Understanding Schizophrenia: Changing the Game with the Oral Microbiome

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This experiment sought to determine if individuals with schizophrenia have observable differences in the genetics of their oral microbiomes compared to healthy individuals. This was done by investigating the significance of oral microbiota phyla and metabolic pathways. The research was performed using genetically sequenced data samples of the human oral microbiomes of six schizophrenics and six healthy individuals from the Integrated Microbial Genomes and Microbiomes (IMG/M) database. To ascertain if distinctions were present between the two oral microbiomes, the data was compared using principal coordinates analysis (PCoA) models, based on phyla composition and protein pathways. Differentiations in the phylogenetic distribution of the samples metagenomes were shown graphically. Additionally, variations between metabolic pathways were identified using Kyoto Encyclopedia of Genes and Genomes (KEGG) models. The PCoA models illustrated a clear division between the samples using spatial separation. The phylogenetic distribution of metagenomes models showed healthy samples had increased amounts of bacteroidetes bacteria, while schizophrenic samples had more firmicutes bacteria. Dissimilarities in phyla between the two oral microbiomes illustrated schizophrenia's affect on phylum diversity. Through analysis of metabolic pathways, schizophrenic samples showed higher concentrations of the metabolic transporters urea and glutamine/glutamate. As a result of the differences between these various analyses, there is a prevalent and observable difference between the oral microbiomes of schizophrenic and healthy individuals. In the future, this research could be developed further regarding how the oral microbiome can be utilized during the diagnosis and treatment of Schizophrenia.

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