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Decoding the microbiome of urban air: Implications for public health and pollution monitoring.

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Introduction

Urban air can act as a vector for antimicrobial resistance (AMR). Airborne microbes may carry resistance genes, which can be transferred to human pathogens through horizontal gene transfer. Construction sites, hospitals, and wastewater treatment plants are potential hotspots for AMR dissemination. Monitoring the resistome—the collection of resistance genes in the environment—could become a critical component of urban health surveillance. Early detection of resistance trends would allow for timely interventions and policy adjustments. Urban air pollution has long been associated with chemical contaminants such as particulate matter (PM), nitrogen oxides (NOx), and sulfur dioxide (SO_2). However, recent research has revealed a biological dimension to air pollution: the urban air microbiome, or aerobiome. This complex community of airborne microorganisms—including bacteria, fungi, viruses, and archaea—plays a critical role in shaping respiratory health, immune responses, and even the spread of antimicrobial resistance. Understanding the composition and dynamics of the urban aerobiome is essential for developing holistic public health strategies and improving pollution monitoring systems [1].

Children growing up in urban areas are particularly vulnerable. Reduced exposure to environmental microbes during early development may impair immune tolerance, increasing the risk of asthma, eczema, and other allergic diseases. Understanding the urban aerobiome could inform public health policies aimed at mitigating these risks. Indoor air quality is often more concentrated in bioaerosols than outdoor air, especially in densely populated urban settings. Buildings, transportation systems, and ventilation infrastructure shape the indoor aerobiome, influencing microbial exposure patterns. The COVID-19 pandemic has intensified interest in airborne pathogen transmission, highlighting the need for microbiome-aware design in public spaces.Smart buildings equipped with microbial sensors and air purification systems could become part of future urban planning. These technologies would monitor microbial load in real time, enabling rapid responses to emerging health threats. Urban air is not sterile; it contains a diverse array of microbial life. Studies using next-generation sequencing (NGS) have identified dominant bacterial phyla such as Proteobacteria, Actinobacteria, Firmicutes, and Bacteroidetes in urban aerosols. These microbes originate from soil, water, vegetation, human activity, and industrial processes. Seasonal variations, geographic location, and pollution levels significantly influence the aerobiome's composition [2].

Despite growing interest, the study of urban aerobiomes faces methodological challenges. Variability in sampling techniques, sequencing platforms, and data analysis pipelines can lead to inconsistent results1. Standardized protocols are needed to ensure comparability and reproducibility across studies. Future research should also explore the functional roles of airborne microbes. Beyond taxonomy, understanding how these organisms interact with pollutants, human hosts, and each other will provide deeper insights into their ecological and health significance. Exposure to airborne particulate matter (PM), especially PM2.5 and PM10, has been linked to microbial dysbiosis in the upper respiratory tract (URT). High levels of PM can carry pathogenic microbes and disrupt the balance of commensal bacteria, increasing susceptibility to respiratory infections, allergies, and chronic conditions such as asthma and chronic obstructive pulmonary disease (COPD). Traditional

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culture-based methods captured only a fraction of this diversity. Modern metagenomic approaches now allow for comprehensive profiling, revealing that biological matter can constitute up to 25% of atmospheric aerosol particles. This biological load is not merely passive—it interacts with chemical pollutants and host organisms, influencing health outcomes [3].

Recent studies show that PM exposure correlates with a decline in beneficial Actinobacteria and an increase in potentially harmful Bacteroidetes and Fusobacteria. These shifts in microbial composition can trigger immune dysregulation and systemic inflammation, contributing to diseases beyond the respiratory system, including neuroinflammation and metabolic disorders. Current air quality monitoring systems focus primarily on chemical pollutants. Integrating microbiome data into these systems could enhance their predictive power and relevance to public health. For example, tracking microbial diversity and abundance alongside PM concentrations may help identify hotspots of microbial risk or resilience [4].

Moreover, microbiome-informed monitoring could guide targeted interventions. Cities could implement green infrastructure, such as urban forests and biofilters, to modulate microbial exposure and improve air quality. These strategies would not only reduce chemical pollutants but also foster beneficial microbial communities. The concept of “Urban Atopy” has emerged to describe the rise of allergic and autoimmune conditions linked to urban microbial exposure. Unlike rural environments, which typically offer diverse microbial stimuli that help train the immune system, urban settings often present a narrow and pathogenic microbial profile. This imbalance can lead to hypersensitive immune responses and chronic inflammation [5].

Conclusion

The urban air microbiome represents a frontier in environmental microbiology and public health. By decoding its composition and dynamics, researchers can uncover hidden drivers of disease, improve pollution monitoring, and design healthier cities. Integrating microbiome science into urban planning and policy offers a promising path toward more resilient and equitable urban environments.

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