

Quantifying strain-level variability in foraging behaviors of rumen bacteria

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Abstract

Ruminants have evolved specialized digestive systems that are great at converting complex carbohydrates into energy. This ability relies on a core bacterial community – the rumen microbiome – that express genes encoding catalytic activities for carbohydrate breakdown. Improving the functional capacity of these microbes has the potential to enhance feed conversion, addressing the challenges of sustainable production of food animals. Our current knowledge of bacterial metabolic pathways relies heavily on indirect techniques: sequencing, computational studies, and in vitro culture. A recent study describes a novel approach to study the direct effects of diet on the rumen microbiome. Using fluorescently labeled polysaccharides (FLA-PS) as a direct method of studying the interaction of microbes with dietary glycans the researchers could visualize carbohydrate metabolism in single bacterial cells within a complex rumen sample. Using this method, they could rapidly assess metabolic phenotype – grouping bacteria into “medium grower” and “high grower” categories. Comparative whole-genome sequencing, RNA-Seq, and enzyme fingerprinting enabled them to identify strain-level variability in carbohydrate utilization predicting individual strategies of nutrient acquisition for each microbial type. This strategy complements next-generation physiology and ‘omics’ approaches to characterize microbial adaptation to prebiotics allowing researchers to measure the effects of interventions to improve ruminant metabolism.