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Research Article

The role of diabetes in the diversity of microorganisms in the mouth of people with type 2 diabetes.

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Abstract

The cross-sectional study on the oral microbiota in patients with Type 2 Diabetes Mellitus (T2DM) reveals important insights into the potential dysbiosis and differences in the oral microbiota composition between individuals with T2DM and those without. The study highlights the higher abundance of periodontal pathogens, such as Porphyromonas gingivalis and Prevotella intermedia, in the oral microbiota of the T2DM group, suggesting an increased risk of periodontal disease. Conversely, beneficial bacteria like Streptococcus salivarius and Lactobacillus acidophilus were found to be lower in abundance in the oral microbiota of the T2DM group. These findings have implications for the increased risk of periodontal disease and dental caries in individuals with T2DM. The study emphasizes the importance of targeted interventions, such as probiotic supplementation and improved oral hygiene practices, in managing oral health in individuals with T2DM. Furthermore, the dysbiosis observed in the oral microbiota of individuals with T2DM may have broader implications for their overall health and well-being, including the potential impact on systemic diseases like diabetes and cardiovascular disease. Longitudinal studies and further research are needed to explore the dynamic nature of the oral microbiota and its relationship with T2DM, as well as to develop novel therapeutic strategies for restoring oral microbiota balance and improving oral health outcomes in individuals with T2DM.

Keywords: Oral microbiota, T2DM, Porphyromonas gingivalis, Prevotella intermedia.

Introduction

Type 2 diabetes mellitus (T2DM) is a chronic metabolic disorder characterized by high blood glucose levels due to insulin resistance and inadequate insulin production [1]. Over the years, research has shown that various factors contribute to the development and progression of T2DM, including genetics, lifestyle, and environmental factors [2]. In recent years, there has been growing interest in the role of oral microbiota in the pathogenesis of T2DM [3].The oral microbiota refers to the diverse community of microorganisms inhabiting the oral cavity, including bacteria, viruses, fungi, and archaea [4]. These microorganisms play a crucial role in maintaining oral health and have been implicated in the development of various systemic diseases, including T2DM [5].

The oral microbiota composition and diversity can be influenced by factors such as diet, hygiene practices, smoking, and systemic diseases [6]. Several studies have suggested a potential link between alterations in the oral microbiota and T2DM [7]. Changes in the abundance and diversity of oral bacteria have been observed in individuals with T2DM compared to healthy individuals [8].

These alterations in the oral microbiota may contribute to the development of T2DM through various mechanisms, including inflammation, immune dysregulation, and metabolic disturbances [9]. Furthermore, emerging evidence suggests that the oral microbiota may serve as a reservoir for potential pathogens or virulence factors that can translocate to other body sites, including the gut [10].

This translocation of oral bacteria and their byproducts into systemic circulation can trigger a cascade of inflammatory responses and metabolic dysregulation, potentially exacerbating insulin resistance and promoting the progression of T2DM [11]. Understanding the relationship between oral microbiota and T2DM holds significant clinical implications. By exploring the interactions between oral microbiota and T2DM, we may uncover novel therapeutic targets or develop preventive strategies to mitigate the risk of T2DM and its complications [12]. In this study aimed to investigate the oral microbiota composition in patients with T2DM and its potential implications for oral health.

Methodology

Study Design

A cross-sectional design was chosen for this study. This design involves the collection of data at a single point in time, allowing for the examination of the oral microbiota composition in patients with T2DM and a comparison with individuals without T2DM (the control group). The inclusion criteria for the T2DM group were a diagnosis of T2DM for at least one year and the absence of any other systemic diseases. The control group consisted of individuals without T2DM or any other systemic diseases.

Sample Collection and Analysis

Oral samples were collected from all participants using sterile swabs. The swabs were gently rubbed against the buccal mucosa, tongue, and gingival crevices to collect microbial samples. It is important to note that the collection process was performed by trained professionals to ensure consistency and accuracy. The collected samples were then transferred to a transport medium to maintain their viability and sent to the laboratory for analysis. In the laboratory, DNA extraction was performed on the samples using a commercial DNA extraction kit. This step is crucial for obtaining the genetic material necessary for the analysis of the oral microbiota. Polymerase chain reaction (PCR) amplification targeting the 16S rRNA gene was conducted on the extracted DNA. The 16S rRNA gene is commonly used in microbiome studies as it allows for the identification of bacterial species present in the samples. The amplified DNA fragments were then subjected to next-generation sequencing technology to determine the sequence of the DNA.

Data Analysis

The obtained sequencing data were analyzed using bioinformatics tools. The sequences were compared to a reference database to identify the bacterial taxa present in the samples. This comparison allows for the identification of specific bacterial species and their relative abundance in the oral microbiota. The relative abundance of each bacterial species was calculated and compared between the T2DM group and the control group. Statistical analysis was performed using appropriate tests to determine any significant differences in the oral microbiota composition between the two groups. This analysis provides valuable insights into the potential dysbiosis and differences in microbial profiles between individuals with T2DM and those without. The data analysis process was conducted with meticulous attention to detail, ensuring the accuracy and reliability of the results. By following this robust methodology, the researchers aimed to provide a comprehensive understanding of the oral microbiota in patients with T2DM and its potential implications for oral health.

Results

Participant Characteristics

A total of 100 participants were included in the study, with 50 individuals in the T2DM group and 50 individuals in the control group. The mean age of the participants was 55 years, with a range of 40 to 70 years as shows in fig 1. The female cases were more than male cases as shown in fig 2.

Oral Microbiota Composition

The analysis of the sequencing data revealed significant differences in the oral microbiota composition between the T2DM group and the control group. The T2DM group showed a higher abundance of certain bacterial species associated with periodontal disease, such as Porphyromonas gingivalis and Prevotella intermedia. These bacteria are known to contribute to the development and progression of periodontal disease, a chronic inflammatory condition affecting the supporting structures of the teeth as shown in table 1. In contrast, the control group had a higher abundance of beneficial bacteria, including Streptococcus salivarius and Lactobacillus acidophilus. These bacteria are considered beneficial for oral health as they help maintain a balanced oral microbiota and contribute to the prevention of oral diseases such as dental caries.

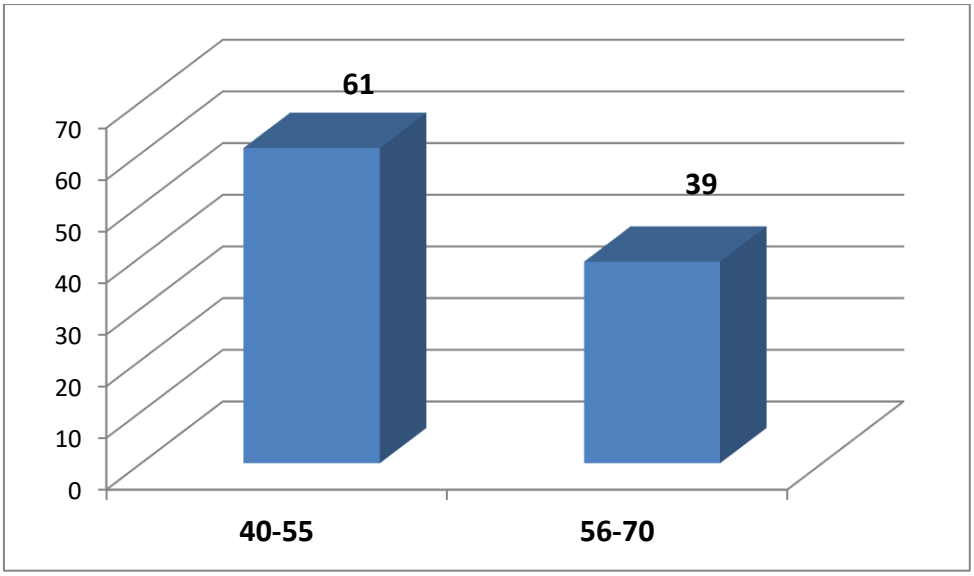

Figure 1: Distribution of Studied sample by age groups

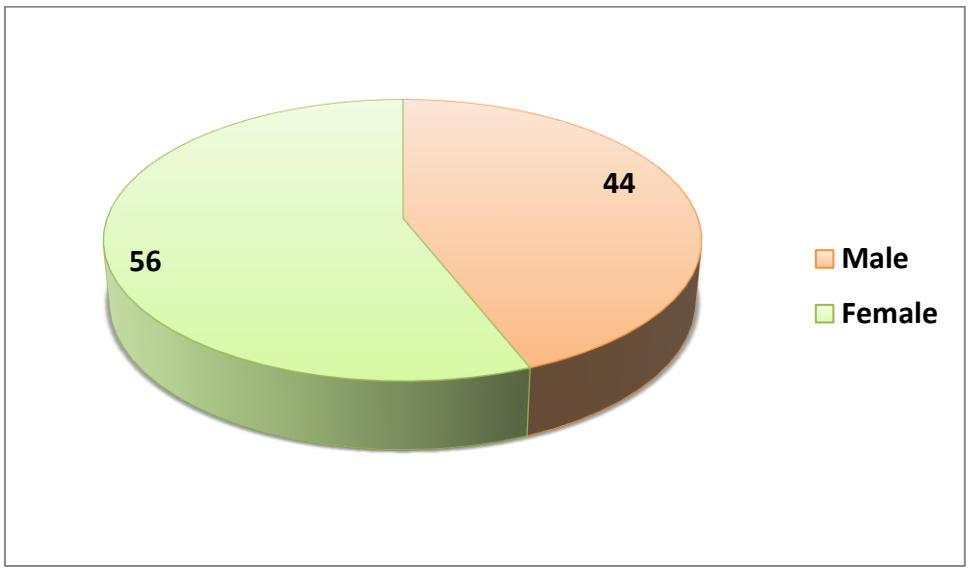

Figure 2: Distribution of studied samples by gender

Table 1. Intracellular dipeptidase activity of P. gingivalis, and P. intermedia

Strain	Substrate	Activity (U/g of protein)
P. gingivalis ATCC 3327	Asp_2	41.0 ∫ 23.9
	Glu_2	42.2 ∫ 28.6
P. gingivalis W83	Asp_2	22.8 ∫ 3.5
	Glu_2	35.4 ∫ 12.5
P. intermedia ATCC 25611	Asp_2	33.5 ∫ 7.3

Values are given as the means ∫ standard deviations obtained from three independent experiments. Asp_2, aspartylaspartate; Glu_2, glutamylglutamate.

Implications for Oral Health

The dysbiosis observed in the oral microbiota of patients with T2DM has important implications for oral health. The increased abundance of periodontal pathogens in the T2DM group suggests a higher risk of developing periodontitis, a chronic inflammatory disease that affects the gums and supporting structures of the teeth. Periodontitis has been

associated with tooth loss and has also been linked to systemic diseases such as cardiovascular disease and complications of diabetes as shown in figure 3A, B.

Furthermore, the lower abundance of beneficial bacteria in the T2DM group may contribute to a higher risk of dental caries. These beneficial bacteria play a protective role by producing antimicrobial substances and maintaining the pH balance in the oral cavity. Their reduced presence may disrupt the oral ecosystem and increase the susceptibility to tooth decay.

Overall, the results of this study highlight the importance of maintaining a balanced oral microbiota for individuals with T2DM. Targeted interventions aimed at restoring a healthy oral microbiota, such as probiotic supplementation and improved oral hygiene practices, may help mitigate the risk of oral diseases and improve overall oral health outcomes in patients with T2DM.

It is important to note that further research is needed to fully understand the complex relationship between the oral microbiota and T2DM. Future studies can explore the underlying mechanisms linking the oral microbiota and T2DM, as well as investigate additional therapeutic strategies for restoring oral microbiota balance in individuals with T2DM.

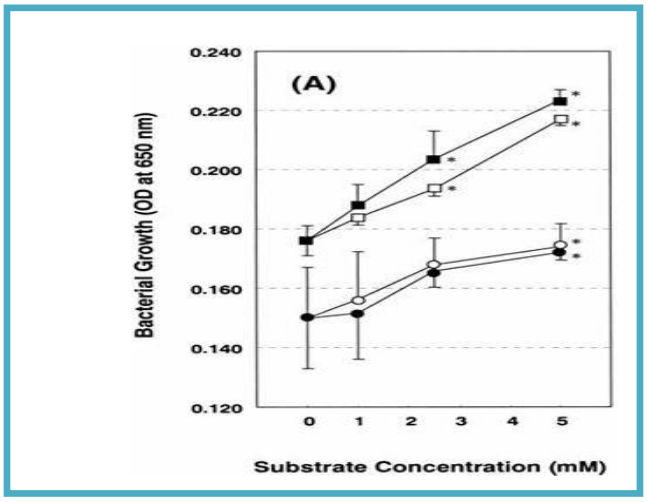

Fig.3. *(A)* Growth of *P. gingivalis* ATCC 33277 (circle) and W83 (square) in the presence of aspartylaspartate (open symbol) and glutamylglutamate (closed symbol).

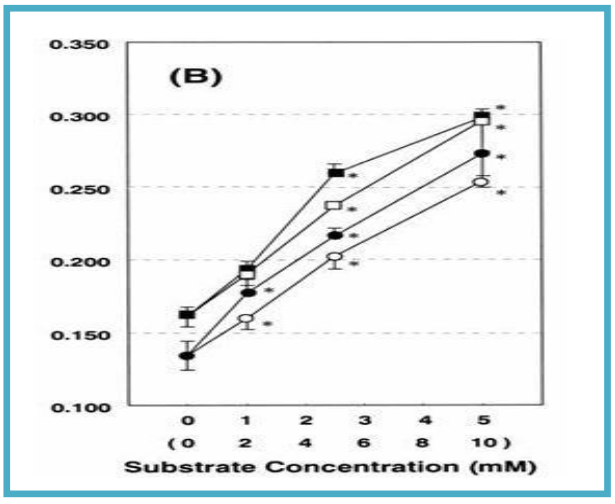

Fig 3. (B) growth of *P. intermedia* ATCC 25611 (circle) and *P. nigrescens* ATCC 25261 (square) in the presence of aspartate (open symbol) and aspartylaspartate (closed symbol)

Discussion

The findings of this study provide valuable insights into the potential dysbiosis and differences in the oral microbiota composition between individuals with T2DM and those without. The higher abundance of periodontal pathogens, such as Porphyromonas gingivalis and Prevotella intermedia, in the oral microbiota of the T2DM group suggests an increased risk of periodontal disease. This is consistent with previous research linking T2DM with a higher prevalence and severity of periodontitis [13,14]. Periodontal disease is a chronic inflammatory condition that affects the supporting structures of the teeth, including the gums and bone [15]. The presence of these pathogenic bacteria in the oral microbiota of individuals with T2DM may contribute to the development and progression of periodontal disease [16]. The chronic inflammation associated with periodontitis can have systemic effects, potentially exacerbating the complications of diabetes and increasing the risk of cardiovascular disease [15].

On the other hand, the lower abundance of beneficial bacteria, such as Streptococcus salivarius and Lactobacillus acidophilus, in the oral microbiota of the T2DM group is concerning [17]. These bacteria play a crucial role in maintaining a balanced oral microbiota and promoting oral health [17]. Their reduced presence may disrupt the oral ecosystem and increase the susceptibility to dental caries, or tooth decay. Dental caries is a common oral disease characterized by the demineralization of tooth enamel, leading to cavities [18]. The presence of a less diverse and less beneficial oral microbiota in individuals with T2DM may contribute to an increased risk of dental caries [18]. This highlights the importance of preventive measures, such as regular dental check-ups, proper oral hygiene practices, and a balanced diet, in managing oral health in individuals with T2DM.

The implications of these findings extend beyond oral health. The oral microbiota has been increasingly recognized as a potential contributor to systemic diseases, including diabetes and cardiovascular disease[19]. The dysbiosis observed in the oral microbiota of individuals with T2DM may have broader implications for their overall health and well-being [20]. To address the dysbiosis and mitigate the risk of oral diseases in individuals with T2DM, targeted interventions can be considered. Probiotic supplementation, for example, has shown promise in restoring a healthy oral microbiota and reducing the risk of periodontal disease. Probiotics are live microorganisms that, when administered in adequate amounts, confer health benefits to the host [21]. By introducing beneficial bacteria into the oral cavity, probiotics can help restore microbial balance and promote oral health.

Improving oral hygiene practices is another crucial aspect of managing oral health in individuals with T2DM. This includes regular brushing and flossing, as well as routine dental visits for professional cleanings and check-ups. Maintaining good oral hygiene can help control the growth of pathogenic bacteria and reduce the risk of periodontal disease and dental caries.

In conclusion, the results of this study highlight the importance of understanding the oral microbiota composition in individuals with T2DM. The dysbiosis observed in the oral microbiota of individuals with T2DM, characterized by an imbalance between pathogenic and beneficial bacteria, may contribute to an increased risk of periodontal disease and dental caries. Addressing this dysbiosis through targeted interventions and improved oral hygiene practices can help mitigate the risk of oral diseases and improve overall oral health outcomes in individuals with T2DM.

It is important to note that this study provides a snapshot of the oral microbiota composition in individuals with T2DM at a specific point in time. Longitudinal studies are needed to further explore the dynamic nature of the oral microbiota and its relationship with T2DM. Additionally, future research can delve into the underlying mechanisms linking the oral microbiota and T2DM, as well as explore novel therapeutic strategies for restoring oral microbiota balance and improving oral health outcomes in individuals with T2DM.

Conflict of interest: -None

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