

## The oral microbiome in children with Crohn's disease exhibits reduced biodiversity compared to healthy children, revealed by 16s profiling

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**Aims:** To identify marker organisms that could identify if a patient is suffering from Crohn's disease. This information may also be used to improve the oral health of patients with Crohn's disease.

**Methods:** The oral microbiome was examined in a cohort of children diagnosed as suffering from Crohn's disease (n=23, CD), inflammatory bowel disease (n=10, IBD), and ulcerative colitis (n=5, UC) respectively. A cohort of 24 children who were attending DDUH were grouped as a healthy control (HC) group. Bacterial DNA was extracted from tongue and buccal swabs and the V1-V2 region of the 16s gene was amplified and sequenced using the MiSeq. Sequences were analysed with the Mothur pipeline.

**Results:** At the phyla level, the tongue of Crohn's patients was found to have significantly lower levels of *Bacteroidetes*, *Proteobacteria* and *Fusobacteria*. Reduced biodiversity of the tongue was reflected by differences in the inverse Simpson's index for both sites (CD tongue=9.39; HC=12.87). Analysis of species richness by rarefaction showed a significant reduction in species richness in CD tongue samples compared to HC tongue samples, whereas species richness in CD buccal was almost as the same as HC buccal. The number of Operating Taxonomic Units (OTUs) identified per sample ranged from 68 to 210. Analysis of community structure and membership using AMOVA showed that the populations on HC and CD tongues were significantly different ( $P < 0.001$ ). Lefse analysis identified 20 OTUs that were significantly enriched on the tongues of healthy children including *Haemophilus parainfluenzae*, *Neisseria flavescens*, *Fusobacterium periodonticum*, *Streptococcus sp.*, *Porphyromonas sp.*, *Actinomyces sp.*

**Conclusion:** Children with Crohn's have an altered microflora that may contribute to their oral health problems. These data could potentially be used to diagnose a patients overall gastrointestinal health.