

# Microbiology of the Gut

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Microorganisms such as bacteria, archaea, fungi, viruses, and protozoa in the gastrointestinal (GI) tract impact many aspects of animals including digestion, efficiency of nutrient utilization, regulation of energy metabolism, GI diseases, control of inflammation and immunity, synthesis of vitamins B12 and K, and possibly psychological state. Clearly, knowledge of the critical roles of bacteria in fermentation for digestion has been studied, but the complexity and biases of culture-dependent methods have made a thorough assessment of the hundreds of bacteria present difficult - particularly since bacteria do not live as individual species or strains in the GI tract but instead as dynamic communities. An explosion of information coinciding with the advent of culture-independent analysis of the microbiome, however, has provided valuable insight as to the microbes present in the GI tract and in other locations of the body. Indeed, sequencing of the 16S rRNA bacterial gene using high-throughput methods has identified a variety of bacterial communities in many species with the majority of information coming from the Human Microbiome Project. Culture-independent measures have greatly expanded what is known about the variation of these bacterial communities as well as their diversity throughout the GI tract and other locations in and on the body. In addition, studies have determined that various bacterial communities exist throughout the GI tract such that an assessment of feces only represents the community of the large intestine. Certainly, bacteria in the rumen, gastric stomach, and small intestine play important functions not assessed through analysis of the fecal microbiome. However, much of the current research has studied the impact of GI microbiome in humans, so fecal material has been the predominant sample type analyzed. Results suggest that the bacterial community in human feces may be related to long-term diet, obesity, and inflammatory status of colon. Development of the GI tract microbiome is rapid after birth, although it likely begins *in utero* as meconium, an infant's first intestinal discharge, is not sterile. The development of the GI tract microbiome is also related to birth mode (vaginal vs caesarian), feeding method (milk vs formula/milk replacer), and antibiotic use. These factors potentially set the basis for the GI bacterial community structure throughout life. As new tools in metatranscriptomics, proteomics, and metabolomics emerge, a more complete picture of the relationships within and functions of GI microbial communities can be elucidated. Understanding the microbial community of the GI tract will likely provide new opportunities to enhance digestion of food/feed while supporting animal health.