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Rumen Metagenome and Metabolome for Optimized Production

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ABSTRACT

Rumen converts lignocellulosic biomass to high-quality food by virtue of the diverse microbiota. The composition of rumen ecosystem is influenced by various factors including diet, individuality, age, geographical location, post-feeding time etc. Earlier culture-based techniques could study rumen microbes partially for the cultivable microbes. But now it is known that about 90% of rumen microbes are unculturable and the knowledge that we have till now seems to be limited. With the advent of new technologies such as next-generation sequencing which studied the whole ruminal ecosystem at one time contributed tremendously to our existing knowledge. Approaches like metagenomics, metabolomics etc. have made it possible to study the structure and function of rumen microbes in their natural environment. Understanding the composition and activity of the microbial community in the rumen is crucial for the improvement of productivity and lessening of environmental pollution in the ruminant livestock industry. Analysis of metabolome and microbiome revealed direct or indirect association for a better understanding of the biochemical and microbial functions of the rumen.

INTRODUCTION

Rumen is the part of the gastrointestinal tract in ruminant animals, where the actual digestion occurs. How does it work? It is filled with several micro-organisms which include bacteria, archaea protozoa, and fungi. The bacteria are most abundant with an estimated population density of 10^{10-11} per mL is of rumen fluid, followed by archaea (10^{8-9} pr mL), ciliate protozoa (10^{4-6} per mL) which contribute up to half of the rumen microbial biomass due to their large size and fungi with 10^{3-5} per mL contributing less than 8% to total biomass (Kamra, 2005; Wang *et al*., 2017). The structure of this microbial community is influenced by many factors, including host species, age, health status, diet, geographical location, and whether the animal has received antibiotic treatment (Dehority and Orpin,1997).

There is a gap between the information on the rumen microbiome and microbial metabolism that needs to be bridged (Bannink *et al*., 2016). Metagenomics and Metabolomics have become an emerging research area that identifies the type of microbes present in the rumen as well as quantitatively measures small molecular metabolites present in biological samples (biofluids or tissues) using high-throughput approaches, such as nuclear magnetic resonance (NMR) (Zhao *et al*., 2014), liquid chromatography-tandem mass spectrometry (LC-MS) (Tian *et al*., 2016), and gas chromatography-mass spectrometry (GC-MS) (Hua *et al*., 2017).

Traditional microbial genomics vs metagenomics

If we go for traditional microbial genomics, we need to sample in rumen followed by isolate the microbes, cultivate them and prepare a DNA for a specific microorganism this is not always possible in the rumen and environmental sample as well. The microbes have a different and specific needs for growth on solid media which increases the workflow and skill requirements in the diagnostic microbiology laboratory. Sometimes, the carbon sources in the culture media are not exactly similar to the requirements of the bacterial growth reflecting success in isolating only limited bacterial members of the community (Nocker *et al*., 2007). Pathogen identification based on the traditional approach using morphology, physiology, chemistry, and biochemical characterization generally requires 2 to 5 days. In addition, phenotypic methods fail to identify the microorganism up to the species or strain level (Bochner, 2009). In some situations, the pathogens are difficult to visualize under a microscope or the organisms are refractory to known culturing methods.

Metagenomics

The word ‘metagenome’ was first used by Handelsman *et al*. (1998) and refers to sequence-based study of collection of all microbial genomes found in a sample. Metagenomics is the application of modern genomics techniques to the study of communities of microbial organisms directly in their natural environments, bypassing the need for isolation and lab cultivation of individual species (Handelsman, 2004).

Metagenomics helps to decode ruminal ecosystem’s role as it prove information about mechanism of compositional variation. It also helps in the identification of those microbes that are not yet to be characterized or identified. Metagenomics analysis also helps to understand about how microbial community composition affect the overall performance of animals.

Metabolomics

“Scientific study of the complete complement of all small molecule metabolites found in a specific cell, organ or organism.” Identification and quantification of the complete set of metabolites in a biological system (Saleem *et al*., 2013).

Application of metagenomics and metabolomics

1. By metagenomics and metabolomics approach we can do analysis of the

microbes and metabolites present in sample.

2. Analysis of microbiota is important to improve animal nutritional strategies and animal health. This knowledge can be used to modulate the rumen microbiota to reduce formation of emission gases.

3. By these techniques we can expend the ruminal database and able to discover the enzyme metabolic pathways.

4. These omics technique also helpful to reconstruct the genome of strictly anaerobic microorganism and applicable to understand the microbial cell to cell interaction.

CONCLUSION

Metagenomics is expanding our knowledge of rumen microbiome diversity, structure, and their function. Lower diversity of rumen microbiome content linked to higher feed efficiency. Marker identified by metagenomic and metabolomic analysis can be used to improve production efficiency of animals.

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