

Improving sustainability of cattle

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Rumen is key for reducing methane emission

To understand on a molecular level what goes on in the rumen is a prerequisite for fully understanding the methane and CO₂ emissions from cattle. To provide such compositional and functional insight of cow rumen function could provide basis for new strategies for reduction of especially methane emission (without losing feeding efficiency).

Molecular data has not yet lead to clarity

The overall composition of the rumen microbiota is well known. It consists of four major groups of microorganisms, two types of prokaryotes, rumen bacteria, archaea; and two types of eukaryotes, rumen fungi and protozoae. DNA-based analysis of microbial composition of rumen microbiota has opened for elucidating the microbial composition to a much deeper level, describing which taxonomic groupings (in which ratios) are present. However, this new knowledge has so far not leveraged into understanding animal-to-animal variations in methane emission. Which again means that we do not yet have sufficient basis for making a knowledge-based and quantifiable strategy for how we can significantly reduce methane emission by breeding or feeding or a combination of both.

New Technology: Microbiota, composition *and* function

The presentation will introduce how we can achieve improved understanding of not just the microbial composition but also the function of the cow rumen. By taking into account all four types of organisms (most studies have confined the DNA analysis to bacteria and archaea); and by going beyond organismal composition, using deep sequencing genomic data as basis for understanding not just which organisms are there, but also elucidating what they do.

Rumen Microbiota Synergy

The rumen bacteria are responsible for most of the enzymatic feed conversion; however, the rumen fungi are responsible for making much more of the biomass accessible for the enzymes of rumen bacteria. Rumen fungi break down the plant tissue and open up the plant cells, providing access to a much bigger part of the feeding materials. The basic mechanisms of these roles will be described. Further, a recently developed DNA/protein analysis technology platform will be introduced. A technology, which opens for elucidating also the composition of the microbiota secretome, responsible for feed conversion, leading to the observed different levels of emissions.

New Strategy Proposed

Early observations of rumen fungi have shown that abundance and composition of rumen fungal flora can be impacted by feeding strategies. Further, recent studies have provided evidence for that special feed additives (or food ingredients) can modify and improve the microbial flora of the non-ruminant gut. The presentation proposes a strategy for attempting reduced methane emission (without compromising efficiency) by feeding based modification of the microbial flora of the rumen; and using advanced, fast track DNA-based analyses to also identify most promising breeding traits. Hereby providing basis for combining targeted breeding and feeding strategies to reach the goal of significantly reduced methane emission.