

**AN OVERVIEW ON RUMEN AND ITS ASSOCIATION WITH MICROBIAL SPECIES**Satyanagalakshmi Karri<sup>1,2</sup>, Suneel Kumar Onteru<sup>2</sup>, Sunita Meena<sup>2</sup>, Vijay A.K.B. Gundi<sup>1\*</sup><sup>1</sup>Department of Biotechnology, Vikrama Simhapuri University, Nellore-524 320, Andhra Pradesh<sup>2</sup>ICAR-National Dairy Research Institute, Karnal – 132 001, Haryana, India\*Corresponding Author Email: [gundi.vijay@gmail.com](mailto:gundi.vijay@gmail.com)**ABSTRACT**

The ruminants harbour a complex microbiome composed of wide variety of bacteria, protozoa, archaea and fungi. The microbes play an important role in digestion of feed particle into utilizable products such as volatile fatty acids and proteins to the host animal. To understand the ruminal function and effect on ruminant, microbial interaction and its role in feed degradation is important. Studies of ruminal microbes represent a key area of research in ruminants, and it is an important to improve our understanding of these complex microbial populations and their interactions. Collectively, the series of studies described here have advanced understanding of the ruminal microbiome, providing detailed information on the microbial communities in fractionates,

**KEY WORDS**

Rumen; microbial interaction; diversity; feed; bacteria.

**INTRODUCTION**

The rumen is an ecosystem that harbours a complex microbiome composed of wide variety of bacteria, protozoa, archaea and fungi (6), among these microbes bacteria are more predominant (13). Microbes survive in the rumen under different constraints which may be either natural or feed associated, as some of the feeds contain a significant amount of anti-nutritional factors, which sometimes limit the growth of some of these microbial inhabitants (37). The major application of microbiome in rumen is to convert feed stuff into digestible compounds that can be used by the host animal (26). This function is of tremendous importance as it allows the conversion of solar energy stored in plant fibre into products, such as milk and meat. Additionally, as the microbiome in the rumen undergoes long-term selection and evolution, the microbes and host form an inter inhibitive and interdependent homeostatic relationship that

has an important role in maintaining host health, improving performance, reducing environmental pollution, and ensuring food and animal product safety (33). Many studies have reported the influences of multiple factors on the composition of rumen microbiota that is affecting the population of certain bacterial groups (35). Therefore, it is important to find the diversity of ruminal bacterial communities.

Ruminants are one of the most successful groups of herbivorous mammals on the planet, with around 200 species represented by approximately 75 million wild and 3.5 billion domesticated individuals worldwide (10). Ruminants are defined by their mode of plant digestion, and have evolved a forestomach, the rumen, that allows partial microbial digestion of feed before it enters the true stomach. In ruminants, the epithelial wall doesn't have glandular cells to secrete digestive enzymes, microbial flora in rumen takes part in feed

digestion by releasing enzymes. These rumen microbes ferment feed to form volatile fatty acids that are major nutrient sources for the host animal and contribute significantly to ruminant productivity. The host also uses microbial biomass and some unfermented feed components once these exit the rumen to the remainder of the digestive tract. Ruminants have evolved various rumen anatomies and behaviours to thrive on a range of plant species, and this flexibility has enabled them to occupy many different habitats spanning a wide range of climates (15). The rumen is an anaerobic fermentation chamber and housing diverse microorganisms such as bacteria, protozoa and fungi. Bacteria play a key role in rumen fermentation, which in turn greatly impact production and health of dairy cows (7).

#### **Rumen development**

After birth, the calves or young ruminants are described as pre-ruminants, as they are not having developed rumen. The establishment of ruminal functions in calves is very rapid between d 1 and 10 after birth, the maintenance of reducing condition of rumen is achieved by microbial flora in rumen from day 2 (5). The first colonized ruminal bacteria were likely facultative anaerobic bacteria (8), which lead to develop reducing environment by consuming oxygen. Subsequently the anaerobic medium in the rumen becomes favourable for the establishment of strict anaerobic bacteria communities (3).

#### **Ruminal bacteria**

Bacteria play an important role in converting feed to nutrients that can be absorbed by the ruminant hosts. Currently, 30 valid bacterial phyla were detected (29); however, two main phyla which tend to dominate the gastrointestinal tract (GIT) are Bacteroidetes and Firmicutes. The phyla Firmicutes were found dominant in ruminant GIT (50) (17) (38). However, several studies have identified Bacteroidetes as the dominant phylum in adult ruminants (18) (30).

The phylum Bacteroidetes bacteria are gram-negative which may be aerobic or anaerobic, and it is generally anaerobic members that belong to the class Bacteroidia (formerly Bacteroides) that are found in all parts of the GIT. As members of the phylum Bacteroidetes possess a wide range of enzymes, especially those which digest carbohydrates or proteins (43).

The phylum Firmicutes bacteria are gram-positive, often form endospores, and are divided into two major classes: Clostridia and Bacilli. Bacteria belonging to the class Clostridia are strict anaerobes and many are characterized as cellulolytic, such as *Butyrivibrio* spp. (51), *Clostridium* spp. (24), or *Ruminococcus* spp. (44). Within the class Bacilli, the major rumen taxa of interest are cellulolytic *Bacillus* species (40) or lactic acid bacteria (order Lactobacilliales), such as *Lactobacillus* spp., *Lactococcus* spp., *Enterococcus* spp., and *Streptococcus* spp.

The phylum Fibrobacteres currently comprises one formal genus, *Fibrobacter* and two cultured species, *Fibrobacter succinogenes* and *Fibrobacter intestinalis*, recognised as major bacteria that are degraders of lignocellulosic material in the herbivores (32) and is not well grouped as they are difficult to culture.

#### **Diversity of bacteria in ruminants**

The study of rumen microbial communities involves prevalence, diversity, their activities, and the relation with each other within the communities and with their rumen host. The diversity studies and cultivation of rumen bacteria started after the development of conventional culture method for anaerobic bacteria, as the majority of rumen microbes are anaerobes (16). The cultivation of pure culture illustrated the metabolic pathways of microbes in rumen. The molecular ecological tools such as 16S rDNA gene amplification, metagenomics enables to study rumen microbial communities without cultivation in laboratory.

By conventional culture method more than 200 bacterial species have been isolated from rumen (36). Culture-independent 16S rRNA gene library demonstrated that bacterial communities are more diverse than cultivated species that may contain 300-400 species (6) and most of the bacterial communities identified in clone library analysis belong to the phyla Firmicutes and Bacteroidetes (50), (22), (6), (27) (45).

In ruminants, the prevalence of phyla Firmicutes and Bacteroidetes difference, many reports suggest that Bacteroidetes were more predominant (42) although other studies have found phyla Firmicutes more dominant (23) (21) (6) but together form as dominant communities in rumen and many factors influence the bacterial diversity.

A Metagenomics study on ruminal diversity revealed that 302 OUTS into 82 genera 304 OTUs of bacteria (6), 1539 OTUs into 74 genus. The meta-analysis of all 16S rRNA gene (rrn) sequences deposited in the RDP database revealed that 5271 operation taxonomic units (OTUs) at species level (21). The advanced pyrotag analysis explore higher diverse species in rumen, (14) observed 1000 OTUs at species level, 1038OTUs at species level 2,409 OTUs in cow, 2593 OTUs at species level (39), 1027 species on alfalfa, 662 species on triticale diet (23), perceptible difference in bacterial communities observed in ruminants (34), (52), with animal species with season geographical regions with growth stage but no difference in diversity with sampling process was observed (25,) (12).

#### **Why rumen studies are important?**

The microbial communities in rumen digest feed particles and endow with >60% of proteins need. The symbiotic relation between microbial communities and ruminants directly impacts the performance of animal. Hence it is important to understand rumen microbial flora, in the form of diversity and functional role in rumen to make

effective management decisions to enhance microbial and animal production.

The direct microscopic observation of rumen estimated  $10^9$ - $10^{11}$  bacterial cells per gram of rumen sample. Thus, culture dependent methods, provided limited information only, as all the rumen bacteria not culturable. The 16S rDNA libraries and metagenomic approaches and T-RFLP (Terminal Restriction Fragment Length Polymorphism) analysis investigated microbial diversity in different environment (1) (7). These 16S rRNA analysis also to rumen microbial diversity studies also(6), (31). In conclusion, this review provides information about ruminants, microbial association with rumen and characterization of rumen bacteria using different methods

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#### **CONFLICT OF INTEREST:**

All authors declared no conflict of interest.

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**\*Corresponding Author:**

**Vijay A.K.B. Gundi<sup>1\*</sup>**

<sup>1</sup>Department of Biotechnology,  
Vikrama Simhapuri University,  
Nellore 524 320, Andhra Pradesh.  
Email: [gundi.vijay@gmail.com](mailto:gundi.vijay@gmail.com)