

Microbiome Associated with Severe Caries in Canadian First Nations Children

Agnello , M., et al. "Microbiome Associated with Severe Caries in Canadian First Nations Children." *Journal of Dental Research* vol. 96, no.12,2017, pp. 1378-1385., doi:10.1177/0022034517718819.

Background

Being in northern Ontario these past few weeks, specifically the coastal communities, I was both saddened and shocked by the prevalence of severe early childhood caries (S-ECC) within this patient population. Most children that come to the clinic are referred to the OR at a very young age for serial extractions of primary teeth and SSC on all posterior teeth. I decided to do this my literature review on both the prevalence of S-ECC, and whether or not there is a possible microbiome associated predisposition that this specific population has.

Young Indigenous children in North America suffer from a higher degree of severe early childhood caries (S-ECC) than the general population. This article explores the possibility that the etiology and characteristics of disease may be distinctive in this patient population. Caries associated microbiome among Canadian First Nations children with severe early childhood caries was investigated.

Introduction

- Early childhood caries (ECC) – Decay involving the primary dentition in children <6 years old. It is considered the most common chronic childhood disease
- Severe early childhood caries - an aggressive form of decay that is over-represented among indigenous children.
- The increased prevalence reflects an underlying oral health disparity within this population
- Major cause of hospital visits for younger children. Requiring extensive dental treatment under general anesthesia
- Children who live in communities with high proportion of First Nations residents have pediatric dental surgery rates nearly 8x higher than those living in communities with a low Aboriginal population (among children ages 1-5)
- Risk factors include known microbial and host-related factors, but also socioeconomic status, (lack of) education and nutrition
- Next generation sequencing was used to analyze plaque microbiome from Canadian First Nations and Métis children with and without S-ECC.
 - Investigated the role of an oral microbiome and different characteristics that

might contribute to its progression

Materials and Methods

- Canadian First Nations children <6 were included in the study.
 - 30 children with S-ECC had severe tooth decay involving primary teeth were recruited on the day of their scheduled dental surgery.
 - 20 caries free children were recruited from the community and assessed
- Information on nutritional habits, oral hygiene habits, socio-economic, and history of previous dental visits was collected
- Plaque samples were collected from each subject by swabbing a sterile interdental brush on all available tooth surface
- Extracted DNA was sent to the Forsyth Institute for library preparation and Illumina sequencing of the amplified V3-V4 16S region

Results

Demographics/Health-Related Questionnaire Data

- The mean age of all children was 40.7 ± 11.6 mo.
- 56.7% of children with S-ECC resided in First Nations communities
- All of the caries-free children lived in the Winnipeg region.
- We found a significant difference in household income between the groups,
 - S-ECC children coming from households with lower incomes
- Children with S-ECC were also bottlefed for a significantly longer duration
 - age in which the child was weaned from the breast was significantly lower

Taxonomic Identification and Relative Abundance

- Plaque samples were obtained from 20 caries free and 30 S-ECC.
- Sequencing generated a total of 3,502,879 sequences after quality filtering
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- 10 phyla, 4 of which were differentially represented in the caries-free versus S-ECC groups:
 - Firmicutes (39.4% vs. 47.2%, $P = 0.01$)
 - Actinobacteria (14.4% vs. 6.8%, $P = 0.002$)
 - Fusobacteria (16.8% vs. 11.3%, $P = 0.008$)
 - TM7 (0.5% vs. 0.24%, $P = 0.008$)
- A total of 95 genera and 290 species were detected
- Most of these species have been associated with either health or caries

- Caries-free group had 5-fold higher *Streptococcus gordonii* and 2-fold higher *Streptococcus sanguinis* than the S-ECC group
- S-ECC group had 7-fold *Haemophilus* species and 9-fold higher levels of a *Porphyromonas* species (HOT 284)
- *Streptococcus mutans* was detected in all samples
 - 3-fold higher amount detected in the S-ECC group as compared with the caries-free group
 - 6 children in the S-ECC group were carrying >5% *S. mutans*
 - 2 children with >10%
 - 1 child with almost 23% of the total species detected.
 - For comparison, in the caries-free group, there was only 1 child with >5% *S. mutans*

Discussion

- First study to use advanced microbial analyses to investigate the oral microbiome of Indigenous children affected by S-ECC
- Knowledge of the importance of the oral microbiome in the etiology of ECC is still lacking
- Indigenous children suffer considerable oral health disparities when compared with other children of the same age
- Stems from the historical and ongoing effects of colonialism and racism that have resulted in major socioeconomic and health care inequities
- There are behavioral and socioeconomic risk factors, including less frequent brushing, bottle-feeding, later age at weaning, and lower household income
- S-ECC is a complex, multifactorial disease with a major microbiological component
- More research should be conducted to determine the underlying causes of extreme oral health disparities in this population

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