Human microbiome and its impact on health in conditions of anthropogenic pollution

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Abstract. The human microbiome plays a crucial role in maintaining physiological homeostasis, influencing immune function, metabolism, and susceptibility to disease. However, increasing exposure to anthropogenic pollutants — including air pollutants, heavy metals, pesticides, and industrial chemicals — has raised concerns about the potential impact of environmental stressors on microbial composition and host health. This article reviews current evidence on how environmental pollution affects the human microbiome, with a focus on the gut, respiratory, and skin microbiota, and discusses the resulting implications for immune response, metabolic function, and disease development. The study synthesizes findings from epidemiological, clinical, and experimental research, highlighting consistent associations between pollutant exposure and microbial dysbiosis, including reduced microbial diversity, shifts in dominant taxa, and alterations in microbial metabolic activity . These changes are increasingly linked to the development of chronic diseases, such as inflammatory bowel disease (IBD), asthma, metabolic syndrome, and neurodegenerative disorders, suggesting that environmental pollution may exert its pathogenic effects through microbiome-mediated mechanisms.

1 Introduction

The human microbiome, a complex and dynamic ecosystem composed of trillions of microorganisms residing in and on the human body, has emerged as a critical determinant of health and disease. Recent advances in genomics, metagenomics, and metabolomics

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have revealed that the microbiome plays a pivotal role in regulating immune function, metabolic processes, and neurological signaling , as well as in protecting against pathogenic infections and maintaining epithelial barrier integrity .

The gut microbiome , in particular, has been extensively studied for its influence on systemic immunity, nutrient absorption, and the production of bioactive metabolites such as short-chain fatty acids (SCFAs), bile acid derivatives, and neurotransmitter precursors . Similarly, the respiratory and skin microbiomes , which are in direct contact with the external environment, are increasingly recognized for their role in modulating allergic responses, inflammatory conditions, and susceptibility to infection .

However, in the context of rapid urbanization, industrial expansion, and environmental degradation , the human microbiome is being exposed to a growing array of anthropogenic pollutants , including air pollutants, heavy metals, pesticides, microplastics, endocrine disruptors , and industrial chemicals . These environmental stressors have been shown to alter microbial composition and functionality , potentially leading to dysbiosis — an imbalance in microbial communities — which is associated with a wide range of chronic diseases and health disorders .

Anthropogenic pollution is now recognized as a major public health concern , with mounting evidence linking long-term exposure to environmental toxins with increased risks of metabolic syndrome, neurodegenerative disorders, respiratory diseases, and autoimmune conditions . Emerging research suggests that many of these adverse health effects may be mediated or exacerbated by changes in the host microbiome , highlighting the microbiome as a potential mediator between environmental exposure and disease development .

Studies have demonstrated that air pollution, including fine particulate matter (PM2.5) and nitrogen oxides (NOx) , can influence gut microbial diversity and function , often leading to reduced abundance of beneficial bacteria and increased presence of pro-inflammatory taxa . Similarly, heavy metals such as lead, arsenic, and cadmium , which are commonly found in contaminated water, soil, and air, have been shown to selectively inhibit or promote specific microbial species , thereby altering microbial homeostasis and host immune responses .

Moreover, chemical pollutants such as bisphenols, phthalates, and perfluorinated compounds , widely used in industrial and consumer products, have been linked to changes in microbial gene expression , gut barrier integrity , and metabolite production , which may contribute to systemic inflammation and metabolic dysfunction .

Despite the growing body of evidence, the mechanisms through which anthropogenic pollutants affect the human microbiome remain incompletely understood , and the long-term health consequences of these microbial alterations are still being explored. The interplay between environmental exposure, microbiome disruption, and disease susceptibility suggests the need for a more integrated approach to studying environmental health risks , one that incorporates microbiome profiling as a key indicator of exposure and response .

This article provides a comprehensive review of current research on the impact of anthropogenic pollution on the human microbiome , with a focus on gut, respiratory, and skin microbial communities . It explores the biological pathways through which environmental toxins may influence microbial balance, discusses the health consequences of pollution-induced dysbiosis , and highlights potential strategies for mitigating these effects , including probiotics, prebiotics, and dietary interventions .

By examining the microbiome as a mediator of environmental stress , this review contributes to the growing understanding of how external pollutants shape internal microbial ecosystems , and how these changes may influence individual and population

health . The findings are relevant for researchers, public health professionals, and policymakers seeking to address the health impacts of environmental pollution through microbiome-informed strategies .

2 Methods and materials

This study employed a systematic review and integrative analysis of peer-reviewed scientific literature to examine the impact of anthropogenic pollution on the human microbiome and its implications for health and disease . The methodology was designed to synthesize current knowledge, evaluate experimental and clinical evidence, and assess the biological mechanisms , epidemiological associations , and intervention strategies related to environmental exposure and microbial dysbiosis.

A multi-database search strategy was used to identify relevant peer-reviewed publications, including original research articles, reviews, meta-analyses, and case studies , published between 2010 and 2024 . The search was conducted in major scientific databases such as PubMed, Scopus, Web of Science, ScienceDirect, and Google Scholar , ensuring broad coverage of both preclinical and clinical research . The search was guided by a set of standardized keywords, including *human microbiome* , *anthropogenic pollution* , *environmental toxins* , *gut microbiota* , *respiratory microbiome* , *skin microbiome* , *dysbiosis* , *air pollution* , *heavy metals* , and *microbial health effects* . These terms were combined using Boolean operators to enhance the precision and comprehensiveness of the search.

To enrich the dataset, the reference lists of key review articles and consensus reports were manually reviewed to identify seminal studies and recent breakthroughs . Particular attention was given to publications from leading microbiome and environmental health research initiatives, including the Human Microbiome Project (HMP), the European Human Exposome Network , and the National Institute of Environmental Health Sciences (NIEHS) , which have significantly advanced the understanding of microbiome-environment interactions .

To ensure scientific rigor and relevance , a set of inclusion and exclusion criteria was applied during the selection of literature. Studies were included if they:
- Focused on the relationship between environmental pollution and microbiome changes
- Utilized human, animal, or in vitro models to investigate microbial composition or function
- Reported empirical findings , including microbiome profiling, metabolomic analysis, or health outcomes
- Were published in peer-reviewed journals and written in English

Studies were excluded if they:
- Were purely theoretical or lacked empirical validation
- Did not address the mechanisms or health outcomes related to microbiome changes
- Focused solely on microbial taxonomy or environmental chemistry without linking to health
- Were limited to abstracts, conference proceedings, or non-peer-reviewed reports

Following the selection process, data were extracted from the included publications using a standardized data extraction protocol that captured key variables such as:
- Study design (observational, interventional, longitudinal)

- Sample size and demographic characteristics
- Methods of microbiota analysis (e.g., 16S rRNA sequencing, shotgun metagenomics, metabolomics)
- Types of anthropogenic pollutants studied (e.g., air pollutants, heavy metals, pesticides)
- Reported microbial taxa and functional pathways
- Health outcomes assessed (e.g., inflammation, metabolic dysfunction, immune response)
- Interventions targeting the microbiome and their reported effects

The extracted data were synthesized to identify common patterns, biological mechanisms, and health implications across different types of pollution and microbial ecosystems. The synthesis was structured around three main dimensions:

1. Microbiome changes in response to environmental pollutants
2. Health consequences of pollution-induced microbial dysbiosis
3. Potential strategies for microbiome restoration and health protection

To ensure methodological consistency and reliability, a quality assessment of the included studies was conducted using a modified version of the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) framework, adapted for microbiome and environmental health research. This assessment evaluated:

- Methodological transparency and reproducibility
- Sample size and representativeness
- Use of validated tools for microbiome profiling and pollutant exposure assessment
- Relevance to clinical or public health outcomes

Only studies with medium to high methodological quality were included in the final synthesis to ensure the validity and generalizability of the findings.

In addition to the literature review, the study incorporated an analysis of selected case studies and experimental models that demonstrated significant findings in microbiome-environment interactions. These studies were selected based on their clinical impact, methodological robustness, and relevance to public health . The selected examples included:

- Cohort studies linking microbial composition to air pollution exposure and respiratory diseases
- Animal models examining the effects of heavy metal exposure on gut microbiota and immune function
- Metabolomic analyses identifying microbial metabolites such as short-chain fatty acids (SCFAs), bile acids, and inflammatory markers in polluted environments

Each case study was analyzed in terms of study design, microbiota profiling methods, pollutant exposure assessment, and health outcomes , providing practical insights into how microbiome research is being applied in environmental health and public policy settings .

To contextualize the findings and explore broader implications, the study also examined ethical, methodological, and translational challenges in microbiome and pollution research. This included a review of guidelines from the World Health Organization (WHO), National Institutes of Health (NIH), and the European Environment Agency (EEA) , with a focus on study design, reproducibility, and public health translation .

The methodology also incorporated an assessment of current trends in microbiome and environmental health research , including the rise of exposome-based studies , multi-omics approaches , and machine learning-based microbiome analysis , which are increasingly

being used to predict health risks, monitor microbial shifts, and personalize interventions in polluted environments.

By combining a rigorous literature review, case study analysis, and evaluation of environmental health frameworks , this research provides a comprehensive foundation for understanding the current evidence, methodological approaches, and future directions in the field of human microbiome and anthropogenic pollution . The methodology supports the development of evidence-based insights for researchers, public health professionals, and environmental scientists working at the intersection of microbiology, toxicology, and human health .

3. Results

The systematic review of scientific literature and case studies reveals a strong and growing body of evidence indicating that anthropogenic pollution significantly affects the composition and function of the human microbiome , with consequent implications for health and disease . Across multiple studies and geographic regions, consistent patterns emerged regarding the impact of environmental toxins on the gut, respiratory, and skin microbiota , and their association with immune dysfunction, metabolic disturbances, and chronic disease .

One of the most frequently reported findings is the alteration of gut microbiota composition in individuals exposed to air pollution, heavy metals, and industrial chemicals . Studies conducted in urban and industrialized settings have shown that exposure to fine particulate matter (PM2.5), nitrogen dioxide (NO_2), and polycyclic aromatic hydrocarbons (PAHs) is associated with a reduction in microbial diversity , shifts in dominant bacterial taxa , and imbalances in microbial metabolic activity . In particular, several studies observed a decrease in beneficial bacteria , such as *Bifidobacterium* and *Faecalibacterium prausnitzii* , which are known for their anti-inflammatory properties and role in gut barrier function , and an increase in potentially pathogenic taxa , such as *Escherichia coli* and *Clostridium species* , which are associated with gut inflammation and dysbiosis .

The analysis also found that heavy metals , including lead, arsenic, and cadmium , have a selective impact on microbial communities , often promoting the growth of metal-resistant strains while suppressing others . For instance, exposure to arsenic-contaminated water was linked to a reduction in *Lactobacillus* and *Bifidobacterium* species , and an increase in *Bacteroides* and *Enterobacteriaceae* , suggesting a shift toward a pro-inflammatory microbial profile . These changes were frequently associated with increased intestinal permeability, systemic inflammation , and altered immune responses , indicating a potential mechanism through which pollution may contribute to chronic disease .

In the context of industrial chemicals , such as bisphenols, phthalates, and perfluorinated compounds , the review identified a clear link between exposure and microbiome disruption . These substances were found to interfere with microbial signaling , alter bile acid metabolism , and promote gut dysbiosis , which in turn may contribute to metabolic syndrome, liver dysfunction, and endocrine disruption . For example, bisphenol A (BPA) was associated with reduced microbial diversity and increased abundance of *Desulfovibrio* species , which are known to promote gut inflammation and insulin resistance .

The results further highlight the impact of pollution on the respiratory microbiome , particularly in relation to urban air quality and industrial emissions . Long-term exposure to air pollutants , especially in highly industrialized and densely populated areas , was associated with alterations in nasal and lung microbial communities , including reduced

diversity and increased presence of opportunistic pathogens such as *Staphylococcus* and *Streptococcus species* . These microbial changes were often linked to increased incidence of respiratory infections, asthma, and allergic rhinitis , suggesting that air pollution may modulate host susceptibility through microbiome-mediated mechanisms .

Similarly, the skin microbiome was found to be sensitive to environmental contaminants , particularly in populations exposed to industrial waste, air pollution, and cosmetic chemicals . Several studies reported a reduction in *Corynebacterium* and *Propionibacterium* species , which are important for maintaining skin homeostasis , and an increase in *Staphylococcus aureus* and *Malassezia* species , often associated with eczema, acne, and inflammatory skin conditions . These findings suggest that environmental pollutants may disrupt the skin's microbial balance , thereby contributing to dermatological and immunological disorders .

The review also explored the functional consequences of pollution-induced dysbiosis , with particular attention to microbial metabolites and host immune responses . Evidence suggests that microbial shifts in polluted environments are often accompanied by changes in the production of short-chain fatty acids (SCFAs), bile acid derivatives, and lipopolysaccharides (LPS) . For instance, reduced levels of butyrate and propionate , which are key anti-inflammatory metabolites, were frequently observed in individuals exposed to air pollution and industrial toxins , and were associated with elevated markers of systemic inflammation , including C-reactive protein (CRP) and interleukin-6 (IL-6) .

In addition to microbial composition, the analysis of microbial gene expression and functional pathways revealed that pollution exposure is associated with changes in microbial metabolism, particularly in carbohydrate utilization, xenobiotic degradation, and stress response pathways. These alterations may affect microbial resilience, host immune signaling, and nutrient absorption, thereby influencing metabolic and immunological health.

Several studies also examined the health outcomes associated with microbiome changes, particularly in relation to chronic diseases . The results indicate that individuals with long-term exposure to anthropogenic pollutants and corresponding microbiome alterations were more likely to develop inflammatory bowel disease (IBD), asthma, metabolic syndrome, and neuroinflammatory conditions , such as Parkinson's and Alzheimer's disease . These findings suggest that the microbiome may act as a mediator or amplifier of pollution-induced pathology , and that microbial profiling could serve as a valuable tool for assessing environmental health risks .

The review further confirms that anthropogenic pollution affects the microbiome in a dose- and duration-dependent manner , with long-term exposure leading to more pronounced microbial shifts and greater health consequences . However, the individual variability in microbiome response to pollution was also evident, likely influenced by genetic background, diet, lifestyle, and pre-existing health conditions .

Despite the promising insights, the results also highlight several limitations and inconsistencies in current research. These include:

- High inter-individual variability in microbiome responses, making it difficult to establish universal microbial signatures of pollution exposure
- Causality versus correlation — many studies report associations but lack longitudinal or interventional evidence of causation
- Methodological differences in microbiome analysis, including sequencing techniques, sample collection methods, and data interpretation frameworks , which can lead to inconsistent findings across studies

- Limited reproducibility of findings across different populations and geographic regions, highlighting the need for standardized protocols and larger, multi-center trials

Overall, the results of this review provide strong support for the role of anthropogenic pollution in shaping the human microbiome , with microbial composition and function emerging as key contributors to pollution-related health risks . These findings suggest that the human microbiome may serve as a sensitive indicator of environmental exposure , and that targeting the microbiome may offer novel preventive and therapeutic strategies for pollution-related diseases .

4. Discussion

The findings of this review provide compelling evidence that anthropogenic pollution significantly influences the human microbiome , with gut, respiratory, and skin microbial communities being particularly vulnerable to environmental stressors such as air pollutants, heavy metals, industrial chemicals, and microplastics . These microbial shifts appear to be closely linked to a range of health outcomes , including metabolic dysfunction, immune dysregulation, and increased susceptibility to chronic diseases , reinforcing the microbiome as a critical interface between environmental exposure and host health .

One of the most consistent observations across the reviewed studies is the alteration of gut microbiota composition in response to urban and industrial pollutants . The reduction in microbial diversity , loss of beneficial taxa , and increase in pro-inflammatory bacteria observed in polluted environments suggest that anthropogenic exposure may disrupt microbial homeostasis , contributing to gut barrier dysfunction and systemic inflammation . These changes align with findings from toxicological and epidemiological studies , which have linked air pollution and heavy metal exposure to gut-related disorders , such as inflammatory bowel disease (IBD) and leaky gut syndrome , as well as metabolic conditions , including obesity and type 2 diabetes .

The role of microbial metabolites , particularly short-chain fatty acids (SCFAs) like butyrate and propionate , further supports this connection. These metabolites are known for their anti-inflammatory and immunomodulatory properties , and their reduction in polluted environments may contribute to heightened systemic inflammation , impaired immune regulation , and neuroinflammatory responses . The observed decrease in SCFA-producing bacteria , such as *Faecalibacterium prausnitzii* and *Roseburia species* , in polluted populations is particularly concerning, as these microbes are considered key regulators of gut and immune health .

The impact of pollution on the respiratory microbiome is another important finding of this review. Given the direct exposure of the respiratory tract to environmental toxins , it is not surprising that air pollution and industrial emissions are associated with microbial imbalances in the nasal and lung microbiota . The observed increase in opportunistic pathogens , such as *Staphylococcus* and *Streptococcus species* , and the reduction in commensal bacteria , like *Lactobacillus* and *Bifidobacterium* , suggest that air pollution may compromise respiratory immunity , increasing the risk of allergies, asthma, and respiratory infections .

Similarly, the skin microbiome , which serves as the first line of defense against environmental stressors , was found to be significantly affected by exposure to industrial toxins and cosmetic pollutants . The loss of skin commensals , such as *Corynebacterium* and *Propionibacterium* , and the increase in pathogenic species , including *Staphylococcus aureus* and *Malassezia* , were frequently associated with skin inflammation and barrier

dysfunction , indicating that pollution-induced dysbiosis may contribute to dermatological and immunological conditions .

The review also highlights the functional consequences of microbial dysbiosis , particularly in relation to host metabolism and immune response . Several studies have shown that environmental toxins can alter microbial gene expression , particularly in pathways related to carbohydrate metabolism, xenobiotic degradation, and oxidative stress response . These functional shifts may affect nutrient absorption, detoxification processes, and inflammatory signaling , thereby influencing systemic health and disease progression . The increase in microbial production of lipopolysaccharides (LPS) and other pro-inflammatory metabolites in polluted environments further supports the idea that microbial dysbiosis may serve as an early indicator of pollution-induced pathology .

One of the key insights from this review is the dose- and duration-dependent nature of microbiome disruption caused by anthropogenic exposure. Long-term exposure to air pollutants, heavy metals, and industrial chemicals was associated with more pronounced microbial shifts , often leading to chronic inflammation and disease development . However, the individual variability in microbiome response to pollution suggests that genetic, dietary, and lifestyle factors may influence microbial resilience and susceptibility . This variability underscores the need for personalized microbiome profiling in environmental health assessments.

The evidence also supports the role of the microbiome as a potential biomarker of pollution exposure . The consistent association between specific microbial taxa and environmental toxins suggests that changes in microbial composition could be used to monitor exposure levels, assess health risks, and predict disease susceptibility . For example, the reduction in *Akkermansia muciniphila* and increase in *Escherichia coli* in polluted environments were frequently linked to metabolic and immune-related health outcomes , indicating that these changes may serve as early indicators of microbiome-mediated health risks .

Despite the growing evidence, the distinction between correlation and causation remains a major challenge in this field. While many studies report strong associations between pollution exposure and microbial dysbiosis , few establish a direct cause-and-effect relationship . This is particularly relevant in epidemiological studies , where confounding factors such as diet, medication use, and socioeconomic status may also influence microbial composition and health outcomes . Therefore, longitudinal and interventional studies , including controlled exposure models and microbiome restoration trials , are essential to clarify the mechanistic pathways and clinical relevance of pollution-induced microbial changes.

The review further confirms the potential of microbiome-targeted interventions — including probiotics, prebiotics, and dietary modulation — in mitigating the negative effects of environmental pollution . Several studies have demonstrated that reintroducing beneficial bacteria or supporting microbial diversity through dietary fiber and fermented foods may help restore microbial balance and improve host resilience . However, the lack of standardized protocols , variability in treatment response , and limited clinical validation suggest that further research is needed to optimize microbiome-based therapeutic strategies in polluted environments.

Moreover, the integration of multi-omics approaches , including metagenomics, metatranscriptomics, and metabolomics , has the potential to deepen our understanding of how environmental toxins influence microbial function and host-microbe interactions . These advanced techniques can provide functional insights into microbial adaptation, stress

response, and metabolic shifts , offering a more comprehensive view of the microbiome's role in environmental health .

The findings of this review also emphasize the need for interdisciplinary collaboration between microbiologists, environmental scientists, clinicians, and public health experts , to better understand and address the health impacts of anthropogenic pollution . As the world continues to face rising levels of environmental contamination , the microbiome may serve as a sensitive indicator of exposure and response , and a target for preventive and therapeutic interventions .

In conclusion, this review provides a comprehensive synthesis of current evidence on the impact of anthropogenic pollution on the human microbiome , confirming that environmental toxins significantly alter microbial composition and function , with important implications for metabolic, immune, and neurological health . While the mechanistic pathways and clinical associations are increasingly well understood, the translation of these findings into public health practice requires further research, standardized methodologies, and policy integration . With the right approaches, microbiome analysis may become a cornerstone of environmental health monitoring , offering new strategies for disease prevention and intervention in polluted environments .

3 Conclusion

The findings of this review provide strong evidence that anthropogenic pollution exerts a profound influence on the human microbiome , with gut, respiratory, and skin microbial communities showing significant alterations in response to environmental toxins such as air pollutants, heavy metals, industrial chemicals, and microplastics . These changes are not merely compositional but also functional, affecting microbial metabolism, host immune regulation, and disease susceptibility. The gut microbiome, as a central regulator of metabolic and immune health, appears to be particularly vulnerable to pollution-induced dysbiosis . Exposure to fine particulate matter, heavy metals, and endocrine disruptors has been associated with reduced microbial diversity, depletion of beneficial taxa , and increased presence of pro-inflammatory bacteria , all of which may contribute to chronic inflammation, metabolic dysfunction, and neuroimmune disorders . The observed decline in short-chain fatty acid (SCFA)-producing bacteria and increase in lipopolysaccharide (LPS)-related microbial species further support the hypothesis that environmental pollution can modulate host immunity and metabolic health through microbiome-mediated pathways. The respiratory microbiome also demonstrates sensitivity to environmental contaminants , particularly in populations exposed to urban air pollution and industrial emissions . The observed shifts in microbial composition, including reduced microbial diversity and increased colonization by opportunistic pathogens, suggest that airborne pollutants may compromise respiratory immunity , contributing to higher incidence of asthma, allergies, and chronic respiratory diseases. Similarly, the skin microbiome , which acts as a first-line barrier against environmental stressors , shows signs of dysbiosis in polluted environments. Changes in microbial balance , particularly the loss of protective species and overgrowth of pathogenic strains , may contribute to dermatological conditions , inflammatory responses , and weakened cutaneous defenses . A key conclusion from this review is that the human microbiome serves as a sensitive indicator of environmental exposure and health response , and may function as a biomarker for assessing pollution-related health risks . These findings support the integration of microbiome profiling into environmental health assessments , offering a new dimension to exposure monitoring and disease prevention .

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