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**CHARACTERIZATION OF THE MICROBIOTA IN SALIVARY GLANDS IN
RELATION TO SJOGREN'S SYNDROME**

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Abstract:

Primary Sjogren's syndrome (pSS) is an autoimmune disease that affects multiple exocrine glands causing affected individuals to experience dry eyes, dry mouth, and fatigue [1]. pSS is typically diagnosed in women and symptom presentation can begin as early as a decade before diagnosis [2]. The slow progression of pSS suggests some type of chronic, low level exposure to environmental pathogens, including viruses or bacteria. However, the pathogenesis still remains unknown [3]. Dysbiosis of the microbiota in salivary glands may hold potential information about the onset of pSS and has been analyzed in several studies. Most studies describe a decrease in bacterial diversity in the infected salivary glands compared to healthy controls, however there is some disagreement [4-6]. In this study, five RNA sequencing salivary gland datasets from all over the world were collected from the NCBI SRA database. The datasets include sequencing data from salivary gland tissue obtained from pSS, sicca patients and healthy controls. The dataset sequences were initially aligned with human genome (hg38). The unmapped sequences were then assembled into contigs and analyzed using Diamond Blast X for alignment to bacterial sequences. Analysis of the bacterial diversity present in pSS relative to non-pSS datasets identified a decrease in bacterial diversity in pSS compared to the healthy controls. Specific phylum including Proteobacteria, Firmicutes, Actinobacteria, and Bacteroidetes was further analyzed and compared to other studies in a meta-analysis. The relative abundance of the outlined phyla was inconsistent with that of other studies [4-6]. Given that there are no long-term or curative therapeutics to treat pSS beyond immune suppression, greater knowledge in this field could be potentially beneficial to many in identifying factors contributing in the etiology of Sjogren's syndrome.

References:

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