

Forsyth team gains new insight on childhood dental disease

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Researchers at The Forsyth Institute have made a significant discovery about the nature of childhood dental disease. The scientific studies led by Anne Tanner, BDS, Ph.D., identified a new pathogen connected to severe early childhood caries (cavities). This bacterium, *Scardovia wiggsiae*, was present in the mouths of children with severe early childhood caries when other known pathogens such as *Streptococcus mutans* were not detected. This research may offer the potential to intervene and halt the progression of disease.

Early childhood caries, ECC, is the most common chronic infectious disease of childhood in the United States. Severe ECC can destroy primary teeth, cause painful abscesses and is the major reason for hospital visits for young children. This condition disproportionately affects disadvantaged socio-economic groups. This research, which will be published in the April issue of *Journal of Clinical Microbiology*, provides new insight on the [microbiota](#) of severe early childhood caries.

Dental caries is caused by an interaction between bacteria, host susceptibility and a [carbohydrate diet](#) that contains large amounts of sugar. Dr. Tanner published an updated evaluation of the diet associated with severe-ECC in collaboration with Dr. Carole Palmer at Tufts University in the [Journal of Dental Research](#) in 2010. The [bacterial species](#) *Streptococcus mutans* is widely recognized as the primary pathogen in early childhood caries. However, it is also present in people without disease and is not detected in all cases of childhood caries. This suggests that other species such as *S. wiggsiae* are also disease causing

pathogens.

"In my work, I have seen the tremendous public health impact of severe early childhood caries," said. Dr. Anne Tanner, Senior Member of Staff, Department of [Molecular Genetics](#), The Forsyth Institute.

"Understanding the causes of severe dental decay in young children is the first step in identifying an effective cure."

Study Details

Severe early childhood caries (ECC), while strongly associated with *Streptococcus mutans* using selective detection methods (culture, PCR), has also been associated with other bacteria using molecular cloning approaches. The aim of this study was to evaluate the microbiota of severe-ECC using anaerobic culture. The microbial composition of dental plaque from 42 severe-ECC children was compared with that of caries-free children. Bacterial samples were cultured anaerobically on blood and acid (pH 5) agars. Isolates were purified, and partial sequences for the 16S rRNA gene were obtained from 5608 isolates. Sequence based analysis of the 16S rRNA isolate libraries from blood and acid agars of severe-ECC and caries-free children had >90% population coverage with greater diversity in the blood isolate library. Isolate sequences were compared with taxa sequences in the Human Oral Microbiome Database (HOMD) and 198 HOMD taxa were identified, including 45 previously uncultivated taxa, 29 extended HOMD taxa and 45 potential novel groups. The major species associated with severe-ECC included *Streptococcus mutans*, *Scardovia wiggsiae*, *Veillonella parvula*, *Streptococcus cristatus* and *Actinomyces gerensceriae*. *S. wiggsiae* was significantly associated with severe-ECC children in the presence and absence of *S. mutans*. Dr. Tanner and her team conclude that anaerobic culture detected as wide a diversity of species in ECC as observed using cloning approaches. Culture coupled with 16S rRNA

identification identified over 74 isolates for human oral taxa without previously cultivated representatives. The major caries-associated species were *S. mutans* and *S. wiggsiae*, the latter of which is a candidate as a newly recognized [caries](#) pathogen.

This study was conducted with collaborators at the Goldman School of Dental Medicine, Boston University, and Tufts University School of Dental Medicine and with Dr. Floyd Dewhirst and resources of the Human Oral Microbiome Database (HOMD) at Forsyth Institute. HOMD links several types of information on oral microbes to a consistent naming system. HOMD contains descriptions of the microbes, their metabolism, and their ability to cause disease along with information on their DNA and proteins, as well as to the scientific literature.

Provided by Forsyth Institute

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