

# Horse Species Symposium: Recent advances in the microbiome and physiology of the hindgut of the horse and dog

**671 Canine intestinal microbiology and metagenomics.** Jan S. Suchodolski\*, *Gastrointestinal Laboratory, Texas A&M University, College Station, TX.*

Recent molecular studies have revealed a complex microbiota in the dog intestine, consisting of thousand bacterial, fungal, and viral phylotypes. Convincing evidence has been reported linking changes in microbial communities to acute and chronic gastrointestinal inflammation, especially in canine inflammatory bowel disease (IBD). Most common microbial changes observed in intestinal inflammation are decreases in the bacterial phyla *Firmicutes* (i.e., *Lachnospiraceae*, *Ruminococcaceae*, *Fecalibacterium*) and *Bacteroidetes*, with concurrent increases in *Proteobacteria* (i.e., *E. coli*). Due to the important role of microbial-derived metabolites for host health, it is important to elucidate the metabolic consequences of gastrointestinal dysbiosis and a better understanding of the physiological pathways is helpful to potentially pinpoint specific diseases. Novel approaches such as shotgun sequencing of DNA allow characterizing functional changes in the bacterial metagenome in gastrointestinal disease. Furthermore, wide scale and untargeted measurements of metabolic products derived by the host and the microbiota in intestinal samples allow a better understanding of the functional alterations that occur in gastrointestinal disease. For example, changes in bile acid metabolism, short-chain fatty acid concentrations, and tryptophan pathways have recently been reported in humans and dogs. Also, metabolites associated with the pentose phosphate pathway were significantly altered in chronic gastrointestinal inflammation and indicate the presence of oxidative stress in dogs with IBD. Better understanding of the interactions of microbial-derived metabolites and the host will yield insights into the pathophysiology of gastrointestinal diseases. Furthermore, some of these metabolic pathways can be targeted to develop better treatment approaches.

**Key Words:** microbiome, metabolome

**672 The microbiome of the horse hindgut.** Véronique Julliard\*, *AgroSup Dijon, Dijon, France.*

The collective genomes of the different microbes (bacteria, fungi, protozoa, yeasts, archaea and bacteriophages) that live inside the horse hindgut compose its intestinal microbiome. This microbiome can be characterized by its microbial community structure (diversity and composition) and function (metabolic activities and resulting end products). It plays a vital role due to its capacity of hydrolysing and fermenting cell-walls into volatile fatty acid that represent an essential energy source for the host. Although not fully understood, it also completes important roles in health and several diseases pathophysiology. Traditionally, the microbes of the horse hindgut were studied using culture dependent techniques. More recently culture-independent methods have been used and have brought new insights. Regarding the ciliate protozoa community, 18S rRNA gene pyrosequencing allowed identifying 15 genera in the feces of pasture-fed horses. Most of these genera had been identified in previous microscopy studies. The 2 clades *Methanobrevibacter ruminantium* and *Methanocorpusculum* and their relatives were showed to dominate the fecal Archaea community using 16S rRNA gene pyrosequencing as it had been reported via cultural techniques. Regarding the bacteria community several studies have been done with molecular methods such as fingerprint techniques or more recently 16S rRNA gene pyrosequencing.

In the cecum and colon, *Firmicutes* and *Bacteroidetes* are the 2 predominant phyla. *Firmicutes* comprise *Clostridium* spp., *Ruminococcus* spp., *Butyrivibrio* spp., and *Eubacteria* spp. that play a major role in fiber degradation. The cellulolytic species *Fibrobacter succinogenes* was identified recently as the second most abundant species in the horse feces. Although a phylogenetic core bacteria community appeared to exist in all regions of the large intestine of healthy horses, strong inter-horse variations on bacteria populations are often reported. The microbiome can also be affected by several factors. The effect of the diet has been the most extensively studied on the microbial community structure and function. Understanding the microbiome changes and the factors in cause can help manipulating the microbiome to improve nutrition and health.

**Key Words:** horse, microbiome, hindgut

**673 Evaluation of the effectiveness of the establishment of an equine research herd with dual cannulation at the ileum and cecum.** Torea L. Bova\*, Cate Mochal-King, Brian J. Rude, Ben C. Weed, Lauren B. Hodge, and Molly Nicodemus, *Mississippi State University, Mississippi State University, MS.*

Cecal and ileal cannulations have been utilized to determine equine digestibility and gastrointestinal physiology, but these cannulations were limited to a single segment of the digestive tract. While these earlier cannulations were successful, the recovery process was difficult for the single cannulation; and thus, the objectives of this case study were to document the post-operative recovery of a dual cannulation surgery in equines and to determine the effectiveness of establishing a dual cannulated research herd. Eight Hackney/Shetland pony cross mares (BW: 200 to 250 kg) were selected for development of a cannulated herd. Initial incisions for placement of the ileal and cecal cannulas were done on the same day. A novel ileal cannula was constructed of a biologically compliant silicone, which included a flange to assist with surgical anchoring to improve stoma formation. For the cecal cannula, a rumen cannula (#7C; Bar Diamond, Parma, ID) was placed into the cecal fistula similar to previous studies. Ileal stomas adhered after 14 d and the cecal stoma at 10 to 14 d post-surgery. Full vital analysis occurred every 4 h for 4 wk post-surgery. Due to granulation at the cecal site, the most common complication for all ponies was increased rectal temperature of 38.9 to 40.9°C from 4 to 10 d post-surgery with a mean ranging from 37.8 to 38.5°C and a standard deviation ranging 0.59 to 1.4. Five ponies showed signs of colic approximately 1 to 2 times during recovery. After surgical recovery, 5 ponies remained healthy during 7 mo of observations, demonstrating vital signs within normal ranges and no colic signs. The 3 ponies that died had intestinal leakage into the abdominal cavity due to lack of adherence of ileum to the body wall resulting in peritonitis within 2 wk post-surgery. Compared with other tubing or polyvinyl chloride options, the current novel ileal cannula design was effective as the ileal cannula design formed a stoma and was easily maintained for the remaining 5 ponies. With a survival rate of 63% at 7 mo post-surgery, the dual cannulation of the ileum and cecum was considered successful.

**Key Words:** equine cannulation, ileum, cecum

**674 Can the microbiome of the horse be altered to improve digestion?** Josie A. Coverdale\*, *Texas A&M University, College Station, TX.*

Common management practices such as high concentrate diets, low forage quality, meal feeding, and confinement housing have an effect on intestinal function, specifically large intestinal fermentation. The microbiome of the equine large intestine is a complex and diverse ecosystem, and disruption of microflora and their environment can lead to increased incidence of gastrointestinal disorder. Digestion in the horse can be improved through a variety of mechanisms such as feedstuff selection, forage quality, feeding management, and inclusion of digestive aids. These digestive aids such as prebiotics and probiotics have been used to improve digestibility of equine diets and stabilize the microbiome of the large intestine. Probiotics, or direct fed microbials, have been widely used in horses for treatment and prevention of gastrointestinal disease. The introduction of these live, beneficial microorganisms orally into the intestinal tract has yielded variable results. However, it is difficult to compare data due to variations in choice of organism, dosage, and basal diet. While there are still many unanswered questions about the

mode of action of successful probiotics, evidence suggests competitive inhibition and enhanced immunity. Lactic acid bacteria such as *Lactobacillus*, *Bifidobacterium*, and enterococci and *Saccharomyces* yeast have all been successfully used in the horse. Use of these products has resulted in improved fiber digestibility in horses offered both high starch and high fiber diets. When high concentrate diets were fed, probiotic supplementation helped maintain cecal pH, decreased lactic acid concentrations, and enhanced populations of cellulolytic bacteria. Similarly, use of prebiotic preparations containing fructooligosaccharide (FOS) or mannanoligosaccharides (MOS) have improved DM, CP, and NDF digestibility when added to high fiber diets. Furthermore, use of FOS in horses reduced disruptions in colonic microbial populations after an abrupt change in diet and altered fecal VFA concentrations toward propionate and butyrate. Potential use of prebiotics and probiotics to create greater stability in the equine microbiome affects not only digestibility but also health of the horse.

**Key Words:** horse, microbiome, prebiotic