Salivary Mucin Degradation by Oral Bacteria

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The Normal Oral Microflora and Biofilms on Teeth

Salivary mucins may act as a site for adherence and nourishment for commensal bacteria. Mucin metabolism by commensal bacteria was tested by an oral microbial enrichment experiment. Bacteria was obtained from 7 sites (front of mouth teeth-inside and outside, back of mouth teeth-inside and outside, top of tongue, inside of cheek, and between bottom front teeth) using a sterile dental brush. Bacteria were inoculated into a modified basal nutrient media supplemented with 1.25% porcine gastric mucin. After inoculation, samples were subjected to 24 and 48h turnovers under O2 and ANO2 conditions. Samples were subjected to p2-p3 PCR and DGGE gels to determine bacterial banding pattern. NMR and amino acid degradation experiments were ran on initial and end 24 and 48h turnovers to assess bacterial metabolism. Cyclic banding was seen for DGGE profiles as the enrichments progressed with ANO2 profiles being more complex than O2. The 48h systems appeared more diverse than 24h systems. DNA banding extraction analyses are on-going. Variations in SCFA within NMR data suggest bacterial cross-talk. The emergence of threonine and serine within the experimental medium suggest the degradation of the apomucin backbone. This study indicates certain oral bacteria possess mucin degrading properties, thus influencing the microbiota within.