RUMINANT NUTRITION: SYMPOSIUM: THE RUMEN MICROBIOME AND NUTRITIONAL HEALTH AND PRODUCTION

0625 [Withdrawn]

0626 The microbiome and health. G. B. Penner[*1], E. Khafipour[2], J. C. Plaizier[2], and L. L. Guan[3], [1]University of Saskatchewan, Saskatoon, Canada, [2]Dep. of Animal Science, University of Manitoba, Winnipeg, Canada, [3]Dep. of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.

The linkage among the microbial community and health outcomes in monogastric species has been well documented along with demonstrated evidence for species-dependent health consequences. While a symbiotic relationship between the microbial inhabitants and the ruminant host has been accepted from the perspective of feed digestion, the mechanisms for host-regulation of the microbial community is not well understood and the influence of individual microbial species on health outcomes has been poorly defined. Major challenges include understanding the structure of the digesta associated and epimural populations and how these populations change across the gastrointestinal tract. Current research efforts are examining the establishment of the microbiome in newborn calves to gain an improved understanding of the colonization process. It is currently accepted that the dominant phyla within the microbiome consist of firmicutes, bacteroidetes, and proteobacteria and that these remain relatively stable for most of a healthy cow's life. However, variations in the composition, proportion, and functional properties of the rumen and intestinal microbiomes exist among individuals. To help understand the relationship between the microbiome and animal health, ruminal acidosis induction protocols have developed and proven to be an excellent model. In fact, it has been demonstrated that changes in the microbial community structure, specifically and increase in *Escherichia coli*, can be related to the systemic immune response induced by ruminal acidosis. However, it is still not clear whether the translocation of antigens induced by ruminal acidosis occurs in the reticulo-rumen or more distally in the gastrointestinal tract. The latter is especially important given the large changes in epithelial barrier function and marked changes in the concentration of lipopolysaccharide across the gastrointestinal tract. An in depth understanding of both the microbiome and host gastrointestinal physiology is key to addressing this challenging area.

Key Words: gastrointestinal tract, health, microbiome

0627 Use of genomics and transcriptomics to identify strategies to lower ruminal methanogenesis. T. A. McAllister[*1], L. L. Guan[2], G. Henderson[3], G. Attwood[3], and P. H. Janssen[3], [1]Agriculture and Agri-Food Canada, Lethbridge, AB, [2]University of Alberta, Edmonton, Canada, [3]AgResearch Limited, Grasslands Research Centre, Palmerston North, New Zealand.

Globally, methane emissions account for 40 to 45% of greenhouse gas emissions (GHG) from ruminant livestock, with more than 90% of these emissions arising from enteric fermentation. Reduction of carbon dioxide to methane is critical for efficient ruminal fermentation, as it prevents the accumulation of reducing equivalents in the rumen. Methanogens exist in a symbiotic relationship with rumen protozoa, fungi and within biofilms associated with feed and the rumen wall. Genomics and transcriptomics are playing an increasingly important role in defining the ecology of ruminal methanogenesis and identifying avenues for its mitigation. Genomic approaches have provided information on changes in abundances as well as the species composition of the methanogen community among ruminants that vary naturally in their methane emissions, their feed efficiency and response to methane mitigators. Sequencing the genomes of rumen methanogens has provided insight into surface proteins that may prove useful in the development of vaccines and allowed assembly of biochemical pathways for use in chemogenomic approaches to lowering ruminal methane emissions. Metagenomics and metatranscriptomic analysis of entire rumen microbial communities are providing new perspectives on how methanogens interact with other members of this ecosystem and how these relationships may be altered to reduce methanogenesis. Identification of community members that produce anti-methanogen agents that either inhibit or kill methanogens could lead to the identification of new mitigation approaches. Discovery of lytic archaeophage that specifically lyse methanogens is one such example. Efforts in using genomic data to alter methanogenesis have been hampered by a lack of sequence information that is specific to the microbial community of the rumen. Programs such as the Hungate 1000 and the Global Rumen Census are increasing the breadth and depth of our understanding of global ruminal microbial communities, steps that are key to using these tools to further define the science of ruminal methanogenesis.

Key Words: ruminal methanogenesis, genomics, transcriptomics

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313

0628   Increasing condensed corn distillers solubles alters the rumen microbiome of beef cattle.

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Five ruminally fistulated steers were used in a 5×5 Latin square design to determine the effects of increasing dietary fat from corn distillers solubles (CDS) on the rumen microbiome. Treatments included a corn-based control (CON), and four levels of CDS (0, 10, 19, and 27%) in a coproduct-based (corn gluten feed and soybean hulls) diet. Fat concentrations were formulated to 3, 5, 7, and 9%, respectively, for diets containing CDS, and all steers were fed to ad libitum intake once daily. After 18 d of adaptation to the diet, ruminal samples were collected 3 h post-feeding and separated into solid and liquid fractions. Bacterial DNA was extracted from the solid fraction after physical homogenization. Real-time quantitative PCR was used to determine dietary effects on the relative abundance of culturable bacterial species. Orthogonal contrasts were used to compare diets formulated to similar fat concentrations (CON and 10% CDS), determine linear, quadratic, and cubic effects of CDS inclusion, and compare CON with all CDS treatments. Of the evaluated species, *Selenomonas ruminantium* was the most prevalent at 0.5 to 1.9% relative abundance. Moreover, *Selenomonas ruminantium* increased with greater CDS inclusion ($P < 0.001$). *Anaerovibrio lipolytica* was affected by treatment ($P < 0.001$); steers fed 0% CDS had eight-fold greater relative abundance than any other treatment. A quadratic effect was observed for *Butyrivibrio proteoclasticus,* with the greatest relative abundance at 0 and 27% CDS and the lowest at 19% CDS. *Butyrivibrio proteoclasticus* was also greater in steers fed 10% CDS compared with CON. *Eubacterium ruminantium* was not affected by treatment but was the second most abundant species evaluated (0.03 to 0.1%). *Fibrobacter succinogenes* was affected by treatment ($P = 0.005$) with a marked decrease for steers fed 19 and 27% CDS, yet relative abundance remained similar for steers fed CON and 10% CDS. *Prevotella bryantii* had a cubic response ($P = 0.005$) to CDS inclusion with the greatest relative abundance for steers fed 10% CDS, followed by the lowest abundance for steers fed 19% CDS. *Megasphaera elsdenii* was affected by treatment ($P < 0.001$); the lowest relative abundance was observed for steers fed CON compared with CDS diets ($P < 0.001$), and the greatest relative abundance was observed for steers fed 19% CDS. Results suggest the rumen microbiome is impacted by substantial changes in dietary CDS.

Key Words: microbiome, distillers solubles, dietary fat

0629   The microbiome composition of the hindgut is altered following weaning in dairy calves: impact of different weaning strategies.

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Composition of calf intestinal microbiota has immediate and long-term effects on health and productivity of the animal. Weaning stress may alter the colonization process due to dietary shifts and environmental factors. The objective of this study was to examine the effects of different weaning strategies on fecal microbiota of dairy calves. Twenty-four male and 20 female Holstein dairy calves were blocked according to gender and birth weight and randomly assigned into a step-down weaning (SW) or an abrupt weaning (AW) treatment at birth. Calves had free access to water and starter intake throughout the experiment and 9 L/d of milk until d 36 of life and weaned on d 49 of life. Calves in SW group were weaned gradually by reducing milk intake from 9 to 4.5 L/d from d 37 to d 48 while the AW calves were abruptly weaned on d 49 by reducing milk intake from 9 to 0 L/d. Fecal samples were collected on d 36 (pre-weaning) and on d 54 (post-weaning) of life. DNA was extracted and V4 region of 16S rRNA gene was amplified and subjected to paired-end Illumina sequencing. The output paired-end reads were merged using PANDASeq assembler and analyzed using QIIME. The resulted operational taxonomic units (OTUs) were aligned to Greengenes database. Alpha-diversity of bacterial community was calculated using different richness estimators. Differences in β-diversity of microbiota across treatments and time points were tested using PERMANOVA. Diversity of fecal microbiota was low before weaning but increased significantly post-wean indicating new species benefited from dietary change. However, different weaning strategies did not affect α and β-diversity measures. Before weaning, firmicutes (49.2%) and bacteroidetes (42.2%), proteobacteria (3.8%), tenericutes (1.7%), and actinobacteria (1.5%) were predominant phyla. Another 16 phyla were present at low abundance, each less than 1% of population. After weaning, the percentage of firmicutes and actinobacteria decreased to 42% and 0.4%, while proteobacteria, and tenericutes increased to 5.6% and 3.9%, respectively. Different weaning strategies did not affect fecal bacterial population at the phylum level. In total, 415 core OTUs, defined as OTUs shared amongst 50% or more of the calves, were different between pre- and post-wean. However, none of the core OTUs was affected by weaning strategies. Data showed fecal microbiota of dairy calves was undergoing a drastic change and became more diversified during the weaning process. However, weaning strategies had no substantial effect.

Key Words: calves, fecal microbiota, weaning

0630 Effects of different dry period managements on rumen microbiome composition. H. Khazanehei[*1], S. Li[1], J. C. Plaizier[1], and E. Khafipour[2], [1]*Dep. of Animal Science, University of Manitoba, Winnipeg, Canada,* [2]*Dep. of Medical Microbiology and Infectious Diseases, Winnipeg, MB, Canada.*

The effects of two different dry period managements on rumen bacterial population were examined during pre- and postpartum periods. Twenty-four Holstein dairy cows were paired according to their expected calving date and randomly assigned to one of the two treatments. Treatments included a 60-d dry period (60-d trt) with separate far-off and close-up diets and a 40-d dry period (40-d trt) during which only the close-up diet was fed. The far-off diet contained 1.28 Mcal/kg NE_l, 14.7% CP, and 50% NDF on a DM basis. The close-up diet contained 1.43 Mcal/kg NE_l, 14.6% CP, and 38% NDF. A common lactation diet was fed to all cows after calving, which contained 1.69 Mcal/kg, 17.6% CP, and 31% NDF. The forage portion of ration consisted of timothy hay, barley, and corn silage, and the concentration portion consisted of soybean, canola, barle, and wheat. Rumen fluid was sampled using stomach tube at wk -2, -1, +1, +2 and +7, relative to calving. DNA was extracted, normalized and used for amplification of the V4 region of bacterial 16S rRNA and subjected to Illumina sequencing. The QIIME pipeline was used for downstream data analyzing. After removing all chimeric reads, sequences were assigned to operational taxonomic units and aligned to Greengenes database. The α- and β-diversity of rumen microbiota were calculated using Chao1 and Unifrac distance matrices, respectively. PERMANOVA procedure was used to compare differences in bacterial communities between treatments and sampling time points. Partial least square discriminant analysis (PLS-DA) of SIMCA was performed to identify taxa associated with each treatment and time point. PERMANOVA analysis revealed significant differences in rumen bacterial composition between pre- and postpartum in the 60-d trt ($P < 0.01$); however, no difference was observed between pre- and postpartum in the 40-d trt ($P < 0.2$). At the genus level, *Bulleidia*, *Coprococcus* and *Ruminococcus* increased in 40-d trt compared with 60-d trt prepartum ($P < 0.05$). After calving, *Olsenella* increased and *Coprococcus*, *Bifidobacterium* and *Treponema* decreased ($P < 0.05$) in the 40-d trt compared with the 60-d trt. At the phylum level, no significant difference was observed between treatments prepartum ($P < 0.9$). However, after calving, spirochaetes and chloroflexi populations decreased ($P < 0.05$) while proteobacteria and firmicutes increased ($P < 0.05$) in 40-d trt compared with 60-d trt. Differences between treatments, at the phylum and genus levels during pre- and postpartum were likely due to longer consumption of close-up diet in the 40-d trt compared to the 60-trt.

Key Words: dairy cow, dry period management, rumen microbiome, illumina sequencing