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Relationship between bronchoscopic culture results and clinical and demographic factors

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ABSTRACT

Introduction: Asthma and Chronic Obstructive Pulmonary Disease (COPD) are prevalent chronic respiratory diseases worldwide. In both conditions, respiratory tract infections are a significant cause of morbidity and mortality. Bronchoscopic sampling is an important diagnostic method for evaluating the microbiological flora. There is limited data on whether the microbiological culture results differ in patients with asthma and COPD from patients without asthma and COPD. This study aimed to investigate potential differences in the respiratory tract microbial profiles of asthma, COPD, and non-asthma/non-COPD patients.

Materials and Methods: This study included patients aged 18 years and older who underwent bronchoscopy between 2019 and 2024. Bronchoscopic samples were collected using the bronchoalveolar lavage method, and the microbiological culture results of these samples were examined in a laboratory setting. All procedures were performed using a flexible bronchoscope under local anesthesia and sedation.

Results: A total of 526 patients were included in the study: 389 Without asthma and COPD, 35 with asthma, and 102 with COPD. The age in the COPD group was significantly higher than in the other groups (p=0.009). There was no difference between gender and procedure indications. Heart failure was more common in the asthma group, and coronary artery disease was more frequent in the COPD group. No significant difference was found between the groups in microbiological cultures (p>0.05).

Conclusion: The bronchial microbial profile in patients with asthma and COPD did not differ from those without these diseases. These findings suggest that microbial colonization is independent of the disease.

Keywords: Bronchoalveolar lavage, bronchoscopy, culture, lung diseases

Introduction

Asthma and chronic obstructive pulmonary disease (COPD) are chronic inflammatory airway diseases with high global prevalence.[1] In both diseases, structural and functional changes are observed in the airway mucosa, increasing patients' susceptibility to infections.[2]

Lower respiratory tract infections are significant causes of morbidity and mortality, leading to hospitalizations and deaths, and can result in more severe clinical presentations, especially in individuals with chronic respiratory conditions.[3] Infections that develop in these patients can alter the microbiological spectrum. Bronchoscopy is a fre-

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quently used invasive procedure for both diagnostic and therapeutic purposes, providing valuable information for microbiological diagnosis through direct sampling from the lower respiratory tract.[4] In recent years, the use of flexible bronchoscopy has become widespread.[5] Evaluating bronchoscopy culture results plays an important role in identifying the causative agent of infection and guiding intensive antibiotic treatment.

The differences in microbiological growth detected in bronchoscopic samples from asthma and COPD patients compared to individuals without asthma-COPD have not been sufficiently elucidated. This study investigated the effect of airway microbial colonization on these diseases by comparing the demographic characteristics, comorbid conditions, and bronchoscopic microbiological culture results of asthma patients, COPD patients, and non-asthma-COPD patients who underwent bronchoscopy.

Materials and Methods

This retrospective study included patients over 18 years of age who underwent bronchoscopy in a tertiary hospital's pulmonology clinic between 2019 and 2024. Patients receiving tuberculosis treatment, those with asthma-COPD overlap syndrome, and those whose cultures were not taken were excluded. The study comprised three groups: Asthma, COPD, and non-asthma/COPD bronchoscopy patients. Patients who underwent bronchoscopy and whose medical records were fully accessible were included in the study. This study was conducted in accordance with the Declaration of Helsinki and ethical committee approval was obtained from Kahramanmaraş Sütçü İmam University, on January 9, 2025 (decision number 21), and patient file records from the hospital information management system were retrospectively reviewed.

The study analyzed patients' demographic data (age and gender), smoking history, concomitant diseases (e.g., diabetes mellitus, hypertension, COPD, etc.), and microbiological culture results of samples taken during bronchoscopy. The obtained data were transferred to a digital environment in an appropriate format for statistical analysis. Information regarding prior antibiotic use was also reviewed from patients' medical records. Data on whether patients had received antibiotic therapy within the two weeks preceding bronchoscopy, as well as the antibiotic type, duration, and treatment setting (ICU vs. non-ICU), were recorded. Patients who had received antibiotics within this period were analyzed separately to assess their potential effect on microbiological culture results and subgroup comparisons were performed between antibiotic-exposed and non-exposed patients. Files containing incomplete or insufficient information were included in the study.

Bronchoscopy procedures were performed in our clinic according to standard protocols, generally using a flexible bronchoscope under local anesthesia and sedation. During bronchoscopy, bronchoalveolar lavage (BAL) was performed in the segmental or subsegmental bronchus corresponding to the radiologically most affected area. A total of 100–150 mL of sterile 0.9% saline was instilled in three to five sequential lavage fractions, each approximately 20–50 mL. The first aliquot was discarded to minimize contamination from the upper airway, and the remaining lavage samples were pooled for microbiological analysis. All procedures were performed using a flexible bronchoscope under local anesthesia with topical lidocaine and conscious sedation (midazolam). To avoid contamination, sterile saline and collection traps were used for each patient, and bronchoscope channels were disinfected and sterilized according to international guidelines between procedures. The collected BAL samples were immediately transported to the microbiology laboratory for culture and further analysis. Indications for the procedure included persistent radiological infiltration, hemoptysis, suspected endobronchial lesions, and chronic cough. Bronchoscopic samplings included bronchoalveolar lavage (BAL), endobronchial biopsy, transbronchial lung biopsy, and brush biopsies. The collected samples were sent to the laboratory for microbiological analysis, and culture results were evaluated retrospectively.

Statistics

All statistical analyses were performed using the Statistical Package for the Social Sciences (SPSS), version 27.0 (IBM Corp., Chicago, IL, USA). The normality of data distribution was evaluated through both visual methods (histograms and probability plots) and analytical tests (Kolmogorov-Smirnov test). Visual and statistical analyses indicated that the continuous variables were non-parametric distributed. Descriptive statistics were used to summarize baseline demographic and clinical characteristics. Continuous variables are presented as medians with interquartile ranges (IQRs), whereas categorical variables are expressed as frequencies and percentages. For multiple group comparisons, the Kruskal-Wallis test followed by the Dunn-Bonferroni post hoc test was applied for continuous variables, and chi-square tests were used for categorical variables. A p-value of <0.05 was considered indicative of statistical significance. Figure 1 was created using GraphPad Prism, version 10.0 (GraphPad Software, San Diego, CA, USA).

Results

A total of 526 patients were included in the study, comprising 389 patients without asthma or COPD, 35 with asthma, and 102 with COPD. The median age was significantly higher in the COPD group compared to patients without asthma or COPD (78 vs. 74 years, p=0.009). No significant difference was observed between groups in terms of gender distribution (p=0.198). The primary indications for the procedure did not differ significantly among the groups (p=0.332). The most common indications across all groups were pneumonia, aspiration pneumonia, and atelectasis. Regarding comorbidities, significant differences were found in the prevalence of heart failure, coronary artery disease, and dementia. Heart failure was significantly more prevalent in the asthma group compared to patients without asthma or COPD (p <0.001). Coronary artery disease was more frequent in the COPD group than in the asthma group (p=0.031). There were no significant differences between groups in terms of intubation rates (p=0.846) or treatment units (outpatient clinic, inpatient ward, intensive care) (p=0.352) (Table 1).

Table 1. Demographic and clinical characteristics of the patients

Variable	Patients with no asthma and COPD (N=389)	Patients with asthma (N=35)	Patients with COPD (N=102)	p
Age, (years), median (IQR)	74.0 (26.0)	77 (26.0)	78.0 (15.0)	0.009*
Gender, (F), n (%)	111 (28.5)	15 (42.9)	29 (28.4)	0.198
Indication for the procedure, n (%)				
Atelectasis	55 (14.1)	4 (11.4)	15 (14.7)	0.332
Mass	27 (6.9)	5 (14.3)	12 (11.8)	
Aspiration pneumonia	113 (29.1)	4 (11.4)	19 (18.6)	
Tuberculosis	26 (6.7)	2 (5.7)	8 (7.8)	
Secretion	40 (10.3)	7 (20.0)	13 (12.8)	
Pneumonia	111 (28.5)	10 (28.6)	33 (32.4)	
Diagnostic	2 (0.5)	0 (0.0)	0 (0.0)	
Cough	2 (0.5)	0 (0.0)	0 (0.0)	
Foreign material	2 (0.5)	0 (0.0)	0 (0.0)	
Hemoptysis	11 (2.8)	3 (8.6)	2 (2.0)	
Comorbidity, n (%)				
Hypertension	181 (46.5)	18 (51.4)	61 (59.8)	0.056
Chronic kidney disease	42 (10.8)	5 (14.3)	9 (8.8)	0.652
Cerebrovascular Disease	136 (35.0)	9 (25.7)	24 (23.5)	0.060
Heart Failure	47 (12.1)	12 (34.3)	26 (25.5)	<0.001Ψ
Coronary Artery Disease	80 (20.6)	4 (11.4)	31 (30.4)	0.031¥
Dementia	105 (27.0)	12 (34.3)	14 (13.7)	0.009¥
Diabetes Mellitus	95 (24.4)	12 (34.3)	19 (18.6)	0.142
Intubated, n (%)	73 (18.8)	6 (17.1)	17 (16.7)	0.846
Unit, n (%)				
Outpatient clinic	47 (12.1)	5 (14.3)	17 (16.7)	0.352
Inpatient ward	50 (12.9)	7 (20.0)	9 (8.8)	
Intensive care	292 (75.1)	23 (65.7)	76 (74.5)	

(*) p<0.05 for patients with no asthma and COPD vs patients with COPD; (Ψ) p<0.05 for patients with no asthma and COPD vs patients with asthma; (¥) p<0.05 for patients with asthma vs patients with COPD; Abbreviations: COPD, Chronic Obstructive Pulmonary Disease.

The overall distribution of microbial growth types including gram-negative bacteria, gram-positive bacteria, and yeast did not significantly differ between groups, whether analyzed as continuous variables or categorical outcomes. For gram-negative bacteria, no significant difference was found in median counts across the groups (p=0.994), and categorical distribution (none, mono, multiple) also showed no significant difference (p=0.181). Similarly, gram-positive bacterial growth did not significantly vary between groups in terms of either median values (p=0.769) or categorical distribution (p=0.817). Yeast or yeast fungi were infrequently detected across all groups, and their distribution was not significantly different (p=0.552 for medians, p=0.598 for categorical levels) (Table 2). Figure 1 illustrates the percentage distribution of microbial growth patterns by group, indicating broadly similar proportions of none, mono, and multi-organism growth across the patient categories.

The comparison of microbial isolates across treatment units revealed that patients in the intensive care unit (ICU) had significantly higher rates of both gram-negative and gram-positive bacterial growth compared to those in outpatient clinics and inpatient wards (p<0.001 for both). While the median values for yeast or yeast fungi remained zero across all units, gram-negative bacteria were less frequently observed in ICU patients, both in mono- and multi-organism growth categories. Similarly, ICU patients showed a lower prevalence of gram-positive bacteria (Table 3).

With regard to smoking history, there were no statistically significant differences in microbial distribution among non-smokers, current smokers, and former smokers (p>0.05 across all microorganism types) (Table 4).

The analysis according to intubation status revealed a significant difference in microbial profiles. Intubated patients had a lower median count of gram-negative bacteria but a significantly higher presence of gram-positive bacteria (p=0.007 and p=0.004, respectively) (Table 5).

Figure 2 highlights a higher concentration of pathogens particularly among ICU patients and intubated individuals, with variations observed across smoking categories and diagnostic groups.

Table 2. Comparison of the number of microorganisms according to the diagnosis

Variable	Patients with no asthma and COPD (N=389)	Patients with asthma (N=35)	Patients with COPD (N=102)	p
Gram-negative bacteria, median (IQR)	1 (0)	1 (1)	1 (0)	0.994
Gram-positive bacteria, median (IQR)	0 (1)	0 (1)	0 (1)	0.769
Yeast or yeast fungi, median (IQR)	0 (0)	0 (0)	0 (0)	0.552
Gram-negative bacteria, n (%)				
None	278 (71.5)	23 (65.7)	77 (75.5)	0.181
Mono	105 (27.0)	9 (25.7)	25 (24.5)	
Multiple	6 (1.5)	2 (5.7)	0 (0.0)	
Gram-positive bacteria,n (%)				
None	96 (24.7)	7 (20.0)	20 (19.6)	0.817
Mono	233 (59.9)	22 (62.9)	67 (65.7)	
Multiple	60 (15.4)	6 (17.1)	15 (14.7)	
Yeast or yeast fungi, n (%)				
None	357 (91.8)	33 (94.2)	95 (93.1)	
Mono	31 (8.0)	1 (2.9)	6 (5.9)	
Multiple	1 (0.3)	1 (2.9)	1 (1.0)	

COPD: Chronic Obstructive Pulmonary Disease; IQR: Interquartile Range.

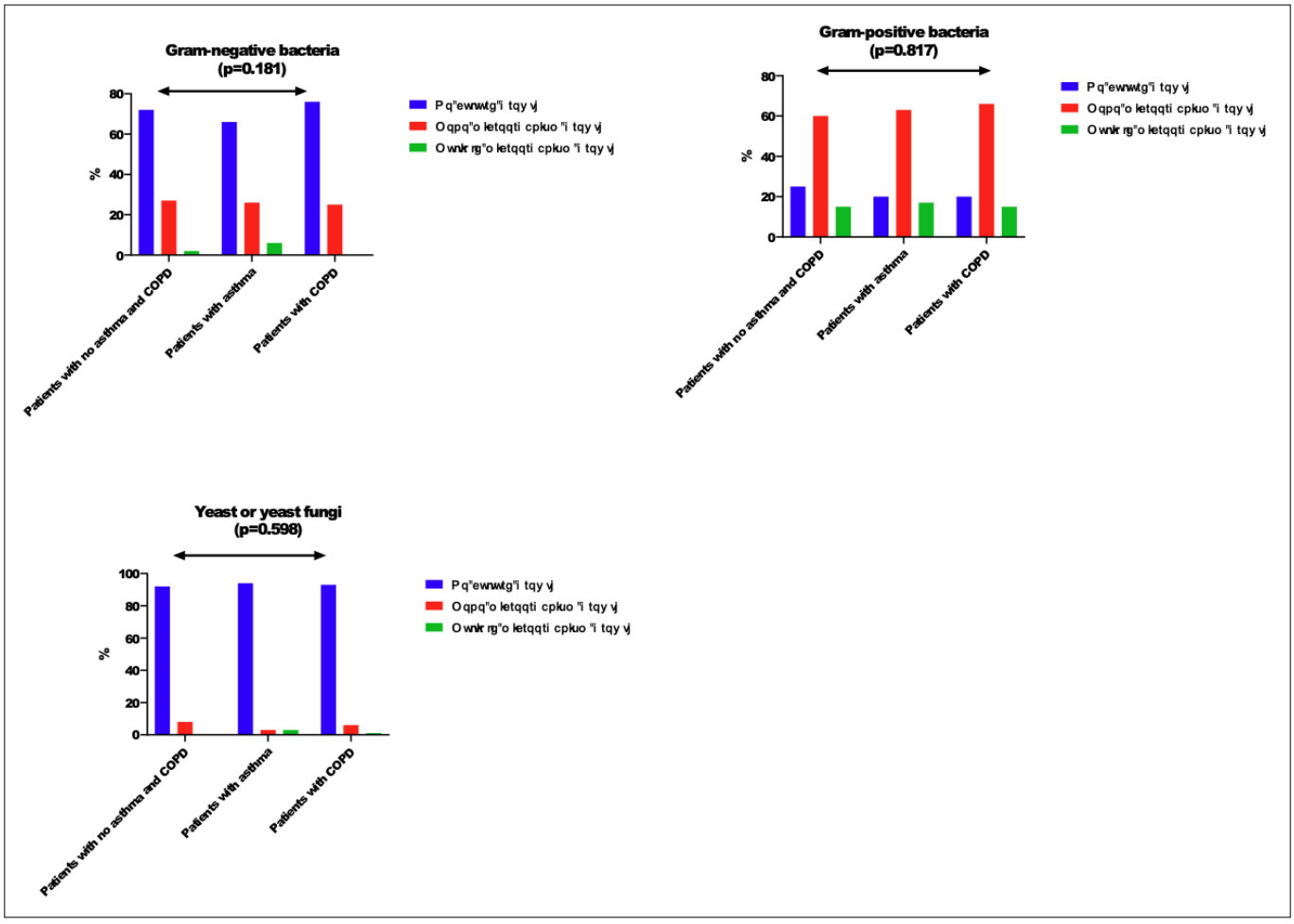

Figure 1. Percentage distribution of microbial growth counts across patient groups.
COPD: Chronic Obstructive Pulmonary Disease.

Discussion

In our study, we compared microbiological growth patterns and clinical variables in patients with asthma, COPD, and those with neither condition among 526 patients who underwent bronchoscopy. Our findings revealed that the respiratory microbiota is shaped more by clinical status (intubation, ICU admission) and care setting rather than by diagnostic groups.

Asthma typically begins in childhood.[6] The aging population increases the risk of chronic obstructive pulmonary disease.[7] Our findings showed that the mean age of patients in the COPD group was statistically higher, supporting the notion that COPD is a disease that increases with age. No significant differences were found between the groups regarding gender distribution and indications for bronchoscopy. This suggests that the microbiological findings observed in our study were not affected by gender-related biases. One of the most significant risk factors for COPD is smoking.[8] In our study, smoking was also significantly higher in COPD patients.

The relationship between asthma and cardiovascular diseases has not been fully elucidated. A study by Nasreen et al. found a higher risk of hypertension in asthmatic patients compared to a control group. Similarly, according to a study by Cristiansen et al., the risk of hypertension increases with asthma severity.[9,10] When comorbidities were evaluated, it was found that the prevalence of heart failure was more common in the asthma group, while coronary artery disease was more frequent in the COPD group. This aligns with the literature indicating that asthma and COPD are associated with systemic inflammation, not just limited to the respiratory system, and can increase the risk of cardiovascular disease. Research has shown that asthma is a risk factor for dementia. In our study, it was found to be significantly higher in the asthma group.[11] The significant difference in dementia prevalence is noteworthy, particularly regarding advanced age and the presence of systemic diseases.

Table 3. Comparison of the number of microorganisms according to the treatment unit of the patients

Variable	Outpatient clinic	Inpatient ward	Intensive care	p
Gram-negative bacteria, median (IQR)	1 (1)	1 (1)	1 (0)	<0.001*Ψ
Gram-positive bacteria, median (IQR)	0 (1)	0 (1)	0 (0)	<0.001*
Yeast or yeast fungi, median (IQR)	0 (0)	0 (0)	0 (0)	0.324
Gram-negative bacteria, n (%)				
None	28	25	69	<0.001
Mono	31	37	256	
Multiple	9	4	67	
Gram-positive bacteria,n (%)				
None	36	44	289	<0.001
Mono	31	22	86	
Multiple	1	0	7	
Yeast or yeast fungi, n (%)				
None	64	58	364	0.222
Mono	3	8	7	
Multiple	1	0	1	

COPD: Chronic Obstructive Pulmonary Disease; IQR: Interquartile Range; (*) p<0.05 for outpatient clinic vs intensive care; (Ψ) p<0.05 for inpatient ward vs intensive care

Table 4. Comparison of the number of microorganisms according to the smoking

Variable	Non smokers (N=492)	Current smokers (N=26)	Former smokers (N=8)	p
Gram-negative bacteria, median (IQR)	1 (0)	1 (1)	1 (1)	0.255
Gram-positive bacteria, median (IQR)	0 (1)	0 (1)	0 (0)	0.485
Yeast or yeast fungi, median (IQR)	0 (0)	0 (0)	0 (0)	0.270
Gram-negative bacteria, n (%)				
None	111	9	2	0.610
Mono	304	15	5	
Multiple	77	2	1	
Gram-positive bacteria, n (%)				
None	355	17	7	0.693
Mono	129	9	1	
Multiple	8	0	0	
Yeast or yeast fungi, n (%)				
None	455	24	7	0.052
Mono	36	1	1	
Multiple	1	1	0	

A study found that in individuals with COPD, the composition of the microbiome changed with different exacerbation subtypes during a one-year follow-up period, encompassing both stable and exacerbation phases, and certain patterns were repeated.[12] In our study, however, microbiological analyses revealed no significant difference between groups regarding the presence of gram-negative and gram-positive bacteria or yeast species. The presence of single or multiple microorganisms also showed a similar distribution. This result suggests that a diagnosis of

Table 5. Comparison of the number of microorganisms according to the intubation

Variable	Non-intubated (N=425)	Intubated (N=96)	p
Gram-negative bacteria, median (IQR)	1 (1)	0 (1)	0.007
Gram-positive bacteria, median (IQR)	0 (1)	1 (0)	0.004
Yeast or yeast fungi, median (IQR)	0 (0)	0 (0)	0.866
Gram-negative bacteria, n (%)			
None	108	11	0.012
Mono	255	67	
Multiple	62	18	
Gram-positive bacteria,n (%)			
None	296	81	0.014
Mono	122	14	
Multiple	7	1	
Yeast or yeast fungi, n (%)			
None	392	89	0.797
Mono	31	7	
Multiple	2	0	

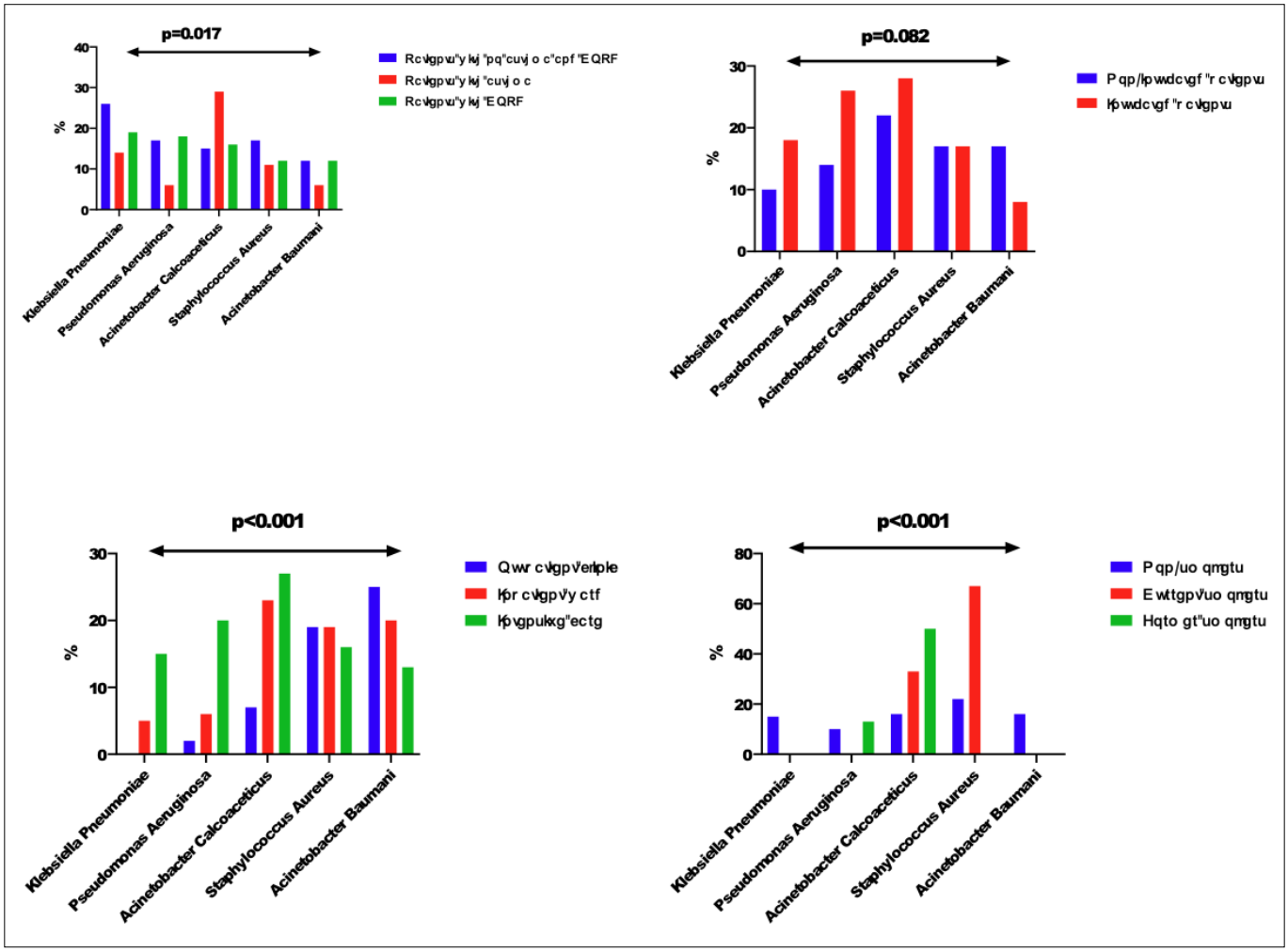

Figure 2. Comparison of the percentage of five most frequently isolated bacterial pathogens among patients according to diagnosis, intubation status, treatment unit, and smoking history.

asthma or COPD does not significantly affect the respiratory tract microbial colonization pattern. While previous studies have presented varying views on the effects of microbial colonization on disease progression in chronic airway diseases, our findings indicate heterogeneity in this area and no significant group differences in terms of microbial diversity.[13] This situation suggests that disease-related structural changes alone are insufficient to explain microbial diversity. It also suggests that microbial load does not change according to diagnosis (presence of asthma or COPD), but is likely influenced by other factors (e.g., ICU stay, intubation, antibiotic use, etc.).

Studies have reported that gram-negative bacteria are dominant in intensive care units, but gram-positive bacteria are also isolated in significant proportions.[14] The significantly higher growth of both gram-negative and gram-positive bacteria in patients hospitalized in the intensive care unit highlights the risk of hospital-acquired infections and the impact of invasive procedures (e.g., mechanical ventilation). Fungal growth was rarely found in ICU patients; this could be related to antifungal prophylaxis, short length of stay, or frequency of sampling.

Despite a low number of gram-negative bacteria in intubated patients, gram-positive bacterial growth is significantly higher. The literature also reports that gram-positive cocci are more frequently isolated in ventilator-associated infections.[15] This indicates that gram-positive pathogens (e.g., MRSA) gain importance in ventilator-associated pneumonias developing after intubation. Intubated patients are usually treated with early broad-spectrum antibiotics. These antibiotics can target gram-negatives and rapidly alter the flora.[16] Consequently, while the gram-negative load decreases, resistant gram-positive bacteria may become dominant. This finding suggests that factors such as whether the patient is in the ICU and whether they are intubated should be considered in empirical antibiotic selection. As this was a retrospective study, information on prior antibiotic exposure was obtained from existing hospital records. Although detailed data on the type, duration, and dose of antibiotics were not consistently available, the presence or absence of antibiotic therapy before bronchoscopy was documented and considered in the analysis. Prior antibiotic treatment particularly in ICU and intubated patients may have contributed to lower culture positivity rates due to partial suppression of bacterial growth. Therefore, antibiotic exposure should be recognized as an important confounding factor when interpreting microbiological growth patterns in retrospective analyses such as this one. Several studies have reported that prior antibiotic exposure can significantly alter the respiratory microbiota by suppressing susceptible bacterial populations and promoting the overgrowth of resistant organisms.[17] In ICU patients, this effect may be even more pronounced due to prolonged hospitalization, mechanical ventilation, and repeated antibiotic courses. Consequently, antibiotic therapy prior to bronchoscopy may reduce bacterial growth in culture, mask potential pathogens, or shift microbial predominance toward multidrug-resistant strains. This should be taken into account when interpreting the microbiological distribution, particularly among critically ill and intubated patients.

Smoking directly affects a person's microbiota, but this varies from person to person.[18] No significant relationship was found between smoking history and microbiological distribution. This finding suggests that smoking increases the risk of infection through indirect effects, such as impairing lung defense mechanisms, rather than directly affecting microbial growth patterns.

It demonstrates that microbiological patterns differ significantly according to the clinical characteristics of patients.[19] Entubation and intensive care unit admission show a strong association, especially with hospital-acquired and multidrug-resistant pathogens.[20] Studies have found a relationship between the intensity of antibiotic use in COPD patients and the growth of gram-negative pathogens such as Pseudomonas aeruginosa, Klebsiella pneumoniae, and Acinetobacter baumannii.[21] In our study, gram-negative bacillus colonization was found to be more prominent in COPD patients due to chronic inflammation and frequent antibiotic use.

A significant contribution of this study is that it shows that intervention and environmental factors, such as intubation and intensive care, have stronger effects on microbial distribution than diagnosis-based differentiation.

The limitations of our study include its retrospective nature and the lack of data regarding previous antibiotic use. Furthermore, the absence of detailed microbiota analyses using molecular methods in addition to microbial culture results limited a more in-depth evaluation of microbial composition. Future studies are recommended to comprehensively examine bronchial microbiota in different patient groups and correlate it with clinical outcomes.

Conclusion

In conclusion, the study reveals that microbial growths are associated more with the treatment unit and intubation status than with diagnostic groups. These data emphasize the importance of considering the patient's clinical status, hospitalization location, and history of invasive procedures in empirical antibiotic selection. Additionally, the clinical significance of microorganisms detected in respiratory tract samples should be carefully evaluated.

Disclosures

Ethics Committee Approval: This study was conducted in accordance with the Declaration of Helsinki, and ethical approval was obtained from the Ethics Committee of Kahramanmaraş Sütçü İmam University Faculty of Medicine (No: 21, Date: 09/01/2025).

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Data Availability Statement: The data that support the findings of this study are available from the Department of Pulmonology, Faculty of Medicine, Kahramanmaraş Sütçü İmam University. However, restrictions apply to the availability of these data, which were used under license for the current study and are not publicly available. Data may be obtained from the authors upon reasonable request and with permission from the relevant institutional administration.

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