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Thumb Infection Caused by *Streptococcus pseudoporcinus*▽

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***Streptococcus pseudoporcinus*, a recently described organism found in the genitourinary tract of women, was isolated from a thumb wound in a male patient subsequent to trauma. This case describes a rarely reported non-genitourinary tract clinical isolate of *S. pseudoporcinus*.**

CASE REPORT

A 33-year-old male patient presented to the Primary Care/Internal Medicine Clinic at the Veterans Affairs Puget Sound Health Care System in Seattle, WA, in June 2006 after he caught his right thumb in a car door the day before. The thumb was painful, with a hematoma under the nail plate, but not fractured. A hole was punched into the nail plate to assist reattachment. The thumb wound was taped with gauze, and the patient was discharged. Eight days later, the patient returned to the clinic with increased right thumb nail pain and an exudate that could be expressed from the wound. The patient did not have a fever or other systemic symptoms. The nail was discolored under the nail plate but the infection did not extend beyond the nail plate. The patient did not have a fever or other systemic symptoms. Purulence from the wound was sent to the clinical microbiology laboratory for Gram stain and aerobic culture. The patient was discharged with a 10-day course of cephalexin and recovered.

Many white blood cells and many gram-positive cocci in chains were observed on the direct Gram stain from the thumb wound purulence. The next day, after incubation at 35°C in a 5% CO_2 atmosphere, there were many (>100) large, wide-zoned beta-hemolytic colonies present as the only isolate. The gram-positive cocci in chains were catalase negative and reacted with the PathoDx group B reagent (Remel, Lenexa, KS) but not the Streptex group B reagent (Remel). The organism was Voges-Proskauer and pyrrolidonyl arylamidase positive, did not hydrolyze hippurate, and had a slight increase in beta-hemolysis with the CAMP test (using *Staphylococcus aureus* strain ATCC 29212). The isolate was sensitive to all antibiotics tested except tetracycline. The organism was identified by the Vitek II gram-positive identification card as *Streptococcus uberis* with 99.00% probability. This result was questioned since *S. uberis* is not found in humans (9) and is reported to hydrolyze hippurate, to be alpha-hemolytic, and to be CAMP test negative. 16S rRNA gene sequencing was performed as described previously (3, 10). A 461-bp sequence was obtained that matched the *S. pseudoporcinus* type strain ATCC BAA-1381 (GenBank accession no. DQ303209) 16S rRNA gene sequence from the NCBI database at all but position 494 of the *Escherichia coli* 16S rRNA gene sequence. The NCBI, Microseq, and BIBI databases were all used to search for comparison sequences, with all confirming the identification. Sequence analysis was performed using Microseq software as previously described (3, 10).

Streptococcus pseudoporcinus was first described in 2006 after several human isolates phenotypically identified as *Streptococcus porcinus* were sequenced and found to be over 2% dissimilar to any other *Streptococcus* species (1). All of these *S. pseudoporcinus* isolates were recovered from female genitourinary tract specimens (1, 8). Up until this time, the designation *S. porcinus* included strains from both animal sources (which retain the name) and human clinical specimens (essentially all are *S. pseudoporcinus*) (5, 7, 11). 16S rRNA gene sequencing clarified the taxonomy (1, 8). Our *S. pseudoporcinus* isolate was from a thumb wound specimen and was initially identified by the Vitek II gram-positive card as *S. uberis*, an animal pathogen that is a common cause of bovine mastitis (9). To our knowledge, *S. uberis* has not been reported from any human clinical cases of disease. *S. uberis* was found as a contaminant of platelets in one instance, although the platelets were transfused to a patient and no transfusion reaction was recorded (14). The accuracy of the identification of this *S. uberis* isolate is also not known, since no information on the identification was given (14). Analysis of the first 500 bp of the 16S rRNA gene sequence indicated that our isolate was identical at all but one position to the *S. pseudoporcinus* strains identified by Bekal et al. and had a 17-bp difference from *S. porcinus* (1). In the first 500 bp, there are 17 mismatches with *S. porcinus* (1); a difference of over 3% is often considered sufficient to separate genera and thus, of course, species (3).

The phenotypic characteristics of *S. pseudoporcinus*, *S. porcinus*, *S. uberis*, and *Streptococcus agalactiae* (group B streptococcus) are shown in Table 1. Because *S. pseudoporcinus* is a beta-hemolytic streptococcus and can be CAMP and Lancefield group B positive and is isolated from the human female genitourinary tract, it could be confused with *S. agalactiae*. However *S. agalactiae* has a narrow zone of beta-hemolysis, is hippurate hydrolysis positive, is bile esculin

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TABLE 1. Phenotypic characteristics of our *S. pseudoporcinus* isolate and *S. porcinus*, *S. dysgalactiae*, *S. agalactiae*, and *S. uberis*

Phenotypic characteristic	Result for[a]:					
	S. pseudoporcinus		*S. porcinus*[b]	*S. dysgalactiae* subsp. *equisimilis*	*S. agalactiae*	*S. uberis*
	Our isolate	Isolates described in the literature				
Hippurate hydrolysis	−	−	v	−	+	+
Voges-Proskauer	+	v	+	−	+	ND
Pyrrolidonyl arylamidase	+	v	v	−	−	−
Esculin hydrolysis	+	+	+	v	−	+
Inulin fermentation	−	ND	−	−	−	v
Lactose fermentation	−	−	v	v	v	+
Mannitol fermentation	+	+	+	−	−	+
Sorbitol fermentation	+	+	+	v	−	+
β-Gluconuronidase	+	ND	+	+	v	v
Streptex group B reagent	−	v	v	−	+	−
PathoDx group B reagent[c]	+	+	v	−	+	−
β-Hemolysis	Large zone	Large zone	Large zone	Large zone	Small zone	−
CAMP test (or gene)	+	+	+	−	+	−

[a] Data are from references 1, 2, 4–8, and 11–13. +, positive; −, negative; v, variable. ND, not determined. All strains on this table ferment trehalose and are leucine aminopeptidase positive.
[b] From the literature and four in-house strains.
[c] We found the PathoDx test was positive for our *S. pseudoporcinus* isolate and four in-house *S. porcinus* strains when the test was performed with extraction but negative when not extracted.

hydrolysis negative, and does not produce acid from mannitol or sorbitol, unlike both *S. pseudoporcinus* and *S. porcinus*. *S. uberis* differs from *S. pseudoporcinus* in that it is either nonhemolytic or is alpha-hemolytic and is hippurate hydrolysis positive (11).

S. pseudoporcinus and *S. porcinus* are phenotypically very similar. Fourteen of 15 reported strains of *S. pseudoporcinus* reacted with group B antibody from the PathoDx Strep typing kit, and our strain did too (8). *S. porcinus* is nearly always Voges-Proskauer positive, while only about half of the described *S. pseudoporcinus* strains have been Voges-Proskauer positive (7). 16S rRNA gene sequencing may be required to definitively differentiate *S. pseudoporcinus* from *S. porcinus*. Isolates that are phenotypically identified as *S. porcinus* should be sequenced to determine if the isolate is in fact *S. pseudoporcinus*. We have described a rare case of a non-female genitourinary tract infection caused by *S. pseudoporcinus*. *S. pseudoporcinus* is an organism found in the urogenital tract of women. The thumb infection in this patient we think was caused after a trauma to the thumb allowed entrance of the organisms, most likely originating from his wife's vagina. Once inoculated into the traumatized tissue, the organism did elicit an inflammatory response, as indicated by the considerable purulence.

Nucleotide sequence accession number. The sequence of the *S. pseudoporcinus* isolate from this study has been deposited in GenBank under accession no. FJ550603.

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