Introduction to the series of papers on animal microbiomes

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There is nothing new except that which is forgotten ... Marie Antoinette

Arguably, the first microbiome study, conducted by Antonie van Leewenhoek with his primitive microscopes, was reported in 1673. For much of the next 300 years, microbiologists worked hard to isolate and study organisms in pure culture. It has only been in the past 30 years that interest has arisen in the study of more complex microbial systems, requiring more powerful methodologies and new approaches.

Studies in the 1990s investigating microbial communities in the environment have led to a tremendous explosion of work on the human microbiome, including the Human Microbiome Project, and the notion of the animal's microbiome as the 'other genome'. Workers studying animal microbiomes are beginning to catch up and are now able to take advantage of the tools and databases in this exciting new area.

Although considerable progress has been made, especially during the past 5 years, what is needed now is hypothesis testing and not merely descriptive studies. It is time to put more emphasis on understanding the dynamics of beneficial microbes as well as the pathogens. In particular, we need to learn how members of the microbiome interact in the animal and, on a mechanistic level, how they affect various host processes. Although most current studies have described the compositions of microbiomes and even tried to infer functional activities based on their genomes, in the future studies that employ metatranscriptomics, proteomics, and metabolomics will allow us to dissect the functional nature of the microbiome. However, in the rush to embrace the latest 'omic' tools, we should not dismiss some of the older methodologies, especially culture, for they too can have value.

There are numerous challenges facing workers in this field. In addition to practical questions such as what is the most useful taxonomic level to study microbiomes in different circumstances – phylum, family, species, gene – and getting sufficient funding to perform these experiments with a large number of animals under controlled conditions without doubt will be a substantial challenge.

This special series of papers in Animal Health Research Reviews brings together expert reviews on a broad range of work in the area of animal microbiomes. And for this, the guest editors are extremely grateful to all of the authors and reviewers who shared their experience, their ideas, and their insights.

Our 'virtual symposium' starts with an excellent overview by Sarah Highlander on various high throughput methods that can be used to study microbiomes. The review by Tomas *et al.* presents a thought provoking review of work on the rat as an animal model for studying human gastrointestinal microbiota. Papers by Minamoto *et al.* and Hooda *et al.* provide outstanding reviews on the current status of our understanding of microbial communities in the feline and canine gastrointestinal tracts. The review by Yeoman *et al.* delves into the special features of the chicken gut microbiota. This issue of AHRR also contains two papers on swine microbiomes. The first, by Isaacson *et al.* provides an up-to-date discussion on swine gastrointestinal microbiome; the second, by Kernaghan *et al.* reviews work that has been done on the microbiome of a little studied tissue, the tonsil of the soft palate. The paper by Costa and Weese provides a very thoughtful critical review of studies on the microbiome of the equine gastrointestinal tract. In the final paper in this series, Taschuk and Griebel take a slightly different tack and offer an insightful detailed discussion of the effects that commensal microbiome have on the development of the mucosal immune system in the ruminant gastrointestinal tract.

As is evident from the papers in this issue of AHRR (Table 1), studies of animal microbiomes are fraught with numerous challenges, but they offer great promise for

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Table 1. Contributors and topics in the 'virtual symposium' on animal microbiomes

Sarah K. Highlander	High throughput sequencing **methods** for microbiome profiling: application to food animal systems
Julie Tomas, Philippe Langella and Claire Cherbuy	The intestinal microbiota in the **rat** model: major breakthroughs from new technologies
Yasushi Minamoto, Seema Hooda, Kelly S. Swanson and Jan S. Suchodolski	**Feline** gastrointestinal microbiota
Seema Hooda, Yasushi Minamoto, Jan S. Suchodolski and Kelly S. Swanson	Current state of knowledge: The **canine** gastrointestinal microbiome
Carl J. Yeoman, Nicholas Chia, Patricio Jeraldo, Maksim Sipos, Nigel D. Goldenfeld and Bryan A. White	The microbiome of the **chicken** gastrointestinal tract
Richard Isaacson and Hyeun Bum Kim	The intestinal microbiome of the **pig**
Shaun Kernaghan, Adina R. Bujold and Janet I. MacInnes	The microbiome of the tonsil of the soft palate of **swine**
Marcio C Costa and J Scott Weese	The **equine** intestinal microbiome
Ryan Taschuk and Philip J Griebel	Commensal microbiome effects on mucosal **immune system** development in the **ruminant** gastrointestinal tract

improved characterization of microbes of microbiomes and enhanced ability to use the information to promote animal health in the future. If nothing else, hopefully, some of the following papers will inspire the reader to think more about the 'microbial gestalt' of their favorite animal species.