



Case report

Skin abscess caused by *Trueperella bernardiae*: Case report and literature review

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ABSTRACT

We investigated a skin abscess caused by *Trueperella bernardiae* in a patient with comorbidities. Initial empirical therapy with Clindamycin did not yield a response, and follow-up culture revealed the presence of *T. bernardiae* through MALDI-TOF and NGS. Since no CLSI or FDA breakpoints have been published for this strain, resistant gene screening of the genetic sequence showed the presence of the erm(X) gene (with 95 % identity). This gene confers resistance to erythromycin, clindamycin, lincomycin, pristinamycin, quinupristin, and virginiamycin. Subsequent therapy with oral amoxicillin/clavulanate led to complete healing.

Introduction

Trueperella bernardiae (*T. bernardiae*) is a coryneform, facultative anaerobic, nonspore-forming, nonmotile, gram-positive coccobacillus. It is catalase and oxidase negative with variable hemolytic activity. Until 1995, *T. bernardiae* was classified under Centers for Disease Control and Prevention coryneform group 2. It was subsequently assigned to the genus *Actinomyces* in 1995, then to *Arcanobacterium* in 1997, and finally transferred to the genus *Trueperella* in 2011 [1,2]. *T. bernardiae* is part of the normal microbiota of human skin and the oropharynx, and it is typically regarded as a contaminant. However, reports of *T. bernardiae* as an opportunistic human pathogen have been increasing. The use of matrix-assisted desorption–ionization time-of-flight mass spectrometry (MALDI-TOF MS) has significantly improved the identification of such microorganisms [3]. In this report, we present a case of *T. bernardiae* skin and subcutaneous tissue infection with abscess formation in a diabetic patient.

Case report description

A 66-year-old male with a medical history of type II diabetes mellitus, hypertension, hyperlipidemia, morbid obesity, and prostate cancer

presented to the Emergency Department (ED) with redness and swelling of the left anterior chest wall at the inframammary fold. He had a previous history of abscess formation at the same location three times before, with the last occurrence a year prior that required incision (I) and drainage (D) without complications.

Clinical examination of the patient was unremarkable except for painful redness on the lower left part of the breast, with no fluctuation or discharge. Treatment with oral Clindamycin and topical Mupirocin was initiated, and he was advised to return in two days for a possible indication of incision and drainage (I & D). The patient returned to the ED with increased pain and worsening redness and swelling of the lesion. His vital signs remained stable, and physical examination revealed a 3.0 × 2.0 cm red swollen area with fluctuation on the left anterior chest wall at the inframammary fold. Blood analysis showed neutrophilic leukocytosis (white blood cell count of $9.59 \times 10^9/L$ with 80 % neutrophils). Incision and drainage revealed purulent exudate, which was sent to the microbiology laboratory for culture. The wound was packed with 1/4" Iodoform ointment, and the patient was referred to the wound care team for further follow-up with instructions to continue the current prescription.

The sample was inoculated on Sheep Blood Agar (SBA), Chocolate Agar (CA), MacConkey Agar (MCA), and thioglycolate broth. All media

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were incubated at 35 °C with 5 % CO₂. No growth was observed on the first day, but rare gram-positive cocci were identified on the second day (Fig. 1), which were sub cultured for further characterization. The observed colonies were nonhemolytic, rounded, and creamy in appearance. Identification by MALDI-TOF MS (BioMerieux VITEK MS, Valencia, CA) confirmed them as *Truperella bernardiae*.

Whole genome sequencing of the isolate was performed on the NextSeq 550 instrument (Illumina) after nucleic acid extraction using the QIAamp DNA microkit (Qiagen, Hilden, Germany) and library preparation using the Nextera DNA Flex prep kit (Illumina, San Diego, CA). A total of 281.78 Mbp reads were obtained from the whole genome sequencing analysis, resulting in 123 contigs with an N50 value of 29,726 bp. The final genome length, determined by de novo assembly, was 2,216,733 bp, with an average coverage of 127.1 × and a G + C content of 65.11 %. The pubMLST Species ID predicted the species as *Truperella bernardiae*, and ANI comparison with *Truperella bernardiae* showed a similarity of 99.72 %. Antimicrobial resistance gene analysis using Resfinder revealed the presence of the erm(X) gene (95 % identity), which confers resistance to erythromycin, clindamycin, lincomycin, pristinamycin, quinupristin, and virginiamycin.

Based on these results, the antimicrobial therapy was switched to oral amoxicillin/clavulanate, which was continued for one week. The patient exhibited a successful clinical response, and at the two-week follow-up, the patient was asymptomatic with complete wound healing.

Discussion

The true incidence of *T. bernardiae* infections remains unknown, primarily due to these bacteria not being identified in clinical samples before the widespread use of MALDI-TOF MS. Consequently, *T. bernardiae* infections were likely misclassified as other bacterial infections. This has made it challenging to establish the pathogenicity and clinical implications of *T. bernardiae*, as only a few cases have been reported [4–6]. In this report, we present a well-documented case of *T. bernardiae* skin and subcutaneous tissue infection with abscess formation.

A review of the literature identified a total of 34 reported cases of human infection, including urinary tract infections [5], skin and soft tissue infections/post-surgical infections [7], diabetic foot infections and prosthetic joint infections [8], joint infections excluding prosthetic joints [9], a case of osteomyelitis which is not peer reviewed [10], bacteremia [11], thrombophlebitis in injection drug users [6], breast abscesses [12], and brain abscesses following otitis media [13]. De novo skin infections without preceding surgical wounds or ulcers were found in only two cases, including this report [14].

In general, these infections are more common in patients with other comorbidities, such as bedridden patients, diabetes mellitus, IV drug use, long-term corticosteroid use, and malignancy. However, a few case reports have documented infections in healthy individuals [12]. Risk factors for *T. bernardiae* infection include immunocompromised status, surgical wounds, long-term non-healing skin ulcers, and joint devices. *T. bernardiae* is frequently reported in multiple bacterial infections, so when infection occurs, it is important to consider the possibility of other rare bacteria causing opportunistic infections.

The treatment of choice for *T. bernardiae* infection has not yet been established due to limited data and CLSI has not published any breakpoints for *Truperella*. In our case, the patient was successfully treated with oral amoxicillin/clavulanate for one week, resulting in complete wound healing without recurrence. Current susceptibility data suggests sensitivity to β-lactams, clindamycin, and vancomycin, with resistance to ciprofloxacin, penicillin G, aminoglycosides, metronidazole, and sulfamethoxazole/trimethoprim reported [9,15].

It is important to consider *T. bernardiae* as a causative agent for skin infection with an associated abscess, in an immunocompromised adult. When such patients are encountered, we should consider infections caused by rare bacteria or opportunistic infections. With the aid of

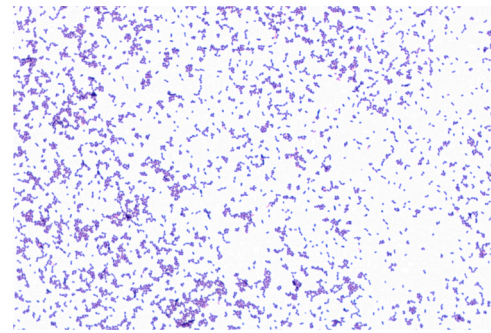


Fig. 1. Gram stain of *T. bernardiae* pure culture.

MALDI-TOF MS technology, organisms like *T. bernardiae* can be identified and probable empirical therapy with β-lactams, clindamycin, and vancomycin could be considered until breakpoints are established. This case highlights the need to further characterize this organism, because it may have greater pathogenic potential than previously recognized, and to further elucidate appropriate antimicrobial therapy.

Ethical approval

N/A.

Consent

NA.

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CRedit authorship contribution statement

Rasha M. Abdelgader and Sarvenaz Karamooz: Data curation, Writing – original draft. **Hosoon Choi and Munok Hwang:** Software, Methodology, Data curation, Writing – review & editing. **Chetan Jinadatha:** Resources, Software, Supervision. **Dharmika H. Navarathna:** Investigation, Methodology, Resources, Software, Supervision, Writing – review & editing.

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