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CASE REPORT

Aspiration Pneumonia Caused by Prevotella Causing Prothorax after Pulmonary Puncture: a Case Report

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SUMMARY

Background: **Aspiration pneumonia in patients in immunocompetent populations is rare, and secondary pyothorax due to puncture operations during treatment has been reported rarely.**
Methods: **We report a confirmed case of aspiration pneumonia caused by Prevotella. The pathogen was detected and confirmed using percutaneous lung puncture and high-throughput next-generation sequencing (NGS).**
Results: **The patient developed secondary pyothorax, severe rash, and exacerbation of symptoms following the lung puncture. Finally, after adjusting the antibiotic regimen and performing chest drainage and washout, the patient's lesions were absorbed, symptoms improved, and the rash disappeared.**
Conclusions: **Prevotella aspiration pneumonia can occur in immunocompetent individuals, and invasive bronchoscopic alveolar lavage may be considered as an option to reduce the risk of infectious organism translocation.**
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KEYWORDS

prevotella, aspiration pneumonia, next-generation sequencing, case report

LIST OF ABBREVIATIONS

AP - aspiration pneumonia
CT - computed tomography
LDH - lactate dehydrogenase
NGS - next-generation sequencing

INTRODUCTION

Prevotella is one of the core members of the oral and intestinal microbiota [1]. The lower respiratory tract is not a sterile environment, but a dynamic balance of mixed microbiota [2]. Prevotella also colonizes the lower respiratory tract and when external and other factors disrupt the equilibrium of the lower respiratory tract, Prevotella takes over and proliferates, causing pneumonia

[3]. The same principle is used in percutaneous lung puncture to introduce custom-made bacteria from the lower respiratory tract into the pleural cavity ecology, thus causing a pyothorax.

CASE PRESENTATION

A 64-year-old man (BMI: 20.0 kg/cm^2) in good physical condition, with a 40-year smoking history (10 cigarettes/day) presented to our institution with recent emaciation and weight loss of 5 kg, cough and bloody sputum for 2 weeks prior, and no fever or chest pain on admission. Chest computed tomography (CT) was performed in the outpatient department on the same day (Figure 1a). Lumpy consolidation lesions could be seen in the posterior base segment of the lower lobe of the left lung, with uneven densities and patchy fuzzy shadows around the lesions. Multiple nodular lesions could be seen in the anterior segment of the upper lobe of the right lung and the lower lobe of the left lung, with fuzzy edges, unobstructed bronchial openings in each lobe, and multiple enlarged lymph nodes in the mediastinum. Complete blood count results indicated leukocytosis (10.85 x 10^9/L) with neutrophilia (76%), and a procalcitonin level of 0.210 ng/mL (Table 1). We considered the possibility of pneumonia; however, tumors could not be excluded since the patient had a long smoking history. Therefore, we ordered a lung biopsy to confirm the diagnosis.

The etiological investigation yielded the following results: sputum smear revealed a few gram-positive cocci, but the sputum culture was negative. The tumor marker level was within the normal range. Given the patient's agreement, guided percutaneous lung puncture was performed, targeting the left lower lobe as the puncture point (day 3). However, on day 4, the patient developed a fever (with a maximum temperature of 38.8°C), tachypnea, and a blood oxygen saturation level of 88% without oxygen supplementation (Figure 2). The patient's symptoms worsened, suggesting an aggravated infection. In response, we modified the antibiotic regimen, administering a combination of piperacillin-sulbactam and levofloxacin. B-ultrasound findings indicated the presence of a small amount of pleural effusion. While awaiting the results of next-generation sequencing (NGS), conservative anti-infection treatment was continued.

On day 5, the patient still had a fever (maximum temperature, 38.7°C) with no improvement in symptoms (Figure 2). Complete blood count results indicated leukocytosis (13.34 x 10^9/L) with neutrophilia (89%) and a procalcitonin level of 3.41 ng/mL (Table 1). The traditional cultures were all negative. The pathology revealed high levels of inflammatory cell infiltration in the lung tissue, organization and tissue cells in the alveolar cavities, and interstitial fiber hyperplasia. The NGS results indicated Prevotella, sequence number 24,740, and Prevotella intermedia, sequence number 13,336 (Table 2). Re-examination of chest radiographs showed an increased amount of pleural effusion. Pleural fluid analysis indicated a glucose level of 255 mg/dL, protein level of 54.20 g/L, lactate dehydrogenase (LDH) level of 3,598 U/L, and white blood cell count of 2,859.0 x 10^6/L. The total serum protein level was 76 g/L, and the serum LDH level was 263 U/L. Empyema was clearly diagnosed, continuous drainage was performed, and urokinase injection was administered with repeated irrigation with normal saline.

DISCUSSION AND CONCLUSION

This is the first reported case of Prevotella infection in an immunocompetent individual, which resulted in the development of pyothorax following pulmonary puncture. The genus Prevotella is named in honor of the notable French microbiologist A. R. Prevotella, who made significant contributions to the study of anaerobic bacteria [4]. Initially, Prevotella microorganisms were classified based on colony morphology, pigmentation depth on blood agar, and they were divided into different species such as Prevotella elaninogenica, Prevotella loescheii, Prevotella denticola, Prevotella intermedia, and Prevotella corporis. Over time, with advancements in genomics, the classification of Prevotella has shifted from DNA-DNA hybridization and G + C content determination to genomic analysis [5]. Currently, approximately 40 genera of Prevotella have been identified. Prevotella is the largest genus in the human oral cavity, with genome lengths ranging from 2.37 Mb to 4.26 Mb and G + C contents varying from 36.4% to 56.1%. Cultivating Prevotella through conventional culture methods can be challenging, and the full sequencing of the 16S rRNA gene is a commonly used method [6]. In the presented case, routine sputum, blood, and pleural fluid cultures did not yield the growth of Prevotella. However, the pathogen was identified using NGS, which is consistent with previous reports.

Until now, it has been widely believed that the lungs are a sterile environment [7]. However, the lungs provide a warm, moist, and humid environment, which, along with the flow of air and mucus, creates a microenvironment conducive to bacterial growth. In 2010, the presence of pulmonary microflora was confirmed through the detection of 16srRNA in the alveolar lavage fluid of healthy individuals [8]. The lung microbiota maintains a dynamic balance through three main mechanisms [9] (Figure 3). First, microorganisms enter the airway through micro-inhalation from the oropharynx. Second, the airway removes microorganisms through ciliary movement, the cough reflex, and the host immune response. Third, the proliferation rate of microbial flora in the airway is regulated. Disruption of this balance can lead to an overgrowth of bacterial colonies, resulting in a shift from Bacteroides to Gammaproteobacteria and the onset of disease [7]. Inflammation increases vascular permeability, causes alveolar exudation, and alters

Table 1. Blood chemistry panel and complete blood count with differential during the hospital course.

	Reference Range	Day 1	Day 2	Day 4	Day 8	Day 11	Day 15
Sodium	**137 - 145 mol/L**	**135**	**137**	**133**	**134**	**134**	**135**
Potassium	**3.5 - 5.1 mol/L**	**3.92**	**3.86**	**4.27**	**3.31**	**4.18**	**5.50**
Chloride	**98 - 107 mol/L**	**102**	**102**	**97**	**93**	**97**	**100**
Glucose	**4.1 - 5.9 mol/L**	**5.81**	**4.37**	**N/A**	**N/A**	**N/A**	**N/A**
Blood urea nitrogen	**3.2 - 7.1 mol/L**	**4.30**	**3.41**	**4.10**	**3.31**	**2.32**	**4.92**
Creatinine	**58 - 110 μmol/L**	**59.2**	**58.7**	**54.4**	**57.1**	**54.3**	**57.1**
Calcium	**2.200 - 2.650 mol/L**	**N/A**	**2.13**	**N/A**	**2.010**	**1.890**	**2.080**
PCT	**0 - 0.050 ng/mL**	**0.210**	**N/A**	**3.41**	**N/A**	**N/A**	**N/A**
CRP	**0 - 6.00 mg/L**	**N/A**	**131.88**	**N/A**	**310.67**	**167.62**	**29.17**
RBC count	**4.30 - 5.80 x 10^{12}/L**	**4.04**	**N/A**	**4.43**	**3.97**	**3.77**	**4.02**
Haemoglobin	**130.0 - 175.0 g/L**	**118.3**	**N/A**	**123.0**	**108.0**	**102.0**	**108.0**
Haematocrit	**40.0 - 50.0%**	**35.08**	**N/A**	**37.90**	**33.50**	**31.90**	**34.00**
Platelets	**125.0 - 350.0 x 10^{9}/L**	**369.1**	**N/A**	**477.0**	**494.0**	**483.0**	**642.0**
WBC count	**3.50 - 9.50 x 10^{9}/L**	**10.85**	**N/A**	**13.34**	**12.86**	**9.26**	**6.04**
Neutrophils %	**40.00 - 75.00%**	**80.04**	**N/A**	**89.00**	**86.60**	**84.40**	**71.50**
Lymphocyte %	**20.00 - 50.00%**	**8.79**	**N/A**	**5.00**	**4.70**	**6.30**	**18.00**
Monocyte %	**3.0 - 10.0%**	**10.4**	**N/A**	**0.8**	**7.1**	**6.7**	**6.6**
Eosinophil %	**0.4 - 8.0%**	**0.5**	**N/A**	**0.03**	**1.0**	**2.0**	**3.2**
Basophils %	**0 - 1.0%**	**0.3**	**N/A**	**0.03,**	**0.6**	**0.6**	**0.7**

Table 2. NGS genetic test report.

Bacteria genus	Sequence numbr	Bacterial species	Sequence number
Prevotella	**24,740**	**Prevotella intermedia**	**13,336**
Streptococcus	**7,247**	**Streptococcus constellatus**	**2,444**
Campylobacter	**5,529**	**Campylobacter rectus**	**3,380**
Treponema	**5,140**	**Treponema lecithinolyticum**	**4,476**
Parvimonas	**4,797**	**Parvimonas micra**	**4,797**

the microecological environment. This, in turn, leads to the proliferation of Gammaproteobacteria and the production of bacterial metabolites, which further nourish Gammaproteobacteria, creating a positive feedback loop that amplifies the inflammatory cycle [10]. The human oropharyngeal microbiome matures within the first two months of birth and consists of Streptococcus, Neisseria, Prevotella, Veillonella, Porphyromonas, and Fusobacterium, similar to the microbiota found in healthy adults [11]. Prevotella is a core bacteria in the oral microbiome that thrives in the lungs and causes disease when stimulated by inflammation. Prevotella, a predominant bacterium commonly found in the oral microenvironment, shows a significant increase in periodontal disease [12]. The patient in this case had early-stage periodontitis. The oral cavity is known to harbor a diverse and complex microbial ecosystem. The influx of Prevotella disrupts the microbial balance, and the inflammatory environment increases vascular permeability and exudation, creating an anaerobic environment that promotes the proliferation of Prevotella. Similarly, in the case of empyema, the lung puncture procedure introduced a large number of bacteria into the pleural cavity, disrupting the microenvironmental balance. Antinozzi et al. found that tobacco use affects the human ecosystem [13]. Although bacterial levels were similar between smokers and non-smokers, the abundance of Prevotella was significantly higher in smokers. Considering the patient's long history of heavy smoking, it is possible that smoking contributed to the Prevotella infection. Addi-

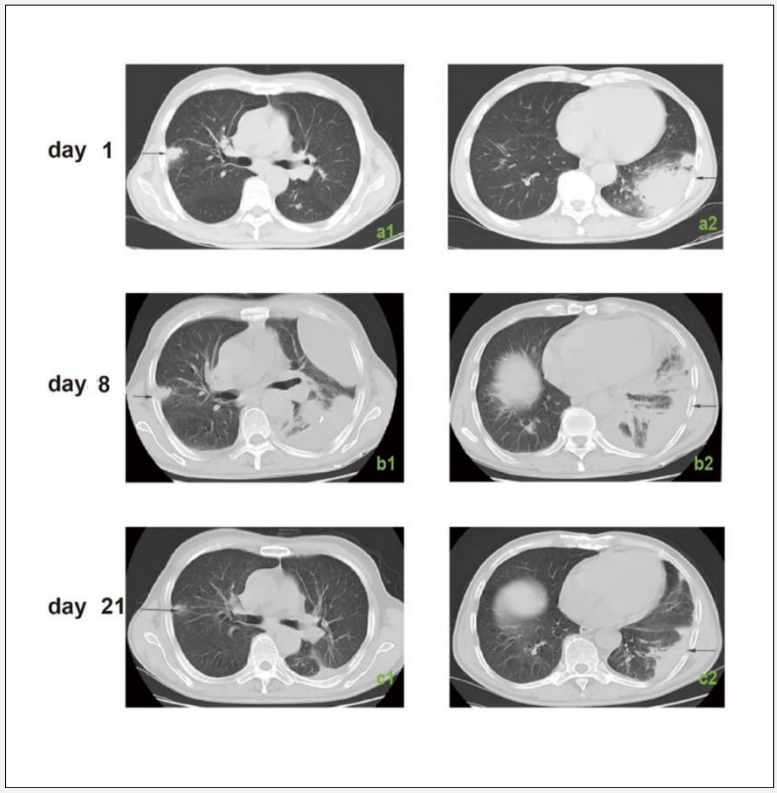

Figure 1. Chest-CT on day 1, day 8, and day 21.

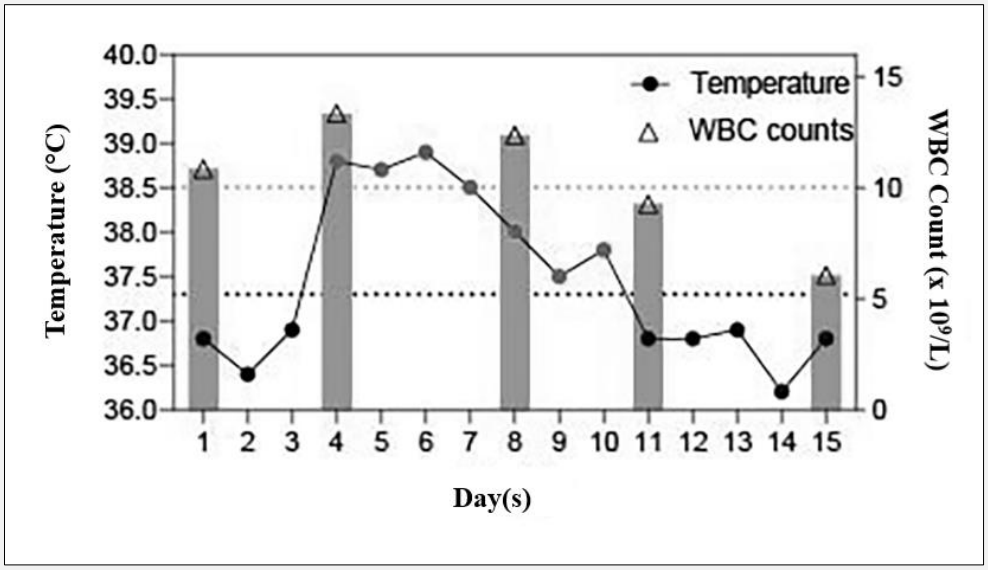

Figure 2. Trend of white blood cell count and temperature of the patient during hospitalization.

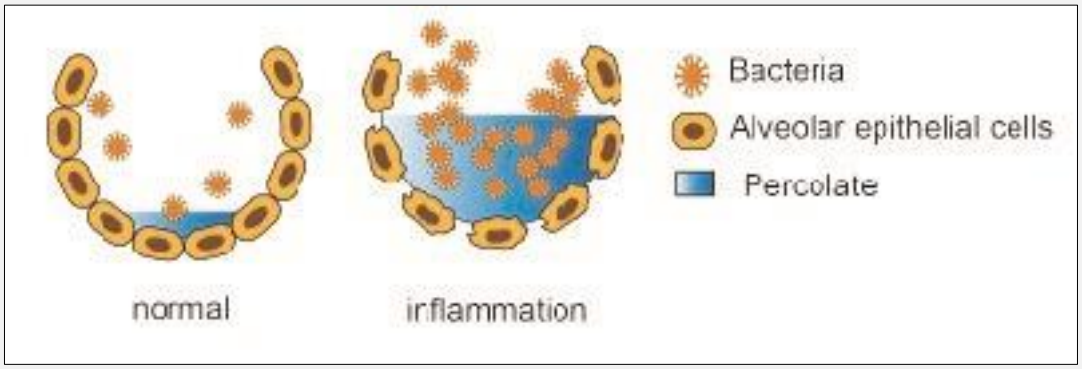

Figure 3. Lung micro ecology (Normal: Lung microbiota maintains a state of dynamic balance in the following three ways: First, microorganisms enter the airway through oropharyngeal micro-inhalation. Second, the airway removes microorganisms through ciliary oscillation, cough reflex, and host immune response. Third, the propagation rate of microbial flora increases in the airway. Bacteria maintain an equilibrium in the lungs. Inflammation: Inflammation increases vascular permeability and alveolar exudate and changes the microecological environment. Gammaproteobacteria proliferate and produce bacterial metabolites, which provide additional nutrients for Gammaproteobacteria, thereby forming a positive feedback cascade that amplifies the inflammatory cycle.)

tionally, recent studies have indicated that dietary habits also influence the oral microbial flora, and nitrite intake can effectively inhibit the growth of anaerobic bacteria [14]. Fresh vegetables, fruits, whole grains, and nuts are rich in nitrites. Poor dietary habits, such as reduced intake of quality protein, foods high in saturated fatty acids, and inadequate consumption of vegetables and fruits, along with a predominance of anaerobic bacteria in the oral cavity, can weaken the body's resistance to infection and increase susceptibility to illness. Therefore, periodontal disease, smoking history, and dietary habits may all contribute to the dominance of Prevotella as a pathogen causing aspiration pneumonia.

A review of the literature suggests that smoking cessation, oral hygiene practices, and a healthy diet can reduce the risk of aspiration pneumonia caused by Prevotella-dominant anaerobic bacteria. Thus, Prevotella can be implicated in aspiration pneumonia even in immunocompetent individuals. Invasive pulmonary puncture procedures can lead to flora translocation and trigger secondary infections. Consideration should be given to performing traumatic small bronchoalveolar lavage to investigate the underlying pathogenesis in such cases.

Ethics Approval and Consent to Participate:
Ethical review and approval was not required for this study. The patient provided written informed consent to participate in this study.

Consent for Publication:
The patient provided written informed consent for study publication.

Availability of Data and Materials:
The original data and materials presented in the study are included in the article/supplementary material. Further inquiries can be directed to the corresponding author.

Declaration of Interest:
The authors declare no competing interests.

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