COMPANION ANIMALS SYMPOSIUM: Microbes and health

K. S. Swanson,*† J. S. Suchodolski,‡ and P. J. Turnbaugh§

*Department of Animal Sciences and †Division of Nutritional Sciences, University of Illinois, Urbana, 61801; ‡Gastrointestinal Laboratory, Department of Small Animal Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, 77843; and §Faculty of Arts and Sciences Center for Systems Biology, Harvard University, Cambridge, MA 02138

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The Companion Animals Symposium on “Microbes and Health” was held at the Joint Annual Meeting of the American Dairy Science Association, Poultry Science Association, Asociación Mexicana de Producción Animal, Canadian Society of Animal Science, and American Society of Animal Science in Denver, CO, July 11 to 15, 2010. This American Society of Animal Science symposium was organized to encourage the participation of animal scientists interested in companion animal biology. The intent was to invite speakers that had expertise not only in studying the trillions of microbes that colonize the gastrointestinal tract and oral cavity of companion animals and humans (i.e., the microbiota), but also in veterinary clinical medicine or molecular biology. Thus, this symposium provided traditional animal scientists with new information pertaining to the emerging set of metagenomic techniques used to study the composition and function of microbial communities and their impact on the physiology of a wide range of animal hosts while providing a platform for increased interaction between the basic and applied scientists in this field.

The program was organized so that the session chair briefly introduced the overall topic of microbes and health, after which invited speakers focused on specific aspects pertaining to microbial phylogeny, metagenomics, and transcriptomics in healthy or diseased populations. The symposium began with a brief presentation by Swanson (Kil and Swanson, 2011), first discussing how microbial communities affect companion animal gastrointestinal development and health. After identifying some of the challenges that exist in studying complex microbial communities, Swanson discussed the strengths of emerging DNA-based assays and the manner by which multiple international human microbiome projects have begun to generate massive reference databases of microbial genes and genomes from multiple body habitats. The presentation concluded with a listing of many of the key areas of study as they pertain to host-microbial interactions in companion animals, including gastrointestinal health, oral health, obesity, urinary tract health, and dermatology.

Buddington and Sangild (2011) began the regular portion of the session by describing the interactions between the host and the most densely populated microbial community, that of the gastrointestinal tract, with emphasis on gut development in young mammals. Although humans and other mammals are born germ free, a complex community of bacteria, many of which are thought to originate from the maternal urogenital tract, rapidly colonize their gut. Large fluctuations in the composition of the gut microbiota are observed throughout the first few months after birth because of an ill-defined collection of selective pressures, potentially including changes in diet, maturation of the gut immune system, ecological interactions among resident microbes, and stochastic effects. The importance of colonization for normal gut development, especially concerning the immune system, has been demonstrated by comparisons of germ-free animal models with colonized ones. Germ-free animals have gut tissue that is overly reactive to stimuli, and they have an increased risk of adverse and inflammatory responses, such as necrotizing enterocolitis. Although attempts to identify bacterial triggers of gastrointestinal diseases, such as inflammatory bowel disease (IBD), have so far been unsuccessful, the technological advances made over the past decade will ideally have a key role in advancing this research field. These findings may lead to a new array of treatment strategies for common diseases through the use of probiotics (i.e., live ingested microbes) and prebiotics (i.e., nondigestible carbohydrates that promote the growth or activity of beneficial microbes).
The next presentation summarized recent molecular-phylogenetic and metagenomic studies that have revealed highly complex microbial communities in the gastrointestinal tracts of dogs and cats (Suchodolski, 2011). Emerging evidence implicates commensal intestinal microbiota in the pathogenesis of various disorders, such as small intestinal dysbiosis and idiopathic IBD. The currently proposed pathogenic mechanism behind IBD involves an abnormal interaction between commensal intestinal microbiota and the intestinal immune system in genetically susceptible individuals. Recent molecular studies have revealed decreased species richness, increases in Proteobacteria, and decreases in Clostridium clusters IV and XIVa in dogs with IBD. Granulomatous colitis of boxer dogs has been associated with the presence of adherent and invasive Escherichia coli. Furthermore, underlying genetic defects in the host innate immunity have been identified in dogs and cats with chronic enteropathies. These include a differential expression of Toll-like receptors in various dog breeds and defects in the gene encoding neutrophil cytosolic factor 2 in boxer dogs with granulomatous colitis, leading to a defunct ability to eliminate intracellular pathogens. These findings point to an abnormal interaction between the innate immune system and commensal intestinal microbiota in the pathogenesis of canine and feline enteropathies and emphasize the importance of developing strategies for maintaining a balanced intestinal ecosystem.

The next presentation was focused on the oral microbiota and periodontal disease in dogs and humans (Marshall-Jones, 2010). More than 500 microbial species inhabit the oral cavity, an environment that contains several unique niches in itself, including the supra- and subgingival locations of the teeth, the tongue, and other soft tissues (e.g., cheeks). The unique aspect of the mouth is the dentition, which provides a solid and permanent fixture on which biofilms may form. Periodontal disease is the most widespread oral disease in dogs (60 to 80%). Although the specific organisms and processes contributing to disease are unclear, dental plaque is considered an etiological agent. Plaque bacteria and their enzymes are thought to initiate a host immune response, including matrix-metalloproteases that lead to tissue damage and inflammation. Detailed knowledge is available regarding plaque formation, microbes, and disease in humans. Little is known in the dog and cat, however. Commensal oral microbes of dogs and cats are quite different from those of humans, based on current knowledge. In fact, the classic periodontal pathogens of humans (e.g., Porphyromonas gingivalis) are often not detected in the mouths of dogs or cats. Thus, the application of human research may be limited in this regard, justifying more research in dogs and cats.

The final presentation (Gootenberg and Turnbaugh, 2011) addressed the potential benefits of merging the study of gutobiotic (i.e., germ-free and intentionally colonized) animal models with culture-independent metagenomic methods to study the human microbiota. These animal models allow researchers to control and closely monitor several important variables, such as dietary macro- and micronutrient composition, microbial exposure, and host genotype. Studies of “humanized” rats, pigs, and mice have demonstrated that the human microbiota can be reproducibly transferred to animal models, maintaining much of the original diversity and functional properties of the donor sample. A recent metagenomic analysis of humanized mice enabled temporal analysis of the effect of dietary shifts on the gut microbiota, the succession of microbial colonization in infant mice, and the biogeography of the gut microbiota along the entire length of the gastrointestinal tract. Although most of the interanimal microbiota transplantation studies to date have focused on human donor samples, these same design principles could be applied to studies in a wide range of animals, with the hope of revealing the mechanisms that govern community assembly, structure, and function across the mammalian phylogeny.

To conclude, the Companion Animals Symposium, “Microbes and Health,” served as an opportunity for animal scientists interested in companion animal biology to interact with some of the world leaders in the gastrointestinal and oral microbiology of companion animals and humans. The importance of the microbial communities inhabiting unique niches throughout the body is beginning to be more widely appreciated, and the recent development of metagenomic tools, coupled with studies of germ-free and colonized animals models (Gootenberg and Turnbaugh, 2011), promises to begin to reveal the molecular mechanisms underlying health and disease. As we learn more about the microbial communities or processes influencing gastrointestinal (Suchodolski, 2011) and oral health (Marshall-Jones, 2010), improved dietary, pharmaceutical, or management strategies may be devised to prevent or treat disease.

**LITERATURE CITED**


