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Case Report

Severe community-acquired pneumonia caused by *Chlamydia pecorum*

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ABSTRACT

Chlamydia pecorum is a zoonotic pathogen. Here, we report the first case of human infection with *C. pecorum*. A man aged 51 years with high fever and dry cough was diagnosed with severe community-acquired pneumonia and respiratory failure. *C. pecorum* was found responsible for the infection, which was detected from bronchoalveolar lavage fluid through metagenomic next-generation sequencing. *C. pecorum* infection was further identified by quantitative polymerase chain reaction and complement fixation test. The patient's condition improved rapidly after targeted treatment. He was a farmer with diabetes mellitus and had a history of close contact with sheep, which might result in *C. pecorum* infection. Our report could provide a direction for the diagnosis and treatment of human *C. pecorum* pneumonia.

Introduction

Chlamydia is a genus of gram-negative, obligate intracellular pathogens, which currently comprise 13 species and three candidate species (Bommana and Polkinghorne, 2019). Most of them have significant impacts on the health of humans or animals. *Chlamydia trachomatis, Chlamydia pneumoniae*, and *Chlamydia psittaci* are the major species that infect humans and can cause a variety of diseases (Elwell *et al.*, 2016).

Chlamydia pecorum infects a wide range of animal hosts, including sheep, goats, cattle, pigs (Walker *et al.*, 2015), and wildlife, such as koalas (Polkinghorne *et al.*, 2013). Infection with *C. pecorum* can present a number of clinical manifestations, such as arthritis, endometritis, conjunctivitis, infertility, enteritis, vaginitis, pneumonia, and mastitis (Jelocnik *et al.*, 2013; Polkinghorne *et al.*, 2013; Walker *et al.*, 2015). These infections are an important source of economic loss for livestock producers (Walker *et al.*, 2018). Nevertheless, there are no case reports of human infection by *C. pecorum.*

Case presentation

A man aged 51 years was admitted to Qitai Hospital of the Sixth Division of Xinjiang Production and Construction Corps (Xinjiang, China). He complained of a 3-day history of high fever, with a temperature up to 39.5°C, and a 1-day history of dry cough. He denied shivers, nasal obstruction, pharyngalgia, dizziness, headache, or chest pain. At the beginning of the illness, he received some medicine orally or intravenously in a local hospital, but his symptoms persisted. The patient had a 4-year history of diabetes mellitus and took metformin and acarbose to control blood glucose levels. As a farmer, he raised more than 40 sheep.

On admission, physical examination showed a temperature of 38.5°C, heart rate of 72/min, respiratory rate of 20/min, PaO_2 of 58 mm Hg, SaO_2 of 90%, and fine crackles in the right lung. A chest computed tomography scan showed consolidation in the right middle lobe and patchy infiltration in the left upper lobe (Figure 1a, c). Bronchoscopy revealed slight edema of the bronchial mucous membrane in the right lung. Laboratory investigations showed white blood cell of 4.90 × 10^9/l (normal 3.5-9.5 × 10^9/l), neutrophil of 3.35 × 10^9/l (normal 1.8-6.3 × 10^9/l), lymphocyte of 1.18 × 10^9/l (normal 1.1-3.2 × 10^9/l), C-reactive protein of 185.10 mg/l (normal 0.068-8.2 mg/l), procalcitonin of 1.266 ng/ml (normal <0.05 ng/ml), erythrocyte sedimentation rate of 85 mm/h (normal 0-15 mm/h), hemoglobin A1c of 10.06% (normal 3.60-6.00%), and fasting blood sugar of 11.73 mmol/l (normal 3.90-6.10 mmol/l).

Serological tests for *Mycoplasma pneumoniae* immunoglobulin (Ig)M, *C. pneumoniae* IgM, *Legionella pneumophila* IgM, and *Mycobacterium tuberculosis* IgG proved negative. No abnormalities were found in the blood culture. Bronchoalveolar lavage was conducted; however, the antiacid staining and culture of bronchoalveolar lavage fluid (BALF) were negative. Considering the symptom

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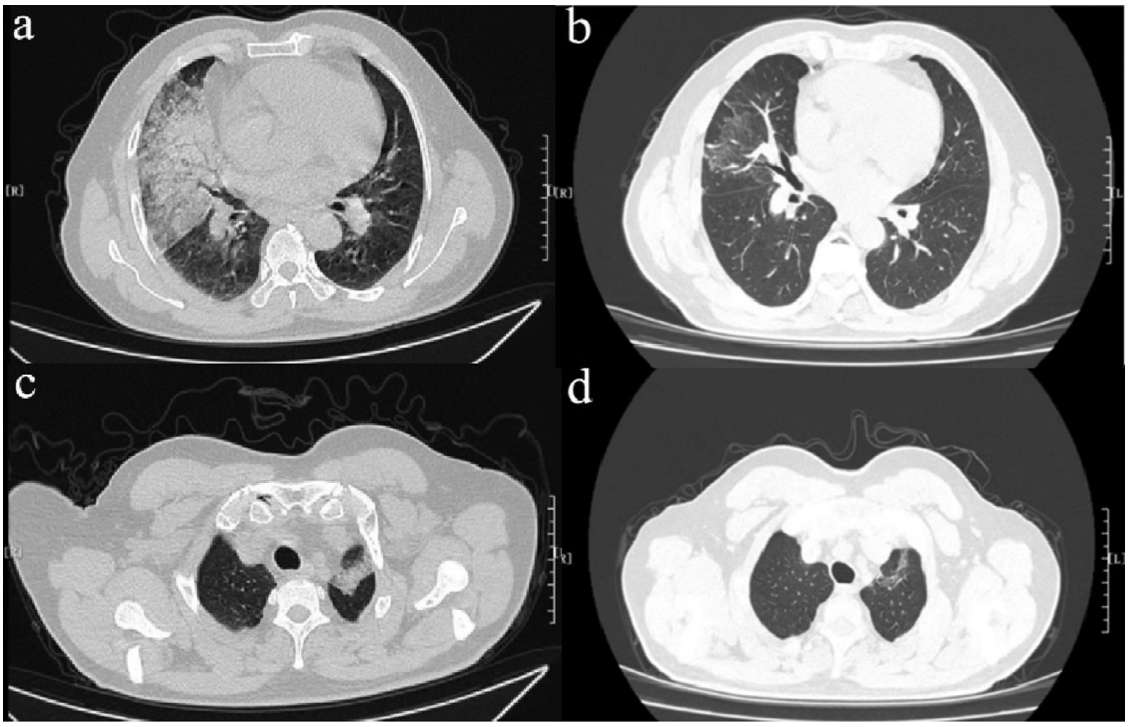

Figure. 1. Images of chest computed tomography. **(a, c)** On the day of admission. **(b, d)** 28 days after discharge.

of persistent high fever and the possibility of rare pathogens infection, the patient's BALF was sent for metagenomic next-generation sequencing (mNGS) (Genskey, Beijing) on the day of admission. A total of 906 unique DNA reads mapping of the *C. pecorum* genome were reported. Some oral microorganisms, such as *Streptococcus infantis, Neisseria elongata, Fusobacterium periodonticum,* and *Veillonella dispar,* were also detected in BALF, but all of their reads did not exceed 70. To confirm the results of mNGS, quantitative polymerase chain reaction (qPCR) amplifying 16S ribosomal RNA gene of *C. pecorum* was performed on the same sample and showed an average critical threshold value of 27 (F-5′-AGTCGAACGGAATAATGGCT-3′ and R-5′-CCAACAAGCTGATATCCCAC-3′) (Walker *et al.*, 2016). The PCR product was verified by sequencing. Serum samples were further analyzed for anti-*Chlamydia* antibodies using the complement fixation test. The antibody titer in the convalescent serum (1: 128, 28 days after discharge) increased remarkably versus the acute-phase serum (<1: 4, on admission), indicating a recent *C. pecorum* infection.

On admission, the patient was diagnosed with severe community-acquired pneumonia and respiratory failure. Empiric treatment with intravenous moxifloxacin (0.4 g every day) was given for 4 days. Body temperature returned to normal within 2 days. On the third day of admission, mNGS analysis revealed the possibility of infection with *C. pecorum.* The patient was discharged the next day and switched to oral doxycycline (0.1 g every 12 hours) and moxifloxacin (0.4 g everyday) for 2 weeks. He had a return visit 28 days after discharge and denied clinical symptoms. Chest computed tomography showed the absorption of the inflammatory sites in the lungs (Figure 1b, d). In addition, *C. pecorum* was not detected again in BALF by mNGS.

Discussion

Chlamydia are common causative organisms of human community-acquired pneumonia. *C. pecorum* has been reported to induce animal pneumonia. A number of cases of cattle pneumonia caused by *C. pecorum* have been demonstrated in the UK (Wheelhouse *et al.*, 2013). *C. pecorum* is also implicated in a few sporadic cases of respiratory disease in sheep (Biberstein *et al.*, 1967). The patient in this case was a farmer and had a history of close contact with sheep, which might result in *C. pecorum* infection. Before the onset of his illness, two of his sheep showed signs of persistent mild conjunctivitis, which is common in *C. pecorum*-infected sheep, but others displayed no signs of ill health (Walker *et al.*, 2018). In addition, diabetes mellitus might also contribute to the patient's infection. History of livestock exposure, high fever, dry cough, and elevated inflammatory biomarkers, coupled with pulmonary consolidation, may guide early clinical diagnosis of *C. pecorum* pneumonia.

Intracellular pathogens are usually difficult to culture and isolate. The general methods to diagnose *C. pecorum* infection are qPCR and complement fixation test. qPCR provides a rapid and definitive diagnosis of *C. pecorum,* which is currently the most widely used method (Walker *et al.*, 2016). mNGS, an emerging technique, represents an unbiased and rapid diagnostic tool that is useful for the diagnosis of unknown diseases (Chiu and Miller, 2019). In the current case, the mNGS reported some unique reads mapping of the genome of *C. pecorum* but not other *Chlamydia,* implying that mNGS might be appropriate for the diagnosis of *C. pecorum* infection. Antibiotic treatment for chlamydial infection is important. *In vitro* susceptibility test of *C. pecorum* to antibiotics showed that macrolides, tetracyclines, and quinolones are all effective (Pudjiatmoko *et al.*, 1998). In this case, the patient was treated correctly, and his condition improved rapidly.

In summary, to the best of our knowledge, we report the first case of *C. pecorum* infection in humans. Human infection with *C. pecorum* might be underreported, underdiagnosed, or misdiagnosed. Microbiologists and clinicians should be aware of the zoonotic potential of *C. pecorum*. It is vital to identify what symptoms can present with *C. pecorum* infection. The mNGS method can help clinicians provide direction for the diagnosis of diseases, especially for rare or difficult cases.

Author contributions

LZC and LH collected clinical and laboratory data. SYW and LJX assisted with data analysis. SFZ integrated the data and wrote the manuscript. All authors read and approved the final manuscript.

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Ethical approval

Written informed consent for publication was obtained from the patient.

Declaration of Competing Interest

The authors have no competing interests to declare.

References

Biberstein EL, Nisbet DI, Thompson DA. Experimental pneumonia in sheep. J Comp Pathol 1967;77:181–92.

Bommana S, Polkinghorne A. Mini review: antimicrobial control of chlamydial infections in animals: current practices and issues. Front Microbiol 2019;10:113.

Chiu CY, Miller SA. Clinical metagenomics. Nat Rev Genet 2019;20:341–55.

Elwell C, Mirrashidi K, Engel J. Chlamydia cell biology and pathogenesis. Nat Rev Microbiol 2016;14:385–400.

Jelocnik M, Frentiu FD, Timms P, Polkinghorne A. Multilocus sequence analysis provides insights into molecular epidemiology of Chlamydia pecorum infections in Australian sheep, cattle, and koalas. J Clin Microbiol 2013;51:2625–32.

Polkinghorne A, Hanger J, Timms P. Recent advances in understanding the biology, epidemiology and control of chlamydial infections in koalas. Vet Microbiol 2013;165:214–23.

Pudjiatmoko Fukushi H, Ochiai Y, Yamaguchi T, Hirai K. In vitro susceptibility of *Chlamydia pecorum* to macrolides, tetracyclines, quinolones and beta-lactam. Microbiol Immunol 1998;42:61–3.

Walker E, Jelocnik M, Bommana S, Timms P, Carver S, Polkinghorne A. Understanding the health and production impacts of endemic *Chlamydia pecorum* infections in lambs. Vet Microbiol 2018;217:90–6.

Walker E, Lee EJ, Timms P, Polkinghorne A. Chlamydia pecorum infections in sheep and cattle: a common and under-recognised infectious disease with significant impact on animal health. Vet J 2015;206:252–60.

Walker E, Moore C, Shearer P, Jelocnik M, Bommana S, Timms P, et al. Clinical, diagnostic and pathologic features of presumptive cases of Chlamydia pecorum-associated arthritis in Australian sheep flocks. BMC Vet Res 2016;12:193.

Wheelhouse N, Longbottom D, Willoughby K. Chlamydia in cases of cattle pneumonia in Scotland. Vet Rec 2013;172:110.