

## Nonruminant Nutrition Symposium: Nutrition and Gut Microbiome

**764 Whole-body systems approaches for gut microbiota-targeted, preventive healthcare.** L. Zhao\*, *Shanghai Jiao Tong University, Shanghai, China.*

Humans are superorganisms whose phenotypes are dictated by 2 integrated genomes, the genetically inherited human genome (23,000 genes) and the environmentally acquired human microbiome (over 1 million genes). The 2 genomes must work in harmonious integration to maintain health. Gut microbiota constitutes the majority of the human microbiome. Bioactive substances (antioxidants, vitamins or various toxins) produced by particular members of gut microbiota may get into bloodstream via enterohepatic circulation or impaired gut barrier to affect host immunity and metabolism. Undigested nutrients from the diet or drugs that arrive in the colon play a dominating role in shaping the structure of the gut microbiome. For example, accumulating evidence supports the new hypothesis that obesity and related metabolic diseases develop because of low-grade, systemic and chronic inflammation provoked by increased antigen load from a diet-disrupted gut microbiota. On the other hand, changes of host health induced by biotic or abiotic perturbations may also disrupt gut microbiota which in return can further deteriorate host health. Due to the tight integration of gut microbiota into human global metabolism, molecular profiling of urine metabolites and gut microbiome can provide an ideal window for reflecting physiological functions of the host. Variations in gut microbiota and urine metabolites can thus be employed as emergent functions for quantitative assessment and monitoring of health at the whole-body level with the advantage of measuring human health based on the results of interactions between the 2 genomes and the environment rather than just host genomic sequences. Large-scale, longitudinal cohort studies in conjunction with these whole-body systems approaches will generate pre-disease biomarkers with predictive power, thus making preventive health management of populations with rapidly changing disease spectrums possible through re-engineering of the imbalanced gut microbiome with specially designed drugs/diets.

**Key words:** gut microbiome, host health, additives

**765 Dietary modulation of the gut microbiota by prebiotics and probiotics.** G. R. Gibson\*, *University of Reading, Reading, UK.*

The human large intestine is an intensively colonized area containing bacteria that are health promoting, as well as pathogenic. This has led to functional food developments that fortify the former at the expense of the latter. Probiotics have a long history of use in humans as live microbial feed additions. In contrast, a prebiotic is a non digestible food ingredient that beneficially affects the host by targeting indigenous components thought to be positive. Dietary carbohydrates, such as fibers are candidate prebiotics but most promise has been realized with oligosaccharides. As prebiotics exploit non-viable food ingredients, their applicability in diets is wide ranging. Main prebiotic targets at the moment are bifidobacteria and lactobacilli (although this may change as our knowledge of the flora diversity and functionality expands). Any dietary component that reaches the colon intact is a potential prebiotic, however much of the interest in the development of prebiotics is aimed at non-digestible oligosaccharides such as inulin type fructooligosaccharides (FOS) and trans-galactooligosaccharides (TOS). Other prebiotics are emerging. Some prebiotics occur naturally in several foods such as leek, asparagus, chicory, Jerusalem artichoke, garlic, artichoke, onion, wheat, banana and oats. However, these foods contain only trace levels, so developments have taken the approach of

removing the active ingredients from such sources and adding them to more frequently consumed products to attain levels whereby a prebiotic effect may occur, e.g., cereals, confectionery, biscuits, infant feeds, yogurts, table spreads, bread, sauces, drinks, etc. The rationale for using probiotics and prebiotics to reduce risk will be reviewed. On the contrary, the role of the gut flora in various clinical states will be briefly discussed. Building upon this information, research will be presented on the generation and testing of a novel prebiotic (TOS) which has led to the development of products designed to improve immune health in the elderly, reduce the symptoms of Irritable Bowel Syndrome and help prevent traveler's diarrhea.

**Key words:** gut microbiome, host health, pro pre biotic

**766 Effect of dietary change on equine and swine gut microbiota.** K. Daly\*<sup>1</sup>, A. Darby<sup>2</sup>, N. Hall<sup>2</sup>, C. Proudman<sup>3</sup>, D. Bravo<sup>4</sup>, and S. P. Shirazy-Beechey<sup>1</sup>, <sup>1</sup>*Department of Molecular and Cellular Physiology, University of Liverpool, Liverpool, UK,* <sup>2</sup>*Department of Functional and Comparative Genomics, University of Liverpool, Liverpool, UK,* <sup>3</sup>*Equine Division, Department of Veterinary Clinical Sciences, University of Liverpool, Liverpool, UK,* <sup>4</sup>*Pancosma, Geneva, Switzerland.*

The large intestinal tracts of mammalian species contain vast populations of microorganisms that interact with each other and co-exist with their host in a mutually beneficial relationship. The total number of these microorganisms (~10<sup>14</sup>) exceeds the number of cells in the body by 10-fold. It is becoming increasingly evident that intestinal microbiota play an important role in maintaining the health and well being of the host. Several environmental factors such as age, disease, antibiotics and diet are known to influence the composition of the microbiota, and subsequent microbial metabolites produced. By far the biggest influence on the composition and activity of the gut microbiota is diet. Domesticated animals, such as the horse, are often fed diets that differ significantly to their natural forage. Indeed, dietary change and the amount of grain fed to horses are two important variables that have emerged from a number of studies as risk factors for acute intestinal disease. Our studies, using molecular biological strategies, have indicated that there are significant modifications in microbiota and fermentation products when horses were maintained on grain based diets, compared to horses maintained on traditional forage; these changes became much more exaggerated in horses affected by a form of dietary-induced intestinal disease. To determine any alterations in gut microbiota that occur during development in piglets, from suckling to weaning, and in response to changes in diet, from hydrolysable to fermentable carbohydrates and addition of nutritional supplements, we have employed a combination of 454 pyrosequencing and 16S rRNA-oligonucleotide hybridization using samples of colonic contents taken from piglets weaned onto various controlled diets. We shall report on the characteristics of microbial transformations that occur.

**Key words:** gut microbiome, host health, pyrosequencing

**767 Dietary manipulation of canine and feline microbiota.** K. S. Swanson\*, *Department of Animal Sciences and Division of Nutritional Sciences, University of Illinois, Urbana.*

The canine and feline colon is inhabited by a complex and dense community of bacteria, archaea, fungi, protozoa, and viruses. A signifi-

cant hindrance to the field has been the inability to effectively identify and quantify microbial species, their metabolic end products, and mechanisms by which they affect host health. Molecular tools, including qPCR, FISH, DGGE, RFLP, and DNA sequencing, have overcome many of the limitations of culture-based techniques. Recently developed high-throughput techniques (e.g., 16S rRNA microarrays; next-generation sequencing) have dramatically changed the research landscape in regards to gastrointestinal microbiology. These techniques are now being used to characterize canine and feline gastrointestinal microbiota and identify the effects of diet, age, and disease on these communities. Continued use of DNA-based techniques to characterize microbial phylogeny and metabolic capacity, along with other technologies to analyze microbial RNA (gene expression), protein, and metabolite profiles, will increase our understanding of host-microbe relationships in pets. Composition of the commensal microbiota is dependent on several factors, including host genotype, age, and diet. The main energy source of colonocytes (i.e., SCFA) is derived primarily from microbial fermentation of carbohydrate-based energy substrates reaching the large bowel. Dietary proteins may also serve as fermentable materials, but result in the production of putrefactive compounds such as ammonia, biogenic amines, and phenols that are implicated as the major odor components of feces and may have negative influences on gut health. The supplementation of dietary fibers, prebiotics, or probiotics has become a popular strategy for improving gut health in humans and pets. In the past couple decades, over 50 peer-reviewed publications have reported the effects of these dietary ingredients in dogs and cats, with many demonstrating beneficial changes in gastrointestinal microbiota, fecal fermentative end products, and stool characteristics. Our current understanding and future research opportunities in this field will be reviewed.

**Key words:** gut microbiome, feline, canine

**768 Rumen microbiota, assessed by evolving techniques.** R. J. Wallace\*, *Rowett Institute of Nutrition and Health, University of Aberdeen, Aberdeen, UK.*

Our present understanding of ruminal microbiology was built initially upon a few epoch-changing advances made many years ago: Gruby and Delafond's (1843) microscopic observations of protozoa; Hungate's (1947) appreciation of the anaerobic nature of the rumen that led to novel culture techniques for the bacteria; Orpin's (1975) realization that some flagellate protozoa were in fact zoospores of anaerobic fungi, until then a contradiction in terms. Isolation and study of pure cultures was invaluable in understanding the likely role of different species of bacteria, protozoa or fungi in the overall fermentation. Cultivation techniques could not deal with more than a very small number of samples, however, in attempting to assess the effects of diet or manipulation on rumen ecology. Even then, it was known that such analyses were flawed by cultivation bias. We have since passed through a period of evolving molecular techniques, based mainly on ss-rRNA gene analyses. Cloning and sequencing provided community analyses that were free from the biases imposed by cultivation techniques. Related techniques for microbiome analysis quickly followed (DGGE, TGGE, RFLP, ARISA). qPCR and FISH enabled groups or species to be quantified. Now, next-generation sequencing has exploded onto the scene. A bacterial genome can be sequenced in an afternoon, and sequencing of the entire community's DNA – the metagenome – is about to become routine. Are these seismic increases in information that we can generate about the rumen microbiota as epoch-changing as the historic discoveries? And can they be used to improve the efficiency of animal production, animal welfare and environmental impact? Very recent genomic and metagenomic results confirm that there is a huge amount that we do not understand about genes and organisms that break down plant fiber. Other studies on fatty acid biohydrogenation have come to a similar kind of conclusion, reaching almost an impasse in identifying key genes and species. We now need equally innovative thinking and technology to ensure that the answer to both questions will be yes.

**Key words:** rumen microbiome, host health