



Periodontal Biofilm in Children with Down Syndrome

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Introduction

Trisomy 21, also known as Down Syndrome (DS), is the most common survivable aneuploidy. The incidence of DS is roughly 1 in 700 births¹. DS has several well-known characteristics including: growth deficiencies, intellectual delays, cardiac defects, hypertension, increased risk for leukemia, early onset of neurodegenerative disease, and immunodeficiencies²⁻⁶. These deficiencies include defective neutrophil chemotaxis, T-cell malfunction, and premature deterioration of the immune system^{7,8}. Thus, people with DS are susceptible to many infections and diseases, such as periodontal disease.⁹

Periodontal disease (PD) is an oral disease of inflammation. The inflammatory response of the body leads to deterioration of the bone in which the teeth reside. Ultimately this response leads to tooth mobility and tooth loss. Much of this can be attributed to a change in the microbial composition in the patient's mouth and gum tissue. These bacteria are found in the biofilm that accumulates on the surfaces of teeth. Typical treatment of PD is the removal of this biofilm. This is accomplished with good oral hygiene and professional scaling and root planing with the goal of a reduction of inflammation.

Periodontal disease takes time to develop and is not routinely found in young children. Due to potential immunodeficiencies, children with DS are at an increased risk to developing periodontal disease much earlier in life.¹⁰

There are several species of bacteria that are associated with PD. These bacteria are well known and studied amongst healthy patients. Oral abscesses also have noted signs of inflammation. Using our current knowledge of the oral microbiome found in patients with PD, we look to compare the biofilm of patients with DS with that of the microbial composition of oral abscesses.

The purpose of this study was twofold:

- (1) To evaluate the microbial composition of periodontal samples from patients with DS.
- (2) To compare the periodontal microbial diversity of children with DS to the microbial composition of dental abscess samples in order to evaluate for trends in an inflammatory environment.

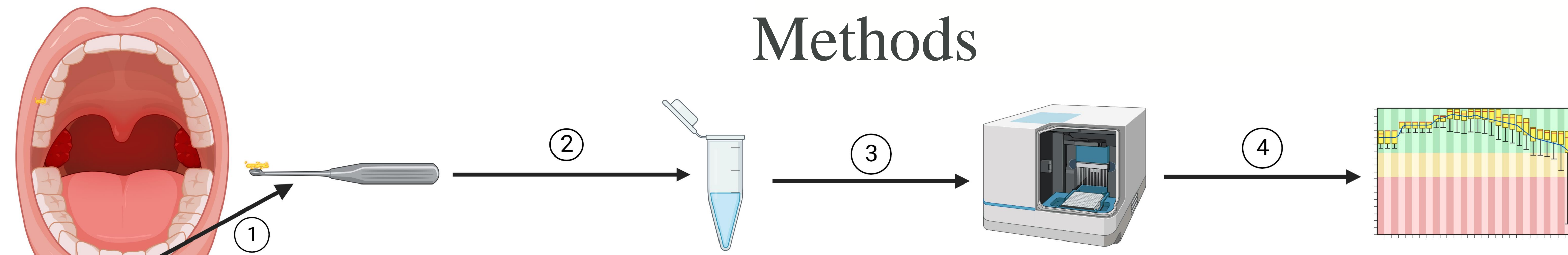


Figure 1. Plaque samples were recorded. Samples were placed in storage medium. The DNA/RNA was collected and sequenced. Community analysis and bioinformatics was completed.

Methods

Discussion

Patients with Down Syndrome (DS) have a higher susceptibility to periodontal disease when compared to non-DS individuals. In this study we determined the microbial composition of periodontal biofilm samples taken from the maxillary molars and mandibular incisors from patients with DS. We then compared these sample profiles to those from previously isolated supragingival plaque samples, and found no significant difference between the samples. When reviewing the data we can see that there is no difference between the groups. This would imply that amongst the different sample sites, the bacterial ecology was not different.

The abscess samples were the least diverse. This was not statistically significant. One thought is that the inflammatory environment likely promotes the growth of certain species.

In evaluating the sites of children with DS, we anticipated detecting less diversity, similar to the abscess samples. This limited diversity would also be noted in sites of periodontal disease. We did not observe a less diverse microbiome.

The lack of differences between samples raises the question of, what contributes to the development of periodontal disease in patients with Down Syndrome? The innate immune system remains a possibility. Further understanding of the immune deficiencies and the oral microbiome in patients with Down Syndrome is needed.

Results

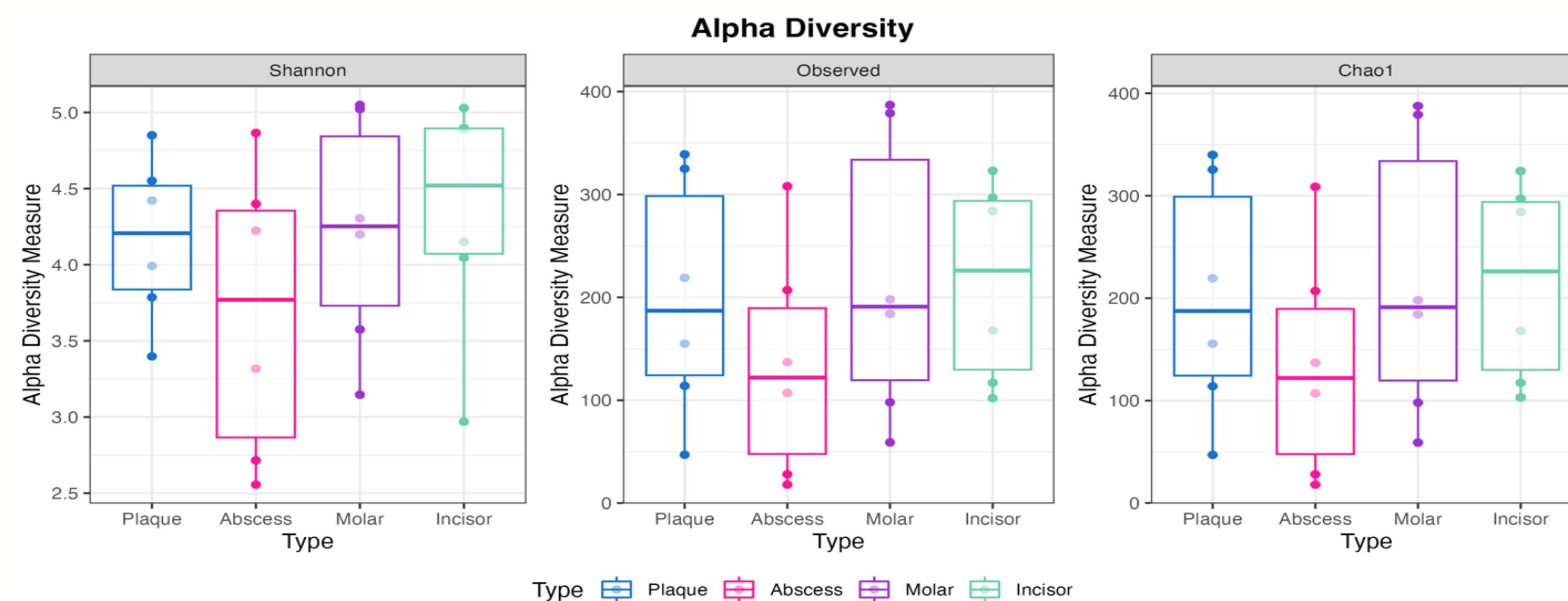


Figure 2. When viewing the α -diversity plots there were no significant differences between any of the groups ($p > .05$).



Figure 3. Principal Coordinate Analysis (PCoA) demonstrating no evidence of clustering.

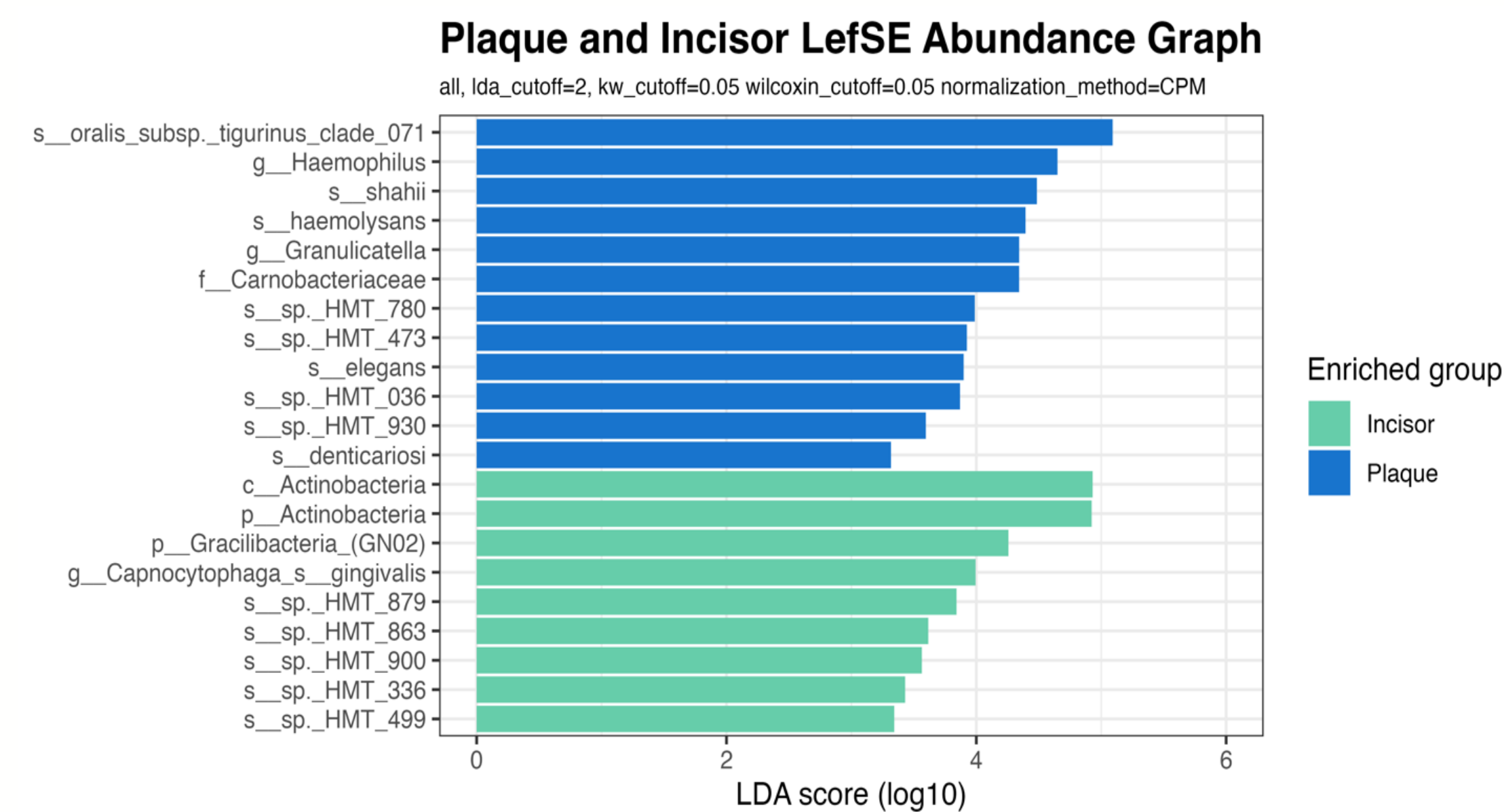


Figure 4. Linear discriminant analysis Effect Size (LefSE) analysis - revealed multiple taxa that significantly enriched in both the DS incisor and control plaque groups at the phylum, family, class, genus and species levels.

Conclusion

When comparing the data recorded, there was no difference in the microbial composition of periodontal plaque samples from children with Down Syndrome and those previously taken from supragingival plaque nor from dental abscesses. There were no trends noted in comparing sites of inflammation, abscess samples, and the Down Syndrome samples.

Our data suggest that the predisposition of children with Down Syndrome to develop periodontal disease may be less on the bacterial ecology and more on other factors attributed with the development of periodontal disease.

One of the limitations of this study was the sample size of patients with Down Syndrome. More research is needed to further evaluate the oral microbiome of children with Down Syndrome, as well as the immune system deficiencies in these patients.

References

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