Eduvest – Journal of Universal Studies
Volume 5 Number 5, May, 2025
p- ISSN 2775-3735-e-ISSN 2775-3727

Interaction of Oral Microbiota and Type 1 Diabetes Mellitus in Children: A Narrative Review

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ABSTRACT

Type 1 diabetes mellitus (T1DM) is a chronic autoimmune disease that frequently affects children, disrupting insulin production and triggering systemic inflammation. Recent studies have indicated that T1DM also influences the balance of the oral microbiota, potentially leading to oral dysbiosis and worsening glycemic control. This narrative review aims to explore the reciprocal relationship between oral microbiota and T1DM in children, focusing on microbiota composition, immune response, and the potential of microbiota-targeted therapies. Using a qualitative synthesis of peer-reviewed literature, this study analyzes patterns of microbiota shifts and their correlation with metabolic parameters and immune markers. The findings reveal that children with T1DM show increased levels of pathogenic oral bacteria such as Streptococcus mutans, P. gingivalis, and Veillonella spp., contributing to periodontal disease, caries, and systemic inflammation. Moreover, chronic hyperglycemia alters salivary composition and mucosal immunity, further promoting microbial imbalance. These changes are linked to immune dysregulation and the acceleration of autoimmunity through the gut–oral axis. The review highlights the need for integrated T1DM management strategies that include oral health monitoring and probiotic-based interventions. Such an approach could help mitigate disease progression and improve the quality of life for children with T1DM.

KEYWORDS *DM T1,microbiota,oral,disbiosis*

Article Info:
Submitted: 05-05-2025 Final Revised: 14-05-2025 Accepted: 19-05-2025 Published: 22-05-2025

INTRODUCTION

Type 1 diabetes mellitus (DM T1) is a chronic autoimmune disease that is usually diagnosed in children and adolescents. The disease is characterized by damage to cells β pancreas, which leads to an absolute lack of insulin and contributes to metabolic disorders as well as an imbalance of the immune system. In recent years, the incidence rate among children has continued to increase globally, including in Indonesia. In 2022, Indonesia recorded the highest number of cases in Southeast Asia, with 41. 817 sufferers, of which 13. 311 of them are under 20 years old (International Diabetes Federation, 2022; Pulungan et al., 2021). In addition to affecting glycemic control, DM T1 also has an impact on the balance of the immune system, increases the risk of vascular complications, and can trigger changes in the body's microbiota, including those found in the oral cavity.

The oral cavity is a dynamic ecosystem, inhabited by a variety of microorganisms, such as bacteria, viruses, and fungi, which are collectively known as the oral microbiota. This microbiota has a very important role in maintaining the environmental balance in the mouth as well as supporting overall systemic health. However, in individuals with T1 DM, there is a change in the composition of the oral microbiota called dysbiosis. This condition can increase the risk of periodontal disease and dental caries. Research shows that children with DM T1 have a high prevalence rate of pathogenic bacteria, such as Streptococcus mutans (S. mutans), Lactobacillus spp., and Veillonella spp., which contribute to the formation of dental caries. In addition, harmful bacterial complexes, including P. gingivalis, Tannerella forsythia, and Treponema denticola, are more commonly found in patients who have poor glycemic control, which is characterized by high HbA1c levels and lack of time in a healthy glucose range (Carelli et al., 2023; Pachoński & others, 2021). The presence of these microorganisms not only affects oral health, but is also closely related to disorders of the immune system as well as the body's metabolism. Thus, a reciprocal relationship is formed between the oral microbiota and glycemic control (Ranbhise et al., 2025).

Therefore, it is important to understand the relationship between oral microbiota and DM T1 in an effort to improve the quality of life of sufferers. This article aims to review the current literature on the interaction between oral microbiota and T1 DM in children, especially regarding changes in the composition of the microbiota, its impact on oral and systemic health, and the possibility of microbiota-based therapeutic interventions in the management of T1 DM. A deeper understanding of these relationships can be the basis for more effective prevention and management strategies, thereby improving the quality of life of children living with T1 DM.

Type 1 diabetes mellitus (T1DM) is a chronic autoimmune disease that frequently affects children and adolescents, disrupting insulin production and inducing systemic inflammation. One underexplored consequence of T1DM is its impact on the oral microbiota—a complex microbial community essential for maintaining oral and systemic health. Emerging evidence indicates that children with T1DM experience oral dysbiosis, contributing to periodontal disease and poor glycemic control. Despite these findings, the reciprocal relationship between oral microbiota and T1DM progression remains poorly understood, especially in pediatric populations.

The growing prevalence of T1DM among children globally, including a surge in Southeast Asia and Indonesia, underscores the urgent need to understand all factors that influence disease progression. Oral health complications—such as gingivitis, periodontitis, and xerostomia—are common in children with T1DM and significantly

reduce their quality of life. Chronic hyperglycemia alters saliva composition and immune defense mechanisms, creating favorable conditions for pathogenic bacteria. These complications are not only local but have systemic implications, influencing glycemic control and autoimmune processes.

Moreover, the oral cavity is not an isolated ecosystem. Dysbiosis here may contribute to gut microbiota imbalance and systemic inflammation via the gut–oral axis and mucosal immune crosstalk. In children with an already dysregulated immune system, this connection can accelerate the progression of autoimmune diseases, including T1DM. Understanding this dynamic interplay is vital to developing comprehensive care strategies that include both metabolic and microbiological management.

Carelli et al. (2023) and Moskovitz et al. (2021) demonstrated that children with poorly controlled T1DM harbor higher levels of Streptococcus mutans, P. gingivalis, and Veillonella spp., all of which are associated with increased risk of caries and periodontal disease. Their work underscores the correlation between poor glycemic control and the abundance of pathogenic oral bacteria.

Kunath et al. (2022) employed a multi-omic approach to reveal significant changes in oral microbiota diversity among children with T1DM, including correlations with gut dysbiosis and systemic inflammatory markers. Similarly, Wang et al. (2024) showed that the presence of specific oral pathogens is linked to HbA1c levels and C-peptide concentrations, reinforcing the clinical relevance of microbiota profiles in T1DM management.

Negrini et al. (2021) and Irie et al. (2023) explored the immunological consequences of oral dysbiosis, showing that increased levels of cytokines like IL-6, IL-17A, and TNF-α contribute to local and systemic inflammation. Their findings support the notion that oral microbiota disturbances in children with T1DM may not only be a consequence but also a contributor to immune dysfunction and metabolic instability.

While numerous studies from developed countries have explored the link between oral microbiota and T1DM, there is limited research focusing on pediatric populations in developing regions like Indonesia. Few studies integrate microbiological data with immunological and metabolic parameters to fully elucidate the bidirectional impact of oral dysbiosis and T1DM progression. Furthermore, the role of environmental, dietary, and cultural factors in shaping this interaction remains understudied, leaving a significant gap in localized, holistic understanding and clinical application.

This narrative review is among the first to consolidate evidence on the interaction between oral microbiota and T1DM in children, with a specific focus on immune pathways and microbiota-host crosstalk. It highlights not only how dysbiosis affects oral and systemic health, but also how the microbiota may serve as both a biomarker and a therapeutic target. The review also proposes microbiota-based interventions—such as probiotics and prebiotics—as adjunctive strategies in T1DM management, opening novel avenues for integrative pediatric care.

The objective of this study is to explore the dynamic relationship between oral microbiota composition and the pathophysiology of type 1 diabetes mellitus in children. It seeks to examine how hyperglycemia-induced dysbiosis affects oral and systemic health, to evaluate the role of inflammatory pathways, and to identify the potential of microbiota-targeted therapies as part of holistic diabetes management strategies.

This study provides valuable insights for pediatricians, dentists, and endocrinologists by emphasizing the critical role of oral microbiota in managing T1DM in children. It encourages the integration of routine oral health assessments into diabetes

care protocols and supports the development of microbiota-modulating therapies. Ultimately, this approach aims to improve both oral and metabolic outcomes, reducing the burden of complications and enhancing the overall quality of life in children with T1DM.

RESEARCH METHOD

This study uses a narrative review design to analyze the current literature on the interaction between oral microbiota and type 1 diabetes mellitus (DM T1) in children. Data were collected from a variety of relevant articles and studies, with a focus on research that addressed changes in the composition of the oral microbiota as well as their impact on the systemic health of children with T1 DM. The inclusion criteria include studies published in peer-reviewed journals, which are relevant to the research theme. Data analysis was carried out qualitatively to identify patterns and relationships between oral microbiota dysbiosis and glycemic control, as well as to pay attention to articles showing the association between pathogenic microbes and oral and systemic complications. The results of the analysis are discussed to understand the clinical implications of these interactions, as well as to explore the potential of microbiota-based therapeutic interventions. This research aims to provide important insights into the importance of maintaining the balance of the oral microbiota in the management of T1 DM in children, as well as to encourage suggestions for further research in this area.

RESULTS AND DISCUSSION

Basic Concepts of Oral Microbiota

Composition of Oral Microbiota in Homeostasis Conditions in Healthy Children

The oral cavity is one of the most complex and dynamic microbiological habitats in the human body, inhabited by more than 700 species of microorganisms, including bacteria, fungi, viruses, and archaea. In healthy children, the oral microbiota forms a balanced community (homeostasis), which plays a role in maintaining oral and systemic health (Zaura & others, 2009).

The dynamics of the oral microbiota in healthy children are influenced by physiological factors such as tooth eruption, dietary changes and external factors such as childbirth type, breast milk, antibiotics, oral hygiene, diet). Research shows the dominance of the genus Streptococcus (S. mitis, S. sanguinis, S. salivarius) which plays a role in the formation of early biofilms and inhibits pathogens through nutrient competition and antimicrobial production. The genus Veillonella that ferments lactic acid, as well as Actinomyces, Rothia, Neisseria, and Granulicatella are commensal microbes that maintain the stability of pH and the structure of oral biofilms (Kageyama et al., 2024).

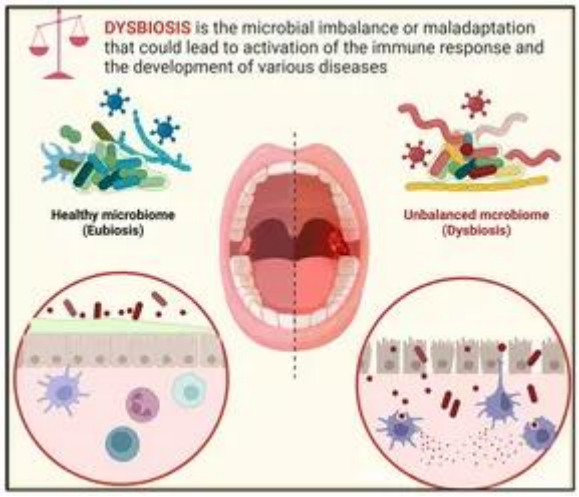
Under conditions of homeostasis, the oral microbiota not only acts as a protective barrier against pathogens, but also plays a role in the regulation of the mucosal immune system, supporting immune tolerance, and maintaining the integrity of oral epithelial tissue. The stability of these microbial communities is determined not only by the presence of a particular species, but also by the proportions and ecological interactions between microbes, which maintain the overall balance of the community (Liu et al., 2022).

The development of next-generation sequencing (NGS) technology has allowed for more detailed mapping of children's oral microbiota, including compositional variations based on geographical, socioeconomic, and genetic factors (Premaraj et al., 2020). These advances provide new insights into understanding the balance of the oral microbiota as well as the factors that can affect it.

One of the main factors that can alter the composition of the oral microbiota is long-term exposure to proinflammatory conditions such as a high-sugar diet or systemic stress, which can lead to changes in the composition of the oral microbiota even before the onset of clinical symptoms of oral disease. In children with systemic predispositions such as DM T1, this condition can accelerate the occurrence of dysbiosis, potentially contributing to systemic inflammatory disorders (Luppi et al., 2024). Thus, understanding the dynamics of the oral microbiota in healthy children is an important foundation for assessing changes that occur in the context of systemic diseases, including type 1 diabetes mellitus (Kunath, Hickl, Queirós, Martin-Gallausiaux, et al., 2022).

The role of the microbiota in maintaining oral and systemic health

The oral microbiota plays an important role in maintaining the balance of the oral cavity and systemic health, especially when the child's immune system is still developing. In addition to maintaining mucosal integrity, this microbiota prevents pathogen colonization through nutrient and spatial competition, as well as producing antimicrobial metabolites as natural protection. More so, the oral microbiota contributes to the development of the mucosal immune system by stimulating immune tolerance and activating non-inflammatory responses, which are important in preventing autoimmune diseases and chronic inflammation. Recent research suggests that oral dysbiosis in children, even in the subclinical stage, can trigger local inflammation that impacts mucosal permeability, thus allowing the translocation of microbes or their products into the systemic circulation. This process has the potential to increase the risk of systemic immunological disorders, including DM T1, which in children often exhibit clinical manifestations along with changes in the commensal microbial community (Liu et al., 2022).



Graphic abstract. A disturbance of the balance between microbes and the immune system that plays a role in systemic homeostasis and its influence on oral and systemic diseases (Liu et al., 2022).

Children's oral microbiota is not only involved in maintaining local balance, but also interacts closely with the microbiota–immune–endocrine axis, which links oral conditions to the body's overall metabolic status (Prince et al., 2023). Therefore, understanding and maintaining the balance of the oral microbiota from an early age is key in the prevention of inflammation-based systemic health disorders in pediatric populations.

Type 1 DM in Children

Pathophysiology and Immunology

Type 1 diabetes mellitus is a chronic autoimmune disease characterized by the destruction of cells β pancreas by the immune system, leading to absolute insulin deficiency. This immune activation triggers a cascade of local and systemic inflammation, which is characterized by an increase in pro-inflammatory cytokines such as IL-1β, IFN-γ, and TNF-α (Li et al., 2021). Children with genetic predispositions, especially the HLA-DR3/DR4 allele, show a higher susceptibility to the initiation of this autoimmunity from an early age, even before clinical symptoms appear. The course of the disease often involves a long period of autoimmune prediabetes, with the positivity of autoantibodies such as IAA, GADA, and ZnT8A, reflecting chronic immune system activation. Along with continued inflammation, metabolic dysregulation occurs due to loss of glucose control, which exacerbates oxidative stress and adds to the systemic inflammatory burden (Pollanen et al., 2022). Chronic inflammatory processes in the pancreas also impact other body systems, including the mucosal microbiota, with far-reaching implications for systemic health and immune–microbiota interactions. In addition to the involvement of the immune system, environmental factors such as viral infections, microbiota dysbiosis, and early life nutrition are believed to play an important role in triggering or accelerating autoimmune processes in vulnerable children. Mucosal microbiota that undergoes dysbiosis can affect mucosal immune regulation, alter immune cell communication, and accelerate the course of the disease towards DM T1 (Dawson et al., 2025).

An Overview of Environmental and Genetic Factors Affecting

Type 1 diabetes mellitus in children is a complex disease that is influenced by the interaction between genetic predisposition and environmental factors. Genetically speaking, certain alleles of the human leukocyte antigen (HLA) complex, specifically HLA-DR3-DQ2 and HLA-DR4-DQ8, have long been known to be major risk factors that increase susceptibility to autoimmunity to pancreatic β cells. However, recent research has also shown the contribution of non-HLA variants, such as INS, PTPN22, and IL2RA, which play a role in the regulation of immune tolerance and T cell activation (Michalek et al., 2024). However, genetic predisposition alone is not enough to trigger the onset of the disease; Environmental factors have a key role in initiating autoimmune processes, especially in children who are genetically susceptible.

Key environmental factors that have been linked to an increased risk of DM T1 include viral infections, especially enteroviruses such as Coxsackie B, early exposure to antibiotics, as well as infant diets, such as early feeding of cow's milk-based formula. In addition, disruptions of the intestinal and oral microbiota are also one of the triggers for increased mucosal permeability, which can trigger an abnormal immune response. Unbalanced colonization of the gut microbiota in the early years of life is associated with excessive activation of the immune system, which can accelerate the progression of autoimmunity to pancreatic β cells (Knip & Hyöty, 2023).

On the other hand, exposure to environmental chemicals, such as pesticides and endocrine disruptor compounds, is also being investigated for their ability to affect the immune system and metabolism in the long term. The combination of infectious factors, nutrition, and microbiota can accelerate autoantibody seroconversion and progression to DM T1, especially in children with high-risk genetic profiles (TEDDY Study Group, 2018).

How Does Type 1 DM Affect the Oral Microbiota?

Effect of hyperglycemia on pH, saliva, local immunity of the oral cavity

Chronic hyperglycemia in children with DM T1 significantly alters the oral environment, triggers changes in the microbiota and increases the risk of oral cavity disease. This condition causes a decrease in the rate of saliva flow as well as levels of IgA, lysozyme, and lactoferrin as a local immune defense, while salivary glucose levels increase, providing nutrients for pathogens such as Candida albicans and S. mutans (Babu et al., 2014). A decrease in saliva pH due to the metabolism of microbes that utilize glucose accelerates enamel demineralization and increases the risk of caries and gingivitis. The condition is exacerbated by local immune dysregulation with an increased but inefficient inflammatory response (Rath, 2024). Children with DM T1 show increased proinflammatory cytokines (IL-6, IL-1β, TNF-α) in saliva and gingiva, which can lead to chronic soft tissue inflammation (Keles et al., 2020). Hyperglycemia creates an immunologically and biochemically dysfunctional oral environment, which supports oral dysbiosis and worsens oral complications in children with type 1 DM.

Changes in Oral Microbiota Profile in Children with Type 1 DM

Chronic hyperglycemia in children with T1 DM causes significant changes in the oral microbiota ecosystem, which is characterized by dysbiosis and an increase in pathogenic bacteria. Studies show that children with type 1 DM have an increased prevalence of periodontopathogenic bacteria, such as P. gingivalis, Aggregatibacter actinomycetemcomitans, and P. intermedia. These bacteria contribute to chronic inflammation of gingival tissue, through the activation of lipopolysaccharides-mediated immune responses (LPS) and interactions with TLR-4 receptors, which can lead to periodontal tissue damage as well as increase the risk of periodontitis (Carelli et al., 2023). In addition, hyperglycemia increases glucose levels in saliva, creating an environment conducive to the growth of acidogenic bacteria, such as S. mutans, Lactobacillus spp., and Actinomyces spp.. These bacteria ferment glucose into acid, lowering the pH of saliva, and accelerating enamel demineralization, thereby increasing the risk of dental caries. Research has also shown that children with poor glycemic control have significant increases in the amount of S. mutans and Veillonella spp., which correlates with glycemic parameters such as HbA1c (Carelli et al., 2023). In another study, there was a decrease in the abundance of Prevotella and Veillonella in children with DM T1, especially in the acute phase of the disease. This decline may reflect a more complex microbiota imbalance, where opportunistic bacteria such as Streptococcus, Granulicatella, Rothia, and Rhodococcus become more dominant. These changes suggest that oral dysbiosis in DM T1 involves not only an increase in pathogenic bacteria, but also a decrease in commensal bacteria that are essential for maintaining oral homeostasis (Moskovitz et al., 2021). Changes in the oral microbiota profile in children with T1 DM reflect a complex interaction between hyperglycemia, immune response, and microbial environment. This dysbiosis not only increases the risk of periodontal disease and caries, but it can also

contribute to systemic inflammation that worsens glycemic control. Therefore, good oral health monitoring and management is essential in the care of children with T1 DM.

Study Data Showing Oral Dysbiosis in Children with Type 1 DM

The oral microbiota of children with DM T1 showed significant changes compared to healthy children. The study by Wang et al. (2024) found the dominance of Streptococcus, Prevotella, Leptotrichia, and Neisseria in the oropharynx, with a positive correlation of Staphylococcus oropharynx and intestinal Ruminococcus_torques_group, as well as the relationship of microbiota variation with HbA1c and C-peptides. A study by Carelli et al. (2023) in 89 children and adolescents with DM T1 found a high prevalence of karyogenic and periodontopathogenic bacteria (Actinomyces spp., Aggregatibacter actinomycetemcomitans, P. intermedia, Lactobacillus spp.), with S. mutans found in 49.4% of samples, mainly with poor glycemic control, as well as an increase in Veillonella spp. which contributes to a decrease in salivary pH and the risk of caries. The research of Kunath et al. (2022) using a multi-omic approach showed oral microbiota dysbiosis in DM T1, characterized by the dominance of certain Streptococcus species and a decrease in microbial diversity, which correlates with intestinal dysbiosis and may affect systemic glucose regulation. Although specific data from Indonesia are still limited, a study by Theodorea et al. (2022) in East Nusa Tenggara examined Veillonella species in dental biofilms of children aged 6–7 years. This study makes an important contribution to the initial understanding of the variation in the oral microbiota of Indonesian children, especially the genus Veillonella, and opens up opportunities for further research on the relationship between nutritional status, oral microbial composition, and its implications for systemic health and disease development.

Does the Oral Microbiota Contribute to the DMT1 Journey?

Recent research shows that the oral microbiota contributes to the course of disease (DM T1) in children through the gut-oral axis mechanism and the cross-interaction of the mucosal immune system (Mucosal immunity cross-talk) and the oral microbiota as a trigger for systemic inflammation or immunity regulators.

Gut-oral axis and cross-interaction of the mucosal immune system

The migration of pathogenic microorganisms from the oral cavity, such as P. gingivalis, to the digestive tract can lead to dysbiosis of the gut microbiota, which contributes to systemic inflammation and insulin resistance. These changes in the gut microbiota trigger an immunological imbalance, which plays a role in the development of DMT1. Animal studies show that oral administration of P. gingivalis alters the composition of the gut microbiota, increases serum endotoxin levels, and triggers chronic inflammation and insulin resistance (Blasco-Baque et al., 2016).

In addition to its impact on the gut microbiota, changes in the oral microbiota also contribute to the regulation of the mucosal immune system. Oral microbiota dysbiosis can affect the mucosal immune system, especially through increased expression of pro-inflammatory cytokines such as IL-17A. Increased expression of IL-17A contributes to local and systemic inflammation, which ultimately worsens glycemic control in children with DM1 (Irie et al., 2023).

In children with DM T1, there is a change in the composition of the oral microbiota, which is characterized by an increase in opportunistic bacteria, such as Streptococcus, Granulicatella, and Rothia. This dysbiosis correlates with increased

HbA1c levels and leukocyte count, suggesting a link between an imbalance of the oral microbiota and systemic inflammation. In addition, pathogenic bacteria such as P. gingivalis can induce the production of pro-inflammatory cytokines, such as IL-6, TNF-α, and IL-8, through activation of the NF-κB and MMP-9 pathways. This process contributes to systemic inflammation and endothelial dysfunction, which can worsen metabolic conditions in DM1 patients (Kunath, Hickl, Queirós, Martin-Gallausiaux, et al., 2022).

In addition to playing a role in systemic inflammation, the oral microbiota also has an important function in modulating the mucosal immune system. The oral microbiota also plays a role in modulating the mucosal immune system. The interaction between oral microorganisms and the immune system can affect the balance between protective immune response and immune tolerance. Oral microbiota dysbiosis can disrupt this immunological balance, trigger chronic inflammation, and contribute to the development of autoimmune diseases, including DMT1. Studies have also shown that changes in the oral microbiota can affect the composition of the gut microbiota through the gut-oral mechanism of the axis, which further impacts systemic immune regulation and contributes to the pathogenesis of DM1 (Negrini et al., 2021).

Clinical Manifestations in the Oral Cavity in Children with Type 1 DM

Children with DM T1 often experience clinical manifestations in the oral cavity, reflecting metabolic and immunological changes resulting from chronic hyperglycemia. These impacts not only affect oral health, but can also worsen glycemic control and increase the risk of systemic complications. In line with the condition, children with DM T1 are more susceptible to gingivitis and periodontitis due to plaque accumulation exacerbated by chronic hyperglycemia. Persistent gingival inflammation can progress to periodontitis, which is characterized by loss of alveolar bone. Studies show that poor glycemic control correlates with increased severity of periodontal disease (Vlachou et al., 2024). In addition to periodontal problems, oral candidiasis often occurs as a result of immunosuppression and insulin use, which increases susceptibility to fungal infections. This condition is characterized by white lesions on the oral mucosa, which can cause discomfort as well as eating disorders (Villarreal et al., 2022).

In addition to fungal infections, decreased salivary flow or xerostomia are also often reported in children with DM T1, which can be caused by dehydration due to hyperglycemia and medication side effects. Xerostomia increases the risk of caries, fungal infections, and taste disorders, making oral conditions more susceptible to various complications (Villarreal et al., 2022).

Furthermore, research conducted by Kunath et al. (2022) revealed a characteristic change in the oral microbiota of individuals with DMT1. These changes are characterized by the dominance of certain Streptococcus species and the presence of a decrease in overall microbial diversity. Interestingly, this change in the composition of the oral microbiota also shows a correlation with the occurrence of dysbiosis in the gut microbiota, and potentially affects the mechanism of glucose regulation in the body systemically.

Clinical Implications and Therapeutic Potential

Understanding the role of the oral microbiota in autoimmune diseases opens up opportunities for therapeutic interventions, such as the use of probiotics, prebiotics, or fecal microbiota transplantation. This approach has the potential to restore the balance of

the oral microbiota as well as improve glycemic control in children with T1 DM. In addition, this strategy can also help reduce the risk of periodontal disease, gingivitis, candidiasis, and xerostomia, which often occur due to oral microbiota dysbiosis and immune dysregulation.

Thus, the oral microbiota plays an important role in modulating the autoimmune response in children with DM T1 through inflammatory mechanisms and interactions with the gut microbiota. Interventions with microbiota manipulation can be a potential strategy in the management of DM T1, especially in minimizing the impact of systemic inflammation and improving mucosal immune balance (Gregorczyk-Maga et al., 2023).

Research Gaps and Advanced Research Opportunities

Although recent research has shown a correlation between oral microbiota, immune response, and DMT1 progression, there are still research gaps that need to be explored further. Most studies still focus on populations in developed countries, while specific data from Indonesia and developing countries are still limited, especially related to variations in oral microbiota based on dietary patterns, environment, and nutritional status (Theodorea et al., 2022).

In addition, the specific immunological mechanisms linking oral dysbiosis to the autoimmune response of DM T1 still require further research. Further understanding of immune system activation and inflammatory pathways such as NF-κB, as well as the role of cytokines in worsening glycemic control, may clarify the impact of the oral microbiota on the progression of T1 DM (Irie et al., 2023).

Although microbiota-based therapeutic strategies, such as probiotics, prebiotics, and fecal microbiota transplantation, are promising as potential interventions in the management of T1 DM, long-term clinical studies are still urgently needed to evaluate their effectiveness in restoring the balance of the oral microbiota and improving glycemic control (Gregorczyk-Maga et al., 2023).

CONCLUSION

The reciprocal interaction between oral microbiota and T1 DM in children shows a complex relationship, in which chronic hyperglycemia creates an environment that supports oral microbiota dysbiosis, while these microbiota changes also affect the systemic immune response and worsen glycemic control, which ultimately accelerates the progression of autoimmunity. Changes in the composition of the oral microbiota in children with DM1 are characterized by an increase in pathogenic bacteria, such as Streptococcus, Prevotella, and Actinomyces, which contribute to periodontal disease, caries, and systemic inflammation. Along with that, the inflammatory response activated by oral dysbiosis not only impacts the local environment, but also interacts with the gut-oral microbiota through the gut-oral axis, thereby exacerbating immune and metabolic dysregulation, confirming that the oral microbiota plays a role in the systemic dynamics that influence the course of DMT1 disease.

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