

To Study the Relationship of Nasal Flora in Patients with Allergic Rhinitis: A Cross-Sectional Comparative Study

Dr. Pankaj Kotiya¹; Dr. Navin Agrawal²; Dr. Chhavi Agrawal³;
Dr. Ajinkya Raverkar⁴; Dr. Sadashiv Parikh⁵; Dr. Kabir Bagga⁶;
Dr. Isha Shrivastava⁷; Dr. Abha Singh⁸

¹Junior Resident, Department of Otorhinolaryngology, Index Medical College Hospital & Research Centre, Indore, Madhya Pradesh, India.

²Professor and Head, Department of Otorhinolaryngology, Index Medical College Hospital & Research Centre, Indore, Madhya Pradesh, India.

³Professor, Department of Otorhinolaryngology, Index Medical College Hospital & Research Centre, Indore, Madhya Pradesh, India.

⁴Assistant Professor, Department of Otorhinolaryngology, Index Medical College Hospital & Research Centre, Indore, Madhya Pradesh, India.

⁵Junior Resident, Department of Otorhinolaryngology, Index Medical College Hospital & Research Centre, Indore, Madhya Pradesh, India.

⁶Junior Resident, Department of Otorhinolaryngology, Index Medical College Hospital & Research Centre, Indore, Madhya Pradesh, India.

⁷Senior Resident, Department of Otorhinolaryngology, Amaltas institute of Medical Science, Dewas, Madhya Pradesh, India

⁸Resident Medical officer, Department of Otorhinolaryngology, Bombay Hospital, Indore, Madhya Pradesh, India

Corresponding Author: Dr. Ajinkya Raverkar

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Abstract:

➤ Background

Allergic rhinitis (AR) is a typical IgE-mediated inflammatory disorder affecting a substantial proportion of the global population. Emerging evidence suggests that alterations in nasal microbiota may influence disease pathogenesis and severity.

➤ Objective

To evaluate the nasal flora in patients with allergic rhinitis, compare it along with the healthy individuals, and also evaluate the relationship between serum IgE levels and allergic rhinitis.

➤ Method

A cross-sectional comparative study was carried out in the Department of Otorhinolaryngology, Index Medical College, Indore, India, from July 2023 to January 2025. 100 patients with clinically diagnosed allergic rhinitis and elevated serum IgE levels were included, along with 100 healthy controls. Nasal swabs were collected from the nasal vestibule, inferior turbinate,

and middle meatus using aseptic techniques. Samples were processed for Gram staining and bacterial culture. Serum IgE values were estimated in all the participants. Statistical analysis was performed using SPSS version 21.0.

➤ Results

The mean age of AR patients group was 35.3 ± 11.9 years, while that of controls was 43.5 ± 14.4 years. Sneezing (75%), nasal obstruction (73%), and nasal itching (60%) were the most common symptoms among AR patients. *Staphylococcus aureus* was isolated significantly more frequently in AR patients than in controls (38% vs. 23%, $p=0.032$). *Staphylococcus epidermidis* was the predominant commensal organism in controls (37%). Serum IgE levels were significantly higher among AR patients (416.04 ± 122.83 IU/mL) compared to controls (71.85 ± 24.38 IU/mL; $p<0.001$).

➤ Conclusion

Patients with allergic rhinitis exhibit significant alterations in culturable nasal flora, particularly increased colonisation by *Staphylococcus aureus*, along with markedly elevated serum IgE levels. These findings favours the role of microbial dysbiosis in allergic rhinitis.

Keywords: Allergic Rhinitis, Nasal Microbiota, Nasal Flora, Serum IgE, *Staphylococcus Aureus*, Dysbiosis.

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I. INTRODUCTION

Allergic rhinitis (AR) is a chronic inflammatory disorder of the nasal mucosa, which is mediated by immunoglobulin E (IgE) following vulnerability to environmental allergens [1,2]. It affects approximately 10–30% of the worldwide population and markedly impairs quality of life manifesting symptoms such as sneezing, rhinorrhea, nasal obstruction, and itching [2,3]. Despite considerable advances in understanding the immunopathogenesis of AR, the contribution of the nasal microbiome to disease development and progression remains incompletely understood.

The nasal cavity harbors a diverse microbial ecosystem that plays a crucial part in maintaining mucosal homeostasis and regulating immune responses [4]. Alterations in microbial composition, commonly referred to as dysbiosis, have been implicated in several inflammatory airway disorders, including allergic rhinitis [5]. Previous studies have demonstrated reduced microbial diversity and increased colonization by potentially pathogenic organisms, particularly *Staphylococcus aureus*, among patients with AR [4–6]. Such microbial alterations may contribute to epithelial barrier dysfunction, persistent inflammation, and symptom exacerbation.

Data regarding nasal microbiota in patients with allergic rhinitis from the Indian population remain limited. Therefore, this study aimed to evaluate the role of nasal flora in patients with allergic rhinitis, compare it with that of healthy individuals, and assess the correlation between serum IgE levels and allergic rhinitis.

II. MATERIALS AND METHODS

After obtaining approval from the Institutional Ethics Committee. This cross-sectional comparative study was carried out in the Department of Otorhinolaryngology at Index Medical College Hospital and Research Centre, Indore, India, between July 2023 and January 2025.

A total of 200 participants were enrolled. Group A consisted of 100 patients aged 15 years or older with clinical features suggestive of allergic rhinitis and elevated serum IgE levels. Group B included 100 healthy individuals without nasal complaints who served as controls. Participants using intranasal steroids, oral antihistamines, or having acute upper respiratory tract infections were excluded.

Serum IgE levels were evaluated in all participants. Statistical analysis was performed using SPSS version 21.0. Continuous variables were expressed as mean $\pm$ standard deviation, whereas categorical variables were presented as percentages. The Mann–Whitney U test and Chi-square test were used where appropriate. A p-value <0.05 was considered statistically significant.

➤ Declarations

- **Ethical Approval:**

Obtained from the Institutional Ethical Committee of Index Medical College, Hospital and Research Centre, Indore.

- **Informed Consent:**

Written informed consent was obtained from all participants.

- Funding:**

No external funding was received for this study.

- Conflict of Interest:**

The authors declare no conflict of interest.

III. RESULTS

A total of 200 participants were listed, out of which 100 patients were with allergic rhinitis and 100 patients were healthy controls.

Table 1. Baseline Attributes of Study Participants

Characteristic	AR Patients (n=100)	Controls (n=100)
Mean age (years)	35.3 ± 11.9	43.5 ± 14.4
Female, n (%)	49 (49%)	47 (47%)
Male, n (%)	51 (51%)	53 (53%)
Rural residence, n (%)	57 (57%)	49 (49%)

Sneezing (75%), nasal obstruction (73%), nasal itching (60%), nasal discharge (50%), and lacrimation (41%) were the predominant symptoms observed among patients with allergic rhinitis.

Table 2. Distribution of Clinical Symptoms in AR Patients

Symptom	Frequency (%)
Sneezing	75
Nasal obstruction	73
Nasal itching	60
Nasal discharge	50
Lacrimation	41

Culture analysis demonstrated markedly non-similarity in nasal flora between the both groups.

Table 3. Distribution of Nasal Flora

Organism	AR Patients (%)	Controls (%)	p-value
Staphylococcus aureus	38	23	0.032
Staphylococcus epidermidis	32	37	>0.05
Streptococcus pneumoniae	24	19	>0.05
No growth	6	21	0.004

Serum IgE levels were significantly elevated among patients with allergic rhinitis.

Table 4. Serum IgE Levels

Group	Mean ± SD (IU/mL)	p-value
AR Patients	416.04 ± 122.83	<0.001
Controls	71.85 ± 24.38	

IV. DISCUSSION

The present study demonstrated significant alterations in nasal bacterial flora among patients with allergic rhinitis. The most important finding was the significantly higher prevalence of *Staphylococcus aureus* among AR patients compared with healthy controls. Similar findings have been described by Greisner et al. and Clausen et al., who observed increased colonization with *Staphylococcus aureus* in patients with allergic airway diseases [4,6].

Staphylococcus aureus has been proposed to contribute to allergic inflammation by producing superantigens and disrupting epithelial barrier integrity, thereby amplifying Th2-mediated immune responses [9]. The increased prevalence

observed in the present study supports the hypothesis that microbial dysbiosis may play a role in the pathogenesis process and perpetuation of allergic rhinitis.

Serum IgE levels were markedly elevated among AR patients, confirming the IgE-mediated nature of allergic rhinitis. Similar observations have been reported in previous studies, highlighting the utility of serum IgE as a reliable biomarker of allergic sensitization [1,2].

Although *Staphylococcus epidermidis* remained a common commensal organism in both the groups, no significant statistically difference was observed. This suggests that the preservation of certain components of the resident microbiota despite ongoing allergic inflammation.

The present findings support the growing body of evidence implicating nasal microbiota in allergic diseases. However, conventional culture techniques identify only a limited proportion of microorganisms. In Addition further advanced molecular approaches such as 16S rRNA sequencing and metagenomic analyses may provide a more comprehensive understanding of microbial alterations associated with allergic rhinitis [5,10].

V. CONCLUSION

Patients with allergic rhinitis exhibit significant alterations in culturable nasal flora characterized by increased colonization with *Staphylococcus aureus* and markedly elevated serum IgE levels. These findings suggest an association between microbial dysbiosis and allergic rhinitis. Further studies employing molecular microbiological techniques are warranted to elucidate the complex interactions between host immunity and the nasal microbiome and to explore potential microbiota-based therapeutic interventions.

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