Journal of Microbiology, Immunology and Infection 57 (2024) 970–971

Contents lists available at ScienceDirect

Journal of Microbiology, Immunology and Infection

journal homepage: www.e-jmii.com

Streptococcus canis infection in Taiwan

Streptococcus canis is a beta-hemolytic Lancefield group G *streptococci* (GGS), recognized for causing severe infections in dogs and cats, with a notable zoonotic potential. Although bacteremia caused by GGS was not uncommon, zoonotic *S. canis* infections in humans have rarely been reported.[1] In Northern Taiwan, Liao et al. reported 106 episodes of GGS bacteremia in 92 patients between 1998 and 2004, with the most common causative agent being *S. dysgalactiae* subsp. *equisimilis* (99 episodes), while only two episodes were caused by *S. canis*.[1] The most common human infection caused by *S. canis* was skin and soft tissue infection, followed by bacteremia, urinary tract infection, osteoarticular infection, pneumonia and asymptomatic carriage. However, there was limited reported case of *S. canis* infection in Taiwan.[1] Herein, we present the unusual case of bacteremia caused by 16S rRNA sequencing confirmed *S. canis* in southern Taiwan.

A 64-year-old man with a history of hypertension, coronary artery disease, nasopharyngeal carcinoma in remission, hyperlipidemia, gout, and chronic hepatitis B presented to the emergency department with insidiously progressive left low back pain for three days. The pain reached to 8 out of 10 on the Visual Analog Scale, causing him unable to walk. There was no recent history of trauma. Fever up to 40 °C was noted upon triage. The physical examinations were unremarkable except systolic heart murmur and tenderness over left pelvis and left para-lumbar spine area without skin redness or palpable mass. Initial laboratory investigations revealed leukocytosis and elevated C-reactive protein levels. The abdominal computed tomography disclosed no obvious abscess nor bone lesion. Empirical antibiotic with cefoperazone/sulbactam was administered after collecting clinical specimens for microbiological investigation. Further transthoracic echocardiogram only demonstrated mild mitral valve regurgitation without heart vegetation, however, the magnetic resonance imaging (MRI) of lumbar-spine demonstrated evidence of infectious/inflammatory processes involving the epidural space, left psoas muscle, and left posterior paraspinal soft tissue of L4-5. Two days later, two sets of blood specimens grew *Streptococcus* spp., which was identified as *S. canis* by Bruker Biotyper matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) system and further confirmed by 16S rRNA. Hence, the antibiotic was shifted to ceftriaxone (2 gm every 12 hours) according to the antibiotic susceptibility test. We obtained blood cultures after 3 days of antibiotic treatment and which were cleared. Tracing back through the contact history, it was found that the patient lives with a dog; however, no evidence of a canine bite or scratch was observed. The patient's low back pain gradually subsided over the 2 weeks of antibiotic treatment. After completion of the 4-week course of treatment, the laboratory data were within normal limits and follow-up of MRI revealed regressive changes.

A previous report from northern Taiwan described a case of primary *S. canis* bacteremia with recurrence in a patient with alcoholic liver cirrhosis, who had no history of dog bites.[1] Here, we report a case of *S. canis* bacteremia involving the epidural space, left psoas muscle, and left posterior paraspinal soft tissue in a cancer patient from Southern Taiwan. Both cases highlight the importance of considering zoonotic pathogens in immunocompromised patients with close contact with pets, even in the absence of obvious exposure.

In a previous report,[1] a probable *S. canis* was identified by a negative β-glucuronidase result and further confirmed using the 16S rRNA method. Similarly, in our case, S. canis was initially identified by MALDI-TOF and subsequently confirmed by 16S rRNA sequencing. However, despite MALDI-TOF being commonly used for microbiological identification in Taiwan,[2–5] *S. canis* can be misidentified by this method.[6] Nybakken et al. reported that *S. dysgalactiae* isolate could be mis-identified as *S. canis* when using MALDI-ToF, according to manual curation of the reference spectra in Bruker's Compass Library DB-7854.[6] All these findings suggests that accurate species identification requires molecular diagnostics, such as 16S rRNA sequencing,[1] which is crucial for proper diagnosis and epidemiological investigations.

In conclusion, this report emphasizes the necessity for clinicians to be vigilant about zoonotic infections and ensure accurate microbial identification to avoid misdiagnosis and enable effective treatment.

CRediT authorship contribution statement

Pei-Yun Tsai: Writing – original draft, Data curation, Conceptualization. **Wan-Hsuan Hsu:** Writing – original draft, Investigation, Data curation. **Yu-Hsin Chiu:** Investigation, Data curation. **Chih-Cheng Lai:** Writing – original draft, Data curation, Conceptualization. **Hung-Jen Tang:** Writing – review & editing, Supervision, Conceptualization.

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https://doi.org/10.1016/j.jmii.2024.09.004
Received 3 June 2024; Received in revised form 24 August 2024; Accepted 14 September 2024
Available online 21 September 2024

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