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Multiple skin abscesses associated with bacteremia caused by
Burkholderia gladioli: A case report

Yi-Ting Wang, Xue-Wen Li, Pan-Yang Xu, Chun Yang, Jian-Cheng Xu

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Abstract

BACKGROUND

Burkholderia gladioli (B. gladioli) is regarded as a rare opportunistic pathogen. Only a few patients with abscesses caused by B. gladioli infections have been reported, and these are usually abscesses at the incision caused by traumatic surgery.

CASE SUMMARY

A 74-year-old male patient with abscesses and pain throughout his body for 1 mo was admitted to our hospital. Some of the abscesses had ruptured with purulent secretions on admission. Color Doppler ultrasound examination of the body surface masses showed mixed masses 75 mm × 19 mm, 58 mm × 17 mm, 17 mm × 7 mm, and 33 mm × 17 mm in size in the muscle tissues of both the right and left forearms, the posterior area of the right knee and the left leg, respectively. Abscess secretions and blood cultures grew B. gladioli. The following 3 methods were used to jointly identify the bacterium: an automatic microbial identification system, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry, and full-length 16S rDNA sequencing. After 27 d of treatment with meropenem, etimicin, trimethoprim-sulfamethoxazole and other antibiotics, most of his skin abscesses were flat and he was discharged without any symptoms.

CONCLUSION

This is the first reported case of multiple skin abscesses associated with bacteremia caused by B. gladioli. Our study provides important reference values for the clinical diagnosis and treatment of B. gladioli infections.

Key Words: Burkholderia gladioli; Multiple skin abscesses; Bacteremia; Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry; Case report

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Core Tip: *Burkholderia gladioli* (*B. gladioli*) is a rare opportunistic pathogen. We report the first case of multiple skin abscesses caused by infection due to *B. gladioli*, and the relevant biological information, identification, and sensitivity to drugs, are also described in detail. The following three methods including an automatic microbial identification system, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry, and full-length 16S rDNA sequencing were jointly used to identify this bacterium. Therefore, the results obtained using the combination of these methods, were more accurate and reliable. This case provides a solid basis for the future clinical diagnosis and treatment of *B. gladioli* infections.

INTRODUCTION

*Burkholderia gladioli* (*B. gladioli*) belongs to the genus *Burkholderia*, which is a group of Gram-negative, aerobic, and non-fermentative bacteria. They were originally identified as plant pathogens in gladiolus and other flowers, and most of them were isolated from soil or water samples. In general, *B. gladioli* is an uncommon opportunistic pathogen in clinical infections. In 1989, Christenson et al. [1] identified a strain that was similar to *Burkholderia cepacia*, in sputum samples from 11 patients suffering from cystic fibrosis. This bacterium did not cause disease and was considered to be able to colonize the respiratory tract, and was identified as *B. gladioli* for the first time in 1995, and showed certain pathogenic ability [2]. *B. gladioli* was cultured from abscess secretions and blood from our patient with multiple skin abscesses and bacteremia in June 2021. The automatic microbial identification system, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS), and full-length 16S rDNA sequencing were used to jointly identify *B. gladioli*, based on bacterial morphology, physiology, and biochemical indicator levels, as well as gene and protein levels. To date, this is the first case of multiple skin abscesses associated with bacteremia caused by *B. gladioli* infection. Following treatment with multiple antibiotics, the patient recovered and was discharged from hospital. In this case report, the clinical characteristics and biological characteristics of *B. gladioli* are reported in detail, and previous case reports of patients infected with *B. gladioli* were analyzed retrospectively.

CASE PRESENTATION

**Chief complaints**
A 74-year-old male patient suffering from abscesses and pain throughout his body for 1 mo was admitted to the First Hospital of Jilin University on June 3, 2021.

**History of present illness**
The patient did not have a fever, cough, or abdominal pain during the disease. On admission, the skin on his left anterior chest, abdomen, and limbs showed red abscesses, which ranged in size from a broad bean to that of an egg. Some of the abscesses had ruptured with purulent secretions and obvious tenderness. Deep ulcers the size of 3 eggs were observed on his right upper limb and left lower limb. Furthermore, the ulcers in his right forearm even reached the muscular layer. Petechiae the size of millet grains or beans, were scattered around his lower limbs, with no signs of fading.

**History of past illness**
The patient suffered from left mandibular lymph node enlargement and underwent surgical incision and drainage 4 mo ago. The patient was hospitalized due to pneumonia 3 years ago.

**Personal and family history**
The patient had no relevant personal and family history.

**Physical examination**
Physical examination showed the following: Body temperature was 36.5°C, pulse rate was 70 bpm, respiratory rate was 20 breaths/min, and blood pressure was 115/54 mmHg.
Laboratory examinations
The initial laboratory examinations on admission showed the following levels: white blood cell (WBC) count was 41.96 × 10^9/L, neutrophil absolute value (NE) was 37.64 × 10^9/L, monocyte absolute value was 2.16 × 10^9/L, red blood cell count was 2.93 × 10^12/L, hemoglobin was 80 g/L, hematocrit was 0.266 L/L, red blood cell distribution width was 24.8%, and high-sensitivity C-reactive protein was 170.26 mg/L.

Imaging examinations
Color Doppler ultrasound examinations of the body surface masses on admission showed mixed masses 75 mm × 19 mm, 58 mm × 17 mm, 17 mm × 7 mm, and 33 mm × 17 mm in size in the muscle tissues of both the right and left forearms, the posterior area of the right knee and the left leg, respectively.

MICROBIOLOGICAL IDENTIFICATION OF THE CAUSATIVE AGENT
The patient’s abscess secretions on admission day 2 and 5 were collected and cultured for general bacteria/fungi at 35°C with 5% CO₂. The bacterial culture showed positive results after 24 h, and no fungi were identified even after 72 h. The bacteria were inoculated into sheep blood and MacConkey agar plates at 37°C. After 36 h, yellowish, round, smooth, moist, slightly raised, and neatly edged colonies appeared on the plates. The bacteria showed a short-rod shape, arranged singly or in pairs under the microscope, and were identified as Gram-negative bacteria based on Gram staining results. Biochemical analysis showed positive results for catalase and dynamic tests, and negative for oxidase and H₂S tests. On admission day 2 and 9, the patient’s blood was added to BACT/ALERT FN Plus Aerobic/F and Anaerobic/F media, respectively, and was cultured in a BACT/ALERT VIRTUO automatic blood culture system. The results of Aerobic/F blood cultures were positive after 36 h, and the colony characteristics, microscopic morphology, and biochemical reactions of this bacterium were consistent with the result of pus cultures, and the results of Anaerobic/F blood cultures were negative. Blood cultures were performed again on admission day 26. The results of Aerobic/F and Anaerobic/F blood cultures were negative after 72 h. The colony and microscopic morphology of B. gladioli are shown in Figure 1A.

In addition, the following 3 methods were used to jointly identify the bacterium in abscess secretions and blood: (1) The VITEK 2 GN cards in the VITEK 2 XL automatic microbial identification system were used for identification (98% probability), and after 4.78 h of analysis, B. gladioli was identified; (2) VITEK MS mass spectrometry (99.9% probability) and MALDI-TOF-MS technology were used to identify the bacterium as B. gladioli, and relevant results of the mass spectromet was are shown in Figure 1B; and (3) Full-length 16S rDNA sequencing was also used to identify this bacterium, and the primers 7F 1540R and 27F 1492R were used for the amplification of 16S rRNA. The PCR products were purified using the SK825 Ezup column bacterial genomic DNA extraction kit and the sequence was determined by the Applied Biosystems 3730XL sequencer. The Ribosomal Database Project database was applied for similarity alignment against this bacterium (NCBI Accession No. DQ513513). The sequence determination results were as follows: the length of the sequence was 1441 bp, the sequence similarity was 99% between this bacterium and B. gladioli. The detailed sequence was as follows:

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CGCCCGTCACACCATGGGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGGAGGA. The above three methods were combined to identify the bacterium as *B. gladioli*. The instruments and reagents used in full-length 16S rDNA sequencing were from Sangon Biotech Shanghai Co., Ltd. Instruments and reagents used in other methods were derived from BioMérieux (Lyon, France).

The Kirby-Bauer method was used to determine the drug sensitivity of the bacterium in abscess secretions and blood. Several colonies were picked and prepared into bacterial suspensions of 0.5 McFarland standard, and then the suspensions were spread on Mueller-Hinton agar plates. The sensitive strips of trimethoprim-sulfamethoxazole (TMP-SMZ), meropenem, and minocycline from Thermo Fisher Scientific were placed on the plates. The plates were inverted after 15 min and incubated at 35°C for 18 h. The diameters of the bacteriostatic zones were measured. The above procedures were in line with the Clinical and Laboratory Standards Institute (CLSI) operating standards. The results of four drug sensitivity tests of abscess secretions and blood cultures are shown in Table 1.

### FINAL DIAGNOSIS

The final diagnosis of the presented case was multiple skin abscesses associated with bacteremia due to *B. gladioli*.

### TREATMENT

The patient underwent 27 d of treatment, and the medications administered during hospitalization are shown in Figure 2.
Table 1 Results of four sensitivity tests by the Kirby-Bauer method

<table>
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<tr>
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<th>Abscess secretion culture (first)</th>
<th>Abscess secretion culture (second)</th>
<th>Aerobic blood culture (first)</th>
<th>Aerobic blood culture (second)</th>
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<td>Diameter of inhibition zone (mm)</td>
<td>36</td>
<td>36</td>
<td>30</td>
<td>26</td>
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<td>TMP-SMZ</td>
<td>28</td>
<td>27</td>
<td>22</td>
<td>25</td>
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<tr>
<td>Meropenem</td>
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<td>Minocycline</td>
<td>26</td>
<td>27</td>
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<td>26</td>
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TMP-SMZ: Trimethoprim-sulfamethoxazole.

Figure 2 The changes in various indicators during hospitalization of this patient. Abscess size: the size of the circle represents the size of the abscess, the larger the circle is, the larger the abscess is, the five sizes of the circles represent 4 cm, 3 cm, 2 cm, 1 cm and 2 mm, respectively; Abscess secretion: the size of the circle represents the amount of abscess secretion, the larger the circle is, the more abscess secretion; NRS: Numerical rating scale, this is a numerical scale for pain, in which the number 0-10 is used to indicate the degree of pain; WBC: White blood count; NE: Neutrophil absolute value.

OUTCOME AND FOLLOW-UP

The patient’s multiple deep ulcers became shallower and a large amount of new granulation tissue was observed on admission day 12. On admission day 18, his skin abscesses were significantly reduced, and there were no secretions after extrusions. Auxiliary examinations showed that the absolute values of WBC and NE were normal. The changes in various indicators during hospitalization of this patient are shown in Figure 2. Most of the skin abscesses were flat on admission day 27 and the patient was discharged. He was instructed to pay attention to wound care and hygiene after discharge. He was asked to take 0.5 g meropenem intravenously 3 times/d, 0.3 g etimicin intravenously once/d, and TMP-SMZ orally twice/d (two tablets each time).

DISCUSSION

In previous studies, all patients with abscesses caused by *B. gladioli* infections were local[2-12], but multiple skin abscesses associated with bacteremia caused by *B. gladioli* were reported for the first time. Basic information of published cases and this case is shown in Table 2. *B. gladioli* is easily neutralized by human serum or complement factors; thus, healthy people are rarely infected with this bacterium[13, 14]. This patient had a history of pneumonia, which provided the same pathological background as in the reported cases of *B. gladioli* infections, most of which were patients with cystic fibrosis and chronic granuloma diseases, suggesting that people with underlying diseases are more susceptible to *B. gladioli*. 
In addition, *B. gladioli* can also easily infect newborns with low immune functions[15]. Consistent with some reports[3,6,8], *B. gladioli* was obtained from the blood and abscess secretions of the patients. It has also been reported that *B. gladioli* was detected in lymph nodes[15], cornea[14], and sputum[16]; therefore, it is possible to improve the detection rates of the bacterium by simultaneously examining the blood, sputum, as well as various other secretions in patients. The patient in this report had no other clinical manifestations except for skin abscesses during hospitalization, which was different from previous cases who had a fever, cough, and other symptoms[8]. Previous studies showed that commercial tests such as the API[7] or VITEK[13] bacterial identification system could mistakenly identify *B. gladioli* as *B. cepacia*. Other studies used cell fatty acid analysis[2] or partial gene sequencing of 16S-23S rRNA[16] to identify *B. gladioli*, but the risks of misidentification always exist. In the clinical laboratory, it is important to timely and accurately identify the bacterium, which is closely related to clinical diagnosis and treatment, and carelessness may delay the diagnosis of diseases. In our laboratory, an automatic microbial identification system, MALDI-TOF MS, and full-length 16S rDNA sequencing were used to jointly identify the bacterium, which overcame the difficulties in the identification process and ensured the accuracy of the identification results.

Drug sensitivity tests were carried out using the Kirby-Bauer method in our laboratory. However, it was difficult for the microbiology laboratory to issue the drug sensitivity reports as the CLSI did not provide the *B. gladioli* drug sensitivity standards. In previous reports, the microtiter dilution method[6] and the E-test method[14] were used to test the drug sensitivity of *B. gladioli*. The results showed that *B. gladioli* was sensitive to TMP-SMZ and meropenem. In some hospitals, patients with *B. gladioli* infections were treated with the above two drugs, and the prognoses were good[2,3]. After treatment with TMP-SMZ and meropenem, combined with other antibacterial agents, the abscesses in our patient were reduced and finally disappeared, and the condition was well controlled. The patient has now recovered from hospital. However, due to the differences between *in vitro* and *in vivo* environments, as well as the differences between drug sensitivity tests *in vitro* and drug efficacies *in vivo*, there will be antimicrobial drug failures and ineffective treatments. As reported by Quon *et al*[17], patients infected with *B. gladioli* can still deteriorate and die, even after treatment with TMP-SMZ and meropenem. It has also been reported that levofloxacin[11], cefazolin and gentamicin[18] were effective in the treatment of patients with *B. gladioli* infections. The above studies suggested that the treatment of
B. gladioli was not limited to certain drugs, and multiple factors should be considered in patients with different clinical symptoms. Nevertheless, at least five people have died due to B. gladioli infections[6,8,16,17,19].

Following a literature review, it was found that the symptoms, identification methods, drug treatments, and outcomes of patients with B. gladioli infections were not the same. The reasons for these differences can be summarized as follows: (1) There were differences in defenses, immune functions, and autologous flora among different populations; (2) There were also differences in the routes and quantity of bacterial invasions; (3) There were differences in the instruments and reagents for the detection and identification of bacteria; and (4) There were differences in the judgment criteria of drug sensitivity used in different laboratories.

CONCLUSION

This paper reports the first case of multiple skin abscesses associated with bacteremia caused by B. gladioli, including the clinical features, laboratory examinations, medications, and outcome. All patients with abscesses caused by B. gladioli infections were analyzed retrospectively. The sensitivity and accuracy of B. gladioli identification results were improved by the combined applications of three identification methods, including an automatic microbial identification system, MALDI-TOF MS, and full-length 16S rDNA sequencing. Our study provides important reference values for the clinical diagnosis and treatment of B. gladioli infections, and is beneficial for the rehabilitation of patients.

FOOTNOTES

Author contributions: Wang YT, Li XW, Xu PY, Yang C, and Xu JC performed the literature review, collected all the data related to the case report; Wang YT wrote the first draft of the manuscript and all authors commented on previous versions of the manuscript; all authors have read and approved the final manuscript.

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