Yokenella regensburgei infection in an immunocompetent host:A case report

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Abstract

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Abstract

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Keywords: Yokenella regensburgei,skin and soft tissue infection,immunocompetent host

Background

Yokenella regensburgei, was firstly identified in 1984, belongs to Enterobacteriaceae [1]. Y. regensburgei is a gram-negative, periplasmic flagellated opportunistic pathogen that is ubiquitous in natural environments such as soil and water. Y. regensburgei and Hafnia alve share similar biochemical properties and thus might be misidentified as the latter by automated bacterial identification systems [2]. It commonly affects immunocompromised patients, such as patients acquired immunodeficiency syndrome and patients undergoing treatment with corticosteroids or immunosuppressors [3-4]. Here, we described the infection of Yokenella regensburgei in an immunocompetent patient.

Case presentation

In May 2022, a 71-year-old female from China suffered from limited mobility and pain for 2 months after a trauma to her left lower leg, and the symptoms aggravated with redness and swelling for 3 days. Two months ago, she hit a tree while doing farm work. The antero- medial part of the leg was broken and bleeding without appreciable erythema or swelling. The next day, the patient was admitted to local hospital and received wound irrigation and antibiotic treatment. Soon, the wound on leg healed but the patient still felt pain occasionally. Three days prior to her admission, she felt more pain in the wound and fever around the wound. There was no obvious exudation and pus around the wound, which was only covered with some scab.

Her body temperature was 36.4°C, with blood pressure of 171/83, a pulse rate of 67 beats per minute, and oxygen saturation was 98% breathing ambient air. Physical examination on admission was unremarkable, except for her left leg wound as described. There was no history of any major illness in the past, which indicated that she was an immunocompetent host.

Blood examinations revealed anemia with hemoglobin of 90g/liter (reference range, 110 to 160 grams/liter). Her white blood cell count was 6.03 × 109 cells/liter (reference range, 4.0× 109 to 10.0 × 109 cells/liter), differential with 69.50% neutrophilic granulocyte (reference range, 50.0% to 70.0%) and 19.70% lymphocytes (reference range, 20.0% to 40.0%). Blood biochemistry results demonstrated serum creatinine of 58μmol/liter (reference range, 45 to 84 μmol/liter), aspartate amino transferase (AST) 19.1U/liter (reference range, 0 to 32 U/liter), alanine aminotransferase (ALT) 16.0 U/L (reference range, 0 to 33 U/liter), albumin 36.8 g/L (reference range, 35 to 52 g/liter), D-dimer was slightly elevated at 0.83ug/ml (reference range, 0 to 0.55 ug/ml) CRP, ESR, renal function and electrolytes were normal. In addition, HbA1c 4.68%, RF negative, ESR 3mm/h, and IgG levels 11.3g/L, and these lab indicators were within the reference ranges, which demonstrated the patient was an immunocompetent host.

The patient was empirically treated with ceftriaxone for 7 days (1 g intravenous every 24h), but her condition did not improve during treatment. The surgical debridement and abscess drainage were performed by surgeons. Wood thorn inside the wound was removed. The wound after the surgery was shown. (fig.1A) Hematic pus was sent for bacterium cultures and a drug susceptibility test. (fig.1B) A Gram smear of the pus revealed numerous leukocytes. Hematic pus was spread onto blood and MacConkey agar plates (Crmicrobio, China) for bacteria inoculation and then observed morphology of bacterial colony with cultured for 24h at constant 36. The colonies were moist, grey-white, semitransparent, regular shaped with slightly elevated and smooth surface. (fig.1C) Gram-negative bacillus can be seen under the microscope. (fig.1D)

In order to identify the species of infected organism, we used the D2Mini semiautomated system (D2Mini, DL Biotech Company, China). The results of a series of biochemical assays revealed it to be Hafnia alve with 99.93% probability. It was positive for glucose, ornithine, lysine, citrate, L-arabinose, raffinose, galactosidase, maltose, cellobiose tests and negative for hydrogen sulfide, urea, arginine, Voges Proskauer, amino acid, malonic, phenylalanine, indole, sucrose, lactose, inositol, melibiose, aesculin, salicin, adonitol, Methylalpha-D- glucopranoside, gelatin, sorbitol tests(DL 96NE, DL Biotech Company, China). Then, it was further exposed again to identification by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry(MALDI-TOF) (Vitek MS, bioMerieux, France). MALDI- TOF analysis identified the colonies as Y. regensburgei. (99.9% confidence interval) Confidence interval of 99.9% is considered acceptable criteria for bacterial identification of gram-negative enteric bacteria.

There were currently no interpretive criteria for susceptibility testing of Yokenella regensburgei. The minimum inhibitory concentrations (MICs) were determined using the agar dilution method following the guidelines of the Clinical and Laboratory Standards Institute (CLSI), and the susceptibility patterns were interpreted according to the CLSI breakpoint criteria of Hafnia alve. The MIC results as shown in Table 1. According to the result for drug sensitivity, antibiotic therapy was switched to cefoperazone/sulbactam and levofloxacin. The patient responded well to the antibiotics and the wounds healed soon(fig.1E). These results also supported that the infected organism was Yokenella regensburgei.

Discussion and Conclusions

Yersinia regensburg belongs to the Enterobacteriaceae family. Yersinia regensburg is mainly distributed in well water and also exists in insect intestinal flora. It can infect humans and has been isolated from human respiratory tract, wounds, blood, urine and feces. This bacterium is described as a gram-negative enterobacteria, without endospores, and possessing peripheral flagellar movement. [1-3] There are biochemical similarities between Y. regensburgei and H. alvei, which can easily be misidentified by automated systems. It has been found that Y. regensburgei has its own unique characteristics. It cannot produce hydroxyproline amidase, tripeptidase or proline deaminase due to its weak catalase positive. Stoke et al. used a series of parameter tests to distinguish between Y. regensburgei and H. alvei. These parameters include hydroxyproline amidase, maltosidase, tripeptidase, proline deaminase, and catalase. Reaction, Voges-Proskauer test and fermentation test of glycerol, melibiose and inositol [4]. According to reports, the Phoenix instrument can accurately identify Regensburg yeast through key tests of citrate utilization and melibiose fermentation. [6] But the detection rate of Yersinia Regensburg did not increase as expected, partly because of different commercial systems. [5,8]

The development of sequencing omics provided a new and powerful method for identifying bacterial species. 16S rRNA gene sequencing is also very useful in bacterial classification. Based on whole genome sequencing analysis, Desiree J et al. obtained more detailed structure and function information of Y. regensburgei. [18] By combining data, the advantages of these technologies can be used to improve the accuracy of identification.

However, due to the high similarity, many researchers have encountered resolution problems at the genus and/or species level in Enterobacteriaceae through 16s rRNA sequencing. [11] MALDI-TOF MS is based on the analysis of protein profiles and has been used in the identification and separation of strains in clinical microbiology laboratories. Its accuracy rate is higher than that of conventional bacterial culture methods. [10] The technique matrix-assisted laser desorption ionization–time-of-flight mass spectrometry is considered to be a promising alternative to the expensive and time-consuming 16s rRNA sequencing method, which has high resolution capability for bacterial strains that are difficult to distinguish. We reported for the first time a case of Yersinia regensburgh infection with no underlying disease and an immunocompetent host, and reviewed the relevant literature. The main details described in these reports are summarized in Table 2. This bacteria can be cultured using standard culture methods. [6-8,12-15], most Yersinia regensburg infections occur in patients with comorbidities such as chronic kidney disease [13] -15], high-dose steroids [6,15] , Liver disease [6,12] and diabetes. [14-15] Patients without underlying diseases are rarely infected with Yersinia regensburg. [16] Almost all cases occurred in hot and humid areas, and our report is no exception. At the same time, cases of Yersinia regensburgh infection were relatively rare, and fewer infected hosts were immunocompetent. At present, only one case Y. regensburgei infected was an immunocompetent host, and the infection after craniotomy causes postoperative secondary osteomyelitis [20]. In general, Y. regensburgei causes life-threatening infections in immunocompromised individuals, especially those infected with human immunodeficiency virus (HIV), immunosuppressive therapy, and organ transplant recipients. [6-8] Other possible risk factors include alcohol abuse. [12] In this case, the laboratory indicators HbA1c, RF negative, ESR, and IgG levels proved that the patient was an immunocompetent host. Stock and colleagues [4] proved that Y. regensburgei possesses the amp C gene and highly inducible β-lactamase, and is inherently resistant to azithromycin and some β-lactam antibiotics. AmpC β-lactamase gene (blaYOC-1) and a conjugating plasmid (pYRW13-125) are present in Y. regensburgei W13. These plasmids confer resistance to multiple antibiotics, including tetracycline, ampicillin (chloramphenicol and florfenicol), and streptomycin. [19] While cefoperazone/sulbactam and levofloxacin still have ability to kill Y. regensburgei, the patient in this study were successfully treated with these antibiotics.

However, there is not enough information to fully understand the pathogenesis and resistance mechanisms of Yersinia regensburg. Although Y. regensburgei can infect immunocompromised hosts, it was worth noting that these immunocompromised hosts suffered tissue damages. When the body's immune system is involved in the repair of tissue damage, its antibacterial immune response may be weakened [21]. Therefore, the prerequisite for Y. regensburgei infection may be still immune abnormality.

In summary, in this case, this patient had no underlying diseases and no systemic symptoms such as fever

and chills. Agricultural activities and stab wounds may be related to Yersinia Regensburg infection. The main cause of chronic non-healing wounds was deep wood thorns. Wound healing is also closely related to immediate debridement, abscess drainage and wound care. Cooperation between clinical microbiology laboratories and surgeons is essential for early diagnosis of Yersinia regensburg, antibiotic selection, and surgical debridement.

List of abbreviations

AST aspartate amino transferase

ALT alanine aminotransferase

MALDI-TOF matrix-assisted laser desorption/ionization time-of-flight mass spectrometry

MICs The minimum inhibitory concentrations

CLSI Clinical and Laboratory Standards Institute

HIV human immunodeficiency virus

Declarations

Ethics approval and consent to participate

The patient in our case has signed the informed consent.

Consent for publication

Written informed consent was obtained from the patient for publication of this case report and any accompanying images.

Availability of data and material

All data generated or analyzed during this study are included in this published article.

Competing Interests

The authors declare that they have no competing interests.

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None.

Authors' contributions

XW and LH managed the case and wrote and revised the manuscript. XW, YZ, YC assisted with the preparation and revision of the manuscript. All authors agree to be accountable for all aspects of the work. All authors take full responsibility for the integrity of the study and the final manuscript. All authors read and approved the final manuscript.

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Figure legends

FIG1: Wound and growth characteristics of Yokenella regensburgei (A): Open wound

after surgical debridement (B) Hematic pus (C) Colonies on MacConkey agar plates (D) Gram-negative bacillus under microscope (E) Healing wound.