

Abstract

Breeding Low Emitting Ruminants: Predicting Methane from Microbes [†]

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Abstract: The greatest source of global anthropogenic methane (CH₄) emissions is from ruminant livestock. Multiple mitigation strategies in livestock are currently being explored. Of these breeding for lower CH₄ emitting ruminants has the advantage of being permanent and cumulative and universally applicable to all classes of livestock. Here, we show that methane emissions can be predicted by the complex community of microbiota sampled from rumens enabling evaluation of systems and individuals. Furthermore, there is evidence that the microbial community is controlled not only by the feed substrate but also by the host itself and that selecting hosts that favour a microbial fermentation with lowered methane emissions changes the energy source to the animal, and in turn both rumen physiology and body composition. Current methods for obtaining microbial DNA and subsequent sequencing of an animal's microbiome, however, are too expensive to implement in commercial selection programs. A methodology that offers fast, low-cost, high throughput profiling of rumen microbiomes using Genotyping-by-sequencing (GBS) has been developed using an unbiased reference free approach to group microbiota. To date, this has been applied to over 4000 sheep samples and validated in cattle. Results show that microbial profiles are heritable and correlated with methane emissions and feed intake. This research is part of a flagship program funded by the global research alliance to disseminate global access to technologies that lower greenhouse gas emissions in ruminant livestock.

Keywords: methane; ruminant; microbiome; environment; breeding; genotyping-by-sequencing; green-house gas



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