardiologie, F-33000 Bordeaux, France

Gaëtane Wirth

CHU Bordeaux, Hôpital Pellegrin, Service des Maladies Infectieuses et Tropicales, F-33000 Bordeaux, France

Carine Greib

CHU Bordeaux, Hôpital du Haut Lévêque, Service de Médecine Interne et Maladies Infectieuses, F-33600 Pessac, France

Laurent Barandon

CHU Bordeaux, Hôpital du Haut Lévêque, Service de Chirurgie Cardiaque, F-33600 Pessac, France

Francis Mégraud

CHU Bordeaux, Hôpital Pellegrin, Laboratoire de Bactériologie, F-33000 Bordeaux, France

Univ. Bordeaux, INSERM, UMR1053 Bordeaux Research in Translational Oncology, BaRITOn, F-33076 Bordeaux, France

Cécile Bébéar

Olivia Peuchant*

Univ. Bordeaux, INRA, USC EA 3671, *Mycoplasma and Chlamydia Infections in Humans*, F-33000 Bordeaux, France

CHU Bordeaux, Hôpital Pellegrin, Laboratoire de Bactériologie, F-33000 Bordeaux, France

Armelle Ménard

CHU Bordeaux, Hôpital Pellegrin, Laboratoire de Bactériologie, F-33000 Bordeaux, France

Univ. Bordeaux, INSERM, UMR1053 Bordeaux Research in Translational Oncology, BaRITOn, F-33076 Bordeaux, France

*Corresponding author. USC EA 3671 Infections humaines à mycoplasmes et à chlamydiae, Centre National de Référence des Infections Sexuellement Transmissibles Bactériennes, Université de Bordeaux, 146 rue Léo Saignat, 33076 Bordeaux Cedex, France. Fax: +33 5 56 93 29 40. E-mail address: olivia.peuchant@u-bordeaux.fr

(O. Peuchant)

13 February 2018

Available online 29 May 2018