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Commensal glycerol metabolism determines oral niche development.

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Abstract

The oral microbiome has coevolved and coexisted in a symbiotic relationship within their own ecology and with the host. Understanding the oral ecosystem and how it promotes a balanced microbiome, is essential to effectively maintain or restore oral health. Of over 700 bacterial taxa, commensals *Streptococcus* and *Corynebacterium* are two of the most prevalent members of the oral microbiome. Surprisingly, the inter-species interactions between both commensals and the effect of such interactions on dental diseases have never been investigated. Therefore, in this study, we aim to understand the molecular mechanism(s) between different taxa interactions, in particularly, *Corynebacterium durum* and *Streptococcus sanguinis*, and the implications on oral diseases. So far, we have discovered a specifically mutualistic interaction that *C. durum* was able to substantially influence the chain morphology of *S. sanguinis*. When Gas Chromatography/Mass Spectrometry (GC/MS) analysis was employed, 3 fatty acids (palmitic, oleic, and stearic acids) were discovered in association with *C. durum* membrane vesicles, resulting in enhancing *S. sanguinis* fitness and survival. Global gene expression profiling of dual species cultures using RNA-seq was further conducted in order to investigate the regulatory effect of lipid metabolism on *S. sanguinis* chain morphology. Of approximately 30 genes as being differentially expressed under the influence of *C. durum*, genes involved *S. sanguinis* lipid metabolism, in particular, glycerol dehydrogenase (*gldA*), its “sister” glycerol kinase (*glpK*), and the neighboring downstream genes were found to be significantly upregulated. Subsequently, *S. sanguinis* fatty acid metabolism-related genes were further characterized and revealed a key role of *S. sanguinis gldA* and a supported role of *glpK* during the mutualistic-interspecies interaction. Overall, our findings have provided new insights into how glycerol metabolism is involved in oral niche development, potentially shaping symbiotic health-associated biofilm communities.

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