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## Role of Rumen microflora in Livestock production

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### Abstract

Rumen microbes include the protozoa, bacteria, archaea and fungi that live inside the rumen, one of the cow's four stomach compartments. They work together to breakdown what the cow eats, turning the feed into energy and feed in the cow. In 1 ml of rumen fluid, approx 25 billion bacteria, 10 million protozoa and 10 thousand fungi that is more than quadrillion of rumen microbes per cow. The microbes are predominantly strict anaerobes due to the physiological conditions within the rumen.

### Introduction

In response to a rapidly growing human population and the economic burden of feed costs, a major goal of the livestock industry is to improve feed efficiency. The conversion of feedstuffs to usable energy depends on assimilation of nutrients, which is contingent upon fermentation by the rumen microbes. The symbiotic relationship between ruminants and rumen microorganisms is paramount to the conversion of low-quality feed to high-quality end products. As the livestock industry faces a challenge to produce more pounds of meat and milk to meet the demands of the growing human population, continued improvements in production efficiency are essential.

The rumen is sometimes called the "paunch". It is lined with papillae for nutrient absorption and divided by muscular pillars into the dorsal, ventral, caudo-dorsal, and caudo-ventral sacs. The rumen acts as a fermentation vat by hosting microbial fermentation. About 50 to 65 percent of starch and soluble sugar consumed is digested in the rumen. Rumen microorganisms (primarily bacteria) digest cellulose from plant cell walls, digest complex starch, synthesize protein from non protein nitrogen, and synthesize vitamin B and vitamin K. Rumen pH typically ranges from 6.5 to 6.8. The rumen environment is anaerobic (without oxygen).



Gases produced in the rumen include carbon dioxide, methane, and hydrogen sulfide. The gas fraction rises to the top of the rumen above the liquid fraction.

### **Development of rumen microflora**

During the first few weeks of life, the rumen is not yet functional and the vast majority of suckled milk from the dam bypasses the rumen through the esophageal groove into the abomasum; the rumen wall villi responsible for nutrient absorption are also not yet developed, and the reticulo-rumen and omasum are rudimentary. Development of the rumen microflora is essential to rumen function, development, and immune response and enables efficient transition from the preruminant to ruminant stage.

### **Rumen Microflora**

**Bacteria:** The most predominant microbes in the rumen belong to the bacterial kingdom and are largely strict anaerobes and account for more than 95% of the population in the rumen. Rumen epithelium-attached bacteria, known as epimural bacteria, are the most distinct from the other bacterial microbes and play important role in host metabolic activity. Epimural bacteria are often facultative anaerobes and can produce urease that they help maintain rumen anaerobiosis. Many bacteria have multiple substrate targets; the main substrates include cellulose, hemicellulose, pectin, starch, and amino acids.

### **Cellulytic Bacteria**

Cellulose is highly prevalent in ruminant forage-based diets; the primary cellulolytic bacteria are *Fibrobacter succinogenes*, *Ruminococcus flavefaciens*, and *Ruminococcus albus*. The most common bacteria that degrade hemicellulose, also ubiquitous in forage diets, include *Butyrivibrio fibrisolvens*, *Prevotella ruminicola*, *Ruminococcus flavefaciens*, and *Ruminococcus albus*. Although cellulose and hemicellulose are the most predominate substrates in a forage-based diet, pectin is also present and is fermented by *B. fibrisolvens*, *P. ruminicola*, *Lachnospira multiparus*, *Succinivibrio dextrinosolvens*, and *F. succinogenes* bacterial species.

### **Starch Fermenting Bacteria**

Rumen bacteria that play a prominent role in starch fermentation are *B. fibrisolvens*, *P. ruminicola*, *F. succinogenes*, *Clostridium* species, *Streptococcus bovis*, *Ruminobacter amylophilus*, *Succinimonas amylolytica*, and *Selenomonas ruminantium*. Other substrates are also present in the rumen beyond the main components of fiber and starch.

### **Aminoacidlytic Bacteria**

Amino acids are readily fermented by bacteria belonging to the genus *Prevotella* to produce adenosine triphosphate (ATP).



### **Archaea**

The rumen archaea are composed primarily of methane-producing microbes, known as methanogen. The majority of rumen archaea (92.3%) belong to the genera *Methanobrevibacter*, *Methanomicrobium*. Most methanogens utilize H<sub>2</sub> and sometimes format to reduce CO<sub>2</sub> to CH<sub>4</sub>, whereas others oxidize methyl groups to CO<sub>2</sub> and ultimately reduce the methyl group to CH<sub>4</sub>. These methanogens rely on the production of H<sub>2</sub> from other rumen microbes (often protozoa), but by utilizing and removing H<sub>2</sub> from the rumen environment, they reduce the inhibitory effects of H<sub>2</sub> accumulation on subsequent fermentation.

### **Protozoa**

Both ciliates and flagellates protozoa are present. Although the number of protozoa in the entire rumen microbial population is low, protozoa comprise nearly 50% of the biomass in the rumen. It has been reported that up to 62% of the cellulolytic activity in the rumen is attributed to protozoa.

### **Fungi**

Fungi may account for 5% to 20% of the microbial biomass in the rumen and harbor enzymes necessary for digestion of plant materials including cellulase, xylanase, and other hydrolases. Fungi play a major role in fiber digestion and due to their complex and substantial enzymatic activity may have competitive advantages over bacteria, specifically digesting plant structural material.

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