CURRENT EXPLORATIONS OF NUTRITION AND RUMEN MICROBIOME OF CATTLE: A COMPREHENSIVE EVALUATION OF THE REVIEW LITERATURE

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The rumen microbiota consists of a great diversity of prokaryotic and eukaryotic microorganisms that allow the ruminants to degrade complex plant fibres and polysaccharides. Understanding the significance of the rumen microbiome in physiological, production, and health-related traits has increased dramatically. This review first aimed to bring current information on the rumen microbial composition of cattle, factors affecting the composition, and the effect of microbial composition on physiology, production, and health into a single document. In addition, it was planned to identify the knowledge gap, barriers, and solutions using existing research findings, and to suggest new research areas to enhance the microbial profile of the rumen. The focus of the review and objectives were identified based on a preliminary literature survey using already published databases during the last 20 years. An advanced literature survey was performed to collect additional information. The microbial profile of the rumen in cattle varied with age, breed, diet as well as individual characteristics, whereas many research had focused on the efficient improvement of the rumen microbiome by changing the diet. Higher feed intake of animals correlated with several bacterial taxa such as Firmicutes. Some bacterial taxa like Bacteroidetes. Firmicutes, and Proteobacteria had a great influence on improving milk yield, fat, and protein contents. Fungal taxa like Aureobasidium, Cryptococcus, and Sarocladium had a great influence on the weight gain of beef cattle. The conflict in microbial relationships also contributes to a number of metabolic illnesses like bloating, acidosis and reticuloperitonitis. The present review summarized that research related to rumen microbial profile to enhance the production and health has become efficient with the advance of molecular approaches. Further, future studies should be directed to individual responses and enhancement of rumen microbiota.

Keywords: Fermentation, Metabolism, Microbiome, Rumen