

Microbiome-metabolome interaction analysis has proven to provide rich information about dental diseases. This study systematically evaluates the metagenomic, metatranscriptomic, and metabolomic data derived from dental plaque samples of 286 individuals from the ZOE 2.0 study. Species-level metagenomics and metatranscriptomics data and metabolomics data in children with Early Childhood Caries (ECC) and without ECC exhibit differential patterns. Through Differential Correlation Mining (DCM) analysis, we locate species groups spanning metagenomics, metatranscriptomics, and metabolomics whose pairwise correlation patterns differ between ECCs and non-ECCs. Verified by the feature permutation test, the level of differential correlation is significantly larger than the background correlation exhibited in each group. Overall, the species identified are largely consistent with findings from previous studies focusing on the differential microbiome abundance and ECC status. The metabolites identified play key roles in metabolic pathways responsible for the development of ECC and agree with the metabolic pathways suggested by microbiome species in the same group.