

Oral Microbiota Changes in Children Undergoing Comprehensive Dental Treatment for Severe Early Childhood Caries

Nivethanan Kamalendran¹, Bernadette Drummond², Nicholas Heng¹, Mary Cullinan¹

¹Department of Oral Sciences, Faculty of Dentistry, University of Otago, Dunedin, Otago, New Zealand

²Paediatric Dentistry, School of Dentistry, University of Leeds, Leeds, UK

Background: Severe Early Childhood Caries (S-ECC) is a leading oral health problem affecting the quality of life of many preschool children. Despite preventive and restorative approaches to manage S-ECC, these children remain at high risk of recurrent dental caries. The purpose of this study was to examine, the oral microbiomes of children before and after comprehensive restorative and preventive dental treatment for S-ECC using next-generation DNA sequencing technology,

Methods: Plaque samples were collected from thirty 2-6 year-old children with S-ECC (dmfs>6) and thirty caries-free (control) children. Children in the S-ECC group were sampled immediately before treatment, 2 weeks and 3 months post-treatment. Bacterial 16S rRNA genes were specifically amplified by PCR from each plaque sample and sequenced using Ion Torrent™ technology. All sequence data were analysed using the QIIME software suite.

Results: Sequence analyses enabled the detection of 103 bacterial species. The most prevalent species in the S-ECC group were *Streptococcus mitis*, *Veillonella dispar*, *Streptococcus mutans*, *Streptococcus oralis*, *Neisseria flavescens*, *Neisseria bacilliformis*, *Prevotella denticola* and *Treponema socranskii*. Conversely, some species including *Actinomyces naeslundii* and *Rothia aeria* were detected at higher levels in the control group. Despite a reduction in the proportions of *S. mutans*, *S. mitis*, *V. dispar*, *N. flavescens*, *N. bacilliformis* and *P. denticola* after comprehensive restorative treatment, no statistically significant differences were observed in bacterial profiles between the time points of each participant in the S-ECC group. Some species (*S. mitis*, *V. dispar* and *R. aeria*) that had reduced levels following treatment did show an increase in levels again after three months, but not to the same levels as in the pre-treatment profile.

Conclusion: Comparing the oral microbiota before and after comprehensive restorative dental treatment revealed changes in bacterial composition. The results also highlighted the unique response of each participant's microbiota following dental treatment.