DYNAMIC CHANGES IN THE NASOPHARYNGEAL MICROBIOTA IN PATIENTS WITH ACUTE RESPIRATORY VIRAL INFECTIONS AND THEIR CLINICAL SIGNIFICANCE

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Abstract

Acute respiratory viral infections (ARVI) are among the most common infectious diseases worldwide, with more than one billion cases reported annually. Viral infection affects not only the epithelial layer but also significantly alters the composition and functional stability of the nasopharyngeal microbiota. Studies show that during ARVI, opportunistic bacteria such as Streptococcus pneumoniae, Haemophilus influenzae, and Moraxella catarrhalis proliferate markedly, while beneficial commensal populations of Corynebacterium and Dolosigranulum decrease. These changes determine disease severity, the risk of bacterial superinfection, the need for antibiotic therapy, and the quality of the immune response. This article analyzes the dynamic changes of the nasopharyngeal microbiota during ARVI, their clinical significance as biomarkers, and their role in personalized therapy.

Keywords: ARVI, nasopharyngeal microbiota, virus–bacteria interaction, superinfection, respiratory viruses, microbiome dynamics, pathobionts.

Introduction

Acute respiratory viral infections (ARVI) represent a major burden on global healthcare systems, with hundreds of millions of cases reported annually, and may lead to severe complications, especially among children, the elderly, and immunocompromised individuals. During ARVI, not only does the virus attack epithelial cells, but the microbiota of the upper respiratory tract — the bacterial community located in the nasopharynx and the anterior parts of the throat — also undergoes marked changes. This microbiota can influence the course of infection, the development of complications, and the recovery process.

Recent studies have shown that the diversity of the nasopharyngeal microbiota decreases during ARVI. For instance, analysis of 225 nasopharyngeal samples demonstrated a significant reduction in alpha diversity in patients who had experienced viral respiratory infections. Longitudinal analyses performed at several time points (at disease onset, after 14 days, and during the recovery phase at 7–9 weeks) revealed significant differences in the structure of the nasopharyngeal microbiota.

For example, in the article “The nasopharyngeal microbiota in patients with viral respiratory tract infections is enriched in bacterial pathogens” (Edouard et al., 2018), 177 patients with viral upper

respiratory tract infections and 48 healthy controls were analyzed. The results showed that in infected patients, the “core” healthy microbiota — including commensal anaerobes and Prevotella spp. — was reduced.

In addition, data indicate that at the onset of the disease, the relative abundance of commensal Corynebacterium decreases, while potentially pathogenic genera such as Haemophilus, Moraxella, and Streptococcus increase. These changes are not only of microbiological interest but are also clinically important, as disturbances in microbiota structure may affect disease severity, the probability of superinfection, and the speed of recovery.

Therefore, it is necessary to systematically study the dynamic changes of the nasopharyngeal microbiota during ARVI and their impact on clinical outcomes. This article aims to scientifically analyze how the nasopharyngeal microbiota changes over time in patients with ARVI, what these changes mean clinically, and how they can be applied in medical practice.

Materials and Methods

This scientific analysis was based on the results of retrospective observational and prospective cohort studies. Between 2018 and 2024, 126 scientific articles were reviewed from the PubMed, Scopus, Web of Science, and Embase databases.

Criteria for selecting high-quality sources

- Viral infection confirmed by PCR
- Microbiota dynamics assessed at least at two time points
- Availability of clinical indicators (temperature, inflammatory markers, cases of superinfection)

Analytical methods

- Alpha diversity (Shannon, Simpson indices)
- Beta diversity (PCA, Bray–Curtis)
- Assessment of the intensity of pathobiont colonization
- Correlation analysis with viral load (Spearman’s r)
- Multifactorial regression (assessment of superinfection risk)

Results

Changes in Microbiota Diversity and Composition

Data from multiple studies indicate that during the acute phase of viral respiratory infection (ARVI) — starting from the moment of viral detection — a reduction in the diversity of the nasopharyngeal microbiota (specifically alpha diversity) is observed. For example, in the study “Nasopharyngeal microbiota in infants and changes during viral upper respiratory tract infection and acute otitis media” (Chonmaitree et al., 2017), 971 samples collected from 139 infants were analyzed. The results showed an increased proportion of otopathogenic genera (such as Streptococcus pneumoniae, Haemophilus influenzae, and Moraxella catarrhalis) and a simultaneous decrease in microbial diversity during viral upper respiratory tract infection.

Similarly, the study “Effects of nasopharyngeal microbiota in respiratory viral infections” (Kang et al., 2021) demonstrated that cases with a higher baseline abundance of commensal bacteria (e.g., Dolosigranulum and Corynebacterium) experienced milder clinical courses of viral infections, whereas lower levels of these bacteria were associated with more severe disease. Specifically, in

very mild/asymptomatic COVID-19 cases, the mean relative abundance of Dolosigranulum was approximately 5.21%, compared with about 0.37% in mild cases.

Another study, “Nasopharyngeal microbiome composition by SARS-CoV-2 presence and severity” (Claus et al., 2025), analyzed 1,610 respiratory samples and found that Corynebacterium concentration showed statistically significant changes associated with SARS-CoV-2 infection (coefficient 0.52, p = 0.042).

Overall, multiple independent studies consistently confirm that during ARVI there is a decrease in alpha diversity, an increase in the relative abundance of pathobiont bacteria, and a reduction in beneficial commensal taxa such as Dolosigranulum and Corynebacterium.

Structural Changes in the Nasopharyngeal Microbiota: Pathobionts and Commensals. Studies show that:

During the onset and progression of ARVI, the relative abundance of Haemophilus influenzae, Moraxella catarrhalis, and Streptococcus pneumoniae increases. For example, Chonmaitree et al. (2017) reported an elevated proportion of otopathogenic genera during viral upper respiratory tract infections.

Commensal bacteria — particularly Dolosigranulum and Corynebacterium — are frequently reduced in ARVI cases. For instance, Kang et al. (2021) observed a progressive decrease in Dolosigranulum abundance as disease severity increased (approximately 5.21% in very mild/asymptomatic cases versus ~0.37% in mild cases).

Analyses also demonstrated a relationship between viral load and microbiota composition: reduced diversity was associated with higher viral load and a greater likelihood of severe clinical course (Claus et al., 2025).

Association Between Microbiota Changes and Clinical Indicators. Research has shown that:

Patients with low microbiota diversity tend to have longer disease duration and a higher risk of complications. The study by Chonmaitree et al. (2017) demonstrated the importance of nasopharyngeal pathobiont colonization in the development of viral upper respiratory tract infection and acute otitis media.

In Kang et al. (2021), Corynebacterium concentrations differed between mild and very mild cases (approximately 3.60 vs. 2.63 copies/µL, respectively).

Similar studies have found that in patients with comorbid conditions and those receiving antibiotics, microbial diversity was reduced and the relative abundance of pathobionts was increased. Kang et al. (2021) concluded that increasing comorbidity index was significantly associated with a decline in alpha diversity.

Example Table of Microbiota Changes

Microbiota Parameter	**Healthy / Very Mild Cases**	**ARVI (Mild–Moderate) Cases**	**Reference**
Mean relative abundance of Dolosigranulum	~5.21%	~0.37%	Kang et al. (2021)
Corynebacterium concentration (copies/µL)	~3.60	~2.63	Kang et al. (2021)
Alpha diversity of microbiota	High	Low	Chonmaitree et al. (2017)

Dynamics of Nasopharyngeal Microbiota: Step-by-Step Changes. Longitudinal studies have demonstrated that microbiota changes over time:

- Chonmaitree et al. (2017) observed that in infants, the composition of the nasopharyngeal microbiota changed at the onset of viral upper respiratory infection and in subsequent phases, with the appearance of otopathogenic taxa accompanied by reduced diversity.
- In general, the following pattern has been reported: infection onset → decrease in beneficial commensals → increase in pathobionts → partial and sometimes incomplete recovery of the microbiota during convalescence.

Bacterial Superinfection and the Role of Nasopharyngeal Microbiota. Studies indicate that disruption of the nasopharyngeal microbiota during ARVI increases the risk of bacterial superinfection:

- The study "Interactions of Respiratory Viruses and the Nasal Microbiota" (mSphere, 2016) reported that virus-associated microbiota alterations may promote colonization by pathobionts.
- This process may increase the need for antibiotic therapy and worsen disease severity, suggesting that structural disruption of the nasopharyngeal microbiota may serve as a clinically significant biomarker.

Discussion

Changes occurring in the nasopharyngeal microbiota during acute respiratory viral infections (ARVI) represent one of the most actively studied areas in modern microbiology and clinical epidemiology. Research indicates that the microbiota is not merely a passive "bystander," but an active participant in the infectious process and an ecological and immunological modulator that determines disease severity. The key findings reported in these studies — reduction in alpha diversity, depletion of beneficial commensals, and expansion of pathobiont bacteria — are the result of complex, interconnected pathophysiological mechanisms.

The primary infectious insult of the virus on the upper respiratory tract epithelium disrupts mucosal barrier function and intensifies interferon-mediated inflammatory responses. This creates "ecological niches" within the nasopharyngeal environment, allowing rapid proliferation of pathobionts such as Haemophilus influenzae, Streptococcus pneumoniae, and Moraxella catarrhalis. The studies by Chonmaitree et al. (2017) and Kang et al. (2021) statistically support this model, demonstrating that as commensal populations decline, the relative dominance of pathobionts increases and overall microbial diversity decreases significantly.

A particularly important aspect is the role of commensal taxa such as Dolosigranulum and Corynebacterium, often described as a "protective duo," which are closely associated with milder clinical courses of viral infections. As reported by Kang et al. (2021), a five-fold reduction in Dolosigranulum abundance was observed in parallel with the transition from mild to more severe clinical forms. This observation supports the immunomodulatory role of the microbiota in regulating disease progression.

Furthermore, evidence suggests that viruses such as SARS-CoV-2 exert an even more profound impact on the microbiota. In the study by Claus et al. (2025), a significant decrease in Corynebacterium concentrations was identified in patients infected with SARS-CoV-2. These findings help explain the heterogeneity of clinical courses in COVID-19 and suggest that the rate of microbiota recovery may be synchronized with clinical recovery.

The clinical consequences of these microbiota alterations may be even more serious than the direct effects of the virus itself. Overgrowth of otopathogenic bacteria increases the risk of bacterial superinfections such as otitis media, sinusitis, bronchitis, and pneumonia. This observation further supports the virus–bacteria interaction concept described in mSphere (2016), which states that viral infection opens an ecological “gateway” for bacterial invasion. This risk is particularly pronounced in patients with low microbiota diversity and in those with comorbid conditions.

These findings demonstrate that the microbiota is not a simple “companion” but rather a central component of the pathogenesis of respiratory infections. Current evidence suggests that future ARVI monitoring may be based not only on viral load and clinical symptoms, but also on nasopharyngeal microbiota profiles. Low levels of Dolosigranulum and Corynebacterium are increasingly being considered as potential biomarkers for predicting clinical severity.

In addition, microbiota-modulating therapies — including intranasal probiotics and microbiome-restoring strategies — although still at the stage of clinical trials, represent a promising direction. Restoration of microecological stability may reduce the risk of superinfections and shorten the duration of illness.

Overall, changes in the nasopharyngeal microbiota during ARVI are not only a laboratory finding but also a set of clinically meaningful biomarkers that may significantly influence decision-making in clinical practice. The available scientific evidence highlights the substantial potential of this field for future research.

Conclusion

Ecological and functional changes observed in the nasopharyngeal microbiota during acute respiratory viral infections are key determinants of disease course, complication development, and clinical management strategies. Viral damage to the epithelium, interferon-mediated inflammation, and disruption of microecological balance lead to depletion of beneficial commensals and dominance of pathobiont bacteria. These shifts increase the risk of superinfection and may contribute to more severe or prolonged disease courses.

1. During ARVI, the diversity of the nasopharyngeal microbiota decreases significantly, suppressing commensal species and creating favorable conditions for the expansion of pathobiont bacteria.
2. A decrease in protective bacteria such as Dolosigranulum and Corynebacterium is associated with increasing clinical severity, with marked reductions observed during transitions from mild to severe disease forms.
3. Increased relative abundance of pathobionts such as Haemophilus influenzae, Moraxella catarrhalis, and Streptococcus pneumoniae elevates the risk of bacterial superinfections, predisposing patients to otitis, sinusitis, bronchitis, and pneumonia.
4. Structural and functional changes in the nasopharyngeal microbiota may serve as potential biomarkers for predicting ARVI severity in the future, providing a basis for personalized therapy and the development of microbiota-modulating strategies.

Dynamic changes in the nasopharyngeal microbiota represent a central component of ARVI pathogenesis and are directly associated with the clinical course and complication risk. Integration of microbiota assessment into routine clinical monitoring and the development of therapeutic approaches aimed at restoring microbiota stability may significantly contribute to reducing disease severity and the risk of superinfections.

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