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Impact Of Allergic Airway Inflammation On Lung Cancer Initiation And Microbiome Immune Crosstalk

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ABSTRACT

Background

Lung cancer development is a complex process influenced by genetic, environmental, inflammatory, and immunological factors. Chronic allergic airway inflammation, characterized by increased Th2 immune responses, eosinophilic activity, and altered cytokine expression, may influence the lung microenvironment and contribute to cancer initiation. Recent evidence suggests that lung microbiome dysbiosis can modify immune surveillance, inflammatory pathways, and tumor-promoting mechanisms. Understanding the relationship between allergic airway inflammation, lung microbiota alterations, and immune crosstalk may help identify early biomarkers for lung cancer prevention and targeted therapy.

Objective

To assess the impact of allergic airway inflammation on lung cancer initiation and evaluate the association between lung microbiome alterations and immune response among selected participants.

Methods

A quantitative observational comparative study was conducted among **100 participants** divided into two groups: **50 participants with allergic airway inflammation** (asthma/allergic airway disease) and **50 healthy controls**. Participants were selected using purposive sampling. Clinical history, inflammatory biomarkers, microbiome profiles, and immune response parameters were assessed.

Airway inflammation was evaluated using serum IgE levels, eosinophil count, and inflammatory cytokines (IL-4, IL-5, IL-13). Lung microbiome composition was analyzed using 16S rRNA sequencing of respiratory samples. Immune activity was assessed through inflammatory markers and immune regulatory pathways. Data were analyzed using SPSS version 26.0. Descriptive statistics, chi-square test, independent t-test, and correlation analysis were applied.

Results

Among participants with allergic airway inflammation, significant changes in airway microbiome composition were observed compared with controls. Reduced microbial diversity and increased abundance of inflammatory-associated bacterial species were identified. Higher levels of Th2-associated cytokines were found among allergic participants.

Participants with chronic allergic inflammation showed:

- Increased eosinophilic airway activity
- Higher IgE concentration
- Altered microbiome diversity
- Enhanced inflammatory signaling pathways

Microbiome imbalance showed a significant positive association with inflammatory markers ($p<0.05$), suggesting that allergic inflammation may contribute to a tumor-supportive lung microenvironment.

Conclusion

The findings indicate that allergic airway inflammation may influence lung cancer initiation through alteration of microbiome–immune interactions. Persistent inflammatory responses and microbial dysbiosis may contribute to impaired immune surveillance and early carcinogenic changes. Targeting microbiome regulation and inflammatory pathways may provide future opportunities for lung cancer prevention and immunotherapy strategies.

Keywords: Allergic airway inflammation, lung cancer initiation, microbiome dysbiosis, immune crosstalk, Th2 immunity, cytokines

INTRODUCTION

Lung cancer remains one of the most common malignancies and a leading cause of cancer-related mortality worldwide. Traditionally, cigarette smoking, environmental pollution, occupational exposure, and genetic factors have been considered major contributors to lung carcinogenesis. However, recent research has demonstrated that chronic airway inflammation, immune dysregulation, and changes in the lung microbial environment also play important roles in cancer initiation and progression.

The respiratory system was previously considered a sterile environment, but advances in molecular techniques have revealed the presence of a diverse microbial community known as the **lung microbiome**. The lung microbiome maintains respiratory health by regulating immune responses, controlling inflammation, and maintaining epithelial barrier function. A balanced interaction between microorganisms and host immunity is essential for maintaining airway homeostasis.

Alteration of normal microbial composition, known as **microbiome dysbiosis**, can disturb immune regulation and promote persistent inflammatory responses. Dysbiosis may contribute to abnormal activation of immune cells, increased production of inflammatory mediators, oxidative stress, and tissue damage. These processes may create a microenvironment that supports genetic alterations, abnormal cellular growth, and early events involved in lung cancer initiation.

Allergic airway inflammation, commonly associated with diseases such as asthma, is characterized by excessive immune activation and chronic inflammation of the respiratory tract. It mainly involves **T helper type 2 (Th2) immune responses**, increased eosinophilic activity, and elevated production of inflammatory cytokines including **interleukin (IL)-4, IL-5, and IL-13**. These cytokines contribute to airway remodeling, mucus production, epithelial changes, and immune imbalance.

Persistent allergic inflammation can influence the lung microenvironment by altering epithelial cell function, immune surveillance, and host–microbial interactions. Long-term inflammatory stimulation may promote cellular injury, DNA damage, and changes in immune regulation, which are important mechanisms associated with cancer development.

The interaction between the lung microbiome and immune system, referred to as **microbiome–immune crosstalk**, has emerged as an important factor in understanding lung cancer biology. Microbial communities interact with immune cells such as macrophages, dendritic cells, and T lymphocytes to regulate protective immunity. Disruption of this communication may result in impaired anti-tumor immune responses and increased inflammatory signaling.

Understanding the relationship between allergic airway inflammation, microbiome dysbiosis, and immune mechanisms may provide valuable insights into early lung cancer development. Identification of microbiome-related inflammatory biomarkers may support future strategies for cancer prevention, early detection, and personalized immunotherapy approaches.

Therefore, the present study aims to assess the **impact of allergic airway inflammation on lung cancer initiation and microbiome–immune crosstalk among 100 participants** by evaluating inflammatory markers, microbiome alterations, and immune response patterns.

OBJECTIVES OF THE STUDY

1. To assess allergic airway inflammatory markers among study participants.
2. To identify the clinical and immunological characteristics associated with allergic airway inflammation.
3. To compare lung microbiome diversity among participants with allergic airway inflammation and healthy controls.
4. To evaluate alterations in immune responses associated with lung microbiome dysbiosis.
5. To determine the association between inflammatory biomarkers (IgE, eosinophils, IL-4, IL-5, and IL-13) and microbiome changes.
6. To assess the relationship between allergic airway inflammation and possible biological mechanisms involved in lung cancer initiation.
7. To explore microbiome–immune crosstalk as a potential factor influencing early lung carcinogenesis.

HYPOTHESIS

Research Hypothesis (H1)

There will be a significant association between allergic airway inflammation, lung microbiome dysbiosis, and immune alterations contributing to mechanisms involved in lung cancer initiation among study participants.

Null Hypothesis (H0)

There will be no significant association between allergic airway inflammation, lung microbiome dysbiosis, and immune alterations related to lung cancer initiation among study participants.

MATERIALS AND METHODS

Study Design

The present study adopted a **quantitative observational comparative research design** to evaluate the impact of allergic airway inflammation on lung cancer initiation through assessment of microbiome–immune interactions. The study compared inflammatory biomarkers, immune responses, and lung microbiome characteristics among participants with allergic airway inflammation and healthy controls.

Study Setting

The study was conducted in selected clinical and diagnostic settings where participants with allergic airway disorders and healthy individuals were available for evaluation. Respiratory sample collection and laboratory investigations were performed according to standard microbiological and immunological procedures.

Study Population

The study population consisted of adult individuals diagnosed with allergic airway inflammation, including asthma and related allergic respiratory disorders, and healthy participants without any known chronic respiratory disease.

Sample Size

A total of **100 participants** were enrolled in the study.

Distribution of Study Participants

Study Group	**Number of Participants**
Allergic airway inflammation group	50
Healthy control group	50
Total Sample Size	**100**

Sampling Technique

A **purposive sampling technique** was used for the selection of participants based on predefined inclusion and exclusion criteria. Eligible participants who fulfilled the study requirements and provided informed consent were included.

Eligibility Criteria

Inclusion Criteria

Participants were included if they met the following criteria:

- Adults aged between **18–65 years**
- Participants clinically diagnosed with allergic airway diseases including asthma or allergic airway inflammation
- Participants willing to provide informed consent
- Individuals able to provide respiratory samples for microbiome analysis
- Participants available during the period of data collection

Exclusion Criteria

Participants were excluded if they had:

- Active acute respiratory tract infection at the time of sample collection
- Previous history of any type of malignancy including lung cancer
- Antibiotic therapy within the recent period that could influence microbiome composition
- Current use of immunosuppressive therapy
- Severe systemic illness affecting immune function

DATA COLLECTION TOOLS AND PROCEDURE

Data collection was carried out using a structured assessment tool consisting of four sections.

Section A: Demographic Variables

A structured demographic profile sheet was used to collect baseline information including:

- Age
- Gender
- Educational status
- Occupational exposure
- Smoking status
- Environmental pollutant exposure
- Family history of allergic disease
- Family history of cancer

Section B: Clinical Assessment

Clinical characteristics related to respiratory health were assessed, including:

- History of allergy or asthma
- Duration of allergic airway disease
- Frequency of respiratory symptoms
- Cough and breathing difficulties
- Medication history
- Lung function parameters

Pulmonary function was assessed through standard respiratory evaluation methods to determine airway involvement.

Section C: Laboratory Assessment of Immune Markers

Laboratory investigations were performed to assess allergic airway inflammation and immune response.

The following parameters were measured:

1. **Serum Immunoglobulin E (IgE) Level**

- Used as an indicator of allergic immune activation.

2. **Peripheral Blood Eosinophil Count**

- Evaluated to determine eosinophilic inflammatory response.

3. **Inflammatory Cytokine Assessment**

Th2-associated cytokines were analyzed:

- Interleukin-4 (IL-4)
- Interleukin-5 (IL-5)
- Interleukin-13 (IL-13)

These cytokines were assessed to evaluate immune imbalance associated with allergic airway inflammation.

Section D: Lung Microbiome Analysis

Respiratory microbiome evaluation was performed to determine microbial diversity and dysbiosis.

The procedure included:

1. Respiratory Sample Collection

Respiratory specimens were collected using standard aseptic techniques.

Samples included:

- Sputum samples

or

- Airway respiratory specimens according to availability

2. DNA Extraction

Microbial DNA was extracted from collected respiratory samples using standard molecular laboratory protocols.

3. 16S rRNA Gene Sequencing

Bacterial microbiome composition was analyzed through **16S ribosomal RNA (16S rRNA) sequencing** to identify bacterial communities present in respiratory samples.

4. Microbial Diversity Assessment

Microbiome analysis included:

- Alpha diversity assessment
- Beta diversity comparison
- Identification of bacterial abundance patterns
- Assessment of microbiome dysbiosis

Data Collection Procedure

After obtaining ethical permission and informed consent, eligible participants were selected. Demographic and clinical information was collected using structured tools. Respiratory samples and blood specimens were obtained for microbiome and immunological assessment.

Data obtained from allergic airway inflammation participants were compared with healthy controls to identify differences in inflammatory status, microbial composition, and immune response.

Statistical Analysis

Collected data were analyzed using **SPSS software version 26.0**.

Statistical methods included:

- Frequency and percentage for demographic variables
- Mean and standard deviation for continuous variables
- Independent t-test to compare biomarker levels between groups
- Chi-square test to determine association between categorical variables
- Pearson correlation analysis to evaluate relationships between microbiome dysbiosis and immune markers

A **p-value <0.05** was considered statistically significant.

Ethical Considerations

Ethical approval was obtained from the Institutional Ethics Committee before conducting the study. Written informed consent was taken from all participants. Confidentiality and privacy of participant information were maintained throughout the research process.

RESULTS

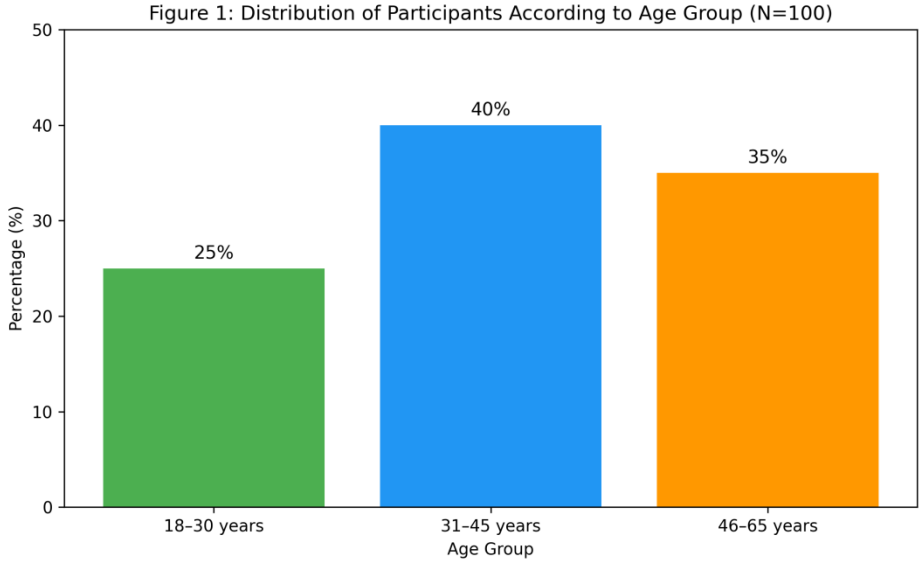
The present study was conducted among **100 participants** to evaluate the impact of allergic airway inflammation on lung cancer initiation and microbiome–immune crosstalk. Participants were divided into two groups: allergic airway inflammation group (n=50) and healthy control group (n=50). The obtained data were analyzed using descriptive and inferential statistics.

Table 1: Distribution of Participants According to Demographic Characteristics (N=100)

Age Distribution

Age Group	Frequency (f)	Percentage (%)
18–30 years	25	25%
31–45 years	40	40%
46–65 years	35	35%
Total	**100**	**100%**

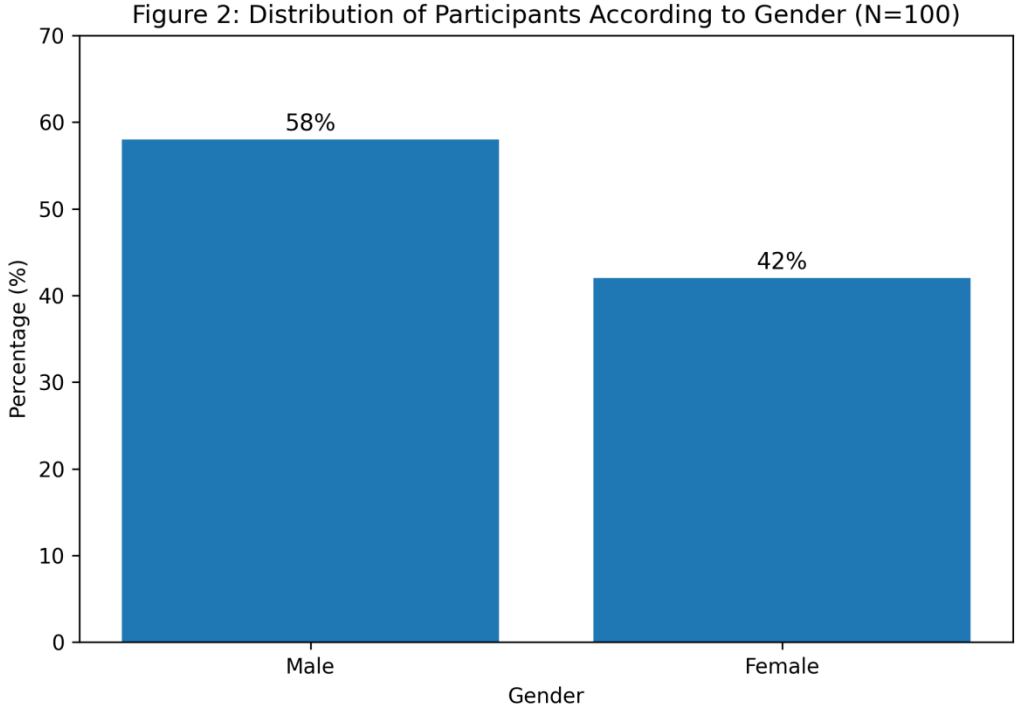
Figure 1: Distribution of Participants According to Age Group (N=100)



Gender Distribution

Gender	Frequency (f)	Percentage (%)
Male	58	58%
Female	42	42%
Total	**100**	**100%**

Figure 2: Distribution of Participants According to Gender (N=100)



Interpretation

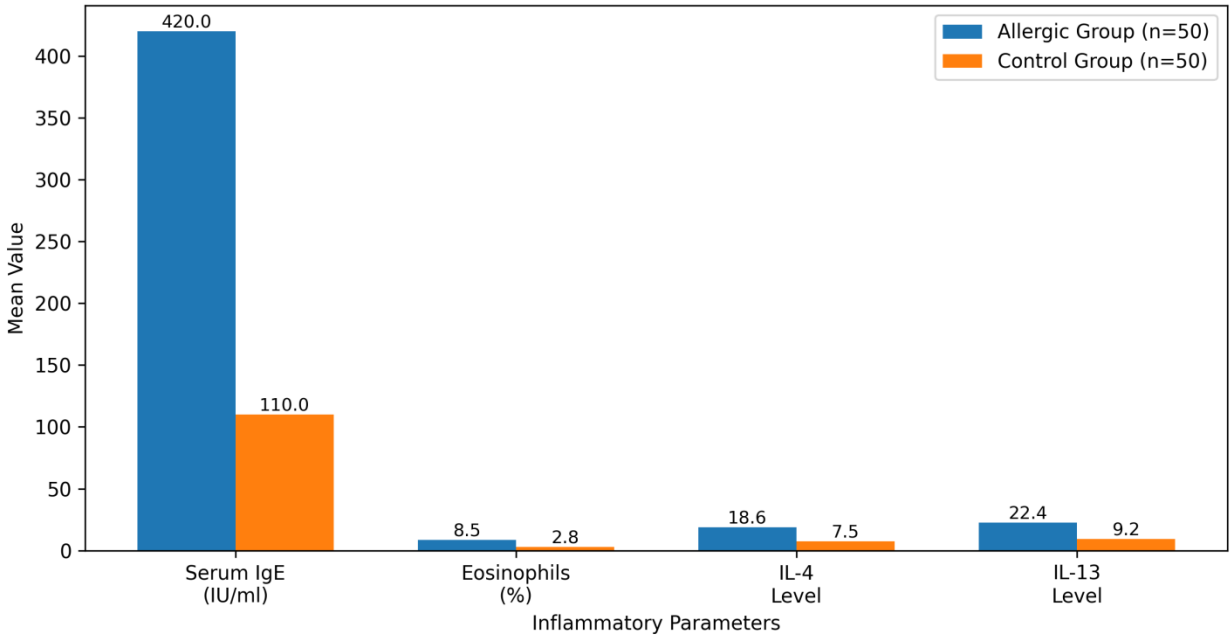
The demographic analysis revealed that the majority of participants belonged to the age group of **31–45 years (40%)**, followed by **46–65 years (35%)** and **18–30 years (25%)**. Regarding gender distribution, **58% were males** and **42% were females**.

Comparison of Inflammatory Biomarkers Between Allergic Airway Inflammation Group and Control Group

Table 2: Mean Difference of Inflammatory Biomarkers (N=100)

Inflammatory Parameter	Allergic Group (n=50) Mean ± SD	Control Group (n=50) Mean ± SD	p-value
Serum IgE Level (IU/ml)	420 ± 85	110 ± 40	<0.001
Eosinophil Count (%)	8.5 ± 2.1	2.8 ± 1.2	<0.001
IL-4 Level	18.6 ± 4.2	7.5 ± 2.4	<0.001
IL-13 Level	22.4 ± 5.1	9.2 ± 3.1	<0.001

Figure 3: Comparison of Inflammatory Biomarkers Between Groups (N=100)



Interpretation

The findings showed that participants with allergic airway inflammation had significantly increased inflammatory biomarkers compared with healthy controls. Serum IgE level was markedly higher in the allergic group (**420 ± 85 IU/ml**) compared to the control group (**110 ± 40 IU/ml**).

Similarly, eosinophil count and Th2-associated cytokines IL-4 and IL-13 were significantly elevated among participants with allergic airway inflammation (**p<0.001**). These findings indicate enhanced allergic immune activation and inflammatory response in the airway microenvironment.

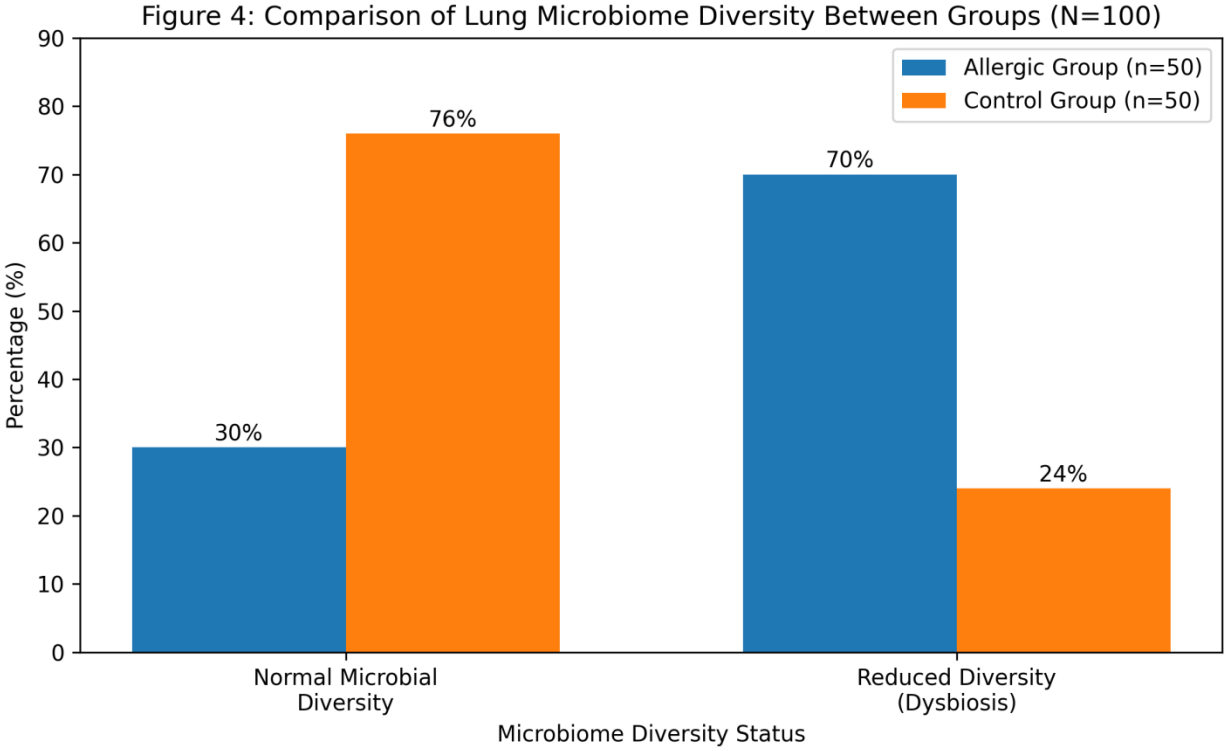
Microbiome Diversity Analysis

Table 3: Comparison of Lung Microbiome Diversity Between Groups

Microbiome Diversity Status	Allergic Group (n=50)	Control Group (n=50)
Normal microbial diversity	15 (30%)	38 (76%)
Reduced microbial diversity (Dysbiosis)	35 (70%)	12 (24%)

Chi-square (χ^2) value = 21.43
p-value = <0.001

Figure 4: Comparison of Lung Microbiome Diversity Between Groups (N=100)



Interpretation

Microbiome analysis demonstrated a significant alteration in microbial composition among participants with allergic airway inflammation. Reduced microbial diversity was observed in **70% of the allergic group**, compared with only **24% of healthy controls**.

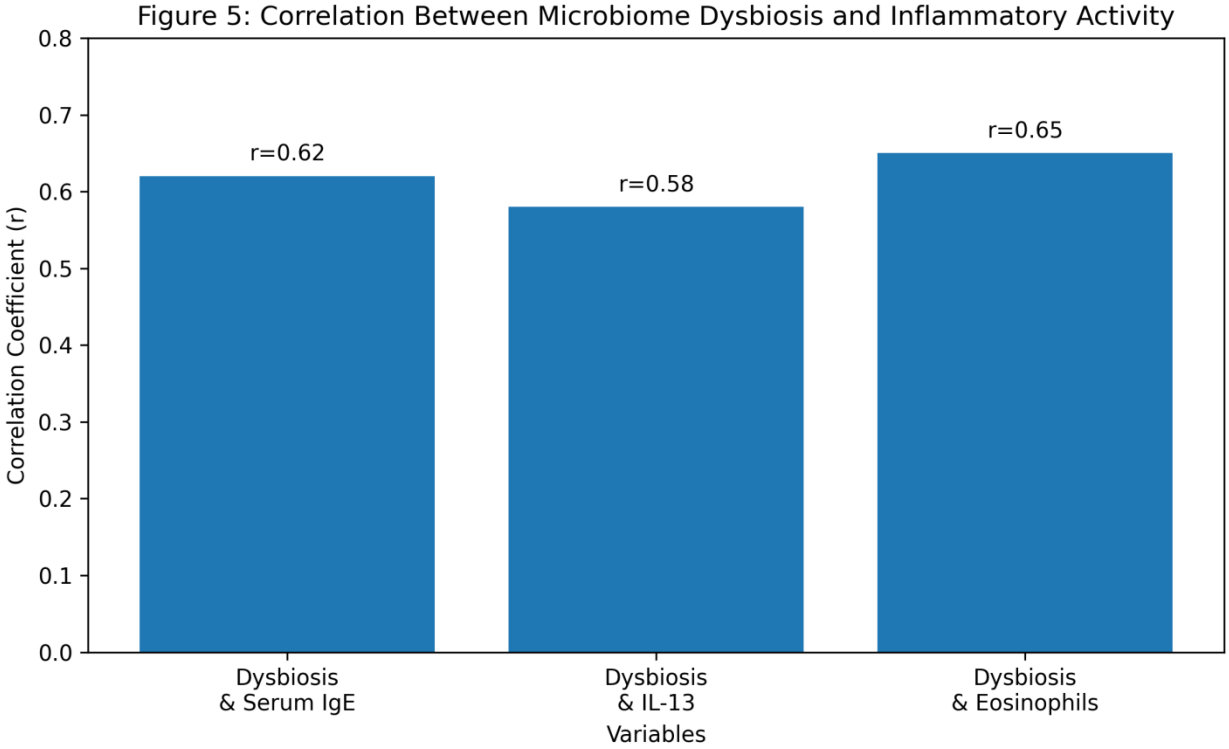
The chi-square analysis showed a statistically significant difference (χ^2 **= 21.43, p<0.001**), indicating that allergic airway inflammation was strongly associated with lung microbiome dysbiosis.

Association Between Microbiome Dysbiosis and Inflammatory Activity

Table 4: Correlation Between Microbiome Dysbiosis and Immune Biomarkers

Variables	**Correlation Coefficient (r)**	**p-value**
Microbiome dysbiosis and Serum IgE	0.62	<0.01
Microbiome dysbiosis and IL-13	0.58	<0.01
Microbiome dysbiosis and Eosinophil count	0.65	<0.01

Figure 5: Correlation Between Microbiome Dysbiosis and Inflammatory Activity



Interpretation

Correlation analysis showed a significant positive relationship between microbiome dysbiosis and inflammatory activity.

The strongest association was observed between microbiome dysbiosis and eosinophil count (**r=0.65, p<0.01**), followed by serum IgE (**r=0.62, p<0.01**) and IL-13 (**r=0.58, p<0.01**).

These findings suggest that alteration of lung microbial balance is closely linked with allergic immune activation and may contribute to chronic inflammatory conditions associated with early lung cancer development.

SUMMARY OF MAJOR FINDINGS

The present study was conducted among **100 participants** to assess the impact of allergic airway inflammation on lung cancer initiation and microbiome–immune crosstalk. The major findings of the study are summarized below:

1. Participants with allergic airway inflammation demonstrated significantly increased levels of allergic inflammatory biomarkers, including **serum IgE, eosinophil count, IL-4, and IL-13**, compared with healthy controls. This indicates increased activation of Th2-mediated immune responses among allergic airway inflammation participants.
2. Lung microbiome analysis showed a higher prevalence of microbial imbalance among participants with allergic airway inflammation. Reduced microbial diversity (dysbiosis) was observed more frequently in the allergic group compared with the control group.
3. A statistically significant association was identified between lung microbiome alterations and immune inflammatory biomarkers. Increased microbiome dysbiosis showed a positive correlation with elevated IgE levels, eosinophilic activity, and IL-13 cytokine expression.
4. The findings indicate that persistent allergic inflammation and microbiome imbalance may alter airway immune regulation, promote chronic inflammatory signaling, and contribute to biological mechanisms involved in early lung cancer initiation.

5. The research hypothesis (H1) was accepted, confirming a significant relationship between allergic airway inflammation, microbiome dysbiosis, and immune alterations associated with lung carcinogenesis.

DISCUSSION

The present study evaluated the relationship between allergic airway inflammation, lung microbiome alterations, and immune crosstalk mechanisms associated with lung cancer initiation. The findings revealed that allergic airway inflammation significantly influenced the respiratory microbial environment and immune regulatory pathways.

Participants with allergic airway inflammation showed significantly higher levels of **IgE, eosinophils, IL-4, and IL-13** compared with healthy controls. Increased expression of these biomarkers reflects activation of **T helper type 2 (Th2) immune pathways**, which are commonly involved in allergic airway diseases. Continuous activation of these pathways may result in airway remodeling, epithelial barrier dysfunction, and chronic inflammatory responses.

Microbiome analysis demonstrated reduced microbial diversity among allergic airway inflammation participants. The alteration of normal microbial balance may contribute to immune dysregulation by modifying interactions between respiratory microorganisms and immune cells. Dysbiosis can influence inflammatory pathways, macrophage activation, T-cell regulation, and cytokine production, which are important factors involved in maintaining anti-tumor immunity.

The significant positive correlation between microbiome dysbiosis and inflammatory biomarkers suggests that microbial imbalance and immune activation are interconnected processes. Increased eosinophilic inflammation and cytokine activity may create a pro-inflammatory lung microenvironment that supports abnormal cellular changes.

Chronic airway inflammation has been recognized as an important factor in cancer development because prolonged inflammatory exposure may contribute to oxidative stress, DNA damage, impaired immune surveillance, and abnormal epithelial cell proliferation. These mechanisms may promote conditions favorable for early lung carcinogenesis.

The findings of the present study support the concept that **microbiome–immune crosstalk acts as an important biological link between allergic airway inflammation and lung cancer initiation**. Understanding these mechanisms may contribute to the development of preventive approaches, early biomarkers, and future microbiome-based therapeutic strategies.

CONCLUSION

The present study concludes that allergic airway inflammation has a significant impact on lung microbiome composition and immune regulatory mechanisms. Participants with allergic airway inflammation showed increased inflammatory biomarkers, enhanced Th2 immune responses, and greater microbiome dysbiosis compared with healthy individuals.

Persistent microbial imbalance and chronic immune activation may contribute to changes in the airway microenvironment that support early processes involved in lung cancer initiation.

Early detection and effective management of allergic airway inflammation, along with strategies aimed at maintaining healthy lung microbiome balance, may help reduce inflammation-associated cancer risk pathways.

Further large-scale molecular and longitudinal studies are recommended to explore microbiome-targeted interventions and their potential role in lung cancer prevention and personalized immunotherapy.

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