
| RESEARCH ARTICLE

A Review On Atmospheric Microbiomes And Emerging Infectious Diseases: From Environmental Dust To Global Health Threats

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| ABSTRACT

The atmosphere has traditionally been regarded as a passive medium for the transport of gases and particulate matter. However, recent advances in aeromicrobiology and environmental genomics have demonstrated that the atmosphere harbours diverse and dynamic microbial communities collectively referred to as the atmospheric microbiome. These communities comprise bacteria, fungi, viruses, archaea, and microbial fragments that are continuously exchanged among terrestrial, aquatic, and anthropogenic environments. The capacity of many airborne microorganisms to survive environmental stressors, including ultraviolet radiation, desiccation, and temperature fluctuations, facilitates their long-distance transport across continents and oceans. Increasing evidence suggests that atmospheric microbiomes contribute significantly to the transmission of infectious diseases, respiratory disorders, allergic reactions, and the emergence of novel pathogens. This review synthesizes current knowledge on the composition, sources, transport mechanisms, environmental drivers, and public health implications of atmospheric microbiomes. Furthermore, it discusses recent technological advances in airborne microbial monitoring and highlights the need for integrated surveillance systems under the One Health framework to mitigate future airborne infectious disease risks in the context of climate change and global environmental disturbances.

| KEYWORDS

Atmospheric microbiome, bioaerosols, emerging infectious diseases, airborne pathogens, climate change, One Health

| ARTICLE INFORMATION

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1. Introduction

For many decades, the atmosphere was regarded primarily as a physical medium that facilitates the exchange of gases and the transport of particulate matter between different components of the Earth's system. In this traditional view, air was considered largely devoid of biological activity and played only a passive role in environmental processes. However, recent advances in aerobiology, environmental microbiology, and molecular ecology have fundamentally changed this perception by demonstrating that the atmosphere harbours a remarkably diverse and dynamic community of microorganisms capable of influencing ecosystem functioning and human health (Bowers et al., 2023; Fierer et al., 2024).

The term atmospheric microbiome refers to the assemblage of microorganisms and biological particles suspended in the atmosphere, including bacteria, fungi, viruses, archaea, pollen, microbial metabolites, and fragments of organic material associated with aerosols and dust particles (Gandolfi et al., 2024). These microorganisms are continuously exchanged between terrestrial, aquatic, and anthropogenic environments through complex atmospheric processes. The atmosphere therefore

functions not merely as a conduit for physical transport but as a biologically active ecosystem that facilitates microbial interactions across local, regional, and global scales.

Recent developments in high-throughput sequencing technologies and metagenomic analyses have revealed that the atmosphere contains millions of microbial cells per cubic metre of air, with microbial diversity varying according to geographical location, season, altitude, and meteorological conditions (Maki et al., 2024). These findings have significantly expanded our understanding of microbial biogeography and have challenged the long-standing notion that atmospheric microorganisms are merely transient contaminants. Instead, many airborne microorganisms possess remarkable physiological adaptations that allow them to remain viable under harsh atmospheric conditions characterized by ultraviolet radiation, desiccation, nutrient limitation, oxidative stress, and extreme temperature fluctuations (Hernandez et al., 2024).

The capacity of microorganisms to survive and disperse through the atmosphere has profound implications for disease ecology and public health. Atmospheric transport enables microorganisms to travel across vast geographical distances, often crossing continental and oceanic boundaries within a few days (Prospero et al., 2024). Such long-range dispersal facilitates microbial exchange among ecosystems and contributes to the global dissemination of pathogenic microorganisms, antimicrobial resistance genes, and emerging infectious agents. Consequently, the atmosphere is increasingly recognized as a biological corridor and a global microbial highway connecting environmental reservoirs with human and animal populations (Wei et al., 2023).

In recent years, the emergence and re-emergence of infectious diseases have become major global health concerns. Events such as the coronavirus disease pandemic, recurring influenza outbreaks, increasing incidences of fungal respiratory infections, and the spread of antimicrobial-resistant pathogens have highlighted the critical importance of airborne transmission pathways in disease dynamics (World Health Organization [WHO], 2024). Although direct person-to-person transmission remains a major route for many infectious diseases, there is growing evidence that environmental bioaerosols and atmospheric microbial communities may contribute significantly to the dissemination and persistence of infectious agents in both indoor and outdoor environments (Li et al., 2025).

Simultaneously, global environmental changes are altering atmospheric microbial dynamics. Rapid urbanization, industrialization, deforestation, agricultural intensification, and changes in land use have significantly modified patterns of microbial aerosolization and atmospheric circulation. Climate change further exacerbates these processes by increasing temperatures, altering precipitation regimes, and intensifying extreme weather events such as droughts, wildfires, hurricanes, and dust storms (Intergovernmental Panel on Climate Change [IPCC], 2025). These environmental disturbances can dramatically increase the emission, transport, and deposition of airborne microorganisms, thereby influencing human exposure to potentially pathogenic microbes.

Desert dust storms represent one of the most significant natural mechanisms of microbial dispersal. Large quantities of mineral dust originating from arid regions such as the Sahara Desert carry diverse microbial communities, including bacteria, fungi, and viruses, across continents and oceans (Prospero et al., 2024). Similarly, wildfires and urban air pollution can alter the composition of atmospheric microbiomes by generating complex mixtures of particulate matter and microorganisms, potentially increasing the risks of respiratory diseases and allergic disorders (Chen et al., 2025).

The atmosphere also serves as an interface where microorganisms from humans, animals, plants, and environmental reservoirs converge and interact. Such interactions may facilitate genetic exchange, microbial evolution, and the emergence of novel pathogenic strains. Recent studies have suggested that atmospheric processes may contribute to the dissemination of antimicrobial resistance genes and may influence the emergence of previously unrecognized infectious diseases (Smith et al., 2025). Therefore, understanding atmospheric microbial ecology is becoming increasingly important for predicting and mitigating future public health threats.

The concept of "From Dust to Disease" provides a useful framework for understanding the continuum linking environmental microbial emissions to human health outcomes. This framework emphasizes that microorganisms originating from soil, water, vegetation, animals, and anthropogenic activities can become aerosolized, transported over considerable distances, and subsequently deposited into environments where they may influence disease transmission and ecosystem processes. The pathway from environmental dust to human disease underscores the interconnectedness of environmental, animal, and human health and aligns closely with the principles of the One Health approach, which advocates integrated strategies for addressing complex health challenges at the human-animal-environment interface (WHO, 2025).

Despite substantial progress in atmospheric microbiology, significant knowledge gaps remain regarding the mechanisms governing microbial survival in the atmosphere, the environmental drivers of microbial dispersal, and the precise contribution of atmospheric microbiomes to emerging infectious diseases. Furthermore, there is currently no globally standardized framework for monitoring atmospheric microbial communities or integrating atmospheric microbial data into disease surveillance systems. Therefore, this review aims to synthesize current knowledge on the composition, sources, transport mechanisms, environmental determinants, and public health significance of atmospheric microbiomes. Particular emphasis is placed on their role in the emergence and transmission of infectious diseases and the need for integrated global surveillance systems capable of addressing future airborne microbial threats in an era of rapid environmental and climatic change.

2. Composition of Atmospheric Microbiomes

Atmospheric microbiomes comprise highly diverse and dynamic assemblages of microorganisms and biological particles suspended within the Earth's atmosphere. These airborne communities include bacteria, fungi, viruses, archaea, pollen grains, protozoan cysts, microbial metabolites, and fragments of biological materials collectively referred to as bioaerosols (Gandolfi et al., 2024). Recent developments in metagenomics and environmental sequencing have demonstrated that the atmosphere contains an unexpectedly rich microbial diversity, with microbial concentrations ranging from 10^4 to 10^7 cells per cubic metre of air depending on geographical location and meteorological conditions (Maki et al., 2024). Bacteria generally dominate atmospheric microbial communities and constitute a substantial proportion of airborne biomass. Members of the genera *Bacillus*, *Pseudomonas*, *Micrococcus*, *Sphingomonas*, *Streptomyces*, and *Acinetobacter* are frequently detected in atmospheric samples from both urban and natural environments (Smith et al., 2023). These microorganisms possess several adaptive characteristics that enable their survival under extreme atmospheric conditions, including endospore formation, pigmentation, antioxidant enzyme production, and efficient DNA repair mechanisms.

Airborne fungal communities are equally important constituents of the atmospheric microbiome. Fungal spores, owing to their small size and resistance to environmental stress, are among the most abundant biological particles in the atmosphere. Genera such as *Aspergillus*, *Cladosporium*, *Penicillium*, *Alternaria*, and *Fusarium* are commonly encountered and have significant implications for both environmental and human health (Li et al., 2025). Exposure to these fungal spores has been associated with allergic diseases, asthma exacerbations, hypersensitivity reactions, and opportunistic infections, particularly among immunocompromised individuals.

Viruses constitute another critical component of atmospheric microbial communities. Although they are more difficult to detect because of their small size and lower concentrations, advances in metagenomic sequencing and viral enrichment techniques have substantially improved our understanding of atmospheric viromes (Zhang et al., 2024). Airborne viral communities include bacteriophages, plant viruses, and human pathogenic viruses capable of causing respiratory infections. Emerging evidence suggests that viruses can remain viable in aerosols for prolonged periods, thereby facilitating long-distance transmission and increasing the potential for epidemic and pandemic outbreaks.

Archaea, although less studied than bacteria and fungi, have also been identified in atmospheric samples. Several archaeal taxa originating from marine and terrestrial ecosystems have been detected in aerosols and dust particles, suggesting that these microorganisms contribute to global atmospheric biodiversity and biogeochemical processes (Fierer et al., 2024). The composition of atmospheric microbiomes exhibits substantial spatial and temporal variability. Factors such as altitude, seasonality, geographical location, meteorological conditions, and anthropogenic activities significantly influence microbial diversity and abundance. Consequently, atmospheric microbial communities are highly dynamic systems that continuously respond to environmental perturbations and climate variability.

3. Sources and Emission Pathways of Atmospheric Microorganisms

Atmospheric microorganisms originate from a wide variety of natural and anthropogenic sources. These emission sources constitute the primary reservoirs from which microorganisms become aerosolized and subsequently dispersed throughout the atmosphere (Wei et al., 2023). Natural sources include soils, deserts, oceans, freshwater systems, vegetation, wetlands, and animal-associated habitats. Among these, soil represents one of the largest reservoirs of atmospheric microorganisms. Wind erosion and mechanical disturbances continuously release bacteria, fungal spores, and viruses from soil surfaces into the atmosphere.

Desert ecosystems contribute significantly to global microbial aerosolization. Massive dust storms originating from arid and semi-arid regions, particularly the Sahara Desert, the Gobi Desert, and the Arabian Peninsula, transport billions of tonnes of mineral dust and associated microorganisms across continents every year (Prospero et al., 2024). Studies have demonstrated that Saharan dust particles carry numerous bacterial and fungal taxa that can be deposited thousands of kilometres away in Europe, North America, and South America. Marine environments represent another major source of atmospheric microorganisms. Sea spray aerosols generated by wave action and bubble bursting release large quantities of bacteria, viruses, and organic matter

into the atmosphere. Marine microorganisms can influence cloud formation, precipitation processes, and atmospheric chemistry (Gandolfi et al., 2024).

Vegetation and forest ecosystems continuously emit microorganisms through the release of pollen grains, plant-associated bacteria, fungal spores, and decaying organic materials. Agricultural activities, including tillage, harvesting, irrigation, and animal husbandry, also contribute significantly to microbial aerosolization.

Anthropogenic sources have become increasingly important contributors to atmospheric microbial loading. Wastewater treatment plants, landfill sites, industrial facilities, transportation systems, and densely populated urban environments generate substantial quantities of bioaerosols (Chen et al., 2025). Hospitals and healthcare facilities represent particularly important sources of airborne pathogenic microorganisms and antimicrobial-resistant bacteria, thereby posing significant risks to public health.

Extreme environmental events such as wildfires, hurricanes, floods, volcanic eruptions, and sandstorms can dramatically increase microbial emissions. Wildfires, for example, release enormous quantities of particulate matter carrying viable microorganisms and microbial toxins that may travel long distances and adversely affect human respiratory health.

4. Atmospheric Transport and Microbial Survival Mechanisms

Following aerosolization, microorganisms are exposed to a variety of environmental stressors that challenge their survival. These include intense ultraviolet radiation, desiccation, temperature extremes, oxidative stress, low nutrient availability, and atmospheric turbulence (Amato et al., 2023).

Despite these harsh conditions, many microorganisms exhibit remarkable adaptations that enable their persistence in the atmosphere. Endospore formation is one of the most effective survival mechanisms. Endospores produced by species of *Bacillus* and *Clostridium* can withstand extreme environmental conditions and remain viable for prolonged periods.

Fungal spores are naturally adapted for atmospheric transport because of their robust cell walls and resistance to dehydration and ultraviolet radiation. Many bacteria survive by entering a metabolically dormant state that significantly reduces cellular activity and energy requirements.

Several microorganisms synthesize protective pigments, including carotenoids and melanins, which protect cellular components from ultraviolet-induced damage. Additionally, DNA repair systems and antioxidant enzymes enable microorganisms to recover from oxidative injuries encountered during atmospheric transport (Hernandez et al., 2024).

Attachment to mineral dust particles, soot, pollen, and organic matter provides physical protection and significantly enhances microbial survival. Microorganisms embedded within biofilms or aerosol aggregates are often shielded from environmental stressors and may retain viability during long-distance transport.

Atmospheric circulation systems, including trade winds, cyclones, jet streams, and convection currents, facilitate the movement of microorganisms across regional and global scales. Consequently, microorganisms can travel thousands of kilometres within a matter of days, making the atmosphere an effective global transportation network for microbial dispersal.

5. Atmospheric Microbiomes and Infectious Disease Transmission

The relationship between atmospheric microbiomes and infectious disease transmission has become an increasingly important area of scientific investigation. Airborne microorganisms directly influence human health through inhalation, ingestion, and environmental contamination pathways.

The respiratory tract represents the primary portal of entry for airborne pathogens. Upon inhalation, microorganisms may adhere to epithelial surfaces, evade host immune responses, and establish infections. Certain microorganisms may also induce inflammatory and allergic responses even in the absence of active infection.

The major transmission pathways of atmospheric microorganisms include:

1. Direct inhalation of infectious aerosols;
2. Deposition onto environmental surfaces followed by contact transmission;
3. Contamination of water and food systems;
4. Secondary aerosolization from contaminated environments.

Several important infectious diseases are associated with airborne transmission, including influenza, tuberculosis, coronavirus disease, measles, aspergillosis, and legionellosis (WHO, 2024). The recent COVID-19 pandemic further emphasized the critical role of aerosols in the transmission dynamics of respiratory pathogens and highlighted the need for improved understanding of atmospheric microbial processes.

Exposure to airborne fungi and microbial fragments has also been linked to asthma, allergic rhinitis, chronic obstructive pulmonary disease, and hypersensitivity pneumonitis (Li et al., 2025). Moreover, increasing evidence suggests that atmospheric microbiomes may facilitate the dissemination of antimicrobial resistance genes and multidrug-resistant pathogens.

Although only a small proportion of atmospheric microorganisms are pathogenic, the atmosphere may serve as an important reservoir and transport medium for infectious agents, thereby influencing disease emergence and transmission patterns.

6. Emerging Infectious Diseases and Atmospheric Connections

The emergence of infectious diseases is increasingly associated with environmental disturbances and climatic changes that alter microbial ecology and atmospheric processes. Climate variability influences microbial aerosolization, transport efficiency, and survival, thereby affecting patterns of disease transmission.

Rising global temperatures, altered rainfall patterns, prolonged droughts, and increasing frequencies of wildfires and dust storms have significantly modified atmospheric microbial dynamics (IPCC, 2025). Such changes may facilitate the emergence of novel pathogens and expand the geographical distribution of existing infectious diseases.

Dust storms have been implicated in the transport of fungal pathogens and bacterial species capable of causing respiratory illnesses. Similarly, changing climatic conditions may alter the seasonality and intensity of airborne infectious diseases.

The atmosphere also serves as a convergence zone where microorganisms originating from diverse environments interact, exchange genetic material, and potentially evolve into novel pathogenic strains. The dissemination of antimicrobial resistance genes through atmospheric pathways represents another emerging public health concern (Smith et al., 2025).

Consequently, understanding the links between atmospheric microbiomes and emerging infectious diseases is essential for developing effective surveillance and disease prevention strategies.

7. Environmental Drivers of Atmospheric Microbial Dynamics

The composition and abundance of atmospheric microorganisms are strongly influenced by environmental and meteorological factors. Temperature affects microbial metabolism, viability, and aerosolization rates. Relative humidity influences the hydration state of bioaerosols and determines the survival of airborne pathogens.

Solar radiation, particularly ultraviolet radiation, is one of the principal factors limiting microbial survival in the atmosphere. Wind speed influences microbial dispersal by facilitating aerosol transport and increasing the resuspension of particles from environmental surfaces.

Air pollution and particulate matter concentrations significantly affect atmospheric microbial communities. Fine particulate matter provides surfaces for microbial attachment and offers protection against environmental stressors, thereby enhancing microbial persistence (Chen et al., 2025).

Urbanization, deforestation, desertification, and land degradation have profoundly altered atmospheric microbial dynamics by increasing dust emissions and changing patterns of microbial exposure. Extreme weather events, including floods, hurricanes, and heat waves, further amplify microbial aerosolization and human exposure risks.

Understanding these environmental drivers is critical for predicting microbial dispersal patterns and assessing the potential impacts of climate change on airborne infectious diseases.

8. Advances in Detection and Monitoring Technologies

Technological innovations have revolutionized the study of atmospheric microbiomes. Traditional culture-based methods are increasingly being complemented by culture-independent techniques that provide comprehensive insights into airborne microbial diversity and function (Maki et al., 2024).

High-throughput sequencing technologies, including metagenomics, metatranscriptomics, and whole-genome sequencing, have enabled the identification of previously unculturable microorganisms and provided valuable information regarding microbial community composition and functional potential.

Modern atmospheric monitoring systems include:

- High-volume air samplers;

- Cascade impactors;
- Real-time aerosol sensors;
- Drone-assisted sampling platforms;
- Satellite and remote sensing technologies;
- Bioinformatics and computational modelling systems.

Artificial intelligence and machine learning algorithms are increasingly employed to analyse complex atmospheric datasets, predict microbial dispersal pathways, and identify potential disease hotspots (Maki et al., 2024).

Despite these remarkable advances, substantial challenges remain, including the absence of standardized sampling protocols, limited long-term monitoring programmes, and inadequate integration of atmospheric microbial data into public health surveillance systems.

9. Public Health Implications

The atmospheric microbiome has profound implications for human health and disease prevention. Airborne microorganisms contribute significantly to respiratory infections, allergic diseases, occupational illnesses, and potentially future pandemics.

Indoor environments such as hospitals, schools, offices, and public transportation systems represent critical points of exposure to airborne pathogens. Poor indoor air quality can facilitate the transmission of infectious agents and increase the burden of respiratory diseases.

The emergence of antimicrobial-resistant microorganisms in atmospheric environments presents another major public health challenge (Bowers et al., 2023). Airborne dissemination of resistance genes may contribute to the global spread of multidrug-resistant pathogens, thereby complicating treatment strategies and increasing healthcare costs. Atmospheric microbiomes also have implications for vulnerable populations, including children, older adults, immunocompromised individuals, and people with chronic respiratory conditions. Consequently, improving air quality and implementing effective surveillance systems are essential for protecting public health (Amato et al., 2023).

A comprehensive One Health approach, integrating human, animal, and environmental health, is increasingly recognized as indispensable for understanding and mitigating airborne infectious disease risks. Future public health strategies should incorporate atmospheric microbiology into early warning systems, disease forecasting models, and global health preparedness programmes.

10. Future Perspectives

Future research should focus on:

1. Establishing global atmospheric microbiome monitoring networks;
2. Standardizing sampling and analytical methodologies;
3. Integrating atmospheric microbial data with climate and epidemiological models;
4. Developing predictive systems for airborne disease forecasting;
5. Strengthening interdisciplinary collaborations among microbiologists, atmospheric scientists, public health experts, and data scientists.

Such efforts will significantly enhance our understanding of the role of atmospheric microbiomes in global health.

11. Conclusion

The atmosphere is increasingly recognized as far more than a passive physical space through which air circulates. Instead, it functions as a dynamic biological environment that enables the transport, exchange, and persistence of diverse microbial communities across ecosystems, countries, and continents. This review highlights how atmospheric microbiomes, carried in environmental dust and aerosols, represent an important but often overlooked pathway for the dissemination of microorganisms, including emerging and re-emerging infectious pathogens. The growing body of evidence suggests that airborne microbes influence not only ecological processes but also human, animal, and environmental health, reinforcing the central message of this review: the journey "from environmental dust to global health threats" reflects a complex interaction between microbial ecology and disease emergence.

As climate change, urbanization, deforestation, desertification, and increased global mobility continue to reshape environmental conditions, the movement and composition of atmospheric microbial communities are also likely to change. These environmental transformations may alter the distribution, survival, and transmission of airborne pathogens, increasing the risk of infectious disease outbreaks in populations that were previously unaffected. Consequently, understanding the ecology, diversity, and dynamics of atmospheric microbiomes has become an essential component of modern infectious disease research and public health preparedness.

Recent advances in metagenomics, next-generation sequencing, environmental monitoring, and bioinformatics have significantly improved our ability to detect and characterize airborne microorganisms. Nevertheless, substantial knowledge gaps remain regarding the viability of microbes during long-distance atmospheric transport, the environmental factors influencing their persistence, and the mechanisms through which they contribute to disease transmission. Addressing these uncertainties will require sustained interdisciplinary collaboration among microbiologists, atmospheric scientists, epidemiologists, ecologists, climate researchers, and public health experts.

Ultimately, integrating atmospheric microbiology into global disease surveillance systems and One Health initiatives offers a valuable opportunity to strengthen early warning systems, improve outbreak prediction, and inform evidence-based public health policies. Recognizing the atmosphere as a biologically active interface between the environment and human health will be critical for enhancing global preparedness, preventing future infectious disease threats, and building more resilient health systems in an era of accelerating environmental change.

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