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GUT MICROBIOME MODULATION AND SICK BUILDING SYNDROME: AN OVERVIEW

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ABSTRACT

Sick Building Syndrome (SBS) is a term used to describe a group of vague symptoms that people living in a building suffer from and cannot be assigned to some particular illness or reason, but are somehow related to the time spent in that building. Traditional research has mainly been concerned with IAQ (indoor air quality), ventilation systems and environmental pollutants, but new studies give more credence to the idea that gut microbiome changes could in part be responsible for the occurrence and severity of SBS symptoms. This article looks into the areas where human gut microbiome, environmental exposures in buildings, and SBS symptoms come together, discussing the possible mechanisms, outcomes, and even the implications for treatment.

INTRODUCTION

Sick Building Syndrome (SBS) has been identified as a major and public health problem since the 1970s, it is estimated to affect 10 to 30 percent of the occupants in buildings in developed countries (Passarelli, 2009; Adedoyin and Ogunsona, 2025a). The syndrome consists of a wide range of symptoms like headaches, fatigue, poor concentration, eye and throat irritation, respiratory problems, skin disorders, and stomach upsets. Generally, these symptoms improve quickly or completely go away when the individual leaves the building which suggests an environmental trigger rather than a disease process existing in the body. Traditional studies on SBS have been mainly focused on the physical and chemical factors in the indoor environment like poor ventilation, volatile organic compounds, particulate matter, living microorganisms (mold and bacteria), electromagnetic fields, poor lighting and thermal comfort. However, the inconsistency in finding specific environmental factors associated with the severity of symptoms has led the researchers to consider other or additional explanation models (Chukwudi, 2024; Adedoyin and Ogunsona, 2025a).

The human gut microbiome, which is the collective term for all the microorganisms that inhabit the gastrointestinal tract, made up of trillions of microbes, has turned out to be a major factor during the human life cycle and even illness (Kuziel and Rakoff-Nahoum, 2022). Not only the gut but also the whole body such as the immune system, brain activities, metabolism, and the level of inflammation throughout the body have been found to be affected by the microbiome. Therefore, it is not far-fetched to suggest that the study of the role of microbiome changes in the case of SBS could well be viewed as the next logical step in the continuation of the present research paradigms since the symptoms of SBS do indeed overlap with those of diseases that have been shown to be influenced by gut dysbiosis e.g. chronic fatigue, cognitive dysfunction, and inflammatory responses (Table 1).

Composition and Function of the Gut Microbiome

The human gut consists of around 100 trillion microbial cells, which are representatives of thousands of species, primarily from the phyla Firmicutes, Bacteroidetes, Actinobacteria, and Proteobacteria. This intricate ecosystem applies its powers and performs metabolic activities like the transformation of food components, vitamin and short-chain fatty acid synthesis, maintaining of the intestinal barrier integrity, immune system training and controlling, and ultimately prevention of the colonization of the gut by pathogens (Goodwin, 2025). The gut microbiome is a very dynamic and versatile ecosystem in terms of its composition and it readily responds to environmental factors. Alterations in microbiome composition are known to be caused by several factors such as diet, antibiotic use, stress, disturbance of circadian rhythm, change in physical activity, and exposure to environmental toxins. Microbiome profiles of individuals show significant variation between persons, though the variation over time is much smaller within one person during stable (homeostatic) conditions (Brody, 2020; Kuziel and Rakoff-Nahoum, 2022).

The gut-brain axis is a two-way communication link between the gut and the brain, connecting them through neural, hormonal, and immunological pathways (Zhang *et al*., 2025). The gut microbiome is one of the factors that affect the axis by means of several mechanisms such as producing neurotransmitters and their precursors, changing vagal nerve signaling, controlling hypothalamic-pituitary-adrenal axis activity, and impacting systemic inflammatory mediators that can reach the brain and alter its function (Talbott *et al*., 2020; Kuziel and Rakoff-Nahoum, 2022; Zhang *et al*., 2025).

Environmental Exposures in Buildings and Microbiome Perturbation

Buildings are very intricate ecosystems where human beings live for around 90% of their time in places with good development (Chukwudi, 2024). The indoor atmosphere is home to a variety of chemical and biological entities that might have a direct or an indirect influence on the gut microbiome.

Chemical Exposures

Volatile organic compounds (VOCs) are the most common indoor chemicals and are found in high concentrations all over the house. These chemicals come from the construction and decoration materials of the house, cleaning agents, and sometimes even from the people living in the house (Adedoyin and Ogunsona, 2025a). The most ordinary VOCs are formaldehyde, benzene, toluene, xylene, and several chlorinated compounds. Indoor VOC exposure leading to acute toxicity is extremely rare, but low-level chronic exposure is what the building tenants usually experience. Also, there is increasing proof that the gut microbiome may be reshaped and affected via the environmental chemicals. Xenobiotics may act as antimicrobial agents and consequently, bacterial community balance get disrupted (Leung *et al*., 2014; Adedoyin and Ogunsona, 2025b). Besides, there are microorganisms that can break down the chemicals found in the environment, and those specific microbial populations may emerge from the different exposure patterns. The bifidobacteria can convert certain compounds into metabolites that have different toxicological profiles from those of the parent compounds since they can effectively carry out biotransformation (Wang, 2019; Adedoyin and Ogunsona, 2025a, 2025b).

Indoor particulate matter and dust harbor a plethora of chemical residues, which include but are not limited to, flame retardants, plasticizers, pesticides, and heavy metals. These chemicals find their way into dust where they linger for a while and are then swallowed in the mouth when a baby licks it, gets food contaminated, or inhales it and the mucociliary clearance is followed by swallowing. Some of the toxicants mentioned above have shown the ability to kill or inhibit microbes in the microbiome or even to exert a controlling effect on the microbiome in laboratory studies (Leung *et al*., 2014; Adedoyin and Ogunsona, 2025a).

Biological Exposures

The indoor mycobiome and bacteriome are primary sources of microbial exposure for the people living and working in the buildings. The buildings, which face moisture issues, are the places where the most fungi (Brambilla *et al*., 2022) and bacteria of all sorts are found, and the air of such places is filled with their spores, fragments, and metabolites (Kumar *et al.*, 2021). People living in the buildings and working there inhale and swallow these particles, which might either interact with the gut microbiome or provoke an immune response that indirectly impacts the microbial communities. Among the fungal species found in water-damaged buildings, some are known to produce mycotoxins and volatile organic compounds that possess antimicrobial properties (Leung *et al*., 2014; Adedoyin and Ogunsona, 2025a). Theoretically, the presence of these compounds might create a situation in the gut where certain microorganisms are preferred, and the others are not because of the different levels of their resistance. The idea of microbial transfer from the built environment to the human microbiome has become a topic of discussion in recent times. Every building has its own microbial flora and fauna that are affected by the patterns of occupancy, ventilation, moisture, and materials. Constant exposure to microbes of a particular building may have an impact on the human microbiome through direct colonization or competition for resources (Leung *et al*., 2014; Adedoyin and Ogunsona, 2025b; Kumar *et al.*, 2021).

Ventilation and Hypoxic Stress

Indoor spaces that have insufficient ventilation see the build-up of carbon dioxide along with decrease in the amount of oxygen available. Nevertheless, the indoor CO2 levels very seldom reach the concentrations where they would impose direct threats to human physiology, however, there is a slowly but surely increase in the evidence that raised CO2 levels may cause cognitive dysfunction and mediate certain physiological processes even at the levels which are already common in the poorly ventilated areas (Plachy *et al*., 2024; Adedoyin and Ogunsona, 2025a). The gut microbiome consists of both types of organisms: those that require oxygen and those that do not, the gradient of oxygen through the intestinal mucosa is one of the main factors that determine the number and type of microbes present. If the oxygen level is altered the changes in the bacterial population might occur more quickly than in the case of the oxygen levels being changed slightly, for instance, modestly. Poor indoor environmental quality triggers the stress response, which might not only affect the gut microbiome directly through mechanisms like stress hormone mediation but also indirectly through changes in the motility of the gastrointestinal tract, mucus production, and immune function (Agarwal *et al*., 2021; Çakmakci Karakaya *et al*., 2025).

Mechanistic Pathways Linking Microbiome Dysbiosis to SBS Symptoms

Neurological and Cognitive Symptoms

The occurrence of neurological symptoms in SBS such as headaches, inability to concentrate, tiredness, and emotional disturbance, is in line with the fact that the gut microbiome has a significant impact on the brain (Huo *et al*., 2020). The microbes of the gut are responsible for the production and metabolism of a wide range of neuroactive substances such as serotonin, gamma-aminobutyric acid (GABA), dopamine, acetylcholine, and histamine. Changes in the manufacturing or supply of these products may be one of the causes of the neurocognitive symptoms associated with SBS. Fermentation of dietary fibers by gut bacteria leads to the production of short-chain fatty acids (SCFAs), among which butyrate, propionate, and acetate have the most significant influence on the brain via different routes (Ekpanyaskul, 2005; Adedoyin and Ogunsona, 2025a). These molecules are capable of penetrating the blood-brain barrier and switching on or off the expression of genes in neurons, hence controlling the neurotransmitter systems and impacting neuroinflammation. A decrease in the production of SCFAs as a result of dysbiosis might lead to the weakening of the cognitive and positive mood respectively (van der Meulen *et al*., 2018; Chukwudi, 2024). The vagus nerve acts as a direct neural pathway linking the gut and brain; thus, the gut microbiota can modulate vagal signaling by means of both mechanical and chemical mechanisms. Changes in the vagal tone that are connected with the disturbance in the microbiome may be a contributing factor to a whole range of symptoms including fatigue, mood alterations, and abnormal functioning of the autonomic nervous system (Huo *et al*., 2020; Adedoyin and Ogunsona, 2025a).

Inflammatory and Immune-Mediated Symptoms

Systemic low-grade inflammation is one of the most plausible mechanisms through which microbiome dysbiosis can cause multiple symptoms of SBS. The gut microbiota is vital for the training and regulation of the immune system and the disruption of this relationship can cause inappropriate immune responses (van der Meulen *et al*., 2018; Chukwudi, 2024). One of the consequences of increased gut permeability, otherwise known as "leaky gut," is that bacterial toxins such as lipopolysaccharides can leak into the bloodstream through the intestines. This, in turn, activates an inflammation process which can affect the whole body. The already-mentioned symptoms of tiredness, joint pain, headache, and impaired cognitive function are often linked to systemic inflammation and may be the case of microbiome-mediated inflammatory responses to the exposure of certain environmental factors in buildings (Huo *et al*., 2020; Adedoyin and Ogunsona, 2025a).

The microbiome is a factor that determines the birth and the effectiveness of regulatory T cells, whose main functions are to keep the immune system in balance and avoid the above-mentioned excessive inflammatory responses. Dysbiosis can weaken the competence of regulatory T cells or even completely incapacitate them, thus causing hyperresponses to the environmental allergens and irritants that are present in buildings (van der Meulen *et al*., 2018). Table 1 presents some of SBS symptoms and potential microbiome-mediated mechanisms, while Table 2 presents building related exposures and potential microbiome effects.

Table 1: Some SBS Symptoms and Potential Microbiome-Mediated Mechanisms.

Symptom Category	Specific Symptoms	Potential Microbiome-Related Mechanisms	Reference
Neurological	Headaches, difficulty concentrating, dizziness, fatigue	Altered neurotransmitter production; reduced SCFA synthesis; impaired vagal signaling; neuroinflammation	van der Meulen *et al*., 2018; EPA, 2006; Chukwudi, 2024;
Respiratory	Throat irritation, cough, chest tightness, nasal congestion	Systemic inflammation; altered immune responses; cross-talk between gut and lung microbiomes	Abbritti, *et al*., 2006; Huo *et al*., 2020; Brambilla *et al*., 2022
Dermatological	Skin irritation, dryness, redness	Systemic inflammation; altered immune function; gut-skin axis disruption	Akinwale *et al*., 2019; Huo *et al*., 2020; Brambilla *et al*., 2022
Ocular	Eye irritation, dryness, burning	Inflammatory mediators; altered tear film composition related to systemic inflammation	Akinwale *et al*., 2019; Huo *et al*., 2020; Brambilla *et al*., 2022
Gastrointestinal	Nausea, bloating, abdominal discomfort	Direct dysbiosis effects; altered motility; intestinal permeability	Akinwale *et al*., 2019; Huo *et al*., 2020; Dujardin *et al*., 2020;

		changes	Brambilla *et al.*, 2022; Chukwudi, 2024
Musculoskeletal	Joint pain, muscle aches	Systemic inflammation; altered pain processing	Akinwale *et al.*, 2019; Huo *et al.*, 2020; Dujardin *et al.*, 2020; Brambilla *et al.*, 2022; Chukwudi, 2024
Psychological	Anxiety, irritability, mood changes	Gut-brain axis disruption; altered neurotransmitter systems; HPA axis dysregulation	Nag, 2018; Huo *et al.*, 2020; Dujardin *et al.*, 2020; Brambilla *et al.*, 2022; Chukwudi, 2024

Table 2: Building-Associated Exposures and Potential Microbiome Effects.

Exposure Category	Specific Agents	Potential Microbiome Effects	Possible Mechanisms	References
Volatile Organic Compounds	Formaldehyde, benzene, toluene, cleaning product chemicals	Altered diversity; shifts in community composition; antimicrobial effects	Direct antimicrobial activity; selective pressure; metabolic substrate effects	EPA, 2006; Nag, 2018; Mayer, 2022; Rani, 2024; Adedoyin and Ogunsona, 2025a
Particulate Matter	Dust, chemical residues, combustion particles	Compositional changes; inflammatory signaling	Ingestion of particles with chemical/microbial components; systemic inflammation	EPA, 2006; Mayer, 2022; Rani, 2024; Adedoyin and Ogunsona, 2025a
Biological Contaminants	Mold spores, bacterial fragments, mycotoxins, endotoxins	Dysbiosis; immune activation; barrier disruption	Direct antimicrobial effects of mycotoxins; inflammatory responses; competitive interactions	EPA, 2006; Dujardin *et al.*, 2020; Mayer, 2022; Rani, 2024; Adedoyin and Ogunsona, 2025a
Poor Ventilation	Elevated CO2, reduced oxygen exchange, accumulation of contaminants	Altered aerobic/anaerobic balance; stress-mediated changes	Oxygen gradient effects; stress hormone responses; accumulated chemical exposures	EPA, 2006; Mayer, 2022; Rani, 2024; Adedoyin and Ogunsona, 2025a
Heavy Metals	Lead, mercury, cadmium (from old materials)	Reduced diversity; pathobiont enrichment	Direct toxicity to beneficial bacteria; oxidative stress; barrier dysfunction	EPA, 2006; Mayer, 2022; Rani, 2024; Adedoyin and Ogunsona, 2025a
Electromagnetic Fields	Low-frequency fields from electrical systems	Uncertain; limited evidence	Potential stress responses; unclear direct mechanisms	EPA, 2006; Nag, 2018; Mayer, 2022; Rani, 2024; Adedoyin and Ogunsona, 2025a

Metabolic and Detoxification Pathways

The microbiome in the digestive tract plays a major role in the metabolism of xenobiotics, as it possesses the enzymatic capacity that makes up for the human liver detoxification systems. The metabolic activity of some species of bacteria can actually make the chemicals in the environment less toxic, or even more toxic (Cox *et al*., 2022). The diversity of the gut microbiome could be a determining factor for an individual's ability to process and thus rid the body of the environmental chemicals that are found in buildings, resulting in increased toxicity. The production of biotransformation products by the gut microbiome impacts the liver detoxification pathways through interactions with the nuclear receptors and transcription factors controlling the enzymes of xenobiotic metabolism. Therefore, dysbiosis may indirectly lead to reduced detoxification capacity by influencing the generation of the very regulatory metabolites that are crucial. The gut flora is also a determinant of energy metabolism and mitochondrial function through numerous pathways. The disturbance of these processes could be a contributing factor to the severe fatigue that patients with Sick Building Syndrome (SBS) often complain about, especially if accompanied by direct mitochondrial poisoning with certain environmental chemicals (Cox *et al*., 2022; Adedoyin and Ogunsona, 2025a).

Individual Susceptibility and Microbiome Variability

One of the long-standing questions in the research on SBS is the large individual differences in the number of symptoms that people show although they have been exposed to the same environmental conditions. Not everyone living in the contaminated buildings will have symptoms, and in the case of those who do have symptoms, the type and intensity will be very different. One of the things that might give rise to this variation in symptoms is the microbiome composition (ElZeina and Hijazia, 2021). The individuals with a less diverse or resilient microbiome may only be able to cope with the environmental changes to a certain, and already low, threshold, whereas those with more diverse or resilient microbiomes may still maintain their equilibrium by developing new supportive relationships with their environment. Genetic differences play a role in the composition of the microbiome and the ability of the individual to react to the exposure. Variants in genes that encode for detoxification enzymes, immune receptors, and inflammatory mediators have a say in each person's reaction to buildings' associated exposures. These same genetic variants may also be implicated in the composition and functioning of the microbiome, thus leading to the emergence of the intricate interactions between genes, environment, and microbiome that decide the susceptibility to SBS (Kumar *et al*., 2021). The combination of factors such as past life experiences, which include, among others, antibiotic treatment, dietary changes, and exposure to infections, deeply imprints the microbiome. These imprints can be regarded as the historical factors that would affect the present-day susceptibility of a person to the environmental changes that lead to a dysbiosis of the microbiome and, as a consequence, the development of symptoms (Kumar *et al*., 2021; Mayer, 2022; Weng *et al*., 2025).

The direct research linking the composition of gut microbiome to SBS is very small thus it becomes a major gap in the literature. Ostensibly, the studies performing microbiome changes in conditions that exhibit symptomatic overlap with SBS provide hints of potential relationships. Investigations done on chronic fatigue syndrome that is very similar to SBS in terms of the ailment, showed distinct microbiome signatures that were less diverse, had a changed Firmicutes to Bacteroidetes ratio and less butyrate-producing bacteria (Brody, 2020; Kumar *et al*., 2021). The declining cognitive ability and fatigue in both conditions might thus be due to shared microbiome-mediated mechanisms among others. Environmental toxicant exposure studies have also pointed out to similar microbiome alterations due to the exposure (Kumar *et al*., 2021; Weng *et al*., 2025). Moreover, in research related to air pollution, changes in the gut microbiome composition have been seen to correlate with exposure level and inflammatory markers. Considering the fact that there is an overlap between outdoor and indoor air contaminants, it can be concluded that the specified pathway may be the way of indoor air quality influencing the gut microbiome. The inquiry into psychological stress and its impact on the microbiome indicates that, stress at work, in most buildings associated with SBS, is at times, the reason for the constant microbiome and symptom changes.

Potential Therapeutic Implications

If the dysbiosis of the microbiome plays a role in the development of SBS, then it would be a wise move to focus on the microbial community in order to find a solution. This could be through methods that are either completely new or by adding them to the existing ones of treating the environment.

Dietary Interventions

Changing one's diet is the easiest way to handle the microbiome. The introduction of more fermentable fibers encourages the good bacteria to flourish and the production of short-chain fatty acids. Following the anti-inflammatory diets may neutralize the inflammatory reactions that would otherwise connect the exposure to the environment with the clinical manifestations. There are certain compounds in food that have the ability to kill or change the microbiome. The polyphenols-group compounds, rich in fruits, vegetables, and beverages like tea and coffee, not only impact the microbiome but also have direct anti-inflammatory actions. Modes of action of omega-3 fatty acids are similar so they toothpaste the microbiome as well as inflammation considering all the sides of SBS pathophysiology (EPA, 2006; WHO, 2006; Igwe *et al*., 2023).

Probiotics and Prebiotics as a Therapeutic Approach

The introduction of microorganisms (probiotics) or the application of substrates that stimulate the growth of beneficial bacteria (prebiotics) also represents a new potential way of treatment. Certain probiotic strains have shown positive impacts on the immune system, the integrity of the intestinal barrier, the production of neurotransmitters, and inflammation (Ji *et al*., 2020; Tochio *et al*., 2021). Nevertheless, individualized treatment methods might be necessary since the effectiveness of probiotics is highly different among strains and formulations. The combination of prebiotics with probiotics, known as synbiotics, might prove to be the best method since it guarantees the nutritional support of the probiotics being introduced. Still, the complicated ecosystem of the intestine suggests that the gut must be invaded by the new bacteria which means they have to drive out the already established ones; thus, the process of getting them accepted in that new environment may turn out to be tedious (DeGruttola *et al*., 2016; Ji *et al*., 2020; Tochio *et al*., 2021).

Changes in Environment and Lifestyle

The process of direct microbiome modification is not the only way to intervention; other factors that support microbiome health have been pointed out as helpful to patients with SBS. Stress relief methods, physical exercise, and sleep quality are among the factors that microbiome composition is influenced and that could make one more resistant to the impact of building-related environmental stressors. Using antibiotics strictly when necessary and avoiding antimicrobial chemicals in personal care products might be a way to maintain the diversity and functioning of the microbiome (EPA, 2006; WHO, 2009; Fu *et al*., 2022). Getting outdoors regularly to different environments and natural places might keep the microbiome diverse by contact with the microbes living in the environment. Table 3 presents proposed microbiome-targeted interventions for SBS.

Table 3: Proposed Microbiome-Targeted Interventions for SBS.

Intervention Type	Microbiome-Targeted Interventions	Proposed Mechanisms	Evidence Level	References
Dietary Modification	High-fiber diet; polyphenol-rich foods; anti-inflammatory diet	SCFA production; diversity enhancement; reduced inflammation	Moderate (indirect evidence)	Xi *et al*., 2020; Zhang *et al*., 2025
Probiotics	Lactobacillus and Bifidobacterium strains; multi-strain formulations	Barrier support; immune modulation; neurotransmitter effects	Low to moderate	Ji *et al*., 2023
Prebiotics	Inulin, fructooligosaccharides, galactooligosaccharides	Selective enhancement of beneficial bacteria; SCFA production	Moderate	Ji *et al*., 2023
Synbiotics	Combined probiotic-prebiotic formulations	Synergistic effects on colonization and metabolic activity	Low	Xi *et al*., 2020; ; Ji *et al*., 2023
Lifestyle Interventions	Stress reduction; exercise; sleep optimization	Indirect microbiome support through host physiology	Moderate (indirect evidence)	EPA, 2006; Fu *et al*., 2022
Environmental Modifications	Reduced antimicrobial product use; outdoor exposure	Microbiome preservation; diversity enhancement	Low	EPA, 2006; Fu *et al*., 2022
Targeted Antibiotics	Selective use for specific pathobiont suppression	Removal of harmful bacteria while preserving beneficials	Theoretical; not yet investigated	D'Accolti *et al*., 2022

Research Gaps and Future Directions

The area where gut microbiome science meets SBS research still has a lot to offer in terms of future research. Prospective cohort studies that look at the microbiome composition in the buildings before, during, and after the occupants develop symptoms would be a good source of information for understanding the relationships in time and the phenomenon of causation. Exposure studies, while difficult to conduct due to ethical and practical reasons, might reveal more about the factors that make certain buildings sick through bacteria and changes in the microbiome. Environmental chambers could be one way to conduct these studies or researchers could compare microbiome profiles in different buildings based on their environmental quality parameters. Combining multi-omics approaches like metagenomics, metabolomics and immune profiling would allow an in-depth characterization of the complex interactions among environmental exposures, microbiome function, host responses, and symptom development. Integrative analyses may help in spotting biomarkers that can predict susceptibility or that can be used for monitoring intervention effectiveness (Adedoyin and Ogunsona, 2025a, 2025b).

Animal models used for mechanistic studies might reveal the exact pathways which are responsible for the influence of environmental exposures on the microbiome and, then, the body. The germ-free and gnotobiotic animal models allow accurate alteration of the microbial communities and the setting of controlled conditions for exposure which cannot be applied in human studies. Another significant area of research is the investigation of the building microbiome and its connection to the health of the occupants. Knowing which microbes associated with the building contribute to or ward off SBS could lead to the alteration of building design, maintenance, and even the removal of such microbes. Microbiome-based interventions developed and validated for SBS necessitate conducting comprehensive clinical trials. The focus of these studies should not only be on the changes in microbiome but also on the corresponding clinical outcomes which will include symptom severity, quality of life, and objective measures of cognitive function and physiological parameters (Belachew *et al*., 2018; D'Accolti *et al*., 2022).

Several challenges complicate the investigation and interpretation of the relationships between the gut microbiome and SBS. One of them is the multifactorial nature of SBS which comes along with a lot of potential contributing factors, as well as very different symptom presentations, thus making it hard to isolate the specific causal pathways. On the one hand, microbiome research itself is surrounded by a lot of methodological challenges which include very high inter-individual variability, temporal dynamics, and the absolute difficulty of establishing causation versus correlation. On the other hand, the absence of standardized definitions and diagnostic criteria for SBS is a major obstacle that complicates studies and makes it hard to compare different populations. Furthermore, the subjective nature of many SBS symptoms together with the possible reporting bias, work as extra hurdles in this clinical research area. In addition, microbiome research involves a lot of technical considerations, such as sample collection and processing methods, sequencing approaches, and bioinformatic analysis pipelines, that tremendously influence the results. The lack of standardization across studies is thus one of the main obstacles that prevents comparison and synthesis of findings. However, the complexity of microbiome-host interactions is great such that changes in microbial composition do not always mean that there is a functional consequence. Functional analyses that examine microbial metabolic activities and host responses provide more mechanistic insights than just doing compositional surveys, however, they require more sophisticated and resource-intensive approaches.

CONCLUSION

The potential role of gut microbiome modulation in Sick Building Syndrome is an emerging area of investigation that nicely intertwines environmental health, microbiology, immunology, and neuroscience. Although studies directly connecting microbiome changes to SBS are still scarce, different disciplines coming together have given rise to some possible paths of coherence that should be explored further. The gut microbiome's impact on the immune response, inflammatory actions, neurotransmitter systems, and metabolic pathways makes it a very likely mediator of the environmental exposures in buildings and the wide range of symptoms associated with SBS. One reason why some building occupants develop SBS while others do not, even under the same environmental conditions, might be explained by the individual differences of microbiome composition and function. Factors like chemical contaminants, biological agents, and poor ventilation, which are often present in buildings with a reported case of SBS, may influence the gut microbiome's composition and functioning directly or indirectly. Long-term exposure to these factors may lead to dysbiosis, and the consequent inflammatory and metabolic processes may produce symptoms similar to those of SBS.

Microbiome dysbiosis might be one of the major factors contributing to the pathophysiology of SBS, and thus, the realization might lead to the invention of new therapeutic ways. Besides traditional environmental remediation efforts, interventions like dietary changes, probiotic supplements, and lifestyle changes that aim to restore and support the microbiome may be used as complementary options. Such methods would be especially helpful for people who still suffer from symptoms even if the environment has improved or for those who cannot stay away from the problematic building. But, there is still a lot of research to be done before it can be concluded that gut microbiome modulation causes SBS. It would be very important to have rigorous prospective studies that look into microbiome changes due to building exposures and symptom development. Also, in-the-lab studies explaining the exact mechanisms of how environmental exposures cause changes in the microbiome and later on physiological effects would help to come to conclusions about causation. Eventually, clinical trials are going to be conducted to test the effectiveness of the therapy in SBS populations through the use of microbiome-targeted interventions. The multifactorial nature of SBS with its myriads of environmental factors, individual susceptibility traits, and diverse symptom presentations indicates that microbiome modulation might be one aspect of a more complex process rather than a direct causal pathway. Therefore, future studies should adopt the complexity through combined approaches considering simultaneous environmental, microbial, immunological, and host genetic factors.

The ongoing progress of microbiome research along with a deeper comprehension of building-occupant interactions has begun to open up an area of research that may even overturn our current approaches towards gaining knowledge about, going in for prevention of, and curing Sick Building Syndrome. Moreover, if these advances are made, they might also lead to better health and increased life quality for millions of people suffering from the effects of poor indoor environmental quality across the globe.

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