Manipulating the rumen microbiome to address challenges facing Australasian dairy farming

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Abstract

Although ruminants evolved as browsing herbivores, today they are farmed around the world under widely varying climatic conditions. In temperate regions, pasture-based dairying systems using highly digestible plant species are common, while in regions with more extreme temperatures, dairying depends on animals fed total mixed rations (TMR) containing high proportions of easily digested carbohydrates in the form of cereal grains combined with digestible forms of protein. The choice of which feeding system is used in any particular dairying situation is driven by the productivity versus costs equation. Economic production of dairy products depends on maximizing the amount produced while reducing the costs of feed and labour. As dairy production systems reach ever higher levels, there is also an increasing need to reduce the impact of dairy wastes on the environment via increased nitrogen use efficiency as well as reduction of emissions of GHG. An understanding of the rumen digestive processes, and the specific roles of rumen microbes, is required in order to maximize the productivity, profitability and sustainability of these farming systems.

Recent advances in high throughput sequencing have provided us with a global census of the rumen microbiomes in 742 samples across 32 species from various geographical locations.
using the 16S rRNA marker gene (Henderson et al., 2015). This has enabled the identification
of the 30 most abundant bacterial groups, of which seven (Prevotella, Butyrivibrio,
Ruminococcus, unclassified Lachnospiraceae, Ruminococcaceae, Bacteroidales, and
Clostridiales) are considered the “core bacterial microbiome”. For the rumen archaea,
members of the methanogen clades Methanobrevibacter gottschalkii and Methanobrevibacter
ruminantium accounted for 74% of the total. The strongest driver of the composition of the
rumen microbiome was found to be the diet of the host animal (Henderson et al., 2015).