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Heterogeneity in clinical patterns of adult lung abscess patients: an 8-year retrospective study in a tertiary hospital

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Abstract

Background The widespread use of broad-spectrum antibiotics has led to changes in both the microbiological and clinical characteristics of lung abscesses. It is necessary to re-evaluate the bacterial spectrum associated with these infections. As a novel method for pathogen detection, metagenomic next-generation sequencing (mNGS) is increasingly being applied in clinical practice. There is limited research evaluating the use of mNGS in patients with lung abscesses.

Methods A retrospective analysis was conducted on patients with lung abscess who were hospitalized between July 2015 and July 2023 at a teaching hospital in China. Patients who underwent both computerized tomography (CT) imaging and conventional pathogen testing were included in the study. The efficacy of pathogen detection using conventional methods was compared with that of mNGS. Additionally, the clinical and radiological features were analyzed to provide a comprehensive understanding of the disease patterns.

Results A total of 782 patients with lung abscess were included in the study and hematogenous abscess accounting for 7.16% (56/782) of cases. The overall hospital mortality rate was 1.53%. The mean age of the patients with lung abscess was 60 years, with a male predominance (80.2%). A significant proportion of patients had comorbid conditions, including diabetes (29.7%) and cardiovascular disease (18.2%). Lung abscesses were predominantly located in the right lung, and pleural effusion was more commonly observed in the deceased group. The detection rate of pathogen via conventional test was lower at 41.8% (327/782). Among patients with positive mNGS results, only 51.9% had pathogens identified through conventional testing methods. *Klebsiella pneumoniae* was the most frequently detected pathogen by conventional culture, while mNGS identified was *Parvimonas micra*. Infections caused solely by anaerobic bacteria or facultative anaerobes were associated with shorter hospital stays. Patient infected with Gram-negative bacilli (GNB) had a higher proportion of liver abscesses (11.8%).

Conclusion Compared to conventional testing methods, mNGS demonstrates superior performance in detecting anaerobic and facultative anaerobic bacteria. The low detection rate of conventional tests may result in an

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underestimation of the clinical significance of anaerobic bacteria infections. In patients with lung abscess caused by GNB, hematogenous dissemination, liver abscess and diabetes were more commonly observed and these patients tended to have longer hospital stays.

Keywords Lung abscess, Pulmonary infection, Pathogen, mNGS

Introduction

Lung abscess is a purulent infection within the pulmonary parenchyma, characterized by the formation of a cavity containing necrotic debris, inflammatory cells, and infectious material. Recent advancements in understanding the etiology of lung abscess have uncovered a spectrum of contributing factors, including pulmonary structural abnormalities, bronchial obstruction and hematogenous dissemination from distant infected sites [1, 2].

Among these factors, infection plays the central role in the development of lung abscess [1, 3, 4]. Despite significant progress in understanding the underlying mechanisms, lung abscess remains a complex and underexplored condition [5]. Diagnosis typically relies on a combination of imaging studies, clinical evaluation, and laboratory tests. Treatment usually involves targeted antibiotic therapy based on the identified pathogen, and timely intervention is crucial to prevent complications and ensure full recovery. The relationship between different pathogens and clinical outcomes highlights the critical importance of accurately identifying the causative agent.

However, conventional diagnostic methods are often proved time-consuming and less sensitive, leading to delayed diagnosis and inappropriate antibiotic use [6–9]. Given the multifactorial etiology of lung abscesses, conventional tests fail to meet clinical needs. Metagenomic next-generation sequencing (mNGS) offers a promising solution for pathogen detection, providing an unbiased and highly sensitive method for identifying the causative agents of infection. Despite its potential, limited research has explored the application of mNGS specifically in the context of lung abscesses [10, 11].

This study aims to analyze the clinical and microbiological heterogeneity of lung abscesses in a tertiary hospital setting, using a comprehensive approach that integrates clinical, radiological, and microbiological data. Identifying distinct clinical subtypes of lung abscess will enhance clinical decision-making and management, ultimately improving outcomes for patients.

Methods

Patients and data collection

This was a retrospective single-center study, which was conducted using the administrative hospital database of China-Japan Friendship Hospital (CJFH), a tertiary teaching hospital. Patients with the diagnosis of lung abscess (ICD-10: J85) between July 2015 and July 2023 were screened. Two independent investigators reviewed all relevant medical records and chest computed tomography (CT) scans.

Patients who underwent both CT imaging and conventional pathogen testing were included in the study. Patients without confirmed abscess, younger than 18 years, or with important data missing were excluded. Meanwhile, we also merged records if the interval between two hospitalizations was less than a week (Fig. S1). Basic information including demographic feature, symptoms, biological results, medical history, radiographic image, microbiologic data were collected.

Patients with confirmed lung abscesses who had suggestive imaging findings and/or positive blood cultures indicative of hematogenous spread were referred as hematogenous lung abscesses. The characteristic imaging features of hematogenous lung abscesses, or septic pulmonary embolism, included multiple small cavities and nodules, often located near the pleura, with or without associated pleural effusion [12, 13].

Microbiological testing

In the study, only patients who underwent conventional pathogen testing were included. The conventional testing methods used at CJFH include culture-based techniques, smear microscopy and GeneXpert test for tuberculosis (details in Table S2, S3). The primary sources of specimens for testing were sputum, bronchoalveolar lavage fluid (BALF), pleural fluid, pus, biopsy tissue and blood. The criteria for microbiological culturing was shown in our previous study [14].

We searched the microbiological laboratory system at CJFH to collect microbiological information about the specimen sources, specimen acquisition methods, and pathogen results. The pathogens were classified based on their characteristics into the following categories: aerobic Gram-negative bacilli (GNB), aerobic Gram-positive cocci (GPC), anaerobe, facultative anaerobe, aerobic Gram-positive bacilli (GPB), aerobic Gram -negative cocci (GPC) and fungi (Fig. S2).

Since mNGS is not covered by insurance and requires out-of-pocket payment, its use was determined by the patient's personal preference. Considering that mNGS can detect a wide range of pathogens, the pathogens identified through mNGS were ranked based on their read counts, and the top five suspected pathogens were included in the analysis. Yeast detected from BALF

Table 1 Baseline characteristics of lung abscess patients

	All (*N* = 782)
Duration of hospital stay, days	13.0 (9.00–20.0)
Age, years	60.0 (51.0–67.0)
Gender, male	627 (80.2%)
Smoking	
Current smoker	206 (26.3%)
Former smoker	175 (22.4%)
Never-smoker	401 (51.3%)
Alcoholism consumption history	253 (32.4%)
Chronic obstructive pulmonary disease	85 (10.9%)
Asthma	28 (3.58%)
Pulmonary embolism	17 (2.17%)
Broncho-esophageal fistula	6 (0.77%)
Bronchiectasis	45 (5.75%)
Interstitial lung diseases	43 (5.50%)
Sinusitis	15 (1.92%)
Immunosuppressive therapy	38 (4.86%)
Diabetes mellitus	232 (29.7%)
Malignancy	
Lung cancer	56 (7.16%)
Other metastatic solid tumor	36 (4.60%)
None	690 (88.2%)
Cardiovascular diseases	142 (18.2%)
Neurological diseases	93 (11.9%)
Kidney diseases	58 (7.42%)
liver abscess	25 (3.20%)
Liver disease	
HBV	19 (2.43%)
Liver cirrhosis	5 (0.64%)
None	81 (10.4%)
Others	677 (86.6%)
Symptoms and signs	
Fever	462 (59.1%)
Cough	578 (73.9%)
Expectoration	532 (68.0%)
Hemoptysis	114 (14.6%)
Chest pain	156 (19.9%)
Loss of appetite	66 (8.44%)
Dyspnea	51 (6.52%)
Intervention	
Bronchoscopy	365 (46.7%)
Ultrasonography-guided	72 (9.21%)
CT guided transthoracic needle	109 (13.9%)
Thoracic drainage	164 (21.0%)
Surgeon	30 (3.84%)

Continuous variable data are presented as mean (SD), median (interquartile ranges, IQR). Classified variable dates are presented as n/N (%), where N is the total number of patients with available data

or sputum, whether by traditional culture methods or mNGS, was considered as a colonizing pathogen (Fig. S3).

Statistical analysis

Continuous variables were described using either means ± standard deviation (SD) or median (interquartile range [IQR]), as appropriate, while categorical variables were presented as counts with percentages (%). To assess differences in characteristics between patients with different pathogens, *t*-tests or chi-square tests were performed, as appropriate. All tests were two-sided, and *P* value of less than 0.05 was considered statistically significant. To correct for multiple comparison of demographic and clinical characteristics between the two groups of study participants with different classes of pathogen, we used a Bonferroni-corrected α threshold of 0·00833. All statistical analyses were performed using SPSS (version 29.0) and R software (version 4.3.1).

Results

Study group and patients' characteristics

A total of 1153 records coded with the diagnosis of 'Lung abscess' (ICD-10: J85) between July 2015 and July 2023 were screened. After excluding the duplicates and readmissions within one week (*n* = 216), patients who did not meet the diagnosis criteria (*n* = 29), those with missing key data (*n* = 25), patients under 18 years old (*n* = 12), and hospitalizations where lung abscess was not the main reason (n = 89), 782 patients were ultimately included in the study (Fig. S1).

The median age of the cohort was 60 years (IQR 51.0–67.0), and they were predominantly male (80.2%, 627/782). Current or former smoker comprised 48.7% of the patients and 32.4% (253/782) had a history of alcohol consumption. Diabetes was the most common comorbidity, followed by cardiovascular disease. The most common symptoms on admission were cough (73.9%, 578/782), expectoration (68.0%, 532/782), and fever (59.1%, 462/782) (Table 1).

Approximately half of the patients underwent bronchoscopy. In addition, 9.21% (72/782) of them underwent ultrasonography-guided transthoracic fine needle aspiration, while 13.9% (109/782) experienced CT-guided transthoracic needle aspiration. Thoracic drainage was performed in 21.0% (164/782) of patients, and 3.84% (30/782) received surgical treatment (Table 1). The median duration of hospital stay was 13 days (IQR 9.0–20.0). A total of 12 patients (1.53%) died during hospitalization.

Radiological features

All patients underwent chest CT scans for diagnostic purposes, enabling the analysis of radiographic

Table 2 The imaging features of patients with lung abscess according to the clinical outcome

Imaging features	All(*N* = 782)	Non-survivor(*N* = 12)	Survivor(*N* = 770)	*P* value
Pleural effusion	340 (43.5%)	10 (83.3%)	330 (42.9%)	0.005
Hema-togenous abscess	56 (7.16%)	0 (0.00%)	56 (7.27%)	1.000
Non- hematogenous abscess				
Right upper lobe	204 (28.1%)	3 (25.0%)	201 (26.2%)	1.000
Left upper lobe	155 (21.4%)	5 (41.7%)	150 (21.0%)	0.169
Right lower lobe	209 (28.8%)	1 (8.33%)	208 (29.1%)	0.209
Left lower lobe	184 (25.3%)	5 (41.7%)	179 (25.1%)	0.329
Right middle lobe	60 (8.26%)	0 (0.00%)	60 (8.40%)	0.613
Multiple lobes	16 (2.2%)	0 (0.00%)	16 (2.24%)	1.000

characteristics associated with lung abscess. Among the total cohort of 782 patients, 340 (43.5%) presented with pleural effusion, which was more commonly observed in the deceased. However, it is important to note that the number of deaths in this study was relatively small ($n = 12$), which may have influenced the statistical proportions. Since pleural fluid tests data were not available, we were unable to differentiate the underlying causes of the pleural effusion.

Of the 56 patients with hematogenous abscess, all had multi-lobar involved. In contrast, among the non-hematogenous abscess patients, lung abscesses were mainly located on the right side, with a high prevalence of right lower lobe (28.8%, 209/726) and right upper lobe (28.1%, 204/726) (Table 2).

Characteristics of microbiological distribution

All patients underwent conventional microbiological testing, yielding a positive detection rate of 41.8% (327/782). mNGS was performed on 102 patients, with 53 patients showing positive results in both conventional testing and mNGS (Fig. 1A). Specimens from various

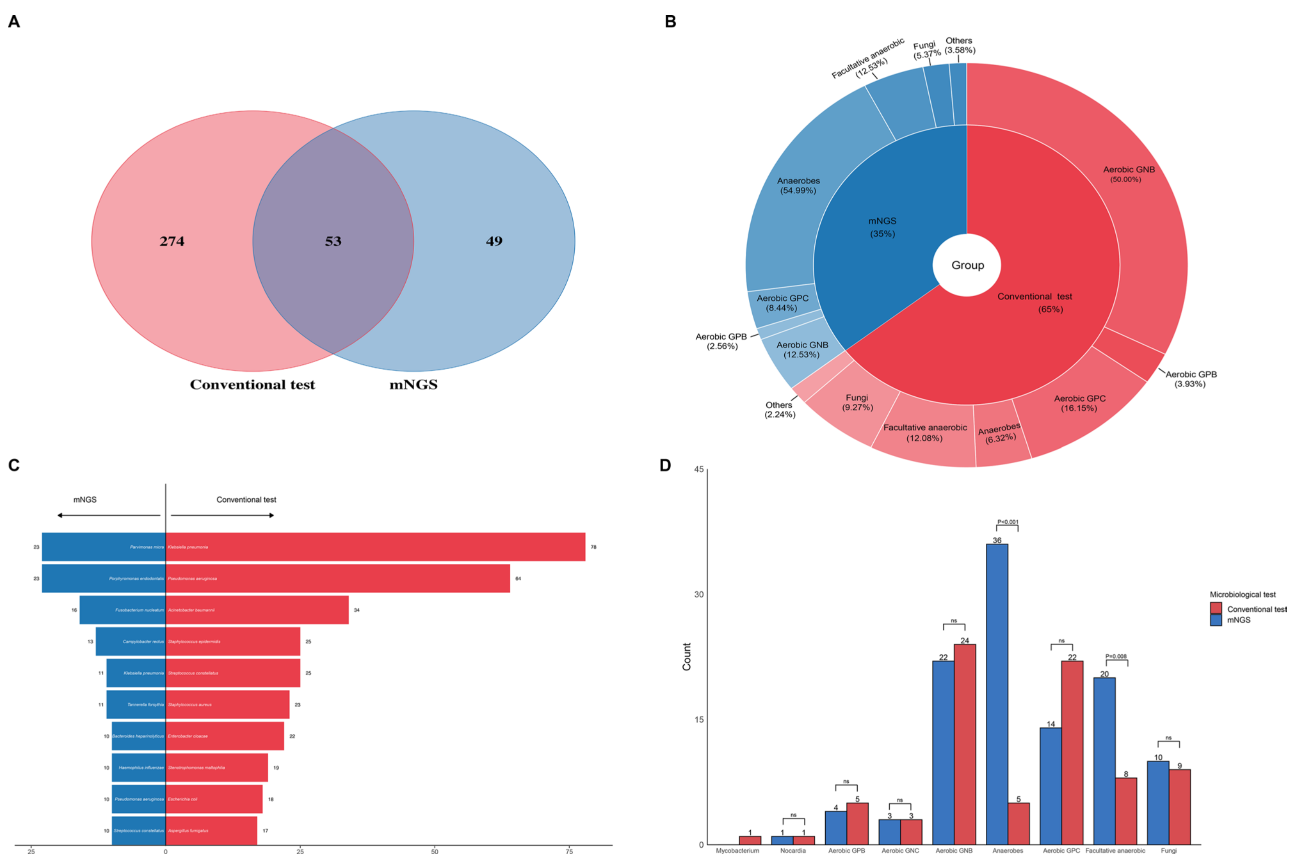

Fig. 1 The heterogeneous pathogens of patients with lung abscess (**A**) The Venn diagram illustration of positive microbiological test results in patients; (**B**) The distribution of detected pathogens in all samples based on different microbial tests; (**C**) the most common pathogens in different microbiological tests; (**D**) Comparison of the diagnostic performance of mNGS with conventional tests. GNB: gram-negative bacilli, GPB: gram-positive bacilli, GPC: gram-positive cocci, GNC: gram-negative cocci

sources were analyzed, including BALF ($n = 428$), sputum ($n = 243$), biopsy tissue ($n = 238$), pleural fluid ($n = 142$), blood ($n = 36$), and others ($n = 15$). In total, 1102 positive entries were identified from 376 patients, with culture-based methods accounting for 65% and mNGS identifying 35% of the pathogens (Fig. 1B, table S1).

The predominant bacteria detected via conventional culture were aerobic GNBs (50%), aerobic GPCs (16.15%) and facultative anaerobes (12.08%). In contrast, mNGS primarily identified anaerobes (54.99%), facultative anaerobes (12.53%), and aerobic GNB (12.53%) as the main bacterial species (Fig. 1C). The detection rate of anaerobic and facultative anaerobic bacteria by traditional culture was significantly lower that by mNGS (Fig. 1D).

Among non-survivor patients, aerobic GNB accounted for 66.7% of the primary types of pathogens, with anaerobes accounted for 11.1%. The most commonly detected pathogens in this group were *K. pneumoniae*, *A. baumannii* and *P. aeruginosa* (Fig. 2A and B). In patients with hematogenous dissemination, a similar pattern was observed, with aerobic GNB being the most prevalent (69.2%). However, there was a significant increase in the proportion of aerobic GPC (18.3%). The most frequently detected pathogens in this subgroup were *K. pneumoniae*, *S. aureus* and *A. baumannii* (Fig. 2A and C).

Among all patients with a potential pathogen detected, *K. pneumoniae* was the most prevalent bacterium, followed by *P. aeruginosa*, *A. baumannii*, *S. constellatus* and *Parvimonas micra* (Fig. 2).

Comparison of clinical and radiological patterns among patients with lung abscess, based on the identified category of potential pathogens

Among the 376 lung abscess patients with a potential pathogen identified, mixed infections accounted for 41.5% (156/376), followed by aerobic GNB (29.3%, 110/376), anaerobe or facultative anaerobe (15.2%, 57/376), and aerobic GPC (7.4%, 28/376) (Fig. S4).

The proportion of patients with a history of alcoholism was significantly higher in the anaerobe or facultative anaerobe infection group compared to other groups. Chronic obstructive pulmonary disease (COPD) was observed in 25% of patients with simple aerobic GPC infections, 10% of patients with simple aerobic GNB infection, 14.7% of patients with mixed infection, and none of patients with simple anaerobe or facultative anaerobe infection. Among the 18 lung abscess patients with concomitant liver abscess, the majority were infected by GNB pathogens (Table 3).

Regarding radiological features, statistically significant differences were observed in all four datasets for abscesses located in the right lower lobe and those exhibiting hematogenous dissemination. Specifically, a statistical difference was found between simple aerobic GNB infection and anaerobe infection when the abscess was situated in the right lower lobe. Similarly, a statistical difference was observed between simple aerobic GNB infection and mixed infection when hematogenous dissemination occurred.

Clinical presentations were comparable across the different pathogen groups. However, patients with exclusive anaerobe or facultative anaerobe infections exhibited less tissue damage compared to the other groups (Table 3). The length of hospital stays for patients infected with anerobic GNB and mixed pathogens infections were 17.0 days (12.0–22.0) and 16.0 days (11.0–28.0), respectively, which was longer than those infected with anaerobe or aerobic GPC.

Discussion

In the pre-antibiotic era, untreated lung abscesses had a mortality rate of 75% approximately, which significantly dropped to less than 10% after the introduction of antibiotic therapy [1, 15]. Our study reported an in-hospital morbidity rate of 1.53%. The mean age of patients with lung abscess was 60 years, with a male predominance, and a significant proportion had comorbidities such as

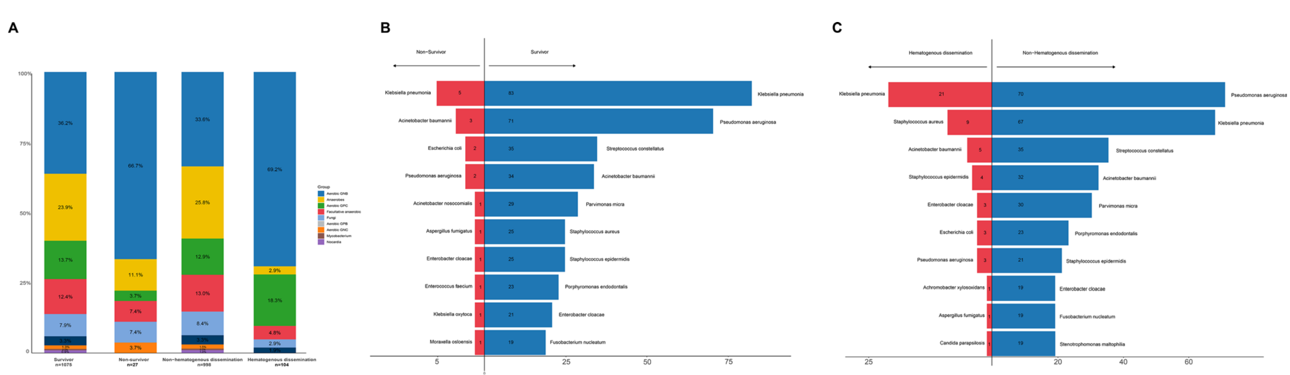

Fig. 2 (**A**) Features of pathogen distribution across various outcome; (**B**) Characterizing pathogen distribution based on clinical outcomes; (**C**) Characterizing pathogen distribution based on hematogenous abscess. GNB: gram-negative bacilli, GPB: gram-positive bacilli, GPC: gram-positive cocci, GNC: gram-negative cocci

Table 3 Comparison of clinical features among patients with lung abscesses, according to bacteriological class of the pathogen(s) isolated

	Aerobic GNB N=110	Aerobic GPC N=28	Anaerobe or Facultative anaerobe N=57	Mixed N=156	P-value
Age, years	61.0 (50.0–67.0)	59.0 (44.0–66.0)	57.0 (49.0–65.0)	60.0 (51.0–68.0)	0.491
Female	24 (21.8%)	9 (32.1%)	5 (8.77%)	31 (19.9%)	0.061
Clinical outcome					
Death	2 (1.82%)	0 (0.00%)	0 (0.00%)	5 (3.21%)	0.696
Length of hospital stay, days	17.0 (12.0–22.0) †	13.0 (9.00–19.0)	13.0 (10.0–17.0) *	16.0 (11.0–28.0)	0.006
Smoking					0.019
Current smoker	23 (20.9%)	5 (17.9%)	22 (38.6%)	34 (21.8%)	
Former smoker	29 (26.4%)	2 (7.14%)	12 (21.1%)	44 (28.2%)	
Never-smoker	58 (52.7%)	21 (75.0%)	23 (40.4%)	78 (50.0%)	
Alcoholism	39 (35.5%)	3 (10.7%) †	28 (49.1%)*	49 (31.4%)	0.004
Dental decay	2 (1.82%)	0 (0.00%)	6 (10.5%)	9 (5.77%)	0.054
Commodity					
Chronic obstructive pulmonary	11 (10.0%)	7 (25.0%)†	0 (0.00%)*	23 (14.7%)	0.001
Asthma	3 (2.73%)	2 (7.14%)	1 (1.75%)	7 (4.49%)	0.516
Pulmonary embolism	6 (5.45%)	1 (3.57%)	0 (0.00%)	2 (1.28%)	0.095
Broncho-esophageal fistula	1 (0.91%)	0 (0.00%)	0 (0.00%)	1 (0.64%)	1.000
Bronchiectasis	11 (10.0%)	3 (10.7%)	1 (1.75%)	10 (6.41%)	0.166
Interstitial lung diseases	3 (2.73%)	1 (3.57%)	3 (5.26%)	12 (7.69%)	0.346
Sinusitis	0 (0.00%)	1 (3.57%)	1 (1.75%)	6 (3.85%)	0.127
Immunosuppressive therapy	4 (3.64%)	1 (3.57%)	1 (1.75%)	16 (10.3%)	0.063
Diabetes mellitus	42 (38.2%)	7 (25.0%)	20 (35.1%)	45 (28.8%)	0.326
Malignancy					0.186
Lung cancer	14 (12.7%)	2 (7.14%)	3 (5.26%)	10 (6.41%)	
None	86 (78.2%)	24 (85.7%)	52 (91.2%)	140 (89.7%)	
Other metastatic solid tumor	10 (9.09%)	2 (7.14%)	2 (3.51%)	6 (3.85%)	
Cardiovascular diseases	21 (19.1%)	3 (10.7%)	9 (15.8%)	24 (15.4%)	0.751
Neurological diseases	14 (12.7%)	2 (7.14%)	8 (14.0%)	21 (13.5%)	0.866
Kidney diseases	12 (10.9%)	1 (3.57%)	2 (3.51%)	16 (10.3%)	0.309
Liver disease					1.000
HBV	5 (4.55%)	1 (3.57%)	2 (3.51%)	2 (1.28%)	
Liver cirrhosis	1 (0.91%)	1 (3.57%)	0 (0.00%)	2 (1.28%)	
None	95 (86.4%)	20 (71.4%)	49 (86.0%)	134 (85.9%)	
Others	9 (8.18%)	6 (21.4%)	6 (10.5%)	18 (11.5%)	
Liver abscess	13 (11.8%) †	0 (0.00%)	0 (0.00%)†	5 (3.21%)	0.002
Symptoms					
Fever	66 (60.0%)	19 (67.9%)	34 (59.6%)	92 (59.0%)	0.852
Cough	78 (70.9%)	20 (71.4%)	42 (73.7%)	119 (76.3%)	0.788
Expectoration	75 (68.2%)	20 (71.4%)	42 (73.7%)	106 (67.9%)	0.856
Hemoptysis	14 (12.7%)	4 (14.3%)	11 (19.3%)	28 (17.9%)	0.608
Chest pain	18 (16.4%)	9 (32.1%)	13 (22.8%)	32 (20.5%)	0.300
Loss of appetite	9 (8.18%)	4 (14.3%)	3 (5.26%)	15 (9.62%)	0.527
Dyspnea	6 (5.45%)	3 (10.7%)	2 (3.51%)	18 (11.5%)	0.152
Imaging features					
Right upper lobe	24 (21.8%)	5 (17.9%)	18 (31.6%)	39 (25.0%)	0.447
Left upper lobe	23 (20.9%)	2 (7.14%)	12 (21.1%)	30 (19.2%)	0.397
Right lower lobe	20 (18.2%) †	10 (35.7%)	21 (36.8%)	46 (29.5%)	0.037
Left lower lobe	27 (24.5%)	7 (25.0%)	10 (17.5%)	48 (30.8%)	0.254
Right middle lobe	9 (8.18%)	2 (7.14%)	3 (5.26%)	10 (6.41%)	0.918
Multiple lobes	3 (2.73%)	0 (0.00%)	0 (0.00%)	7 (4.49%)	0.378
Hematogenous dissemination	18 (16.4%) *	5 (17.9%)	2 (3.51%)	9 (5.77%)	0.004
Pleural effusion	56 (50.9%)	15 (53.6%)	26 (45.6%)	85 (54.5%)	0.707

Table 3 (continued)

	Aerobic GNB *N* = 110	Aerobic GPC *N* = 28	Anaerobe or Facultative anaerobe *N* = 57	Mixed *N* = 156	*P*-value
Laboratory findings					
Leukocyte (x10^9/L)	9.66 (6.99-14.0)	10.7 (8.10–15.5)	8.70 (6.95–12.5)	9.95 (6.66–13.9)	0.496
Neutrophil (x10^9/L)	7.61 (4.62–11.6)	8.73 (5.13–12.8)	76.4 (62.5–83.9)	7.64 (4.78–11.9)	0.504
Lymphocyte (x10^9/L)	1.31 (0.90–1.75)	1.43 (0.95–1.80)	1.48 (1.15–1.89)	1.28 (0.87–1.77)	0.324
Platelet (x10^9/L)	258 (188–389)	290 (232–380)	295 (235–341)	290 (207–409)	0.411
Hemoglobin (g/L)	115 (99.0-130)	124 (104–133)	123 (109–135) *	113 (99.0-124)	0.008
C-reaction protein (mg/L)	8.24 (2.20–14.8)	12.9 (7.82–21.1)	3.50 (0.66–9.69)	9.56 (2.46-16.0)	0.043
Procalcitonin (ng/mL)	0.42 (0.22–1.92)	0.36 (0.22–0.96)	0.26 (0.18–0.70)	0.36 (0.19–0.82)	0.304
AST (U/L)	19.5 (16.0-27.8)	25.5 (16.8–36.2) †	16.0 (12.0–24.0) *	21.5 (16.2–32.5)	0.003
ALT (U/L)	23.5 (15.0-39.8)	27.0 (19.5–39.0)	21.0 (12.0–32.0)	25.5 (15.0-41.5)	0.157
Albumin (g/L)	34.7 (6.82)	33.9 (7.75)	38.4 (35.1–41.1) *	35.2 (30.9–39.1)	0.017
BUN (mmol/L)	4.93 (3.67–7.32)	4.75 (3.34–6.64)	4.63 (3.66–5.85)	4.88 (3.82–6.68)	0.425
Creatine (μmol/L)	60.9 (49.9–77.2)	68.4 (53.7–77.4)	65.9 (56.3–76.8)	62.2 (48.8–79.9)	0.509
PT (s)	14.3 (13.4–15.1) †	14.1 (13.4–15.5)	13.8 (13.1–14.6)	14.1 (13.4–15.0)	0.043
APTT (s)	40.8 (38.0-44.5)	43.0 (39.5–49.9)	40.9 (37.2–45.0)	42.5 (38.3–48.4)	0.077
DD (μg/mL)	1.90 (0.70-3.00) †	2.20 (0.92–3.38)	1.04 (0.45–1.77) *	1.83 (0.71–3.03)	0.018

Abbreviations ALT: Alanine aminotransaminase, AST: Aspartate aminotransferase, TBIL: Total Bilirubin, DBIL: Direct Bilirubin, BUN: Blood urea nitrogen, PT: Prothrombin time, APTT: Activated Partial Thromboplastin Time, DD: d-dimer. GNB: gram-negative bacilli, GPB: gram-positive bacilli, GPC: gram-positive cocci. Continuous variable data are presented as mean (SD), median (interquartile ranges, IQR). Classified variable dates are presented as n/N (%). * $P < 0.0083$ for comparison of co-infeciton with other groups. †$P < 0.0083$ for comparison of Anaerobe or Facultative anaerobic with aerobic GNB or aerobic GNC

diabetes and cardiovascular disease, consistent with findings from previous studies [4, 16].

Common presenting symptoms on admission included cough, expectoration, and fever; but not all patients exhibited these typical symptoms. Therefore, it is crucial to consider both clinical presentations and imaging features for accurate diagnosis [17, 18]. The most frequently affected location was the right upper lobe followed by the right lower lobe, which aligns with findings from other studies [16, 19, 20]. Additionally noted was a higher incidence of pleural effusion among deceased individuals. Hematogenous dissemination was characterized by multiple peripheral nodules and its occurrence was closely related to the patient's immune status. Diabetes mellitus and liver abscesses were significantly more prevalent in the hematogenous dissemination group, and the pathogens detected were predominantly aerobic GPC and aerobic GNB, which is consistent with previous research [21].

The treatment of lung abscess typically involves targeted antibiotic therapy against the specific pathogen responsible for the infection, making accurate identification of the potential causative agent crucial. However, conventional culture methods exhibit a detection rate lower than 41.8%. Among patients with positive mNGS results, only 52.0% (53/102) were also identified as positive by traditional culture techniques. This discrepancy is likely due to the limited ability of conventional methods to detect anaerobic and facultative anaerobic bacteria. Previous studies have shown that antibiotic usage significantly reduces the detection of anaerobes via traditional culture techniques [22]. While mNGS is less affected by the antibiotics use [9]. Several studies have highlighted the advantage of mNGS in diagnosing anaerobes and mixed anaerobic infections [10, 23].

Previously, anaerobic bacteria, mainly related to aspiration and poor oral hygiene, were considered as the main causative organisms of lung abscess [24, 25]. However, recent researches have shown that aerobic GNB are now more commonly identified in patients with lung abscesses [3, 15, 19, 26]. Our study, which included the largest cohort of patients with lung abscess undergoing mNGS testing, found that conventional culture methods predominantly identified GNB, especially *K. pneumoniae*. In contrast, mNGS primarily detected anaerobe followed by facultative anaerobe and GNB. This suggests that the low detection rate of traditional culture methods may underestimate the harm caused by anaerobic bacteria.

Infections caused exclusively by anaerobic bacteria or facultative anaerobes tend to be associated with shorter hospital stays and relatively improved laboratory indicators. This may be attributed to the early administration of broad-spectrum antibiotics [27]. In contrast, infections caused solely by aerobic GNB or GNC exhibit a significantly higher proportion of hematogenous dissemination, particularly in cases with *K. pneumoniae* and *S. aureus*. Furthermore, infections caused by aerobic GNB exhibit a notable prevalence of liver abscesses. Over the past three decades in China, *K. pneumoniae has increasingly replaced Escherichia coli* as the predominant pathogen in liver abscess infections, now accounting for more than 80% of reported cases [28–30].

This study has several limitations. First, as a retrospective, single-center investigation, it is subject to potential bias in data collection. Second, while mNGS has been shown to have a significantly higher positivity rate compared to conventional microbiological methods, there is currently no standardized approach for interpreting mNGS results. This poses challenges in distinguishing between colonization and infection, particularly with non-sterile specimens like BALF [31]. Morever, further prospective studies are needed to determine whether mNGS can effectively reduce the inappropriate use of broad-spectrum antibiotics. Lastly, as lung abscess patients typically receive broad-spectrum antibiotic treatment upon symptom onset, the obtained pathogen results may not accurately reflect their actual conditions. Future prospective studies are required to validate the findings presented in this study.

In conclusion, the use of antibiotics has significantly reduced the mortality rate of lung abscess compared to previous decades. mNGS demonstrates superior performance in detecting anaerobic or facultative anaerobic bacteria in patients with lung abscess compared to conventional tests, providing crucial evidence for clinical decision-making. The low detection rate of traditional culture may underestimate the harm caused by anaerobic bacteria. Patients with GNB are more likely to experience hematogenous dissemination and have longer hospital stays.

Abbreviations

mNGS	Metagenomic next-generation sequencing
BALF	Bronchoalveolar lavage fluid
GNB	Gram-negative bacilli
GPB	Gram-positive bacilli
GPC	Gram-positive cocci
GNC	Gram-negative cocci
CT	Computed tomography
SD	Standard deviation

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12890-025-03487-2.

Supplementary Material 1

Author contributions

BC and HL conceived and designed the study. RLZ, JPY and HL analyzed and interpreted the data. RLZ, HL, XS and ZYW drafted the manuscript.

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Data availability

This data is not publicly accessible. However, it can be provided upon a reasonable request directed to the corresponding author.

Declarations

Ethical approval

The study is approved by the ethics committee of China-Japan Friendship Hospital (2019-122-K84) and the database was anonymized. The requirement for informed consent was waived by the ethics committee of China-Japan Friendship Hospital due to the retrospective nature of the study. All procedures were performed in accordance with the principles of the Declaration of Helsinki.

Informed consent

The need for informed consent was waived because of the study's retrospective design.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

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References

1. Kuhajda I, Zarogoulidis K, Tsirgogianni K, Tsavlis D, Kioumis I, Kosmidis C, Tsakiridis K, Mpakas A, Zarogoulidis P, Zissimopoulos A, et al. Lung abscess-etiology, diagnostic and treatment options. Ann Transl Med. 2015;3(13):183.
2. Puligandla PS, Laberge J-M. Respiratory infections: pneumonia, lung abscess, and empyema. Semin Pediatr Surg. 2008;17(1):42–52.
3. Wang J-L, Chen K-Y, Fang C-T, Hsueh P-R, Yang P-C, Chang S-C. Changing bacteriology of adult community-acquired lung abscess in Taiwan: Klebsiella pneumoniae versus anaerobes. Clin Infect Dis. 2005;40(7):915–22.
4. Montméat V, Bonny V, Urbina T, Missri L, Baudel J-L, Retbi A, Penaud V, Voiriot G, Cohen Y, Prost ND et al. Epidemiology and Clinical Patterns of Lung Abscesses in ICU: A French Multicenter Retrospective Study. CHEST 2023;0(0).
5. Gadkowski LB, Stout JE. Cavitary pulmonary disease. Clin Microbiol Rev. 2008;21(2):305–33. table of contents.
6. Li G, Sun J, Pan S, Li W, Zhang S, Wang Y, Sun X, Xu H, Ming L. Comparison of the performance of three blood Culture systems in a Chinese tertiary-care hospital. Front Cell Infect Microbiol. 2019;9:285.
7. Austin B. The value of cultures to modern microbiology. Antonie Van Leeuwenhoek. 2017;110(10):1247–56.
8. Sin MLY, Mach KE, Wong PK, Liao JC. Advances and challenges in biosensor-based diagnosis of infectious diseases. Expert Rev Mol Diagn. 2014;14(2):225–44.
9. Miao Q, Ma Y, Wang Q, Pan J, Zhang Y, Jin W, Yao Y, Su Y, Huang Y, Wang M, et al. Microbiological Diagnostic performance of Metagenomic Next-generation sequencing when Applied to Clinical Practice. Clin Infect Dis. 2018;67(suppl2):S231–40.
10. Zhang Y, Song P, Zhang R, Yao Y, Shen L, Ma Q, Zhou J, Zhou H. Clinical Characteristics of Chronic Lung Abscess Associated with Parvimonas micra diagnosed using Metagenomic Next-Generation sequencing. Infect Drug Resist. 2021;14:1191–8.
11. Zhu X, Yu S, Kang Q, Qiu Y, Tian M, Cao E. Campylob acter r ectus infection leads to lung abscess: a Case Report and Literature Review. Infect Drug Resist. 2021;14:2957–63.
12. Ye R, Zhao L, Wang C, Wu X, Yan H. Clinical characteristics of septic pulmonary embolism in adults: a systematic review. Respir Med. 2014;108(1):1–8.

13. Dodd JD, Souza CA, Müller NL. High-resolution MDCT of pulmonary septic embolism: evaluation of the feeding vessel sign. AJR Am J Roentgenol. 2006;187(3):623–9.
14. Yan M, Zou X, Wang Y, Wang C, Wang Y, Liu Z, Shang L, Cui X, Cao B. Impact of Metagenomic Next-Generation sequencing of Bronchoalveolar Lavage Fluid on Antimicrobial stewardship in patients with lower respiratory tract infections: a retrospective cohort study. J Infect Dis. 2024;229(1):223–31.
15. Maitre T, Ok V, Calin R, Lassel L, Canestri A, Denis M, Hamidi M, Tavolaro S, Verdet C, Parrot A, et al. Pyogenic lung abscess in an infectious disease unit: a 20-year retrospective study. Ther Adv Respir Dis. 2021;15:17534666211003012.
16. Vaarst JK, Sperling S, Dahl VN, Fløe A, Laursen CB, Gissel TN, Gjoerup PH, Bendstrup E. Lung abscess: clinical characteristics of 222 Danish patients diagnosed from 2016 to 2021. Respir Med. 2023;216:107305.
17. Hirshberg B, Sklair-Levi M, Nir-Paz R, Ben-Sira L, Krivoruk V, Kramer MR. Factors Predicting Mortality of patients with Lung Abscess. Chest. 1999;115(3):746–50.
18. Moreira JS, Camargo JJP, Felicetti JC, Goldenfun PR, Moreira ALS, Porto NS. Lung abscess: analysis of 252 consecutive cases diagnosed between 1968 and 2004. J Bras Pneumol. 2006;32(2):136–43.
19. Mohapatra MM, Rajaram M, Mallick A. Clinical, Radiological and Bacteriological Profile of Lung Abscess - An Observational Hospital based study. Open Access Maced J Med Sci. 2018;6(9):1642–6.
20. Hraiech S, Ladjal K, Guervilly C, Hyvernat H, Papazian L, Forel JM, Lopez A, Peres N, Dellamonica J, Leone M, et al. Lung abscess following ventilator-associated pneumonia during COVID-19: a retrospective multicenter cohort study. Crit Care. 2023;27(1):385.
21. Jiang J, Liang Q-L, Liu L-H, Cai S-Q, Du Z-Y, Kong J-L, Chen Y-Q. Septic pulmonary embolism in China: clinical features and analysis of prognostic factors for mortality in 98 cases. BMC Infect Dis. 2019;19(1):1082.
22. Jin X, Li J, Shao M, Lv X, Ji N, Zhu Y, et al. Improving suspected pulmonary infection diagnosis by Bronchoalveolar Lavage Fluid Metagenomic Next-Generation sequencing: a Multicenter Retrospective Study. Microbiol Spectr. 2022;10(4):e02473–02421.
23. Guo W, Gao B, Li L, Gai W, Yang J, Zhang Y, Wang L. A community-acquired lung abscess attributable to odontogenic flora. Infect Drug Resist. 2019;12:2467–70.
24. Bartlett JG. Anaerobic bacterial infection of the lung. Anaerobe. 2012;18(2):235–9.
25. Bartlett JG. The role of anaerobic Bacteria in lung abscess. Clin Infect Dis. 2005;40(7):923–5.
26. Takayanagi N, Kagiyama N, Ishiguro T, Tokunaga D, Sugita Y. Etiology and outcome of community-acquired lung abscess. Respiration. 2010;80(2):98–105.
27. Mansharamani N, Balachandran D, Delaney D, Zibrak JD, Silvestri RC, Koziel H. Lung abscess in adults: clinical comparison of immunocompromised to non-immunocompromised patients. Respir Med. 2002;96(3):178–85.
28. Yin D, Ji C, Zhang S, Wang J, Lu Z, Song X, Jiang H, Lau WY, Liu L. Clinical characteristics and management of 1572 patients with pyogenic liver abscess: a 12-year retrospective study. Liver Int. 2021;41(4):810–8.
29. Qu T-t, Zhou J-c, Jiang Y, Shi K-r, Li B, Shen P. Wei Z-q, Yu Y-s: clinical and microbiological characteristics of Klebsiella pneumoniae liver abscess in East China. BMC Infect Dis. 2015;15:161.
30. Siu LK, Yeh K-M, Lin J-C, Fung C-P, Chang F-Y. Klebsiella pneumoniae liver abscess: a new invasive syndrome. Lancet Infect Dis. 2012;12(11):881–7.
31. Li N, Cai Q, Miao Q, Song Z, Fang Y, Hu B. High-throughput metagenomics for identification of pathogens in the clinical settings. Small Methods. 2021;5(1):2000792.

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