

Subject – Insights into the bovine rumen microbiome

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Abstract - Ruminants have the remarkable ability to convert human-indigestible plant biomass into human digestible food products, due to a complex microbiome residing in the rumen compartment of their upper digestive tract. However, the rumen microbiome is also responsible for the

production of one of the most potent greenhouse gasses, methane, and contributes about 18% of its total anthropogenic emissions. Recent studies have linked microbiome structure to host genetics and phenotype (methane emissions, rumen and blood metabolites, and milk production efficiency). These phenotypes can be predicted from the microbiome using machine learning algorithms. Another study performed by our group showed that rumen microbiome components are tightly linked to cows' ability to extract energy from their feed, termed feed efficiency. We therefore assume that the rumen microbiome comprises different community states, some of which are linked with low feed efficiency and high methane production, while others are linked to lower methane emissions. Another aspect of our research deals with the temporal dynamics of the rumen microbial community and whether these ecosystems could undergo structural changes during life. Such an ability would render us the possibility to manipulate microbial communities towards a more favorable community state. This proof of concept was shown to be possible during an experiment in which early perturbation had a long term effect on community composition. Taken together, our studies along with the cooperation with RumenEra, take us one step closer towards microbial engineering of environmentally favorable dairy cows.