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Gut-brain-oral dysbiosis: A comprehensive review

Geetanjali Jadhav[1], Rahul Hegde[2], Yashraj J Jadhav[3], Anand Shigli[4], Pawan Herkar[5] ✉

Highlights

- This study explores the intricate interactions within the gut-brain-oral microbiome axis, emphasizing the role of microbial dysbiosis in shaping health outcomes.
- Microbiome dysbiosis contributes to dental caries and neurodevelopmental outcomes, emphasizing the bidirectional relationship between oral and systemic health via the gut-brain axis.
- These findings highlight the potential of microbiome-targeted strategies to improve oral health and reduce systemic risks in children.

[1] *Associate Professor, Department of Pedodontics and Preventive Dentistry, D Y Patil Dental School, India*
[2] *Professor, Department of Pedodontics and Preventive Dentistry, D Y Patil Dental School, India*
[3] *Resident, Department of Ophthalmology, Mahadevappa Rampure Medical College, India*
[4] *Professor, Department of Pedodontics and Preventive Dentistry, D Y Patil Dental School, India*
[5] *Assistant Professor, Department of Pedodontics and Preventive Dentistry, D Y Patil Dental School, India*

Correspondence:
Department of Pedodontics and Preventive Dentistry, D Y Patil Dental School, India
E-mail address:
pavanherkar@gmail.com

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Abstract

The gut-brain axis is a bidirectional communication system between the gut and central nervous system, mediated by the nervous, hormonal, and immune systems. This connection plays a critical role in overall health and has been linked to oral health conditions such as dental caries. Specific bacteria within cariogenic biofilms are associated with an increased risk of dental caries, and emerging evidence suggests that the gut microbiome may influence biofilm formation. Dysbiosis in the gut can alter immune responses, affecting the body's ability to manage cariogenic bacteria and contributing to caries susceptibility, particularly in children. The composition of the gut microbiome in early childhood is crucial, as it influences immune system development and oral microbial ecology, determining long-term dental health outcomes. Psychological stress, which interacts with the gut-brain axis, has also been correlated with higher susceptibility to dental caries. Stress can dysregulate immune pathways, exacerbate inflammation, and contribute to oral biofilm imbalance. Furthermore, disruptions in the oral microbiota can have systemic consequences. Dysbiosis in the gut-brain-oral axis may trigger inflammatory responses linked to both neurodevelopmental and systemic health conditions. In conclusion, the gut-brain axis and the gut microbiome play pivotal roles in dental health by modulating immune responses, stress interactions, and microbial balance. Understanding these relationships is essential for developing preventive and therapeutic strategies, particularly in pediatric populations. This review aimed to delineate the relationship between the gut-brain axis, oral microbiome, and dental caries, focusing on how dysbiosis and immune responses influence caries susceptibility, particularly in children.

Keywords: Gut-Brain Axis; Oral Microbiome; Dysbiosis; Pediatric Dentistry; Dental Caries

INTRODUCTION

The oral cavity's complex microbiota and its interaction with the immune system significantly influence overall health. Dental caries and dysbiosis, or imbalances in the oral microbiota, are common diseases affecting the oral cavity. Additionally, the oral cavity is considered a component of the gut-brain axis, with dysbiosis of the oral microbiota implicated in the development of dental caries. This state is characterized by rapid changes and involves multiple heterogeneous microbial communities, each with specific roles in distinct physical locations.[1] After birth, the oral mucosa is colonized by bacteria and fungi transmitted through various means, including parent-to-parent contact, parent-to-child interactions, food, and horizontal transmission from caregivers and peers. During infancy, as permanent and deciduous teeth begin to erupt, the oral microbial community continues to develop, evolving into a complex and diverse pathobiotic microbiome.[2] The prenatal interaction between the maternal environment and the microbiome influences postnatal development, innate and adaptive immunity, and long-term health outcomes. Importantly, the oral cavity facilitates access to microbial communities within the body, enabling the use of biomarkers—such as metabolites, inflammatory markers, and microbial by-products in saliva—for diagnosing, predicting, and monitoring oral diseases.[3]

Recent studies[4–6] suggest that early alterations in the oral environment and the establishment of a healthy oral microbiome play a crucial role in shaping oral health and disease in children, similar to the well-documented association between the microbiome and health in adults. Conditions such as childhood caries, gastrointestinal diseases, and infections that disrupt and harm oral bacteria are among those influenced by the oral microbiome. Long-term studies are required to establish definitive relationships between the oral microbiome and oral or general health. Screening for these associations is best achieved through advanced diagnostic tools, including Next-Generation Sequencing (NGS), Quantitative PCR (qPCR), Metagenomic Analysis, Salivary Biomarker Analysis, Microbial Culturing, 16S rRNA Gene Sequencing, and Point-of-Care devices such as portable diagnostic kits. These tools are particularly valuable for monitoring vulnerable populations, such as infants and children.[7]

Researchers are also finding applications of the microbiome with a focus on microbial manipulation. In the simplified gut microbiome of the infant, the single-species bacterial intervention is effective in modulating the risk of infection[8]. Even though the research related to the effects of the dynamic nature of the oral microbiome of bacteria in the body is incomplete at present, we can say that in the future, we will be able to have a better understanding of the oral cavity and gut by having a better knowledge of the tools through which diabetes in children gets diagnosed[9-10].

The primary aim of this study is to gather comprehensive knowledge about the developing oral microbiome in young children, particularly during early childhood, and to profile the bacterial species present within this dynamic ecosystem. Furthermore, it seeks to explore the predictive value of the oral microbiome for identifying risks of future dental and oral diseases. Understanding these microbial patterns and their interactions could pave the way for early diagnosis, targeted prevention, and innovative therapeutic strategies to improve long-term oral health outcomes.

This review aimed to delineate the current perspective of understanding the relationship among gut, brain, and oral microbiota and its participation in pathogenesis in conditions of dysbiosis.

METHODS

Keywords like gut-brain axis, oral microbiome and brain health, dysbiosis, neurological diseases, gut microbiota, dental health, and cross-talk between the gut, brain, and brain were used to access research databases, including Scopus, PubMed, Web of Science, and Google Scholar.

The review maintains methodological rigour by following MOOSE (Meta-analysis of Observational Studies in Epidemiology) or PRISMA (Preferred Reporting Items for Meta-Analyses & Systematic Reviews) recommendations. This has explicit inclusion/exclusion criteria for selected papers, detailed descriptions of the search strategy, and databases used (PubMed, Scopus, Web of Science, Google Scholar). Quality evaluation measures were also considered.

Review Question

How does dysbiosis within the gut-brain-oral microbiome axis influence dental and neurodevelopmental health outcomes in children, and what potential therapeutic interventions can address these effects?

Primary Outcome

To determine the relationship between microbiome dysbiosis within the gut-brain-oral axis and its impact on pediatric oral and neodevelopmental health.

Secondary Outcome

To identify specific microbial profiles within the oral microbiome that can serve as early biomarkers for risks associated with dysbiosis-related health conditions.

Study Selection

Figure 1 presents the flowchart of the study describing the study selection process and the risk of bias assessment table are incorporated to make the review more transparent and reproducible. Definitive inclusion criteria were used to direct the process of study selection so that a comprehensive and relevant analysis of the association between the microbiome and ASD, ECC, OSA, IBS, etc., was ensured. Studies were selected based on relevance to the gut, brain, and oral microbiota of the mentioned populations, with emphasis on studies involving mechanisms and clinical consequences of dysbiosis.

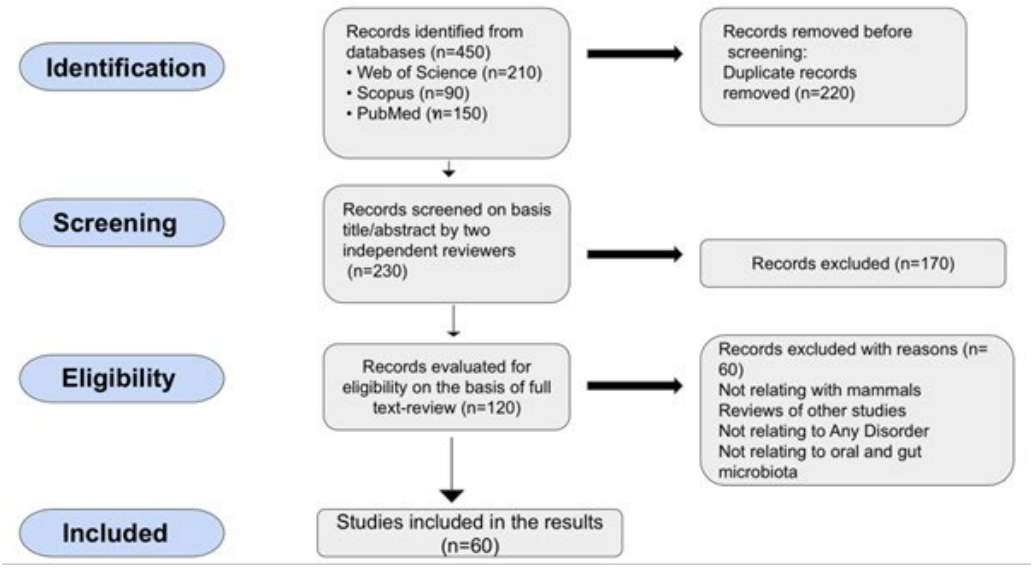

Figure 1. STROBE flowchart illustrating the review process: identification, screening, eligibility, and inclusion

Transparency Measures

To ensure the systematic review was both comprehensive and reproducible, the study selection process was outlined using a PRISMA flowchart and a risk-of-bias assessment table. These tools enhance methodological transparency by visually and systematically documenting the inclusion and exclusion decisions.

Inclusion Criteria

Clear and definitive inclusion criteria were meticulously applied to select relevant studies, enabling a focused exploration of the interplay between the microbiome and conditions such as Autism Spectrum Disorder (ASD), Early Childhood Caries (ECC), Obstructive Sleep Apnea (OSA), and Irritable Bowel Syndrome (IBS). This rigorous approach ensured the review maintained its scope, emphasizing mechanisms of microbiota-related dysbiosis and its clinical implications.

Key Areas of Focus

The selected studies focused on associations among the gut, brain, and oral microbiota, aiming to elucidate mechanisms underlying dysbiosis and its clinical implications across diverse populations. Emphasis was placed on research exploring the biological pathways and interactions within the microbiome relevant to the conditions studied. The design and methodology incorporated significant findings from the microbial community, including insights into pathways linking microbiota alterations to neurodevelopmental changes. Studies investigating mechanisms by which microbial dysbiosis exerts systemic effects—such as inflammation or metabolite production—were prioritized. Additionally, the review highlighted potential therapeutic interventions targeting the microbiome. This comprehensive approach provides valuable insights into the relevance of the microbiome-gut-brain axis for diagnosis and treatment.

Bias Selection and Quality Assessment

The study selection and analysis were meticulously conducted to minimize potential biases in the findings. Common sources of bias included heterogeneity in study designs, variability in microbiota evaluation methods, and inconsistent reporting of outcomes, all of which could affect the comparability and generalizability of the results. Figure 2 summarizes the key biases and their effects on the studies' conclusions. To mitigate these biases, several strategies were employed, including the use of only peer-reviewed articles and the application of standardized criteria for study inclusion.

Risk-of-Bias Traffic Light Plot

Each cell in the plot includes text indicating the degree of risk associated with a specific criterion: Low, Moderate, High, or None. The legend clearly defines the colors corresponding to each risk level, allowing for quick and easy interpretation. (Generated using the ROBVis-Risk Bias Assessment tool.) The following methodological criteria were employed to assess the quality of the selected studies: allocation concealment, blinding of outcome assessment, selective reporting, random sequence generation, and deviations from intended treatments.

Oral Microbial Development in Early Infancy

The critical developmental stage spanning the first two years of life is characterized by the gradual establishment of the oral microbial community. While microbial colonization in humans was traditionally believed to begin at birth, recent evidence suggests that the presence of bacteria in amniotic fluid and the placenta may indicate that

microbiome formation is initiated in utero.[11] Research has identified *Streptococcus*, *Fusobacterium*, and *Neisseria* as common inhabitants of the placental environment, forming the foundation for microbiota colonization after birth.[12]

Early Microbial Colonization and Its Dynamics

Oral microbial colonization begins to accelerate immediately after birth, driven by initial exposure to caregivers, feeding practices, and environmental factors.[13] Newborns first acquire transient microbial communities, which gradually evolve into stable and diverse populations as they mature. Sequencing studies, such as the work by Mason et al.[14], have identified early colonizers in the oral cavity, including *Streptococcus salivarius* and *Staphylococcus epidermidis*, which dominate the oral environment. These bacteria thrive due to their ability to utilize nutrients present in breast milk and their compatibility with mucosal surfaces. As infants grow, microbial diversity and abundance increase, influenced by dietary changes and anatomical developments such as tooth eruption. The emergence of teeth introduces new niches for colonization,[15] allowing the proliferation of species like *Streptococcus mutans*, which preferentially adhere to tooth surfaces.

Microbial Composition During the Primary Dentition Stage

During the primary dentition stage, the oral microbial community undergoes significant changes. Initially dominated by facultative Gram-positive bacteria, the microbiota transitions to include facultative Gram-negative anaerobes such as *Fusobacterium* and *Veillonella*.[16] The presence of teeth provides attachment sites for these bacteria, shaping the microbial ecology of the oral cavity. By the age of seven, the oral microbiome stabilizes, comprising approximately 600 operational taxonomic units (OTUs),[17] reflecting increased microbial diversity and complexity.

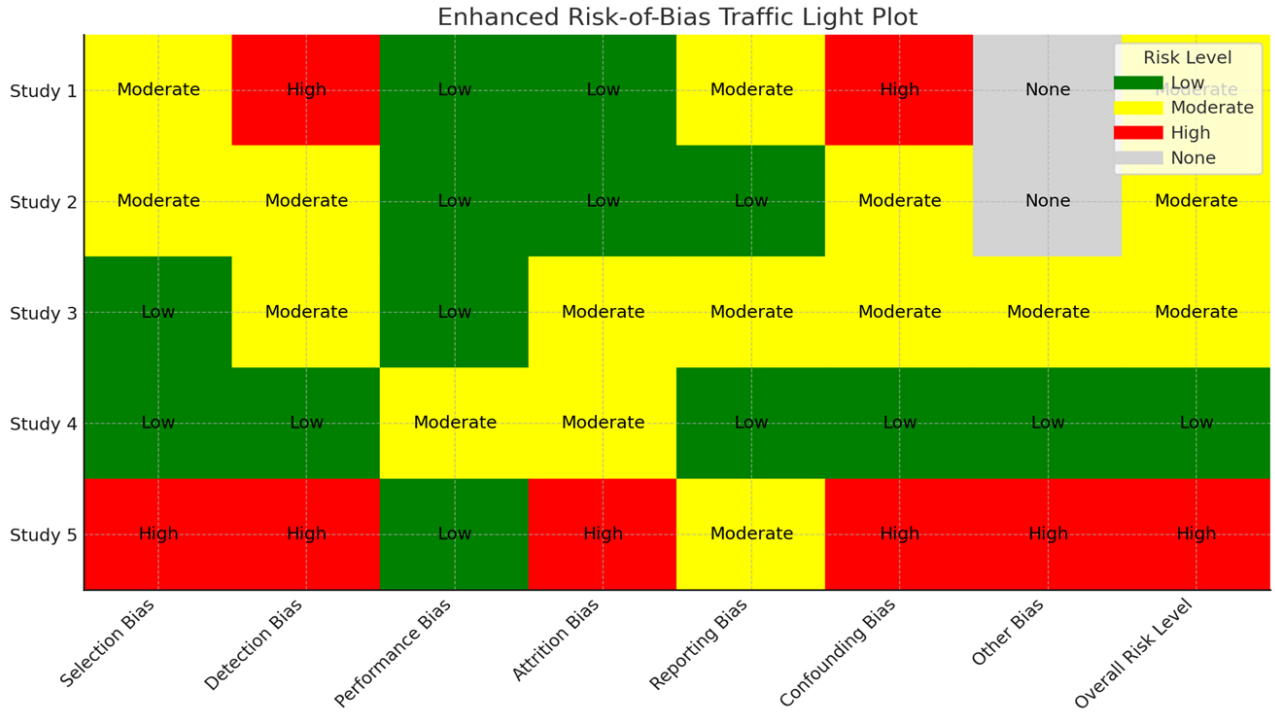

Figure 2. Traffic light plot showing the risk of bias levels across various bias categories for the studies reviewed

Factors Affecting Oral Microbiota Development

Factors influencing the development of the oral microbiota include dietary habits, environmental exposures, genetic predispositions, and oral hygiene practices, each playing a pivotal role in shaping microbial composition.

Inherited Factors

Genetic predisposition partially influences an individual's oral microbiome. Twin studies have demonstrated a correlation between genetic makeup and microbial similarity, though diet and health conditions exhibit a stronger association with microbial resemblance.[18] Specific genetic markers have been linked to the presence of bacteria such as *Prevotella* and *Pasteurellaceae*, suggesting that host genetics do play a role in shaping microbial colonization patterns.[19]

Vaginal vs. Caesarean Delivery

The mode of delivery significantly influences the initial composition of an infant's microbiota. Vaginally delivered infants acquire microbial communities resembling their mother's vaginal flora,[20] whereas those delivered via caesarean section develop microbiota more akin to maternal skin flora. These early microbial differences can have long-term effects on immune system development and susceptibility to oral diseases.

Feeding

The type of feeding plays a critical role in shaping the oral microbiota from the very beginning. Breastfed infants develop a distinct microbial profile compared to formula-fed infants.[21–22] By the age of one, these profiles tend to converge, becoming more similar. However, the early microbial exposures associated with breastfeeding may have lasting benefits, including protection against oral infections and systemic diseases.

Health Consequences of Oral Microbial Communities

1. Early Childhood Caries (ECC)

ECC is one of the most prevalent oral health issues affecting children. The condition is primarily driven by the overgrowth of *Streptococcus mutans*, which adheres to tooth surfaces and produces acids that demineralize enamel.[23] Other species, such as *Veillonella* and *Lactobacillus*, contribute to the cariogenic process by metabolizing lactate, thereby enhancing acid production. The Industrial Revolution marked a turning point, with increased production and consumption of rice and sugar leading to a dietary shift. This change favored the proliferation of cariogenic bacteria like *Streptococcus mutans*, fueling the rise of ECC and other dental pathologies.

Predictive Studies and Longitudinal Research

Longitudinal studies have consistently identified high *Streptococcus mutans* (S. mutans) counts as a reliable predictor of ECC risk. For instance, Fontana et al.[25] studied 329 American children at approximately 26 months of age and found that infants with over 10510^5105 colony-forming units of *S. mutans* per milliliter of saliva were at significantly higher risk for ECC. Similarly, Piva et al.[26] conducted a two-year study involving 163 Brazilian children aged 3 to 4 years, observing a strong correlation between elevated *S. mutans* counts and caries development. These findings highlight the potential of *S. mutans* as a predictive marker for ECC.[24–26]

Expanding the Microbial Landscape

While *Streptococcus mutans* (*S. mutans*) is a key contributor to the pathogenesis of ECC, other bacterial species also play significant roles. A variety of microorganisms have been associated with ECC, including *Streptococcus salivarius*,

Streptococcus sobrinus, *Streptococcus parasanguinis*, *Scardovia wiggsiae*, *Streptococcus exigua*, *Lactobacillus salivarius*, *Parascardovia denticolens*, *Porphyromonas* species, *Actinobacteria*, and *Veillonella*. This highlights the multifactorial nature of ECC, involving a complex interplay among microbial communities. For instance, Gross et al.[28] conducted a study sequencing plaque samples from 36 children with severe ECC (S-ECC) and 36 caries-free (CF) children. Their findings revealed that most S-ECC cases were dominated by *S. mutans*. Conversely, children with low or undetectable levels of *S. mutans* exhibited high concentrations of other bacterial species, such as *S. salivarius*, *S. sobrinus*, and *S. parasanguinis*. These results suggest that while *S. mutans* is a significant contributor to ECC, other microbes can independently drive caries development.[28]

Role of Veillonella in ECC Development

Among lesser-studied bacteria, *Veillonella* has emerged as a significant contributor to the progression of ECC. Unlike *Streptococcus mutans* and other acidogenic species, *Veillonella* has been identified as a predictor of future tooth decay in children with no prior history of caries.[29] This bacterium is particularly notable for its ability to metabolize lactate, a byproduct of carbohydrate fermentation by *Streptococcus* species. The close proximity of *Veillonella* to acid-producing bacteria within biofilms suggests a synergistic relationship that exacerbates tooth demineralization.[30]

Veillonella's metabolic role in recycling lactate to produce weaker acids provides insight into its unique phenotype and its potential to contribute to ECC independently of *S. mutans*. This novel understanding highlights the microbial interactions that drive caries development, offering new opportunities for targeted preventive strategies.

Social And Environmental Factors

In addition to microbial dynamics, social and environmental factors influence ECC prevalence. Studies have shown reduced social disparities in the oral microbiota of children with caries compared to their healthy counterparts[31]. These findings highlight the multifaceted nature of ECC, where biological, environmental, and social determinants interact to shape disease outcomes.

2. Systemic Health Conditions

Dysbiosis in the oral microbiome has been linked to various systemic health conditions, including obesity, celiac disease, and inflammatory bowel disease (IBD). Research indicates that children with IBD exhibit lower diversity in their oral microbiota, highlighting a potential connection between oral health and systemic inflammation.[32] This reduced microbial diversity suggests that the state of the oral microbiome may either reflect or influence systemic immune-related disorders. These findings emphasize the importance of maintaining oral health as a critical component of overall well-being.

3. Communication and Developmental Disorders

These disorders are characterized by challenges in social communication and behavior. Alterations in the gut and oral microbiota have been linked to such conditions.[33] Salivary microbiome may serve as non-invasive biomarkers for early diagnosis, offering valuable insights into the "microbiome-gut-brain axis." Shifts in the oral microbiome have been observed in disorders like autism spectrum disorder (ASD), with distinct microbial profiles correlating with developmental and gastrointestinal symptoms. These biomarkers present a promising, noninvasive approach for early ASD detection while deepening our understanding of the complex

interplay between the microbiome, gut, and brain.[34]

Microbial Diversity

Reduced diversity in the salivary microbiota is frequently observed in individuals with autism spectrum disorder (ASD).[35] The loss of microbial variety may indicate disruptions in the microbiome-gut-brain axis, which is closely linked to neurological development.

Specific Microbial Species

In individuals with autism spectrum disorder (ASD), increased levels of certain bacteria, such as *Prevotella* and *Selenomonas*, and decreased levels of beneficial bacteria, like *Streptococcus*, have been identified.[36] These microbial imbalances may affect both oral and gut health, ultimately influencing brain function.

Metabolites Produced by Oral Microbiota

Short-chain fatty acids (SCFAs), metabolites produced by bacterial activity within the microbiome, have been suggested as potential biomarkers.[37] Imbalances in SCFA levels may disrupt neural signaling pathways associated with ASD.

Inflammatory Markers

Alterations in the oral microbiota may lead to increased inflammation, as reflected by elevated levels of biomarkers such as cytokines or immune proteins in saliva.[38] These inflammatory changes could have implications for systemic health.

Bacterial Pathways

Dysregulation of bacterial metabolic pathways, particularly those involved in amino acid metabolism, may provide valuable insights into the microbiota-related alterations linked to ASD.[39]

4. Oral Microbiome in Pediatric OSAS

Research has explored the relationship between the oral microbiome and pediatric obstructive sleep apnea syndrome (OSAS) using advanced 16S rRNA gene sequencing techniques. The analysis included the oral microbiota of 30 children diagnosed with OSAS and 30 healthy controls.[40] The findings revealed significant differences in microbial composition between the two groups. Specifically, bacterial genera such as *Veillonella* spp., *Prevotella* spp., *Moraxella* spp., *Campylobacter* spp., *Butyrivibrio* spp., *Thermus* spp., *Pseudomonas* spp., and *Achromobacter* spp. were more than twofold higher in children with OSAS compared to healthy controls.[40–41]

Such differences suggest that alterations in the oral microbiota may either contribute to or result from the pathophysiology of pediatric OSAS. To further explore these connections, the research was extended to include urinary metabolite profiles from the same cohort of children. Metabolomic analysis revealed associations between shifts in oral microbial communities and disruptions in urinary metabolites among children with OSAS.[42] These findings suggest potential systemic implications of microbial imbalances in affected patients. However, while these associations are promising, further longitudinal studies are necessary to establish causal relationships and elucidate the underlying mechanisms driving these interactions.

Obesity Factor in Paediatric OSAS

Unlike adult OSAS, where obesity is a well-established risk factor, the association between pediatric OSAS and obesity remains inconclusive. The interaction among OSAS, obesity, and oral microbial imbalances in young children is complex.

Comprehensive research examining the interplay between diet, microbiota composition, and OSAS is essential to better understand these relationships.

Future Directions and Unsolved Questions

Despite significant advancements in understanding pediatric OSAS, many questions remain unresolved. Prospective studies are needed to determine whether the observed differences in oral microbiota are causative or merely correlative. Additionally, exploring how microbial imbalances interact with factors such as malnutrition and systemic health is crucial for developing a more holistic approach to managing OSAS in children.

Transmission and Evolution of Oral Microbes

The transmission of microbes to infants occurs through direct contact with caregivers during feeding or from environmental exposure. Within days of birth, an infant's oral microbiome closely resembles that of the mother, influenced by breastfeeding and close physical contact.[44] Horizontal transmission from peers and caregivers further shapes the developing microbiome during early childhood. By the age of three, microbial communities diversify significantly, reflecting dietary transitions and interactions with broader environmental factors.[45] This diversification facilitates the formation of specific niches within the oral cavity, such as the tongue, teeth, and mucosa, each supporting distinct bacterial populations.

Oral Microbiota as Indicators of Health and Disease

Predictive Potential

The structure of the oral microbiome offers valuable insights into a child's overall health status.Specific bacterial species have been linked to a higher risk of conditions such as ECC and systemic diseases. Regular monitoring of the oral microbiome could enable the early detection of these conditions, potentially before their clinical onset.

Oral-Systemic Dysbiosis

Imbalances in the oral microbiome aren't limited to local illnesses; they can also flag systemic health issues[47]. This includes specific bacteria in the oral cavity, leading to obesity in infants. Certain microbial signatures have now been linked to diseases as diverse as Crohn's disease.

CONCLUSIONS

The development of the oral microbiome is a dynamic process influenced by genetic, environmental, and lifestyle factors. From birth, microbial communities in the oral cavity undergo significant changes driven by feeding practices, anatomical development, and interactions with caregivers. A deeper understanding of these processes may enable the identification of strategies to optimize oral health and prevent disease. Future research should aim to harness insights from the oral microbiome to develop innovative diagnostic tools and therapeutic interventions.

This review explores key findings on the relationship between oral and gut bacteria. Evidence suggests that bacterial dysbiosis correlates with the presence of bacterial pathogens and is linked to neuroinflammatory features in the gut microbiota. However, the precise mechanisms underlying this association remain unclear. Notably, a bidirectional relationship has been proposed between intestinal dysbiosis and the accumulation of beta-amyloid in the brain.[48]

A significant concern is the role of the oral microbiome in disease prevention and its potential contribution to systemic pathologies. Pathogenic

bacteria such as *Porphyromonas gingivalis* have been shown to transport amyloid peptide plaques from peripheral sites to the liver.[49] In the liver, macrophages can facilitate the movement of β-amyloid to the brain, triggering neuroinflammation and accelerating pathological progression. Particularly notable are specific microbiota and their metabolites, which play a key role in the pathogenesis of disorders linked to the microbiota-gut-brain axis. Prolonged exposure to these interactions promotes a pro-inflammatory state, exacerbating cognitive decline during subsequent episodes.[50]

Limiting Factors

The mouth serves as the gateway to the gut, and while its microbial ecology is not inherently a risk factor for disease, it represents an important diagnostic feature. Recent advancements in salivary biomarker diagnostics and oral microbiome analysis have facilitated the identification of bacterial pathogens linked to various conditions, including dental caries, periodontal disease, autoimmune disorders, diabetes, and malignancies.[51] Although much emphasis has been placed on the relationship between the gut microbiome and health, oral microbes offer unique advantages for diagnostics. The non-invasive collection of oral samples makes them particularly suitable for diagnostic testing, especially in vulnerable populations such as infants and children. Buccal samples, therefore, hold significant promise as a valuable diagnostic tool.

While the detection of the aforementioned pathogens is promising, several obstacles hinder a comprehensive understanding of the oral microbiome and its pathogens in children. Much of the existing evidence is derived from cross-sectional or case-control studies with small sample sizes, limiting the ability to establish correlations between oral bacterial communities and diesase severity. Most available case-control and retrospective studies have primarily focused on *Streptococcus mutans* and ECC. However, research examining the oral microbiome of children with systemic diseases, such as autism, irritable bowel syndrome (IBS), and celiac disease (CD), has been unable to establish a definitive relationship between dental caries and these conditions due to study design limitations.[52] Consequently, it remains unclear whether changes in the oral microbial community can predict the onset of systemic diseases or indicate future disease development.

Members of the microbiome, including bacteria and viruses, play critical roles in oral health and disease. Future research should prioritize examining interactions between different microbial species to gain a more comprehensive understanding. Current pediatric microbiome studies have primarily relied on 16S rRNA amplicon sequencing, which limits analysis to taxonomic diversity and composition. To advance the field, studies should focus on the metabolic activities of the microbiota that drive host-microbiota interactions within the oral environment. This approach could elucidate the molecular basis of these interactions and identify metabolic or pathogenic mechanisms as potential therapeutic targets.

Studies of the oral microbiota in healthy individuals have revealed differences across various groups, highlighting regional, ethnic, and racial diversity. However, the influence of racial diversity on the development of the oral microbiota in term infants remains underexplored. Additionally, the interactions between the oral microbiota, colonization of other body sites, immunity, and early health are complex, characterized by bidirectional and nonlinear relationships. This complexity poses challenges to fully understanding and critically evaluating these interactions.[53]

Future Trends

There is a pressing need for further research on disease-specific microbial biomarkers and their integration into sensitive, targeted, and cost-effective diagnostic and prevention programs. Such efforts could harness the potential of the oral microbiota to enhance human health outcomes. In children, the oral microbiota complements the human genome, proteome, transcriptome, and metabolome, positioning it as a critical component of precision and personalized medicine in the future.[54]

Advancements in microbiome research are expected to transform the understanding of oral health and its connections to systemic diseases, paving the way for innovative diagnostic and therapeutic strategies.

Non-invasive diagnostic tools leveraging oral microbial data have the potential to enable early identification of conditions such as autism spectrum disorder (ASD) and inflammatory bowel disease (IBD). Early detection could significantly reduce the burden of these diseases through timely interventions. Longitudinal studies are essential to fully realize the potential of the oral microbiome as a biomarker for health.[55]

Future personalized strategies for managing the oral microbiome may include the use of probiotics or diet-specific modifications, offering promising avenues to prevent both oral and systemic diseases.[56]

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