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WORK EXPERIENCE & EDUCATION

2012-Present Current affiliation (Shinshu University)

1994-2012 The National Federation of Dairy Co-operative Associations.

Received Agricultural Ph.D. degree from Hokkaido University in 2011

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“Dynamics and functionalities of animal intestinal microflora explored with molecular approaches”

The resident microbiota in animal gastrointestinal (GI) tract is one of the most complex ecosystems usually containing up to 10^{14} bacteria classified into more than 500 species. The microbial activity of this community has an important metabolic and protective function in the GI tract and thus plays a major role in the nutrition and health of the host. For many years, descriptions of bacterial diversity in the GI tract were based mainly on the use of anaerobic culture techniques but this area has been received renewed interest due to the development of various molecular techniques, especially those based on the 16S rRNA genes. These technologies not only provided a phylogenetic framework of the GI tract microbiota, the majority of which has not yet been cultured, but also advanced insights into the impact of host and environmental factors on the microbiota community structure and dynamics.

However, our understanding of this complex community and its interactions with the host is still far from complete. For instance, little is known about how members of the indigenous microbiota interact with their mammalian hosts to establish mutually beneficial relationships. Novel high-throughput molecular technologies such as metagenomics approaches and microarrays have enabled rapid progress in characterizing the taxonomic composition, metabolic capacity, and immunomodulatory activity of the human gut microbiota, allowing us to establish its role in human health and disease. Furthermore, these approaches have shown that the prokaryotic genomes of the human microbiota encode a spectrum of metabolic capabilities beyond that of the host genome, making the microbiota an integral component of human physiology.

Microbial community in the rumen of cattle is also of great interest because of possible links to economically or environmentally important traits : enhanced digestion of polymeric feed components and methane emission. Metagenomic analyses of rumen microbiome have unveiled numerous novel genes coding for enzymes involved in digestion and metabolism of feed components. Advances in such technology thus highlight the promise of the approaches for characterizing the community structure and linking this with the functions of the rumen microbiota. It provides an unprecedented opportunity to achieve the enzymatic machinery involved in the degradation of plant structural polysaccharides as well as the mitigation of methane emission.

Here, a critical summary is provided of current molecular ecological approaches for studying the GI microbiota and exploring further integrity of its function.