

Molecular Identification of Streptococcus Mutans from Patients with Dental Caries using PCR and Gene Sequencing

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Dental caries is the most prevalent oral disease in the world. Even in Sri Lanka, its prevalence is considerably high with a huge negative impact on our society and economy. *Streptococcus mutans* is the major bacterial etiological agent of dental caries. Precise identification of *S. mutans* from saliva or dental biofilms is important in the preparation of clinical isolates for testing the efficacy of oral healthcare formulas against dental caries and its risk assessment in vulnerable populations based on their counts in saliva. Since oral microbiome contains numerous species of *Streptococci* with subtle changes in morphological and biochemical characteristics, precise identification of *S. mutans* based on these characteristics is a tedious task. This study aims to precisely identify *S. mutans* from dental biofilms using PCR and gene sequencing. DNA was extracted using an optimized chemical method. Using species-specific *Sm479F/R* primers, a segment of the *HtrA* gene of *S. mutans* was amplified. Agarose gel electrophoresis of the PCR product confirmed the presence of a 479-bp PCR amplicon. Sequencing of the PCR product and alignment of it with sequences available in the NCBI database showed that it has 97.8% identity to the *S. mutans* reference sequence. Among the 32 *Streptococcus* bacteria isolated from clinical samples on Mitis Salivarius agar, 23 were confirmed to be *S. mutans*. In conclusion, PCR with species-specific primers *Sm479F/R* is an effective method for precise identification of *S. mutans* among multitude of *Streptococci* in the oral cavity. The *S. mutans* clinical isolates confirmed in this study can be used to test the efficacy of oral healthcare formulas. Further, this PCR can be improved to quantify *S. mutans* in saliva and utilized in population screening for risk assessment of dental caries, which may help early interventions to prevent the occurrence of dental caries in high-risk individuals.

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