

Oral bacterial microbiome in association with potential prediabetes using different criteria of diagnosis

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Objective: This study aimed to find a potential biomarker that can be used to diagnose prediabetic condition by comparing the salivary bacterial microbiomes between Thai dental patients with normoglycemia (NG) and those with potential prediabetes (PPG) conditions.

Method: Thirty-three subjects were randomly recruited. Demographic data were collected along with oral examination and unstimulated salivary collections. The salivary bacterial microbiomes were identified by high-throughput sequencing on the V3–V4 region of the bacterial 16S rRNA gene. Microbiomes in this study were composed of 12 phyla, 19 classes, 29 orders, 56 families, 81 genera, and 184 species. To check the validity of the selection criterion for prediabetes, we adopted two separate criteria to divide samples into PPG and NG groups using glycated hemoglobin A1c (HbA1c) or fasting plasma glucose (FPG) levels.

Results: Using the HbA1c level resulted in the significant reduction of *Alloprevotella*, *Neisseria*, *Rothia*, and *Streptococcus* abundances in PPG compared with those in NG (p -value < 0.05). On the other hand, the abundance of *Absconditabacteriales* was significantly reduced whereas *Leptotrichia*, *Stomatobaculum*, and *Ruminococcaceae* increased in the PPG group when the samples were classified by the FPG level (p -value < 0.05). It is implied that the group classifying criterion should be carefully concerned when investigating relative abundances between groups. However, regardless of the criteria, ***Rothia* is significantly dominant in the NG groups, suggesting that *Rothia* might be a potential prediabetic biomarker.**

Limitation: Due to the small sample size of this study, further investigation with a larger sample size is necessary to ensure that *Rothia* can be a potential biomarker for prediabetes in Thai people.