Childhood Obesity And MetS are associated with Oral Microbial Dysbiosis

Ada Reyes, DDS[1], Ahmed Sidahmed[1], Muna Hakim, BDS[1], Sydney Woods, BA[1], Ashutosh Mangalam, MS PhD[2], Shailesh Shahi, MS PhD[2], Natayla Guseva, PhD[2], Kecia Leary, DDS MS[1], Karin Weber-Gasparoni, DDS MS PhD[1], Lauren Kanner, MD[2], Vanessa Curtis, MD[2], Sukirth Ganesan, BDS PhD[1],

University of Iowa College of Dentistry[1], University of Iowa Carver College of Medicine[2]

Objective:
The aim of this study is to determine the alterations in the microbial composition and associated changes in the inflammatory milieu in the oral environment in children with components of metabolic syndrome compared to healthy obese and non-obese children.

Methods:
Supragingival and subgingival plaque were collected using curettes and sterile paper points from 45 patients belonging to three groups 1) Metabolic syndrome (MetS), 2) Metabolically Benign Obesity (MBO), and Normal Weight Healthy controls (NWH). Gingival Crevicular Fluid (GCF) was collected using filter paper strips. All the participants were dentally healthy and frequency-matched forage, gender, type of dentition, and ethnicity. Diagnosis of MetS and MBO was based on the International Diabetes Federation. After GCF elution, levels of proinflammatory cytokines and adipokines were analyzed using the multiplex assay. Bacterial DNA was isolated, V3-V4 hyper variable regions were amplified, and 16Ssequencing was performed on Illumina Miseq 2x300bpPE platform. The generated sequences were annotated against the SILVA database. Statistical comparisons were made using Tukey HSD.

Results:
Both the obesity and the MetS groups showed a significant decrease in bacterial diversity than healthy controls. Additionally, several oral health-associated bacterial genera such as streptococcus (non-caries related), actinomyces were decreased in the obesity and MetS groups compared to the normal weight cohort. The proinflammatory cytokine MMP-9 that is associated with adipocytes in obesity is significantly increased only in GCF of obesity and MetS patients.

Conclusion:
Decrease in health-associated bacterial members along with an increase in obesity-associated cytokine, MMP-9 in otherwise orally healthy patients with MetS and obesity indicate at-risk-for-environment before the onset of oral clinical disease. These disturbances in the microbiome and inflammatory cytokines may be the underlying cause for increased risk for oral diseases and poor oral health in patients with obesity and MetS. Identification of obesity-associated cytokine MMP-9 adipokines in GCF that mirrors the systemic levels indicate the potential use of GCF as a biomarker for MetS and Obesity.