

ZOOBOTIC *STREPTOCOCCUS CANIS* INFECTION IN SINGAPORE

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Dear Sir,

Streptococcus dysgalactiae (*S. dysgalactiae*) subspecies *equisimilis* is a Lancefield Group G streptococcus (GGS) that is responsible for a variety of human infections, including pharyngitis, skin and soft-tissue infections, septic arthritis, osteomyelitis, and bacteraemia. *Streptococcus canis* (*S. canis*), a phenotypically similar close relative, causes pyogenic infections in dogs and cats. However, zoonotic *S. canis* infections in humans have been reported.⁽¹⁾ It has been suggested that the actual number of *S. canis* infections in humans may be underestimated, as GGS is not routinely identified at the species level.⁽¹⁾

According to the Agri-Food and Veterinary Authority of Singapore, the number of dog licences issued in Singapore increased from 35,125 in 2000 to 60,440 in 2014.⁽²⁾ Our study aimed to investigate whether *S. canis* formed a significant proportion of GGS isolated in our laboratory. All large-colony beta-haemolytic GGS isolated for a period of one year, from 19 August 2013 to 19 August 2014, were identified at the species level using MALDI-TOF (Bruker Singapore Pte Ltd, Singapore). Any suspected *S. canis* isolates were confirmed by sequencing of the *16S* rDNA gene.

During the study period, 181 GGS were isolated. The majority were identified as *S. dysgalactiae* subsp. *equisimilis*. One isolate (DM12402_14) was identified by MALDI-TOF as *Streptococcus castoreus* with a score of 2.273. The second- and third-choice identifications were *S. canis* and *S. dysgalactiae* subsp. *dysgalactiae*, with scores of 2.249 and 2.150, respectively. The isolate DM12402_14 was identified by API® 20 Strep (bioMérieux Singapore Pte Ltd, Singapore) as most likely to be *S. canis* (99.1%, Profile 0063405), with *S. dysgalactiae* subsp. *equisimilis* (0.7%) as the second-choice identification. The VITEK® 2 (bioMérieux Singapore Pte Ltd, Singapore) identified the DM12402_14 isolate as *S. dysgalactiae* with 97% probability. However, *S. canis* is not included in the VITEK 2 database. A 1.3 kb fragment of the *16S* rRNA gene was amplified, sequenced and submitted to the National Center for Biotechnology Information's Basic Local Alignment Search Tool and the 16SpathDB 2.0 database. The closest matches were with *S. canis* (99% Genbank accession number EU075063.1, 99.8% Genbank accession number DQ303184.1.1).

There were two limitations to this study. Firstly, only three *S. canis* reference spectra exist in the MALDI-TOF database (MBT 3.0). Secondly, *16S* rRNA gene sequencing was not performed on all GGS. Therefore, it is possible that some *S. canis* were missed.

DM12402_14 was isolated in a mixed culture with *Neisseria canis* from the hand of a 20-year-old man. The patient sustained multiple abrasions and puncture wounds over his right thumb and thenar eminence after his hand was caught in the wheel of a bicycle during an accident. He presented the following day with cellulitis of the right hand. His wounds were debrided and he completed a course of oral amoxicillin and clavulanate potassium with good outcome. Although the patient did not volunteer any information about animal contact at presentation, he recalled at follow-up, after the culture results were known, that his wounds had come into contact with his pet dog, a Siberian husky.

S. canis is not a common cause of GGS infection in humans in Singapore. Although misidentification at the species level does not greatly affect the treatment, availability of low-cost methods of bacterial identification like MALDI-TOF may reveal previously unsuspected zoonotic causes of streptococcal soft-tissue infections of the upper limb.

Yours sincerely,

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