

UNIVERSITI TEKNOLOGI MARA

**ORAL BACTERIOME ANALYSIS
USING METAGENOMIC
SEQUENCING IN ELDERLY
INDIVIDUALS WITH DIABETES
MELLITUS FOR THE PREDICTION
AND CONTROL OF DENTAL
CARIES**

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ABSTRACT

Background: Dental caries among the elderly is on the rise due to increased life expectancy and the trend of retaining natural teeth longer. The oral cavity harbours a diverse microbial community even in health, but systemic conditions such as diabetes mellitus (DM) can disrupt this balance, inducing dysbiosis and promoting dental caries. **Objectives:** To determine the prevalence of caries in elderly with DM and to identify the taxonomic distribution of the oral bacteriome in elderly diabetics using 16S metagenomic sequencing. **Methods:** In Phase I, cross-sectional study involving participants aged 60 years and older with DM was conducted at public health clinics in Kuala Lumpur and Selangor. Participants underwent assessments including a structured questionnaire and oral health screenings. Phase II involved collection of unstimulated saliva samples from participants to characterise the oral bacteriome through 16S rRNA gene amplication and next-generation sequencing. **Results:** A total of 111 participants were recruited in Phase I. Participants with poorly-controlled DM had a higher mean DMFT score of 16.51 compared to those with well-controlled DM, with a mean score of 13.19 ($p=0.007$). In Phase II, saliva samples were collected from 40 patients from the previous phase. Alpha diversity did not reveal any significant differences in bacterial richness or diversity among the groups ($p>0.05$). Similarly, the beta diversity analysis revealed no significant differences in the composition of microbial communities across the groups ($p>0.05$). Distinct microbial patterns were observed where *Streptococcus*, *Veillonella*, *Prevotella_7*, and *Corynebacterium* were enriched among elderly with poorly controlled DM and having active caries. In contrast, *Bulleidia*, *Peptococcus*, and health-associated taxa such as *Kocuria* and *Gemellibacter* predominated in well-controlled DM caries-free subjects, suggesting systemic glycaemic regulation promotes a balanced, commensal-rich oral microbiome. **Conclusion:** Caries prevalence was notably higher in the elderly with poorly controlled DM. This study offers valuable insight into the taxonomic composition of the oral bacteriome in elderly individuals with diabetes mellitus and caries, laying the groundwork for future development of targeted preventive and therapeutic strategies.

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CHAPTER 1

INTRODUCTION

1.1 Research Background

With the global trend of ageing populations, Malaysia is projected to become an ageing nation by 2030, with individuals aged 60 years and above constituting 15% of the total population. The increased life expectancy and the retention of natural teeth among the elderly have led to a surge in dental caries prevalence. Studies revealed that 95.4% of Malaysian older adults aged 60 and above suffer from dental caries, highlighting a critical public health challenge. Simultaneously, diabetes mellitus (DM) remains a pressing health issue in Malaysia, with the prevalence steadily rising over the decades. DM is associated with significant systemic and oral health complications, including periodontal disease, changes in salivary composition, and an increased risk of dental caries. However, the specific relationship between DM and dental caries, particularly in the elderly, remains underexplored.

Dental caries, a polymicrobial disease, is influenced by the delicate balance between eubiosis and dysbiosis of the oral microbiome. Recent advancements in genomic techniques, particularly next-generation sequencing (NGS), have enabled a deeper understanding of the microbial composition of the oral cavity and its role in health and disease. Saliva, as a reservoir of oral microbiota, offers a non-invasive means to study these microbial communities. Previous research has predominantly focused on children and adults, with limited studies examining the oral microbiome in specifically elderly diabetic individuals. Existing studies often exclude subjects with active dental caries, leaving a significant gap in understanding the interplay between DM, oral microbiota, and caries development.

Elderly individuals with DM are at a higher risk of microbial dysbiosis due to compromised immunity and changes in the oral microenvironment, such as altered salivary glucose levels and reduced salivary flow. These changes create favourable conditions for the proliferation of cariogenic bacteria, including *Streptococcus mutans* and *Lactobacillus* species. Emerging evidence suggests that the diversity and abundance of certain bacterial taxa, such as *Aggregatibacter*, *Neisseria*, and *Veillonella*, are higher in diabetics than in non-diabetics. These findings underscore the need for