

***Abiotrophia defectiva* Degrades Mucins in the Oral Cavity**

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Background: The oral cavity harbors a diverse microbial community that is continually exposed to mucin-rich saliva. Salivary mucins contribute to lubrication, microbial clearance, and protection of the oral epithelium. In the gastrointestinal tract, many bacteria degrade mucin glycans and use the released sugars as nutrients. Mucin-degrading bacteria may not consume all liberated sugars, allowing these nutrients to support neighboring microbes through metabolic cross-feeding. Thus, mucin degradation could influence the composition, spatial organization, and activity of oral microbial communities. However, the bacteria responsible for mucin degradation in the oral cavity remain poorly characterized. We therefore sought to identify and characterize oral mucin-degrading microbes. **Methods & Results:** To assess the mucin-degrading capacity of the oral microbiome, we queried the Integrated Microbiome Genome Database, which contains >100,000 bacterial genomes. Interestingly, we found that the oral commensal bacterium *Abiotrophia defectiva* had multiple enzymes for removing mucin glycans. We found that all the *A. defectiva* genomes had the enzymes to remove sialic acid (EC 3.2.1.18), fucose (EC 3.2.1.51), GlcNAc (EC 3.2.1.52), GalNAc (EC 3.2.1.97), and Galactose (EC 3.2.1.22). However, it did not have the enzymes to remove sulfate (EC 3.1.6.14). To explore the ability of *A. defectiva* to consume mucus in vitro, we grew *A. defectiva* ATCC 49176 in a chemically defined medium, ZMB1, with intact human salivary mucus or varying concentrations of mucin oligosaccharides. As expected, we found that *A. defectiva* had robust growth with glucose, and it was also able to grow with human salivary mucus. It also could use galactose, GlcNAc, GalNAc, and mannose to support its growth. Interestingly, it did not use fucose or sialic acid. Since *A. defectiva* had the enzymes to remove fucose and sialic but did not consume them, we next explored the cross-feeding of *A. defectiva* with oral *Streptococcus* and *Fusobacterium* species as well as the effects of their secreted products on oral cells. **Conclusions:** We identified *A. defectiva* as a mucin-degrading microbe that is capable of changing the dynamics of the oral microbiome, potentially influencing overall oral health.