The microbiomes attached to fresh perennial ryegrass adapt to changing ecological niches

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Video Byte

Keywords: Microbiome, rumen, bacteria, archaea, biofilm, temporal, colonisation, metatranscriptome, energy harvesting, digestion, ecology, niche, network analysis, gene expression

Posted Date: October 13th, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-967795/v1>

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Abstract

The rumen is the largest compartment of the ruminant forestomach and houses a complex microbiome. That microbiome greatly influences gut energy harvesting capacity. Improving our understanding of the mechanisms that influence energy harvesting capacity could be used to optimize ruminant feed efficiency and management. Thus, researchers recently examined temporal ecological interactions at the plant-biofilm interface by incubating fresh perennial ryegrass in cattle rumens and analyzing the bacterial diversity and gene expression at several time points. Network analysis identified two sub-microbiomes. They represented the primary (<4h) and secondary (>4h) colonization phases. Several of the most transcriptionally active microbial families didn't interact with either sub-microbiome, which suggests non-cooperative behavior. Conversely, the putative keystone families of each sub-microbiome had low transcriptional activity. This may suggest that these groups are “cheating” and utilizing the energy harvesting capacity of other microbes to survive. These results expand our ecological understanding of microbial energy harvesting within the rumen and provide information that may be used to streamline the microbiome for optimized energy harvesting.