Microbial endocrinology represents the intersection of 2 seemingly disparate fields, microbiology and neurobiology, and is based on the shared presence of neurochemicals that are exactly the same in structure in the host as well as in the microorganism. The ability of microorganisms not only to respond to but also to produce many of the same neurochemicals that are produced by the host, such as during periods of stress, has led to the introduction of this evolution-based mechanism which has a role in the pathogenesis of infectious disease as well as the microbiota-gut-brain axis. Production of neurochemicals by microorganisms usually employs the same biosynthetic pathways as those utilized by the host, indicating that acquisition of a neurochemical-based signaling system in the host may have been acquired due to lateral gene transfer from microorganisms. Such recognition of a shared signaling system suggests that there is a common mechanism by which the host may interact with the microbiota in a microbiota-gut-brain axis. Production of neurochemicals by microorganisms usually employs the same biosynthetic pathways as those utilized by the host, indicating that acquisition of a neurochemical-based signaling system in the host may have been acquired due to lateral gene transfer from microorganisms. Such recognition of a shared signaling system suggests that there is a common mechanism by which the host may interact with the microbiota in a bi-directional fashion influencing aspects of both stress and health. In the case of infectious disease pathogenesis, the consideration of a microbiota-endocrinology–based mechanism in which infectious bacteria can directly respond to host-derived neurochemicals such as those present during periods of stress has demonstrated, for example, that the prevalent use of catecholamine-based synthetic drugs in the clinical setting contributes to the formation of biofilms in indwelling medical devices leading to increased morbidity and mortality. At the same time, the ability of the microbiota to produce neurochemicals that constitute the host’s own neuronal signaling systems means that a common pathway exists for the microbiota to influence host neurophysiology. Currently, we have little understanding of the neurochemical environment of ruminants, whether that within the rumen microbiota or the host tissue. Application of a microbial endocrinology-based approach may lead us to the identification of novel mechanisms by which the ruminant interacts with its microbiota and thereby provide new approaches to health and disease management.

Key Words: neurochemicals, bacteria, stress

The rumen and intestines in the cattle digestive tract house 2 complex, symbiotic microbial communities, which are established early in a calf’s life and have complementary roles in cattle health and productivity. It is unclear how these vital relationships between microbes and host cells are maintained throughout life, but the ability of prokaryotic and eukaryotic cells to communicate with one another by direct contact or through secreted or shed chemical substances may be a factor. Commensal microflora of the intestinal tract shape gut immunity and enteric nervous system development, and are essential for feed assimilation and energy production. Some bacteria produce neurotransmitter substances, and microbial products such as exotoxins and pathogen-associated molecular patterns are recognized by host cells in the intestinal mucosa. The host in turn may influence establishment and maintenance of ruminal and intestinal microbial communities. Neurotransmitters and other chemical signals secreted into the intestinal lumen may influence bacterial growth and virulence. Epithelial cells in the rumen wall and intestinal mucosa are key points of microbe-host contact regulated by nerves and hormones. In the intestinal mucosa, the sympathetic neurotransmitter and stress hormone norepinephrine increases bacterial internalization into Peyer’s patches, the inductive site for gut immunity. Norepinephrine enhances non-intimate adherence of Escherichia coli to colonic epithelial cells and promotes vectorial transport of secretory immunoglobulin A across the small and large intestinal mucosae, which stabilizes mucosa-associated bacteria. Stress activation of the sympatho-adrenomedullary system has profound effects on the digestive tract and on the microbial communities housed within it. Knowledge of the bidirectional communication between host cells and prokaryotic bacteria is steadily increasing for the intestinal tract, but is lacking with respect to the rumen. By understanding the cellular and chemical factors that impact ruminal and intestinal microbial populations, we can potentially identify targets and develop strategies for maintaining the well-being and enhancing the productivity of cattle and other ruminants.

Key Words: microbe-host interaction, norepinephrine, epithelium

Rumen microbiology research has evolved in the last decade to understand their diversity, metabolic functions and different interactions between host and microbes, particularly with the intervention of molecular biology techniques. To date, hundreds to thousands of microbial phylotypes have been identified from various rumen systems using the culture-independent molecular-based approaches. Exploring compositional and functional characteristics of the rumen microbiome can improve the understanding of its role in rumen function. Recent research has applied targeted high-throughput sequencing to assess the microbiota by the determination of presence or absence of unique microbial taxa. However, such information does not provide the functional aspect of the microbiota, such that this type of research is lacking in ruminants. In the past, we have developed various approaches aiming at enhancing the functional outcomes of rumen microbiota. First, we have developed a pipeline to enhance the outcomes of rumen metagenomic data set using a microbial genome reference based approach. Second, we developed a method to study the active rumen microbiomes at both taxonomic and functional levels using total RNA-sequencing based metatranscriptomics approach. These methods were then applied to study rumen microbiome from cattle raised under different dietary feeding, with different feed efficiencies and/or methane emissions. The in-depth understanding of rumen microbiome from numerous animal trials provides a more thorough understanding of rumen microbial metabolic functions and how they can be affected by various factors. Such knowledge is vital for enhancing nutrient utilization and improving animal productivity through enhanced rumen function.

Key Words: rumen microbiome, metagenomics, metatranscriptomics