CASE REPORT

Successful Treatment of Severe Community-Acquired Pneumonia caused by Chlamydia Psittaci: a Case Report

Xiao Zhou, Guoqiang Bai, Lei Dong, Haizhou Zhuang, Meili Duan

Department of Critical Care Medicine, Beijing Friendship Hospital, Capital Medical University, Xicheng District, Beijing, China

SUMMARY

Background: Community acquired pneumonia is a common and deadly condition, which remains a major cause of morbidity and mortality throughout the world. Chlamydia psittaci pneumonia is responsible for less than 5% of community-acquired pneumonia with a fatality rate of 1%. Nonetheless, it is underestimated due to low awareness of the disease and atypical clinical presentation in a majority of the cases. Metagenomic next-generation sequencing can help us diagnose and clarify the etiology in time.

Methods: We reported a case of an 85-year-old man who presented with intermittent fever and cough with wheezing for 4 days and did a review of related literature.

Results: The patient was admitted to our department due to severe CAP and multiple organ dysfunction. After admission, we applied an empirical antibiotic strategy, performed intubation and invasive ventilation, fluid resuscitation, vasoactive drugs and supportive care. On the third day of admission, metagenomic next-generation sequencing results of blood and bronchoalveolar lavage fluid suggested Chlamydia psittaci. We made a diagnosis of severe Chlamydia psittaci pneumonia and adjusted antibiotics to minocycline combined with azithromycin two days after admission. The patient was successfully cured with a good prognosis.

Conclusions: Detecting the pathogen as early as possible and achieving accurate diagnosis are essential in infected patients. We can benefit from careful application of metagenomic next-generation sequencing.

KEY WORDS

community acquired pneumonia, Chlamydia psittaci, metagenomic next-generation sequencing, case report

LIST OF ABBREVIATIONS

CAP - community acquired pneumonia
CP - Chlamydia pneumoniae
MP - Mycoplasma pneumoniae
C. psittaci - Chlamydia psittaci
mNGS - metagenomic next-generation sequencing
BALF - bronchoalveolar lavage fluid
Tmax - peak body temperature
SpO2 - pulse oxygen saturation
WBC - white blood cell
GR% - percentage of neutrophils
CRP - C reactive protein
PCT - procalcitonin
INTRODUCTION

Community acquired pneumonia (CAP) is a common and deadly condition, which remains a major cause of morbidity and mortality throughout the world [1,2]. The main pathogens for CAP are Streptococcus pneumoniae, Hemophilus influenzae, Mycoplasma pneumoniae, Chlamydia pneumoniae, Chlamydia psittaci, viruses (rhinovirus, adenovirus, coronavirus), and fungus [3]. According to epidemiological survey in our country, Chlamydia pneumoniae (CP) and Mycoplasma pneumoniae (MP) are essential atypical pathogens in CAP [4,5]. However, there are still a large number of patients with CAP in whom the etiology is difficult to determine. These patients are therefore delayed in treatment which leads to poor prognosis.

CP is an important respiratory pathogen, causing pneumonia, pharyngitis, sinusitis, and bronchitis [6]. Chlamydia psittaci (C. psittaci) is an obligatory intra-cellular Gram-negative bacterium that typically infects birds, but could occasionally cause psittacosis in humans [7]. C. psittaci enters the body mainly through the respiratory tract by inhaling aerosolized bacteria when exposed to infected secretions, droppings, or feathers. C. psittaci is responsible for less than 5% of community-acquired pneumonia [8,9]. However, C. psittaci pneumonia in humans is underestimated due to low awareness of the disease and atypical clinical presentation in a majority of the cases [7].

Metagenomic next-generation sequencing (mNGS) is a culture-independent and rapid method for direct identification of all microorganisms in clinical specimens. We reported a case of sever C. psittaci pneumonia complicated by sepsis and multiple organ dysfunction. The patient was diagnosed through mNGS of blood and bronchoalveolar lavage fluid (BALF).

We present the following case in accordance with the CARE reporting checklist.

CASE PRESENTATION

An 85-year-old man was admitted to the hospital due to intermittent fever and cough with wheezing for 4 days in March 2021. The patient had a fever (the peak body temperature T_max 41.6°C) after catching a cold 4 days ago, accompanied with chills, fatigue, cough with purulent sputum difficult to cough up, and chest tightness. He went to a community hospital nearby and was treated with cephalosporin. With poor response to antibacterial treatment, he then went to the emergency department of our hospital. Physical examination in emergency room revealed a temperature of 37°C, a heart rate of 169 beats/min, a blood pressure of 140/93 mmHg and a pulse oxygen saturation (SpO_2) of 84%. Blood routine test showed white blood cells (WBC) 13.32 x 10^9/L (reference range, 3.5 - 9.5 x 10^9/L), percentage of neutrophils (GR%) 95.2% (reference range, 40 - 75%), C-reactive protein (CRP) 334.04 mg/L (reference range, 0 - 8 mg/L), procalcitonin (PCT) 20.80 ng/mL (0 - 0.5 ng/mL). Blood gas showed PH 7.227, PO_2 43 mmHg, PCO_2 42.2 mmHg (FiO_2 21%). Chest computer tomography (CT) examination revealed double pneumonia lesions (see in Figure 2A). He was diagnosed “Community acquired pneumonia, type I respiratory failure”, and received antibiotics of imipenem and non-invasive ventilator assisted ventilation. The patient’s SpO_2 at once rose to 95 - 96%, but it was difficult to maintain. As the condition of the ventilator continued to rise, the patient developed somnolence. Then he was admitted to the intensive care unit (ICU). Physical examination on admission revealed blood pressure of 69/47 mmHg, coma and wet rales in the lower lung. Acute Physiology and Chronic Health Evaluation (APACHE II) score was 37 and Sequential Organ Failure Assessment (SOFA) score was 14. The patient had a history of hypertension, type 2 diabetes, and silicosis for 30 years which did not affect daily life. Blood pressure was well controlled, but blood sugar was high with fasting blood glucose fluctuating between 10 - 11 mmol/L. The patient kept 7 - 10 birds for 10 years, and he denied a history of contacting with epidemic areas, smoking or drinking.

After admission, we performed intubation and invasive ventilator, fluid resuscitation, and administered vasoactive drugs to improve hypoxia and hypotension immediately. We used imipenem and moxifloxacin as an empirical anti-infection strategy, and collected blood, sputum, urine, and fence for pathogenic examination as soon as possible. In order to increase the detection rate of pathogens, we performed bronchoscopy after intubation, and collected BALF at lingual lobe of left lung. BALF and blood were sent to bacterial culture and mNGS at the same time. On the third day of admission, the mNGS results of blood and BALF suggested C. psittaci. The number of sequences was 4 in blood sample while 2,210 in BALF sample. Other etiological results reported later, including sputum culture (-), urine culture (-), blood CMV-DNA (-), EBV nucleic acid (-), Toxoplasma IgM antibody (-), Rubella virus IgM antibody (-), Herpes simplex virus type I + II IgM antibody (-), IgM antibody of Mycoplasma pneumoniae (-), IgM antibody of Legionella pneumophila (-), IgM antibody of Rickettsia Q fever (-), IgM antibody of Chlamydia pneumoniae (-), IgM antibody of adenovirus (-), IgM antibody of respiratory syncytial virus (-), IgM antibody of influenza virus type A and B (-), IgM antibody of parainfluenza virus type 1,2,3 (-), G test (-), and nucleic acid and antibody of COVID-19 (-). We made a diagnosis of severe Chlamydia psittaci pneumonia and adjust-
The initial CT scan (on admission) showed air-space consolidation with inflammatory exudation in the middle lobe of the right lung and ground glass shadow in lower lobe of left lung (A). On follow-up, the consolidation and ground glass shadows were reduced (day 7 after admission) (B) and completely absorbed (2 months after onset) (C). This image was published with the patient’s consent.
In our department was ultra,
our e mNGS results of both blood and BALF two outcomes and minimize
ment fixation test At the same time, we should clearly recognize the limi-
tional methods. Therefore, it allows for quick iden-
from sampling, nucleic acid extraction, library sequenc-
In addition, mNGS takes only approximately 24 h
fections, particularly for severe pneumonia in ICU [15].

Several outbreaks of C. psittaci infections in humans have occurred in different countries over the past 20 years. Some studies have reported that C. psittaci was more pathogenic than other Clamydia species. Moreover, C. psittaci predisposes to severe inflammatory re-
se and causes high mortality [10]. C. psittaci pne-
umonia occurs mostly in young people, and more than half have a history of bird exposure. However, there are

The prevalence of C. psittaci in poultry sold in markets was 13% in chickens, 39% in ducks, and 31% in pigeons [11]. Recommended treatment for C. psittaci pneumonia includes tetracycline, macrolide, and quinolones. The prognosis of patients depends on the severity, comor-
biditys, and the timing of treatment and care. Most pa-
tients improve within 48 hours of treatment, and 1% of
cases die [12,13]. C. psittaci pneumonia can be diagnosed meeting any one of three criteria [12]: (1) isolation of C. psittaci from respiratory secretions; (2) a four-fold or greater in-
crease in antibody titre between serum samples collect-
ed 2 weeks apart, using a complement fixation test
(CFT) or micro-immunofluorescence (MIF); and (3)
IgM antibody against C. psittaci titer detected by MIF
of 1:16 or higher. However, conventional detection
methods have some limitations. Pathogen isolation and
culture are time-consuming and require high-level labo-
atory conditions, which make it difficult to carry out
routinely. The monitoring of antibody titer is suitable
for retrospective diagnosis, with a low value of early
diagnosis. In recent years, metagenomics has played an
increasingly important role in pathogen detection. mNGS allows identification of all microorganisms in
environmental or clinical samples by high-throughput
sequencing and genomics analysis of total DNA [14].
Recent work has highlighted mNGS as the most prom-
ing approach for the comprehensive diagnosis of in-
fecions, particularly for severe pneumonia in ICU [15].
In addition, mNGS takes only approximately 24 hours
from sampling, nucleic acid extraction, library sequenc-
ing, data processing, and reporting compared to con-
ventional methods. Therefore, it allows for quick iden-
tification of pathogens in case of unexplained diseases.
At the same time, we should clearly recognize the limi-
tations of mNGS, such as lack of recognized standards,
unclear relationship between sequencing results and
treatment, difficulty of monitoring drug resistance
genes, and high cost of testing. Therefore, mNGS has
not become a routine detection technique for chlamydia
infection. But it is certain that mNGS can provide clues
for timely diagnosis of etiology.
In this case, mNGS of blood and BALF was performed
for rapid and accurate diagnosis. While BALF, sputum,
and blood cultures were all negative during hospitaliza-
tion, the mNGS results of both blood and BALF two
days after admission confirmed the presence of C. psit-
taci. Limited by laboratory conditions, we did not per-
form PCR testing. However, through the verification of
standardized treatment, we believe that this patient can
be diagnosed with C. psittaci pneumonia. We followed
the principles to treat this patient and helped the patient
achieve a satisfactory prognosis owing to timely diag-
nosis and accurate treatment.
A critical review of the literatures showed that studies
on the use of mNGS to diagnose C. psittaci are limited.
Doctors used blood specimens, BALF or the biopsy of
lung tissue for mNGS detection in the studies [7,9,11,
13]. Patient's outcomes were not always good. The case
of severe C. psittaci pneumonia in our department was
treated successfully due to timely diagnosis and stan-
ard anti-infection and supportive care.
Detecting the pathogen as early as possible and achiev-
ing accurate diagnosis are essential in infected patients,
which can improve patients’ outcomes and minimize
the use of nontargeted antibiotics. We can benefit from
careful application of mNGS.

Acknowledgment:
The authors express special thanks to BGI Beijing who
helped this work.

Availability of Data and Materials:
All data generated or analyzed during this study are in-
cluded in this published article.

Ethics Approval and Consent to Participate:
This study was approved by the ethics committee of
Beijing Friendship Hospital (No. 2021-P2-268-01).

Consent for Publication:
Written informed consent was obtained from the patient
for publication of this case report and any accompany-
ing images.

Declaration of Interest:
The authors declare that they have no competing inter-
ests.
References:


