Mitigating Ruminal Methanogenesis Through Genomic and Transcriptomic Approaches

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Abstract : According to FAO, enteric methane (CH_4) production is about 44% of all greenhouse gas emissions from the livestock sector. Ruminants produce CH_4 as a result of fermentation of feed in the rumen especially from roughages which yield more CH_4 per unit of biomass ingested as compared to concentrates. Efficient ruminal fermentation is not possible without abating CO_2 and CH_4. Methane abatement strategies are required to curb the predicted rise in emissions associated with greater ruminant production in future to meet ever increasing animal protein requirements. Ecology of ruminal methanogenesis and avenues for its mitigation can be identified through various genomic and transcriptomic techniques. Programs such as Hungate1000 and the Global Rumen Census have been launched to enhance our understanding about global ruminal microbial communities. Through Hungate1000 project, a comprehensive reference set of rumen microbial genome sequences has been developed from cultivated rumen bacteria and methanogenic archaea along with representative rumen anaerobic fungi and ciliate protozoa cultures. But still many species of rumen microbes are underrepresented especially uncultivable microbes. Lack of sequence information specific to the rumen's microbial community has inhibited efforts to use genomic data to identify specific set of species and their target genes involved in methanogenesis. Metagenomic and metatranscriptomic study of entire microbial rumen populations offer new perspectives to understand interaction of methanogens with other rumen microbes and their potential association with total gas and methane production. Deep understanding of methanogenic pathway will help to devise potentially effective strategies to abate methane production while increasing feed efficiency in ruminants.

Keywords : Genome sequences, Hungate1000, methanogens, ruminal fermentation
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