

Companion Animals Symposium: Microbes and Health

291 Introduction: Microbes and health. K. S. Swanson*, *University of Illinois, Urbana.*

Despite human claims to superiority, it can be legitimately argued that microbes rule the world. Whether it is an ocean reef, a landfill, or a gastrointestinal tract, invisible communities of highly active and adaptable microbes prosper. Over time, mammalian species developed a symbiosis with microbes that are now important inhabitants not only in the intestines, but also in the mouth, skin, and vaginal tract. In the gut, commensal microbes are a critical element for the development of the gut-associated lymphoid tissue, pathogen resistance, nutrient digestion (fermentation), and intestinal epithelial cell gene expression. Proper balance is key, however, as microbial imbalances contribute to inflammatory bowel diseases, gastrointestinal cancers, and other intestinal disorders. Microbial colonization also plays a crucial role in oral disease, which is now the most common form of disease in dogs and cats. Recent evidence also suggests a role of intestinal microbiota on the metabolic phenotype and disease risk (e.g., obesity, metabolic syndrome) of the host. A significant hindrance to studying gut microbiota has traditionally been the inability to effectively identify and quantify microbial species. Researchers have been reliant upon microbial culturing methods that are not only laborious, time-consuming, and often inaccurate, but also greatly limited in scope. High-throughput, DNA-based methods have been developed recently and have changed the research environment dramatically. Recent experiments using these techniques have begun to characterize the identity and metabolic activity of the entire gastrointestinal microbiota and their association with health and disease. Despite this recent progress, more research is needed to provide deeper coverage of the oral and intestinal microbiomes, evaluate effects of age, genetics, or environment (e.g., diet) on its composition and activity, and identify its role in disease.

Key Words: microbe, gastrointestinal health, oral health

292 Bacterial influences on mammalian gut development. R. K. Buddington*, *University of Memphis, Memphis, TN.*

The interactions between the gastrointestinal tract (GIT) and the resident bacteria play critical roles in influencing GIT development and the health and nutrition of young mammals and begin at birth when the sterile GIT is colonized by bacteria from the environment, particularly the maternal urogenital tract. Postnatal changes in the bacterial assemblages continue for months and are the result of shifts in dietary inputs, maturation of GIT and host physiology, and interactions among the resident bacteria. The interactions between the bacteria and the developing GIT are evident from the different patterns of GIT gene expression for gnotobiotic and conventional animals. Although postnatal development progresses smoothly for most animals, the overly reactive mucosal immune system of the immature GIT and the unstable assemblages of bacteria increase the risk of adverse and damaging inflammatory responses, such as neonatal necrotizing enterocolitis (NEC). Attempts to identify specific bacteria as causative agents of NEC have been inconclusive. The association of NEC with fermentation of undigested components of the diet and altered proportions of volatile fatty acids suggest bacterial metabolites may be better predictors of NEC risk than species composition. This presentation describes how the development, health, and disease resistance of the GIT are responsive to management of the bacterial assemblages. Antibiotic induced disturbances in the developing assemblages of bacteria can have profound and long-term adverse impacts on the GIT and the host. Encouraging results have been achieved by administration of probiotics

to accelerate acquisition of bacterial assemblages that promote health. However, to be effective probiotics must be matched with the unique GIT environment of each host, and perinatal exposure is essential for colonization and long-term persistence. Prebiotics are an alternative that represent metabolic substrates for specific health promoting bacteria and include galactooligosaccharides, fructooligosaccharides and other complex carbohydrates.

Key Words: gastrointestinal, neonatal, infant

293 Microbes and gastrointestinal health of dogs and cats. J. S. Suchodolski*, *GI Laboratory, Texas A&M University, College Station.*

Recent molecular studies have revealed a complex microbiota in the canine and feline intestine, compromising several thousand bacterial, fungal, and viral phylotypes. The microbiota plays an important role in the development of the immune system. Studies have demonstrated a microbial dysbiosis in humans, cats and dogs with inflammatory bowel disease (IBD). In humans, the microbiota is implicated as inflammation develops in areas with the highest bacterial counts and antibiotic therapy improves clinical signs in a subset of patients. In rodent models with genetic susceptibility, intestinal inflammation develops only in the presence of bacteria. Current theories for the development of chronic intestinal inflammation favor a combination of environmental factors, the intestinal microbiota, and a genetic susceptibility of the host (e.g., polymorphism in the NOD2/CARD15 in Crohn's disease). New evidence suggests that genetic susceptibility predisposes to infection with enteric organisms. Polymorphisms in specific genes (e.g., interleukin-8, lactoferrin) have been associated with diarrhea in humans. It is suspected that intestinal inflammation causes a dysbiosis toward gram-negative bacteria, perpetuating the disease in genetically susceptible hosts. Most common microbial changes observed in intestinal inflammation are a decrease in the bacterial phyla *Firmicutes* and *Bacteroidetes*, with concurrent increases in *Proteobacteria*. Individuals with intestinal inflammation show a reduced diversity of *Clostridium* clusters XIVa and IV (i.e., *Lachnospiraceae*, *Ruminococcaceae*, *Faecalibacterium prausnitzii*), suggesting that these bacterial groups, important producers of short-chain fatty acids, may play an important role in promoting intestinal health. Similar changes (i.e., reduction in *Clostridium* clusters XIVa and IV) have been observed in dogs and cats with IBD. Boxer dogs with histiocytic ulcerative colitis harbor adherent and invasive *Escherichia coli* (AIEC) that share similarities to AIEC isolates obtained from ileal tissues of humans with Crohn's disease. Underlying genetic susceptibilities are currently an area of intense research in companion animals with chronic enteropathies.

Key Words: 16S rRNA gene, pyrosequencing, IBD

294 The oral microflora and periodontal health in dogs. Z. Marshall-Jones*, *Waltham Centre for Pet Nutrition, Waltham-on-the-Wolds, Melton Mowbray, Leicestershire, UK.*

The microbial ecology of the oral cavity is rich with over 500 species estimated to be represented. This diversity may be enhanced by the variety of niches available. Biofilms reside both on the dentition, as dental plaque, and the oral mucosa including the buccal mucosa and the tongue with its undulating papillae providing a range of microenvironments. Salivary microbial populations meanwhile exist in a planktonic niche outside of these biofilm communities.

Studies suggest periodontal disease is the most widespread oral health disease in dogs with between 56 and 80% of dogs estimated to have periodontal disease. Although the specific organisms or processes involved are unclear, the aetiological agent of periodontal disease is considered to be dental plaque. Virulence determinants including enzymes secreted by plaque bacteria are thought to initiate the host immune response, including the activation of host matrix-metalloproteinases, which are the major cause of tissue damage and inflammation. Despite the relatively detailed knowledge regarding plaque formation and the microorganisms associated with disease in humans, the oral microflora in dogs is relatively undescribed. Several studies have assessed the species in the canine oral cavity and detected substantial differences in the oral flora of dogs compared to humans. Studies of canine plaque and saliva have found as little as 28% of organisms identified by 16S rRNA gene sequence are indigenous to the human oral flora. In one such study over half of the taxa cultured were novel species with no similar organisms represented in the GenBank database. The classic human periodontal pathogens, including *Porphyromonas gingivalis*, *Tannerella forsythensis*, and *Aggregatibacter actinomycetemcomitans* were not detected in canine subgingival plaque. Disparity between *Porphyromonas* isolates from humans and companion animals were initially detected as differences in the catalase activity between human *P. gingivalis* (catalase-negative) and veterinary isolates. The veterinary *P. gingivalis*-like organisms are now thought to represent a related species *Porphyromonas gulae*. The potential of these species in disease causation is however unclear.

295 Using “humanized” mice to study the effect of diet on the human gut microbiome. P. Turnbaugh*, *Harvard University, Cambridge, MA.*

Unraveling the interrelationships between diet, energy harvest, and the gut microbial community (microbiota) and its gene content (microbiome) is confounded by large variations in microbial ecology between individuals. We created an animal model of the human gut ecosystem by transplanting fresh or frozen adult human fecal microbial communities into germ-free C57BL/6J mice. Metagenomic analysis of the temporal, spatial and intergenerational patterns of bacterial colonization showed that these humanized mice were stably colonized, and reproduced much of the bacterial diversity of the donor’s microbiota. Switching from a low-fat, plant polysaccharide-rich diet to a high-fat/high-sugar “Western” diet shifted the structure of the microbiota within a single day, changed the representation of metabolic pathways in the microbiome, and altered microbiome gene expression. Reciprocal transplants involving various combinations of donor and recipient diets revealed that colonization history influences the initial structure of the microbial community, but that these effects can be rapidly altered by diet. Humanized mice fed the Western diet have increased adiposity; this trait is transmissible via microbiota transplantation. Humanized gnotobiotic mice will be useful for conducting proof-of-principle “clinical trials” that test the effects of environmental and genetic factors on the gut microbiota and host physiology.

Key Words: gut, microbes, diet