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Pregnancy-Associated Lung Abscess from a Migratory Childhood Foreign Body: A Case Report and Literature Review

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Case Report

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Abstract

Background: This research aimed to verify the effect of sequencing technology in the detection of special pathogenic bacteria. Diagnosis of specific infectious pathogens, nucleic acid extraction, library construction and metagenomic next-generation sequencing.

***Case presentation*:** this study involved the sample from a patient with pneumonia complicated with acute empyema. Her cultures were negative. But her chest was still pain and difficulty in drainage with pleural effusion. Pleural effusion was sent for mNGS. A large amount of anaerobic bacterias and *Streptococcus* species were detected. A diagnosis of pneumonia complicated with acute empyema was made. After antibiotic treatment, the patient's chest pain disappeared.

Conclusions: From this research, mNGS maybe help identify pathogens and treat them early in the future, which can improve prognosis.

1. Introduction

Pneumonia is a common infectious disease in clinic, and its mortality rate ranks first among infectious diseases, especially severe pneumonia, with a mortality rate of 50%[1–3]. Common categories of pneumonia include Community-acquired pneumonia (CAP), Hospital-acquired pneumonia (HAP), Ventilator-associated pneumonia (VAP), Health care–associated pneumonia (HCAP)[4]. CAP generally refers to pneumonia acquired outside a hospital[5]; HAP generally refers to pneumonia acquired more than 48 hours after admission[6]. VAP generally refers to pneumonia acquired after using a mechanical ventilation[7]. HCAP generally refers to pneumonia acquired in lower-acuity health care settings such as nursing homes and dialysis centers[8]. As it is impossible to determine whether the patient is infected with pneumonia in or out of hospital, and there is no significant difference between the two clinically and epidemiologically, there is no strict distinction between the above four types of pneumonia.

Studies show that bacterial infections are the main cause of pneumonia in developing countries. So far, it has been reported that there are many epidemic diseases affecting human severe pneumonia, such as *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, *Hemophilus parainfluenzae*, etc[9, 10]. In prospective microbiology studies, 30–50% of pneumonia cases are caused by *Streptococcus pneumoniae*. The second most common cause is *Haemophilus influenzae* type b (Hib), followed by *Staphylococcus aureus* and *Klebsiella pneumoniae*[11]. According to the guidelines, the diagnosis of pneumonia needs to meet the following points: new lung infiltrates on chest imaging, respiratory decline, fever, productive cough[12, 13]. The traditional diagnostic method for pneumonia includes using auscultatory signs, in particular crepitations, cultures, polymerase chain reaction (PCR), Procalcitonin testing[8, 14–16]. Most patients infected pneumonia can benefit from antimicrobial therapy while the pathogens are detected. For the present, identifying pneumonia cases and instituting appropriate antibiotic therapy are

effective ways to reduce the mortality of pneumonia[17–19]. However, aetiological diagnosis is only achieved in half of pneumonia cases due to the limitations of testing technology. Another part of patients could not determine the pathogen of infection pathogen, thus delaying the illness, resulting in death[20, 21].

Since microbial culture positivity rates for respiratory tract samples are low, probably because of antibiotic therapy prior to sampling, non-culture-based rapid laboratory methods are urgently needed to compensate for this deficiency and help direct patient management in the future[22, 23].

In recent decades, metagenomic next-generation sequencing (mNGS) is a rapidly developing new technology for etiological diagnosis[24–26]. In some infectious diseases (e.g., blood infection, central nervous system infection, lung infection, and focal infection), it plays an important role in etiological diagnosis, especially the identification of anaerobic and rare pathogens, for example, mycoplasma, chlamydia, parasite, virus[27–30].

mNGS not only has the advantages of conventional culture, but also show many excellent properties (e.g., short turn-around times, high sensitivity and specificity analysis)[29, 31]. Furthermore, unrecorded pathogens can be detected by mNGS technology in the first place, along with identification of non-culturable pathogens[32]. In the future, mNGS technology could become the primary method of identifying, predicting, and preventing infectious diseases[33–35]. Clinicians may also be more inclined to use mNGS technology.

This study is aimed to explore the value of mNGS in diagnosing pathogen in infected patients with pneumonia[36]. For this purpose, we described that why the patient was sent for mNGS and assessed the most recent information on no cultivation and cultivation methods for detecting respiratory pathogens such as anaerobion[37–39]. Besides, we explored the application of second-generation sequencing technology in respiratory illness.

The conclusions of this review are that for most of the pathogens that cause pneumonia, there is the possibility of using rapid methods that may help clinicians to use a better-targeted antibiotic treatment.

2. Methods

2.1. Materials Rescription

The case involved a 34-year-old woman in her 19th week of pregnancy. Due to 3-day history of fever, pain in the thorax, dyspnea, and productive cough, she was admitted to Affiliated Hospital of Jining Medical University of Shandong Province, in China, on January 22th, 2022.

On admission, physical examination showed a sane, okay patient; her temperature was 37.0 ℃, pulse rate 114 bpm, respiratory rate 20 breaths/min, and blood pressure 122/74. Laboratory investigations

revealed that white blood cell count (WBC) 13.80 x 10^9/L (reference range 3.5–9.5), C-reactive protein (CRP) 217.51 mg/L (reference range 0–6), erythrocyte sedimentation rate (ESR) 112 mm/H (reference range 0–20), procalcitonin 0.135 ng/mL (PCT) (reference range 0–20). Computed tomography of the chest revealed that enlargement of right hilum, obstruction of right lower lobe bronchial opening, lesion of right lower lobe and right sided pleural effusion. The patient had undergone a puncture to the chest due to chest pain on January 24th, 2022. Thoracocentesis revealed pus. Samples of pleural effusion were sent for microbial culture. Pathogen of pleural effusion for culture was no detective but a large amount of anaerobic bacterias were detected by mNGS. The patient was diagnosed with lung abscess and empyema. Clinicians recommended mixed infections and treat them with antibiotics.

But, two weeks later, the patient continued to have chest pain and difficulty in drainage with pleural effusion. Considering the sequencing results, the patient underwent electronic bronchoscopy in order to further identify the cause and guide treatment on February 7th, 2022. The automatic pencil lead was found at the opening of the basal segment of the right lower lobe. After that, the pleural fluid drained smoothly. The patient coughed less sputum and no longer had chest pain. The patient underwent an intramniotic injection of rivanol to induce labor on February 13th, 2022. She was discharged in a week.

The patient was in good condition during the follow-up three months later. No significant abnormalities were found in WBC, CRP, PCT.

2.2. Specimen Collection and Processing

In this research, specimen collection and processing were shown in Fig. 1.

2.3. Preparation of DNA Libraries and Sequencing

The DNA libraries were preparation using the PMseq™ High-throughput DNA Detection Kit (Huada Biotechnology Co., Ltd., Wuhan, China). The process, such as DNA fragmentation, endrepair, adapter-ligation, and unbiased PCR amplification was performed strictly in accordance with the instructions[40].

2.4. Sequencing analysis and determination of pathogens

All statistical analyses were carried out with reference[40]. Some datas, such as adapter contamination, low quality and low-complexity reads, were quality filtered. Next, Burrows-Wheeler Alignment (Version: 0.7.10) was used to map the filtered sequences to a human reference database [41]. The rest of the data was assembled by using the PMSEQ bioinformatics analysis software and were classified by simultaneously aligning to the PMDB pathogen metagenomics database containing 17500 pathogens. So far, the PMDB pathogen metagenomics database contains 10,989 bacterial genomes or scaffolds (196 Mycobacterium and 159 mycoplasma, chlamydia, rickettsia), 1,179 fungi related to human diseases, 5,050 whole-genome sequences of viral taxa, and 282 parasites associated with human infection.

3. Results and Discussion

Pneumonia is a major health problem, being associated with high morbidity and mortality[42]. It is also the leading infectious disease cause of mortality among all ages worldwide. Pneumonia have an associated parapneumonic effusion. Pneumonia complicated with acute empyema is up to 57%[43].

In this case, patient presented with symptoms of cough, expectoration and chest tightness. Computed tomography of the patient's chest revealed that enlargement of right hilum, obstruction of right lower lobe bronchial opening, lesion of right lower lobe and right sided pleural effusion. Findings revealed pneumonia. Routine blood testing results were shown in Table 1. Results of microbial culture (blood, sputum, balf) were negative. The doctor diagnosed the patient with infection. The patient underwent a puncture to the chest due to chest pain, thoracocentesis revealed pus. Samples of pleural effusion were sent for microbial culture. Results of culture were negative. In contrast, in addition to *Porphyromonas endodontalis*, *Streptococcus constellatus*, *Streptococcus anginosusa*, *Fusobacterium nucleatum*, a large amount of anaerobic bacterias (*Parvimonas micra* and *Dialister pneumosintes*) were detected by mNGS. The patient was diagnosed with lung abscess and empyema.

Streptococcus constellatus is a gram-positive coccus and belongs to *Streptococcus anginosus* group. It is widely distributed in the external environment, the body surface, mouth, nose and intestine of human and animal, and is also one of *streptococcus pyogenes*, which can cause endocarditis [3], pneumonia [4], Lemierre syndrome [5], etc. The symptoms of its infection include shortness of breath, chest pain, cough, and fever, but it is rarely reported in empyema cases to be caused by *Streptococcus constellatus*.

Two species of anaerobic bacteria were detected by NGS. The one is *Parvimonas micra*, a gram-positive coccus obligate anaerobicity. It is widely distributed in the mouth and is one of the suspected pathogens of periodontitis. Moreover, it can also cause systemic pyogenic infection, oral and maxillofacial anaerobic bacteria infection, such as, abdominal abscess, liver abscess, endocarditis, suppurative arthritis, meningitis, bacteremia, root periarthritis and pericoronitis. However, we have not found any reports on *Parvimonas micra*-related pneumonia. Because the lung is an oxygen-containing organ, it is an unsuitable environment for fastidious *Parvimonas micra*.

Table 1
The patient's white blood cell (WBC) count during hospitalization.

Inflammatory makers	**Jan.22**	**Jan.30**	**Feb.06**	**Feb.13**
WBC(mg/L)	13.80	15.66	6.93	6.76
PCT(ng/mL)	0.135			0.174
CRP(10^9/L)	217.51	80.92		8.00

The other detected anaerobe is *Dialister pneumosintes*. It is a non-spore-forming, non-motile, non-fermentative, gram-negative anaerobic bacilli and widely distributed in the external environment as well as the body surface, mouth, nose and intestine of humans and animals, and is also one of streptococcus pyogenes, which can cause endocarditis, pneumonia, Lemierre syndrome, etc.

In this experiment, the patient has severe chest pain, pleural effusion with difficulty in drainage. Cultures were negative. Then, pleural effusion sample was positive by mNGS. As a result, *Porphyromonas endodontalis*, *Streptococcus constellatus*, *Streptococcus anginosusa*, *Fusobacterium nucleatum* and a large amount of anaerobic bacterias (*Parvimonas micra* and *Dialister pneumosintes*) were detected. The patient improved in 3 weeks after initiating antibiotic treatment (linezolid, Imipenem and Cilastatin Sodium. As shown in Table 2, laboratory findings of patient (WBC 6.76; CRP 8.00; PCT levels 0.174) were coming back to normal on February 13th.

Drainage of pleural effusion is more difficult on February 4th. Combined with the sequencing results, the doctor ran an electronic bronchoscopy again and took out an automatic pencil lead at the opening of the basal segment of the right lower lobe. After that, the pleural fluid drained smoothly. The patient coughed less sputum and no longer had chest pain. The patient underwent an intramniotic injection of rivanol to induce labor on February 13th, 2022. She was discharged in a week.

In this report, there are several reasons that why it is difficult to detect pathogen in samples. Firstly, these pathogens are hard to identify by routine culture due to their slow and strict anaerobic growth; Secondly, the patient was already on medication before pathogen identification, thereby increasing the chances of a negative culture; Finally, mNGS for detecting pathogenic bacteria are significantly better than that of culture due to its sensitivity and specificity. Another some factors also increase the difficulty of clinical examination. Therefore, it is necessary for the rapid and effective laboratory tests.

In June 2020, chinese experts published an expert consensus for the application of China's mNGS technology in the pathogen diagnosis in clinical moderate and severe infections (first edition). This consensus described the expert consensus of etiology diagnosis based on mNGS in the scope of detection, rules and applications in clinical moderate and severe infections, and also looked forward to the improvement of its clinical application in the future.

Several studies report the capacity of mNGS to detect pathogens. For example, the clinician suspected the patient of bacterial infection although conventional microbiological tests (CMT) were negative. Samples was sent for mNGS and were given to positive. So, mNGS was more suitable than CMT to detect pathogens (e.g., *herpesvirus type 6*, *Pneumocystis jirovecii*, and *Stenotrophomonas maltophilia*) in some cases. Besides, mNGS may be used to exclude fever as a sign of infection and reduce the abuse of antibiotics in these infected patients.

However, mNGS still has certain. Firstly, there is no uniform standard for experimental procedure, and it is difficult to distinguish between pathogens and colonizing bacteria[44]. Secondly, the use of antibiotics drug will affect the diagnostic results of mNGS. Additionally, RNA in all patient samples was not almost sequenced due to the high cost; therefore, infection caused by RNA viruses (such as human immunodeficiency virus, Influenza A virus) may have been partially undetected. Finally, it is especially hard to distinguish contaminant, colonizer and pathogen using mGNS in severe infections. Besides, the cost of mNGS is higher, and patients cannot afford to pay it. It is not conducive to the development of clinical work and cannot help in learning how mNGS can be implemented in real-world clinical settings.

4. Conclusions

These studies suggest that mNGS is superior to traditional laboratory testing methods and took shorter time. We believe that mNGS will soon become a candidate for clinical diagnosis in infected patients. The mNGS is likely a potential technology for rapid detection of pathogens in the future, particularly in the context of opportunistic pathogens and mixed infections, or in cases with negative CMT results. So, in order to better serve the clinic, we still need more study how to the identify pollutants, colonizers or pathogens in the future.

Declarations

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Author' contribution

XMJ, JX and MJY designed the study, performed laboratory experiment, MK and LQJ analyzed and interpreted the data and prepared the manuscript. XTW contributed the study design and manuscript preparation. All authors read and approved the final manuscript.

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Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Ethics approval and consent to participate

The study was conducted with the informed consent of the pregnant woman and passed the ethics review of this hospital (2025-12-C021).

Consent for publication

Written informed consent for publication of the clinical details and/or clinical images was obtained from the patient. A copy of the consent form is available for review by the Editor of this journal.

Competing interests

The authors declare no competing interests.

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Figures

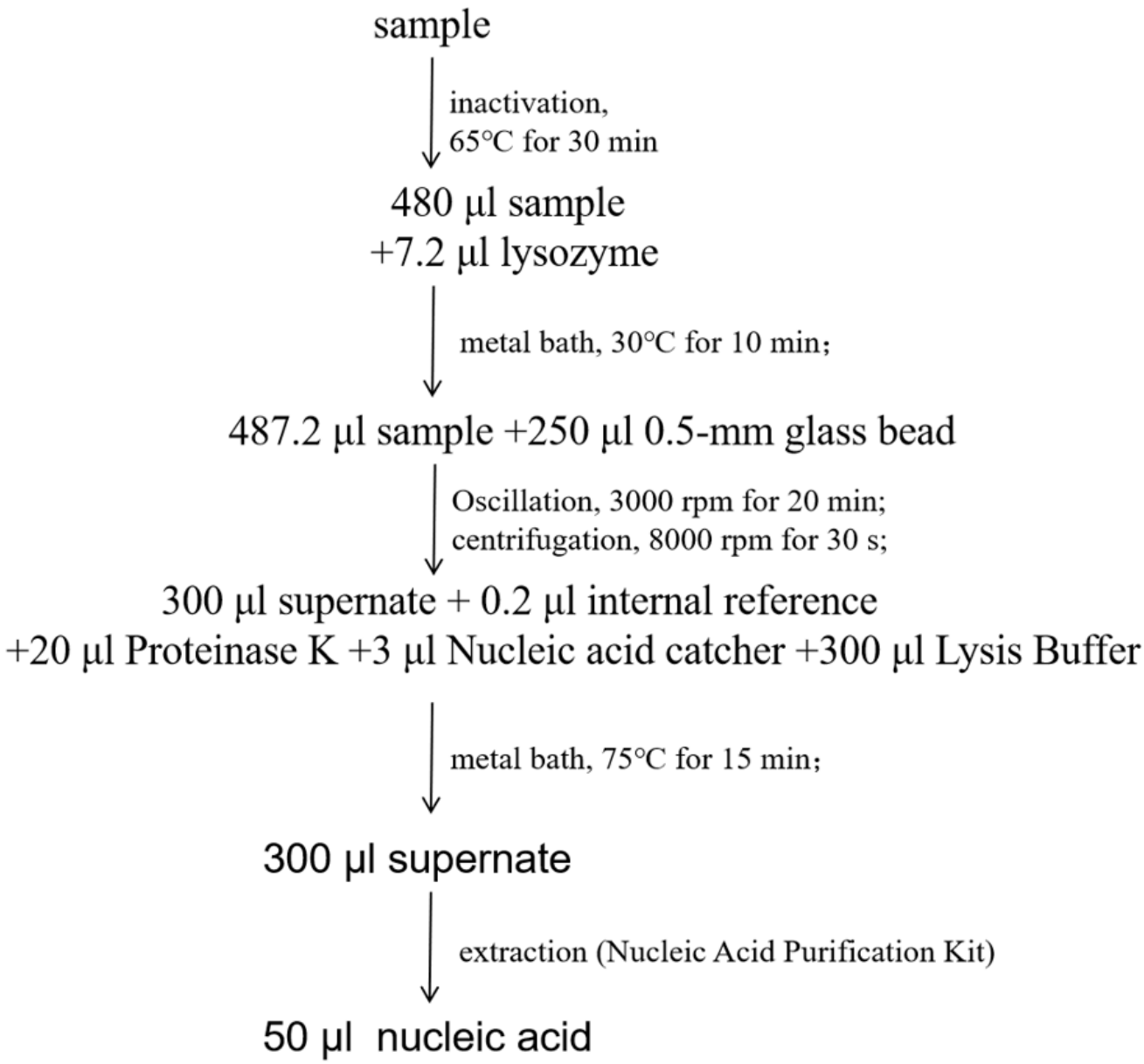


Figure 1

Sample preprocessing and nucleic acid extraction flowchart