digestibilities for CB1, CB2, and PB for each feed; and 3) endogenous matter production for each feed. Then, similar to ELS, NE, ME, and DE are computed from TDN. In the MLS, CH, is computed based on the stoichiometric relationship of VFA produced in the rumen. The BCNRM includes an optimizer to assist with diet formulation and balancing, an ability to perform stochastic modeling, and a table generator that allows the user to create tables of nutrient requirements through an optimization procedure. The BCNRM was compared with NRC (1996, 2000) levels of solution 1 (L1) and 2 (L2) using data from 20 experiments (n = 2539 pen-fed animals). For ME-allowable gain, ELS and L1 predictions were nearly identical ( $r^2$  of 0.999, root of mean square error (RMSE) of 0.018 kg/d, and accuracy (Cb) of 0.998). The MLS predictions tended to be greater than L2 predictions by approximately 0.158 kg/d, though there was a strong correlation between them ( $r^2$  of 0.999 and Cb of 0.9). The opposite was observed for MP-allowable gain, and MLS and L2 predictions were nearly identical (r<sup>2</sup> of 0.999, RMSE of 0.023 kg/d, and Cb of 0.998) while ELS and L1 predictions differed by 0.234 kg/d  $(r^2 \text{ of } 0.975 \text{ and Cb of } 0.9)$ . A stochastic simulation (n = 5000)predicted 122 and 97 g CH<sub>4</sub>/d for ELS and MLS, respectively, with a 67% prediction overlap.

Key Words: computer, modeling, simulation, spreadsheet

## NON-NUTRITION: THE FUTURE OF NUTRITION?

**1029** Why the intersection of microbiology and neurobiology matters to animal health: microbial endocrinology as a means to examine the hostmicrobiota interface. M. Lyte\*, *Iowa State University, Ames.* 

Microbial endocrinology represents the intersection of two seemingly disparate fields, microbiology and neurobiology, and is based on the shared presence of neurochemicals that are exactly the same in structure in the host as well as in the microorganism. The ability of microorganisms not only to respond to but also to produce many of the same neurochemicals that are produced by the host, such as during periods of stress, has led to the introduction of this evolution-based mechanism that has a role in the pathogenesis of infectious disease as well as the microbiota-gut-brain axis. Production of neurochemicals by microorganisms usually employs the same biosynthetic pathways as those utilized by the host, indicating that acquisition of a neurochemical-based signaling system in the host may have been acquired due to lateral gene transfer from microorganisms. Such recognition of a common shared signaling system suggests that there is a common mechanistic pathway by which the host may interact with the microbiota in a bi-directional fashion influencing aspects of both disease and health. In the case of infectious disease pathogenesis, the consideration of a microbial endocrinology-based mechanism in which infectious bacteria can directly respond to host-derived neurochemicals, such as those present during periods of stress, has demonstrated, for example, that the prevalent use of catecholamine-based synthetic drugs in the clinical setting contributes to the formation of biofilms in indwelling medical devices, leading to increased morbidity and mortality. At the same time, the ability of the microbiota to produce neurochemicals that constitute the host's own neuronal signaling systems means that a common pathway exists for the microbiota to influence host neurophysiology. One of the most prevalent examples by which neurochemical production by microbiota may influence the host's brain and ultimately behavior can be seen with the increasing use of probiotics as a means to influence behavior. Numerous probiotics in current use produce large amounts of neurochemicals, such as GABA, which are known to have well-recognized roles in behavior. That both the host and microorganism produce and respond to the same neurochemicals means that there is bi-directionality contained within the theoretical underpinnings of microbial endocrinology. Such a shared pathway argues for a role of microbiota-neurochemical interactions in animal health.

Key Words: gut endocrinology, microbiome

## **1030** The gut microbiome as a virtual endocrine organ: implications for host physiology and behavior. G. Clarke\*, University College Cork, Cork, Ireland.

The gut microbiome exerts a marked influence on multiple aspects of host physiology including not just host metabolism and body composition but also brain function and behavior. This impact relates to its ability to produce or indirectly control a large range of hormonal agents that can play a regulatory role in the activity of local and distal systems and organs. Dysfunction of the hypothalamic-pituitary-adrenal (HPA) axis in particular has been a striking consequence to disrupting the gut microbiota in preclinical studies. The translational relevance of these findings is apparent in stress-related disorders, such as irritable bowel syndrome. Unlike other endocrine organs, however, the gut microbiota exhibits compositional plasticity and can itself be subject to fluctuation as a result of stressors or dietary factors with implications for the associated functionality. This includes stress experienced prenatally, postnatally, and during adulthood. Farm animals regularly encounter a variety of such stressors related to handling practices, weaning, housing systems, and transport that potentially affect welfare and productivity. While optimizing nutrition to promote the gold standard assembly and maturity of the microbiota is one option to counteract the detrimental impact of stress exposure, more targeted interventions may be necessary at various critical points of control across the lifespan. Understanding how best to manipulate the gut microbiota to control host physiological and behavioral responses could have important implications in multiple settings, including the prevention or treatment of stress-related disorders. Expanding this research to farm animals may pave the way for new strategies to enhance animal health and to meet farm production targets.

**Key Words:** endocrinology, gut physiology, microbiome

### 1031 Threats to gut health in production animals.

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Demand for meat protein is steadily increasing due to an expanding population and increasing wealth in populous nations. With finite supplies of arable land under increasing pressure, productivity gains through increased efficiency of animal production are essential for future food security. However, regulations and public opinion have restricted the use of hormone supplements and antibiotics for growth enhancement. There is thus a focus on other non-nutrient additives, including phytonutrients. The gastrointestinal mucosa is a major determinant of feed conversion efficiency, as it represents the first line of defense against enteric pathogens and is susceptible to disruption by events, such as weaning, environmental (notably heat) stress, and infection. Heat stress is increasing with global warning and a shift of agricultural production into tropical regions; in feedlot cattle and in intensive pig faming, it can cause decreases in feed intake and growth, and in extreme cases may result in death. The gut leakiness of heat exposure is associated with oxidative stress in the intestine, which is manifested by compromised glutathione peroxidase activity and increased levels of oxidized glutathione. A further threat to gut health is rapid and early weaning. Rapid weaning is required to maintain breeding productivity and effective herd management. However, it causes stress that is not associated with gradual weaning, which occurs for animals in the wild. The weaning transition in farmed pigs is accompanied by adverse changes in intestinal morphology, including villus atrophy, increased crypt depth, reduced absorptive capacity, and reduced brush border enzyme activity. The weaned animals lose weight, some animals die, and those that lose significant weight lag behind their litter mates in weight gain. In pigs, first litters show greater post-weaning deficits. The third major threat, which is exacerbated by heat or post-weaning stress and by intensification of production, is reduced resistance to enteric pathogens. Intestinal bacterial infections can reduce average growth rates by as much as 40%. The major hormone that promotes mucosal growth and repair is glucagon-like peptide 2 (GLP-2), which is released from L-type enteroendocrine cells. These cells bear receptors that are potential targets for food additives. In addition, a number of phytonutrients and other food additives have antioxidant or mucosal protective qualities, for example cinnamaldehyde and selenium. There is need to further advance understanding of mucosal biology and the actions of non-nutrient additives in production animals to improve gut health, animal health, and productivity.

Key Words: gut health, mucosal integrity, heat stress, weaning, enteritis

1032 The gut microbiome and its role in the development and function of newborn calf gastrointestinal tract. N. Malmuthuge<sup>1</sup>, G. Liang<sup>2</sup>, P. J. Griebel<sup>3</sup>, and L. L. Guan<sup>\*1</sup>, <sup>1</sup>Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, <sup>2</sup>University of Alberta, Edmonton, AB, Canada, <sup>3</sup>Vaccine and Infectious Disease Organization, University of Saskatchewan, Saskatoon, SK, Canada.

Microbial colonization plays important roles in neonatal gut health. However, studies on gut microbial composition and how it can shape host function during early life in ruminants are limited. Here, we report some of our recent efforts in studying host-microbial interactions in neonatal calves focusing on small intestines collected from animals from soon after birth to 6 wk of age. The use of molecular-based approaches revealed extensive colonization of the gut with active microbiota during birth. Composition of the newborn gut microbiota was significantly different from the maternal microbiota in the birth canal and the environmental microbiome. Further differences in diversity were observed between tissue-attached (epimural) and content-associated microbiomes. Epimural communities consisted primarily of Pseudomonadaceae and Propionibacteriaceae, whereas Propionibacteriaceae, Prevotellaceae, Ruminococcaceae, and Lachnospiraceae dominated luminal contents. Within the first week of life, Veillonellaceae and Lachnospiraceae dominated epimural communities, while Bacteroidaceae, Clostridiaceae, and Lactobacillaceae dominated content communities. Investigation of calf small intestinal transcriptomes using RNA-seq revealed that the expression of immune-related genes at birth was different from three other developmental stages (week 1, 3, & 6) in the jejunum and ileum. The expression of genes related to tight junction proteins, antimicrobial peptides, NOD-like receptors, regulatory T cell markers, and cytokines underwent dynamic changes within the first week of life along with the observed changes in microbiome. This suggests that the first week postpartum is a critical developmental period for the intestinal epithelial barrier, and development of the mucosal immune system may be responding to the changing microbial composition. This conclusion is supported by evidence of strong correlations between expression of mucosal immune-related genes and total bacterial population in different gut regions at different ages. This study provides evidence that the establishment of the small intestinal-specific microbiota begins during birth, and its composition deviates significantly from the dam's microbiota. This process may be modulated primarily by host selection. The establishment of such "individualized" gut microbiota may be an important regulator of gut tissue and immune function development. Our findings provide fundamental knowledge regarding host-microbial interactions in neonatal calves and may support future development of more effective strategies to improve neonatal gut health.

Key Words: calf, gut health, mucosal immunity

1033 From pre- to post-weaning: the adaptations of the gastrointestinal tract of the young calf. M. Steele\*1, S. J. Meale<sup>2</sup>, K. Wood<sup>3</sup>, and G. B. Penner<sup>4</sup>, <sup>1</sup>Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, <sup>2</sup>INRA, Unité Mixte de Recherches sur les Herbivores, St Genès Champanelle, France, <sup>3</sup>Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, <sup>4</sup>Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada.

The ruminant gastrointestinal tract (GIT) faces the challenge of protecting the host from luminal contents and pathogens while supporting the absorption and metabolism of nutrients for growth. The GIT of the calf in early-life undergoes some of the most rapid microbial and structural changes documented in nature, and it is these adaptations in GIT function that make the young calf susceptible to gastrointestinal disease and disorders. Despite these challenges, the GIT of the calf has a certain degree of plasticity and can sense nutrient supply and respond to bioactive ingredients. For example, the pre-weaned calf can adapt to meal size by altering abomasal emptying as a means of controlling nutrient delivery to the intestine, thereby stabilizing blood metabolites. Despite this plasticity, research has historically focused on the transition during weaning and characterizing ruminal papillae development using microscopy. Through the use of molecular-based approaches, we have recently shown that delaying the age of weaning and providing a step-down weaning protocol is associated with a more gradual shift in ruminal microbiota to a post-weaned state. In addition to ruminal adaptations during weaning, nutrient flow to the lower gut changes dramatically during weaning, coinciding with a wide array of structural and microbiological changes. A study examining structural and gene expression changes suggests that the lower gut of the dairy calf undergoes alterations that may reduce barrier function when solid feeds are consumed. Additionally, a recent in vivo calf study revealed that the weaning transition increases total gut permeability of the calf. Interestingly, some evidence suggests that the upper and lower gut are able to communicate with the forestomach, meaning that a nutrient can be sensed in the lower gut and cause subsequent adaptations in the forestomach. An improved understanding of how diet, microbiota, and functional ingredients interact to impact growth and barrier function of the intestinal tract would greatly benefit the industry. A mechanistic understanding of such adaptations would also aid in the formulation of specific management regimens and provision of the functional ingredients required to support or enhance gut function in young calves.

**Key Words:** calf, gastrointestinal tract, weaning, functional nutrition

**1034** Metabolic effects of dietary pungent spices on the gut in animal models. K. Srinivasan\*, Department of Biochemistry and Nutrition, CSIR-Central Food Technological Research Institute, Mysore, India.

The beneficial influence of pungent spices was examined in experimental rats on (i) the fluidity of intestinal brush border membrane (BBM), (ii) the activity of intestinal membrane bound enzymes, and (iii) ultrastructural alterations in the intestinal epithelium. Groups of Wistar rats were maintained on dietary black pepper (0.5%), red pepper (3.0%), ginger (0.05%), and spice bioactive compounds-piperine (0.02%) and capsaicin (0.01%)-for 8 wk. A membrane fluidity study using an apolar fluorescent probe showed increased BBM fluidity in all of the spice fed animals. This was corroborated by decreased cholesterol: phospholipid ratio in jejunal and ileal regions of the intestine. These dietary spices stimulated the activities of BBM enzymes-glycyl-glycine dipeptidase, leucine amino peptidase, and  $\gamma$ -glutamyl transpeptidase in jejunal mucosa, suggesting a modulation in membrane dynamics due to the apolar spice bioactive compounds interacting with surrounding lipids and hydrophobic portions in the protein vicinity. Scanning electron microscopy of the intestinal villi in these spice treatments revealed alteration in the ultrastructure, especially an increase in microvilli length and perimeter, which would mean a beneficial increase in the absorptive surface of the small intestine, providing for an increased bioavailability of micronutrients. Thus, dietary spices-black pepper, red pepper, and ginger were evidenced to induce alteration in BBM fluidity and passive permeability property, associated with the induction in the increased microvilli length and perimeter, resulting in an increased absorptive surface of the small intestine. Everted segments of duodenum, jejunum, and ileum portions of small intestines isolated from rats fed piperine, capsaicin, and ginger containing diets for 8 wk were examined for ex vivo uptake of iron, zinc, and calcium from incubations containing digesta of finger millet. A higher uptake of iron, zinc, and calcium by the intestinal segments from spice-fed animals was observed. The increase in the mineral uptake was the highest for calcium with >100%. Higher in vitro absorption of  $\beta$ -carotene in the intestines was evidenced in all spice-fed animals. Dietary piperine and ginger increased the uptake of  $\beta$ -carotene by 147 and 98%, respectively, while increases in absorption were 59 and 27% in black pepper and red pepper fed animals, respectively. An animal study conducted to evaluate the influence of dietary spice compounds—piperine, capsaicin, and ginger—on the absorption of orally administered  $\beta$ -carotene and its conversion to vitamin A revealed significantly increased  $\beta$ -carotene concentration in the serum, liver, and intestine of piperine and ginger fed rats, suggesting improved absorption of  $\beta$ -carotene. Retinol concentration was not however changed in these animals, suggesting that bioconversion of  $\beta$ -carotene to vitamin A was not similarly influenced. The higher intestinal uptake of iron, zinc, and  $\beta$ -carotene as a result of consumption of pungent spices could encourage a strategy to reduce the deficiency of these micronutrients prevalent in populations dependent on plant-based foods.

Key Words: gut health, nutrient absorption, spices

# **1035** Phytonutrients as non-nutritive feed additives to enhance growth and host immunity in broiler chickens. H. Lillehoj<sup>\*1</sup> and S. Oh<sup>2</sup>, <sup>1</sup>ARS USDA, Beltsville, MD, <sup>2</sup>USDA, Beltsville, MD.

The gut represents a continuously evolving ecosystem where a dynamic interaction between host immune, neuroendocrine, and enteroendocrine cells and the gut microbiota influences normal physiological development and homeostasis. New antibiotic regulatory policies and cage-free rearing systems in poultry production now challenge animal scientists to think outside of the box to develop alternative strategies for sustainable animal agriculture. This presentation will discuss using dietary phytonutrients to enhance poultry growth and modulate innate immunity against enteric pathogens. Phytochemicals are non-nutritive, plant-derived chemicals, many with disease-preventing properties. A growing body of scientific evidence has demonstrated that many of the health-promoting activities of phytochemicals are mediated through their ability to improve host defense against microbial infections and tumors. During the last 10 yr, our research has provided science-based evidence for the beneficial effects of certain phytochemicals in the poultry immune system. Many of these phytonutrients are now commercially used to increase poultry growth and reduce disease-associated losses. Furthermore, our latest study demonstrated that dietary phytonutrients influence the intestinal microbiome through "crosstalk" with the host immune system to maintain gut homeostasis and gut health. These studies collectively suggest that dietary feeding of certain phytonutrients reduces the negative consequences of enteric diseases, in part, through alteration of the gut microbiome.

Key Words: plant extracts, poultry, immunity

# 1036 Phytonutrients as additives in ruminants: the unexpected target organ. J. Oh<sup>1</sup>, E. H. Wall<sup>2</sup>, D. M. Bravo<sup>2</sup>, and A. N. Hristov<sup>\*3</sup>, <sup>1</sup>The Pennsylvania State University, University Park, <sup>2</sup>Pancosma, Geneva, Switzerland, <sup>3</sup>Department of Animal Science, The Pennsylvania State University, University Park.

Plants produce an extensive array of organic compounds derived from secondary metabolism that may be useful in animal nutrition because of their chemical makeup. These plant-derived bioactive compounds, also referred to as phytonutrients or phytobiotics, have been shown to express antimicrobial activities against a wide range of bacteria, yeast, and fungi and have been investigated as rumen modifiers in animal nutrition. Reports have concluded that phytonutrients may inhibit deamination of amino acids and methanogenesis in the rumen and shift fermentation toward propionate and butyrate. Responses, however, have been highly variable. Most of the experiments have been conducted in vitro. Although in vitro data are useful for screening purposes, the true value of phytonutrients for altering rumen microbial fermentation and ultimately enhancing animal production must be assessed in vivo and in long-term experiments. Some phytonutrients, due to their phenolic nature, are likely less susceptible to microbial degradation in the rumen and, similar to observations in monogastric species, may exhibit activities postruminally. For example, depending on dose, 15 to 30% of capsaicin from capsicum oleoresin administered intraruminally was estimated to escape ruminal degradation. Thus, phytonutrients, such as garlic, curcumin, and capsicum, which have modulatory effects on both the innate and adaptive immune systems in monogastric animals, may exhibit similar properties in ruminants if protected from ruminal fermentation. This opens a new area of research on the effects of phytonutrients on the immune system, physiology, and health of ruminant animals. Studies with dairy cows have shown that some phytonutrients delivered postruminally increase subtype T cells in peripheral blood (CD4+) related to adaptive immunity. More recent reports indicated that capsicum increased energy-corrected milk yield and facilitated immune cells related to acute phase responses in high-producing dairy cows. In another study with dairy cows, a rumen-protected capsicum product tended to increase milk yield and increased feed efficiency. Increased insulin sensitivity during a glucose tolerance test in that study suggested that capsicum may redirect glucose for lactose synthesis and milk production. Data also suggest that capsicum may be enhancing fat mobilization in early lactation. Further research is needed to elucidate the effect and mode of action of phytonutrients on immune function and animal energetics. Overall, the effects of phytonutrients on immunity, health, and productivity of ruminant animals observed in short-term, crossover studies are encouraging but need to be confirmed in long-term, production experiments.

**Key Words:** phytonutrients, postruminal effect, immune response, insulin sensitivity, dairy cow

## **1037** Non-nutrients in swine health and production. Y. Liu\*, University of California, Davis.

Demand for animal proteins in human food consumption is rising globally at an unprecedented rate. Swine products occupy an important position in the structure of animal proteins. Thus, the improvement of swine health in future swine production systems will be critical to increase global food production. A group of health technologies have been applied to powerfully improve swine health and production, including age segregation, all-in/all-out pig flow, biosecurity measures, sanitation, vaccination, and others. In addition, the regular use of antibiotics in pig diets has been proven to improve health and productive performance, as shown by volumes of scientific literature and decades of practical experience. Recently, a novel concept, non-nutrients, was illuminated to describe a group of dietary compounds, which has no nutrient contribution to animals but has physiological activities beyond provision of bioavailable nutrients. Antibiotics are also counted in the category of non-nutrients. Emerging evidence suggested that these non-nutrients provided benefits for animal health and production through different modes of action: regulating nutrient digestibility or absorption and modulating microbial ecology in the digestive tract and/or immune responses. For example, dietary supplementation of artificial sweeteners prevents enteric disorders and enhances the growth and performance of early weaned pigs by increasing the expression of the intestinal glucose transporter SGLT1 and glucose absorption. Different types of exogenous enzymes, such as phytase, xylanases, proteases, etc., may be used in swine diets to improve nutrient digestibility of all stages of pigs when certain endogenous enzymes are insufficient. Interest is growing in the use of probiotics and/or prebiotics to increase the populations of desired microbes in the digestive tract and thereby provide benefits on pig health and performance. They may achieve this goal either by continuously introducing the target microbes into the digestive tract or by providing substances that specifically favor the growth of the target microbes over competitors. Moreover, plant extracts can be additional tools that producers use to keep pigs healthy and reduce the impacts of disease. Dietary supplementation of certain plant extracts may enhance the disease resistance of pigs by improving gut mucosal integrity and optimizing immune response. In the near future, the importance of using non-nutritional dietary components for maintaining pig health will be increased, as such use of antibiotics will be progressively restricted in many countries.

Key Words: health, non-nutrients, pigs

## 1038 Manipulation of gut morphology and gut immunity in swine using novel, naturally sustainable bioactives. T. Sweeney<sup>\*1</sup> and J. O'Doherty<sup>2</sup>, <sup>1</sup>School of Veterinary Medicine, University College Dublin, Dublin, Ireland, <sup>2</sup>School of Agriculture and Food Science, University College Dublin, Dublin, Ireland.

As health and environmental regulations increase the constraints on the use of in-feed antibiotics and minerals in swine husbandry, the search for novel bioactives from sustainable natural resources increases. A wealth of chemodiversity in nature has arisen from plants and animals developing protective molecules to survive in varying complex biosystems. Many of these molecules have anti-inflammatory, antimicrobial, and/or antioxidant properties, which help the host to survive a wide spectrum of environmental challenges. We hypothesize that these non-nutritive molecules can be used in the diet to support the developing gastrointestinal tract of the piglet. The mammalian gastrointestinal tract is a dynamic environment, where a symbiotic relationship exists between the immune system, the resident microbiota, and the digestive system. The development of the immune system begins in-utero and is further developed following the colonization of the GIT with microbiota during birth and postnatal life. The early establishment of this relationship is fundamental to the development and long-term maintenance of gut homeostasis, with unfavorable alterations in the composition of the microbiota, known as dysbiosis, being implicated in many conditions. The weaning period of the piglet under modern husbandry conditions is very prone to dysbiosis in the gastrointestinal tract, resulting in a period of post-weaning diarrhea. It involves complex dietary, social, and environmental stresses that interfere with gut development and is characterized by a reduction in feed intake and growth, atrophy of small intestine architecture, up-regulation of intestinal inflammatory cytokines, alterations in GIT microflora, diarrhea, and heightened susceptibility to infection. In this review, we discuss advances in our understanding of the immune mechanisms by which the dynamic interplay of the intestinal microbiota and its host normally favors a homeostatic, symbiotic relationship, and how feeding novel, naturally sustainable bioactives from marine flora and fauna and milk can be utilized to support this symbiotic relationship in times of challenge. The overall aim of our research program is to provide dietary support to ensure an appropriate level of immune reactivity in the gut to accommodate the presence of beneficial and dietary microorganisms, while allowing effective immune/inflammatory responses to clear pathogens. A variety of natural sustainable bioactives has been identified that target different components of the gastrointestinal tract environment. Modes of action vary from commensal microbial stimulants, targeted antimicrobial activity, gut barrier repair, mucosal structure (villous architecture, absorptive capacity, nutrient transporters), and mucosal anti-inflammatory activity. Interestingly, ingestion of combinations of these bioactives can enhance bioavailability lower down in the colon.

**Key Words:** swine, natural, sustainable, bioactive, gut health

## PHYSIOLOGY AND ENDOCRINOLOGY

1039 WS Influence of sampling location and pregnancy on composition of the microbiome associated with the reproductive tract of the ewe.
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R. L. Ashley, and S. L. Ivey, New Mexico State University, Las Cruces.

The objective of this study was to investigate the microbiome of the vagina, uterus, and embryo and determine the effects of pregnancy status and a maternal pregnancy recognition antagonist treatment. We hypothesized that location, pregnancy status, and maternal pregnancy recognition antagonist treatment would result in significant differences in the bacterial microbiome of the reproductive tract in sheep. Mini osmotic pumps were placed surgically into the uterus and loaded with control (PBS, n = 9) or treatment (AMD3100, n = 7). AMD3100 is an antagonist for maternal pregnancy recognition. Samples were collected for microbiome analysis from the vagina, uterus, and embryo. AMD3100 and PBS had no effect on microbiome composition (P > 0.98). Sampling location had the greatest effect on bacterial population (P > 0.01). Firmicutes, Proteobacteria, and Actinobacteria were the most predominant phyla (P < 0.01) present in the vagina while Proteobacteria, Firmicutes, and Actinobacteria were present in the uterus (P < 0.01). The genus of bacteria present in the uterus and vagina supported the phylum data. Corynebacterium was more prevalent than *Finegoldia* in the vagina (P < 0.01), while the prevailing genus in the uterus was *Bradyrhizobium* (P < 0.01). The pregnancy status of ewes did not differ by phylum; however, the genus *Finegoldia* was greatest in nonpregnant ewes (P < 0.01). Treatment effects were not observed on embryo microbiome phylum (P < 0.90) or genus (P < 0.88). Results show further research is needed to understand the relationship between the reproductive tract microbiome and ewe fertility.

Key Words: metagenome, sheep, uterus, vagina

1040 Use of doppler ultrasound and infrared thermography to evaluate scrotal insulation in Braford bulls. F. A. Barca Junior<sup>1</sup>, C. Koetz Junior<sup>\*1</sup>, G. R. Pereira<sup>2</sup>, S. R. Menegassi<sup>2</sup>, F. Morotti<sup>3</sup>, J . O. Barcellos<sup>2</sup>, L. A. Claus<sup>3</sup>, and M. M. Seneda<sup>3</sup>, <sup>1</sup>UNOPAR, Arapongas, Brazil, <sup>2</sup>NESPRO/UFRGS-Federal University of Rio Grande do Sul, Porto Alegre, Brazil, <sup>3</sup>UEL- Universidade Estadual de Londrina, Londrina, Brazil.

The objective of this study was to evaluate the flow dynamics of scrotal surface temperature (SST) by infrared thermography in Braford bulls submitted to scrotal insulation. In addition, bulls were also evaluated for velocity parameters (V), pulsatility index (PI), and resistance index (RI) using Doppler ultrasound. All procedures were approved by the Ethical Committee for Care and Use of Experimental Animals (Project 19656/2014/58, CEUA/UEL). All animals had a breeding soundness examination at the beginning of the experiment. Eight Braford bulls were used at the age of 18 mo and randomly divided into four different groups, as follows: the control group not subjected to insulation (CON; n = 2), scrotal insulated bulls for 72 h (G72, n = 2), scrotal insulated bulls for 96 h (G96, n = 2), and scrotal insulated bulls for 120 h (G120, n = 2). Infrared thermography and Doppler data were collected at four different periods: after removal of scrotal insulation (M0), 10 min after removal of scrotal insulation (M10), 30 min after removal of scrotal insulation (M30), and 60 min after removal of scrotal insulation (M60). Data were analyzed using ANOVA, t test (paired), and Pearson correlation with a significance level of 5%. No differences were observed between insulated treated groups. Rectal temperature (38.5  $\pm$ 0.4) was higher compared to scrotal surface (32.7  $\pm$  0.8; P < 0.05). Scrotal insulated animals showed higher testicular temperature at M0 ( $33.0 \pm 0.7$ ) compared to M10, M30, and M60 periods  $(30.2 \pm 1.3, 31.6 \pm 1.5, 30.6 \pm 1.0, respectively;$ P < 0.05). We observed no difference in PI and RI indexes between evaluation periods after scrotal insulation. However, blood flow velocity (cm/sec) showed differences between M10 (17.1  $\pm$  4.22) compared to the M0, M30, and M60 periods  $(12.5 \pm 5.1, 14.3 \pm 4.5, 14.3 \pm 2.9, \text{respectively}; P < 0.05)$ . A positive correlation (93.1%) was observed between PI and RI (P < 0.05) variables. The scrotal insulation changes the temperature and the blood flow velocity; however, after 60 min of insulation, these parameters are already reestablished. We conclude that Doppler ultrasound can be used to evaluate scrotal blood flow variations during scrotal heat stress induction in Braford bulls.

**Key Words:** Doppler ultrasonography, infrared thermography, scrotal insulation