Native valve endocarditis caused by *Streptococcus oligofermentans*: a case report

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**Introduction:** Viridans group streptococci (VGS), which are commensal flora in the oral cavity, can act as opportunistic pathogens causing serious infections such as infective endocarditis (IE). Species identification of these organisms is difficult because of variability in phenotypic traits among strains of the same species.

**Case presentation:** We report a case of endocarditis in a 64-year-old male patient caused by *Streptococcus oligofermentans*, which was identified by 16S rRNA gene sequencing. *S. oligofermentans* is a commensal of the oral cavity and rarely causes disease. This is the second report of IE caused by *S. oligofermentans*.

**Conclusion:** Molecular methods are necessary to ascertain the identity of VGS strains, particularly those that rarely cause human disease.

**Keywords:** 16S rRNA gene PCR; infective endocarditis; *Streptococcus oligofermentans*.

**Abbreviations:** IE, infective endocarditis; VGS, viridans group streptococci.

Received 18 November 2014
Accepted 28 April 2015
identity with S. oligofermentans (GenBank accession no. KP119845). The patient recovered after treatment with intravenous vancomycin and ceftriaxone for 4 weeks, and was discharged from the hospital.

S. oligofermentans was first described as a new Streptococcus sp, of the mitis group of VGS by Tong et al. (2003) during a survey of oral acid-producing bacteria in dental plaque and saliva of caries-free patients with nasopharyngeal carcinoma. The organism derives its name from the fact that it ferments few sugars, typically only glucose and sucrose. Our isolate appeared to be different because it did not hydrolyse hippurate or ferment sucrose but was similar in all other phenotypic characters to the isolate described by Tong et al. (2003). The organism has been isolated from healthy tooth surfaces, has a weaker ability to produce acid and demineralize hydroxyapatite, and is not considered to be a pathogen. To the best of our knowledge, only one case of endocarditis caused by S. oligofermentans has been reported so far (Matta et al., 2009). This case was reported in 2009 in a 43-year-old female who presented with fever, arthralgia, a systolic murmur and a forearm abscess. The excised mitral vegetation as well as pus from the abscess were culture negative; however, direct 16S rRNA gene PCR from the clinical specimens and gene sequencing confirmed the presence of S. oligofermentans. In the present case, the organism was isolated from multiple blood cultures, phenotypically characterized and its identity confirmed by 16S rRNA gene amplicon sequencing. The patient recovered with intravenous antibiotic therapy. Recent phylogenetic studies have shown that S. oligofermentans is closely related to Streptococcus sinensis and a new phylogenetic clade, the 'sinensis group' has been proposed which includes Streptococcus sinensis, Streptococcus oligofermentans and Streptococcus cristatus (Teng et al., 2014). 16S rRNA gene PCR, although useful for identification of VGS is considered less accurate than other molecular methods such as multilocus sequence analysis (Naveen Kumar et al., 2014).

Identifying VGS by biochemical methods may be difficult, especially in the case of rare species, and hence molecular methods should be used to ascertain the identity of strains isolated from serious infections.

Acknowledgements

This study was approved by the institutional human ethics committee.

References


Fig. 1. α-Haemolytic, opaque yellowish colonies of S. oligofermentans.