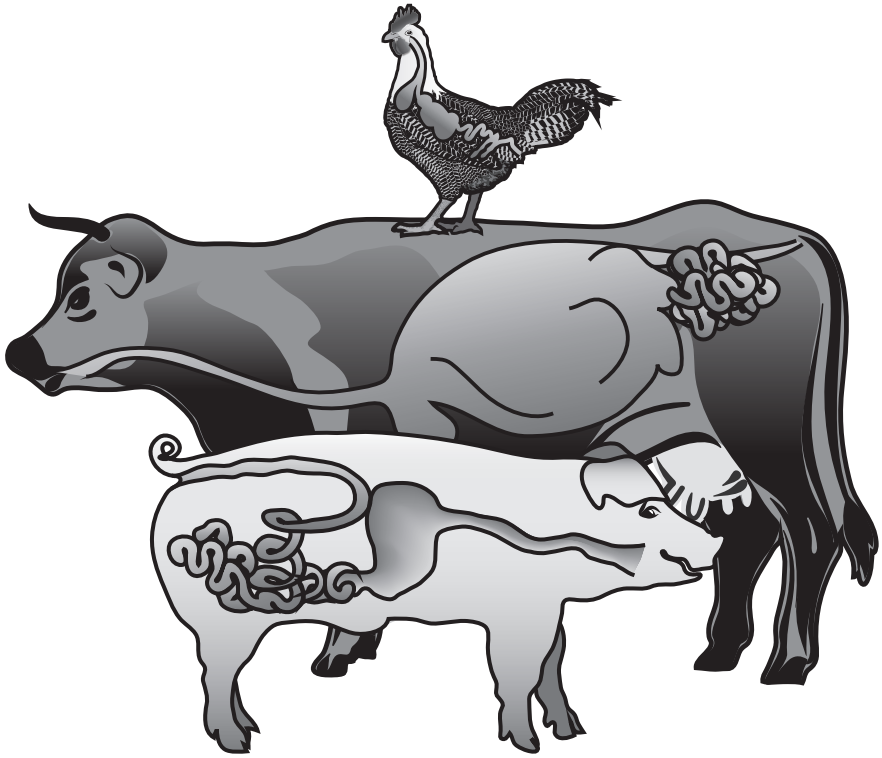
Symposium on Gut Health
in Production of Food Animals
November 13–15, 2017, St. Louis, Missouri



Program and Abstracts
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WELCOME

On behalf of the Organizing Committee for the 6th Symposium on Gut Health in Production of Food Animals, I welcome you back to St. Louis, Missouri! After a very successful 5th Symposium here in 2016, we decided a return trip was in order. I look forward to another scientifically and socially rewarding meeting in 2017.

The aim of the Symposium is to bring together a group of scientists from academia, government, and industry to discuss the role of gut health in animal production and the essential role that the gut plays in establishing and maintaining animal health. The overall aim of the conference is to promote the unifying concepts that the gut drives animal health and performance. Although the gastrointestinal tract is frequently described simply as ‘‘the gut,’’ it is actually made up of (1) an epithelium; (2) a diverse and robust immune arm, which contains most of the immune cells in the body; and (3) the commensal bacteria, which contain more cells than are present in the entire host organism. Understanding of the crosstalk between ALL of these interrelated components of the gut is what cumulatively makes the gut the basis for the well-being of animals and the motor that drives their performance. The abstracts submitted to the Symposium are defining these links and mechanisms that inter-connect the three components of the gut and how each can be manipulated to improve animal health.

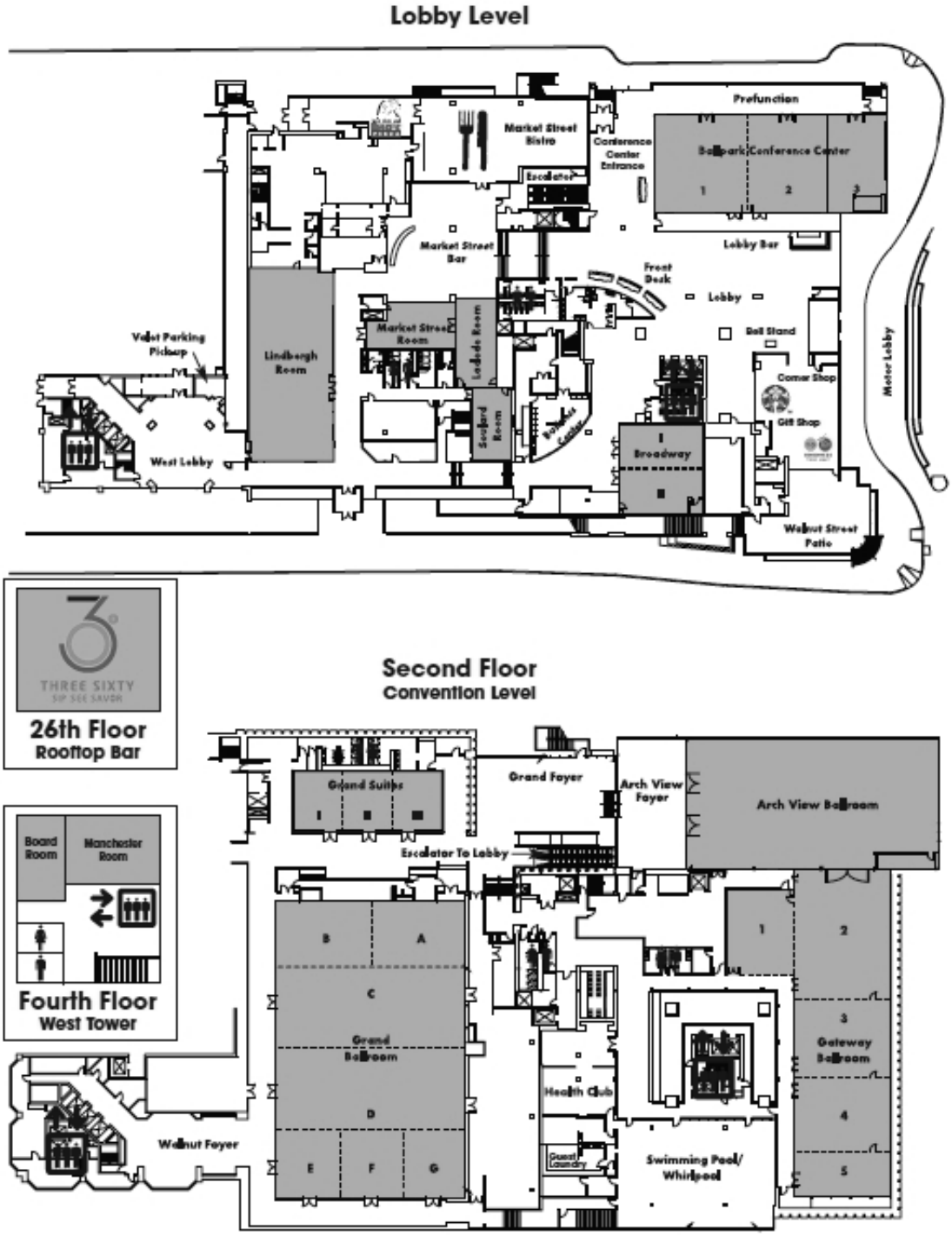
As in the past, this year we have invited four distinguished plenary speakers that will cover current research topics in avian, porcine, and bovine gut health. Please take advantage of the presence of these scientists to engage in productive talks and develop collaborations between different laboratories in order to further the science of gut health.

Likewise, I encourage all of you to please take advantage of the informal nature of the symposium—it was planned this way to encourage interaction between scientists. I again ask that senior researchers make a special effort to engage with the graduate students who are attending and presenting. Remember that, whatever your research specialty or food animal commodity, we are all working together to improve food quality for the consumer.

Welcome again and enjoy the Symposium and your stay in St. Louis!

Mike Kogut
Chair, Organizing Committee

Hilton St. Louis at the Ballpark



Program

Sunday, November 12

5:00 pm – 7:00 pm Registration: Grand Foyer

Monday, November 13

7:00 am – 8:00 am Hot Breakfast Buffet: Arch View Ballroom
Sponsored by King Techina Group

7:00 am – 5:00 pm Registration: Grand Foyer

SESSION 1

Chair: Mike Kogut, USDA-ARS
Salons A, B, and C

8:00 am – 9:00 am Intracellular homeostasis and its impact in gut health and adaptation. (Abstract 100)
A. Laarman, University of Idaho, Moscow, ID.*

9:00 am – 9:30 am The effect of coccidiosis and decreased feed intake on growth parameters of broilers as well as the expression of genes associated with nutrient uptake. (Abstract 101)
K. B. Miska and R. H. Fetterer, USDA/ARS, Beltsville, MD.*

9:30 am – 10:30 am Biogeographical differences in the influence of maternal microbial sources on the early successional development of the bovine neonatal gastrointestinal tract. (Abstract 102)
C. J. Yeoman[*1], S. L. Ishaq[1], E. Bichi[2], S. K. Olivo[1], J. Lowe[2], and B. M. Aldridge[2], [1]Montana State University, Bozeman, MT, [2]University of Illinois, Urbana-Champaign, IL.*

10:00 am – 10:30 am Coffee Break: Grand Foyer
Sponsored by KWS Lochow GMBH

10:30 am – 10:45 am Profiling the vaginal microbiome of sows of different parities. (Abstract 103)
H. Tran[*1], B. de Rodas[1], and T. Johnson[2], [1]Purina Animal Nutrition, Gray Summit, MO, [2]University of Minnesota, St. Paul, MN.*

10:45 am – 11:00 am Interaction of beef calf health, performance and environmental impact by modifying the gut through natural feed additives. (Abstract 104)
D. McClellan[*1], J. K. Bamford[2], R. Bechtel[3], K. Eng[4], and D. Hutcheson[5], [1]McClellan Consulting Service, Fremont, NE, [2]Inco Digestive, Haxtun, CO, [3]Advanced Agricultural Testing, Baden, ON, Canada, [4]Biolite, Winston, NM, [5]Animal Agricultural Consulting International, Scroggins, TX.*

11:00 am – 11:15 am Interrelationship between *Eimeria* species and *Clostridium perfringens* in the chicken intestine. (Abstract 105)
C. Wang, W.-Y. Yang, H.-Y. Lu, Y.-J. Lee, and J. A'arabi, Department of Basic Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, MS.*

11:15 am – 11:30 am Transcriptome changes in neonatal calves treated with artificial dosing of rumen content from adult donor cow. (Abstract 106)
W. Li[*1], M. Cox[2], J. H. Skarlupka[2], A. J. Steinberger[2], A. Edwards[3], and C. Riehle[4], [1]USDA Dairy Forage Research Center, Madison, WI, [2]Department of Microbiology, University of Wisconsin-Madison, Madison, WI, [3]Department of Biology, University of Wisconsin-Madison, Madison, WI, [4]Department of Genetics, University of Wisconsin-Madison, Madison, WI.*

11:30 am – 11:45 am A *Bacillus* direct-fed microbial, alone and with protease, improves barrier integrity in an in vitro porcine intestinal epithelial cell culture model. (Abstract 107)
L. Payling[*1], *J. Liljavirta*[2], *S. Latvala*[2], *P. Nurminen*[2], *and M. Walsh*[1], [1]*Danisco Animal Nutrition, Marlborough, Wiltshire, UK,* [2]*DuPont Nutrition and Health, Kantvik, Finland.*

11:45 am – 12:00 pm Effect of *Bacillus* spp. direct-fed microbial on leaky gut, bone mineralization, serum peptide YY levels, and ammonia excretion in turkey poults fed a rye-based diet. (Abstract 108)
G. Tellez[*1], *J. Maguey*[2], *M. A. Michel*[3], *M. Baxter*[1], *G. Tellez Jr.*[1], *P. A. Moore*[4], *S. Dridi*[1], *A. D. Wolfenden*[1], *B. M. Hargis*[1], *and J. D. Latorre*[1], [1]*University of Arkansas, Fayetteville, AR,* [2]*FES Cuautitlan UNAM, Cuautitlan, Mexico,* [3]*FCV Universidad del Nordeste, Corrientes, Argentina,* [4]*USDA-ARS, Fayetteville, AR.*

12:00 pm – 1:00 pm Lunch (provided): Arch View Ballroom

Sponsored by SilvaTeam

1:00 pm – 3:00 pm Poster Session: Grand Foyer

SESSION 2

Chair: Mike Kogut, USDA-ARS
Salons A, B, and C

3:00 pm – 4:00 pm Why resist: Antibiotic alternatives in swine. (Abstract 109)
C. Loving, USDA-ARS National Animal Disease Center, Food Safety and Enteric Pathogens, Ames, IA.*

4:00 pm – 4:30 pm Comparison of multiple *Clostridium perfringens* strains and their influence on necrotic enteritis. (Abstract 110)
K. M. Wilson[1], *W. N. Briggs*[1], *K. M. Chaser*[1], *A. D. Duff*[1], *J. D. Latorre*[2], *B. M. Hargis*[2], *J. R. Barta*[3], *and L. R. Bielke*[*1], [1]*Ohio State University, Columbus, OH,* [2]*University of Arkansas, Fayetteville, AR,* [3]*University of Guelph, Guelph, ON, Canada.*

4:30 pm – 5:00 pm Genetically modified *Lactobacillus casei* could be a bio-therapeutic for enteric bacterial infections. (Abstract 111)
M. Peng and D. Biswas, University of Maryland, College Park, MD.*

5:00 pm – 5:15 pm Microbial modifying properties of reused litter and iodinated water in poultry production. (Abstract 112)
D. Pepin and B. Willing, University of Alberta, Edmonton, AB, Canada.*

5:15 pm – 5:30 pm Aqueous citrus extract supplementation affects gut microbiota and histological parameters of broiler chicken. (Abstract 113)
R. Djezzar[1], *M. el Amine Benrbia*[*2], *and P. Chicoteau*[2], [1]*Veterinary School Algiers, Algiers, Algeria,* [2]*Nor-Feed, Beaucouzé, France.*

5:30 pm – 5:45 pm Transcriptome changes in neonatal calves treated with artificial dosing of rumen content from adult donor cow. (Abstract 114)
W. Li[*1], *M. Cox*[2], *J. H. Skarlupka*[2], *A. J. Steinberger*[2], *A. Edwards*[3], *and C. Riehle*[4], [1]*USDA Dairy Forage Research Center, Madison, WI,* [2]*Department of Microbiology, University of Wisconsin-Madison, Madison, WI,* [3]*Department of Biology, University of Wisconsin-Madison, Madison, WI,* [4]*Department of Genetics, University of Wisconsin-Madison, Madison, WI.*

7:00 pm – 9:00 pm Reception: Arch View Ballroom
Sponsored by DSM Nutritional Products

Tuesday, November 14

7:00 am – 8:00 am Hot Breakfast Buffet: Arch View Ballroom
Sponsored by Biomin America

7:00 am – 5:00 pm Registration: Grand Foyer

SESSION 3

Chair: Mike Kogut, USDA-ARS
Salons A, B, and C

8:00 am – 9:00 am The poultry gut: Signals integrator, generator, and target for intervention. (Abstract 115)
R. Arsenault, University of Delaware, Newark, DE.*

9:00 am – 9:30 am Evaluation of *Campylobacter jejuni* isolates to experimentally colonize and selective media to enumerate from poults. (Abstract 116)
M. Sylte[1], T. Looft[1], M. Inbody[1], E. Meyer[1], T. Johnson[1,2], Z. Wu[3], Q. Zhang[3], and E. Line[4], [1]USDA-ARS National Animal Disease Center, Ames, IA, [2]Purdue University, West Lafayette, IN, [3]Iowa State University, Ames, IA, [4]USDA-ARS National Poultry Research Center, Athens, GA.*

9:30 am – 10:00 am Enteric bacterial toxin neutralization by Calibrin-Z. (Abstract 117)
F. Chi[2], H. Xue[1], S. Ching[1], M. McPherson[1], S. Johnston[2], E. DeBoer[1], and R. Cravens[2], [1]Oil-Dri Corporation of America, Chicago, IL, [2]Amlan International, Chicago, IL.*

10:00 am – 10:30 am Coffee Break: Grand Foyer
Sponsored by KWS Lochow GMBH

10:30 am – 11:00 am A mixture of organic acids and botanicals ameliorates and prevents the damage induced by an inflammatory challenge in Caco-2 cell cultures. (Abstract 118)
B. Rossi[1], B. Tugnoli[1], A. Piva[1,2], and E. Grilli[2], [1]Vetagro S.p.A, Reggio Emilia, Italy, [2]DIMEVET, University of Bologna, Ozzano Emilia (Bologna), Italy.*

11:00 am – 11:30 am Forskolin and butyrate act synergistically in protecting chickens from necrotic enteritis by inducing host defense peptide synthesis. (Abstract 119)
Q. Yang[1], K. Robinson[1], B. Chen[1], R. Arsenault[2], and G. Zhang[1], [1]Oklahoma State University, Stillwater, OK, [2]University of Delaware, Newark, DE.*

11:30 am – 12:00 pm Effect of replacing antibiotic growth promoters with polyphenolic botanical extracts and essential oils in feed of laying hens on performance, health, Newcastle disease titer, and some blood parameters. (Abstract 120)
A. A. Tahir[1], A. Hasnain[1], S. Waheed[1], O. Tarar[2], and T. Ali[1], [1]University of Karachi, Karachi, Pakistan, [2]PCSIR, Karachi, Pakistan.*

12:00 pm – 1:00 pm Lunch (provided): Arch View Ballroom
Sponsored by Vetagro Inc.

SESSION 4

Chair: Mike Kogut, USDA-ARS
Salons A, B, and C

1:00 pm – 1:30 pm Favoring gastrointestinal health of pigs—Benefits of dietary concepts including rye as the main cereal? (Abstract 121)
J. Kamphues[1], R. Grone[1], M. Kolln[1], and A. v Felde[2], [1]University of Veterinary Medicine, Hanover, Germany, [2]KWS Lochow GmbH, Bergen, Germany.*

1:30 pm – 2:00 pm Inactivation of *Salmonella* and *Clostridium* by Alquermold Natural L, a fungicide/bactericide. (Abstract 122)
S. Goyal[*1], *H. Aboubakr*[1], *C. Domenech*[2], *J. Pie*[2], *and A. Tesouro*[2], [1]*University of Minnesota, St. Paul, MN,* [2]*Biovet SA, Tarragona, Spain.*

2:00 pm – 2:30 pm Spray-dried plasma—A review of a unique functional protein ingredient on intestinal health. (Abstract 123)
J. Campbell, J. Polo, and J. Crenshaw, APC Inc, Ankeny, IA.*

2:30 pm – 3:00 pm Use of a novel methodology to validate that β-mannanase (Hemicell HT) reduces feed-induced inflammatory responses and alters metabolism in the avian gut. (Abstract 124)
M. A. Martinez-Cummer[*3], *R. Arsenault*[2], *and M. H. Kogut*[1], [1]*USDA-ARS, Southern Plains Research Center, College Station, TX,* [2]*University of Delaware, Newark, DE,* [3]*Elanco Animal Health, Greenfield, IN.*

3:00 pm – 3:30 pm Coffee Break: Grand Foyer
Sponsored by Nutriad Inc.

3:30 pm – 3:45 pm The effects of different feed additives on bird performance and the gastrointestinal microbiome of *Salmonella*-challenged broilers. (Abstract 125)
T. Johnson[*1], *P. Karnezos*[2], *N. Evans*[2], *and M. Sims*[3], [1]*University of Minnesota, Saint Paul, MN,* [2]*PMI Nutritional Additives, Shoreview, MN,* [3]*Virginia Diversified Research Corp, Harrisonburg, VA.*

3:45 pm – 4:00 pm Microbial metabolite deoxycholic acid attenuates necrotic enteritis. (Abstract 126)
H. Wang, JD Latorre Cardenas, G. Tellez, B. Hargis, and X. Sun, University of Arkansas, Fayetteville, AR.*

4:00 pm – 4:15 pm Effect of synbiotic supplementation on intestinal development and integrity of broilers. (Abstract 127)
C. Pender[*1], *G. R. Murugesan*[1], *and D. Koltes*[2], [1]*Biomin America Inc, San Antonio, TX,* [2]*Iowa State University, Ames, IA.*

4:15 pm – 4:30 pm Effects of Varium on expression of intestinal barrier, antioxidant and pro-inflammatory cytokine genes in young broiler chickens with experimental necrotic enteritis. (Abstract 128)
S. Ching[2], *S. Oh*[1], *H. Lillehoj*[1], *S. Johnston*[3], *M. Herpfer*[2], *E. DeBoer*[2], *and H. Xue*[*2], [1]*USDA-ARS, Beltsville, MD,* [2]*Oil-Dri Corporation of America, Chicago, IL,* [3]*Amlan International, Chicago, IL.*

4:30 pm – 4:45 pm Impact of exogenous carbohydrases on intestinal and peripheral inflammatory status in nursery pigs fed a higher fiber, lower energy diet. (Abstract 129)
Q. LI[*1], *N. Gabler*[1], *C. Loving*[2], *C. Sparks*[3], *and J. Patience*[1], [1]*Iowa State University, Ames, IA,* [2]*USDA-ARS-National Animal Disease Center, Ames, IA,* [3]*Huvepharma Inc, Peachtree City, GA.*

4:45 pm – 5:00 pm Development of a chicken enterocyte culture to study its functional physiology. (Abstract 130)
A. Gupta[*1], *R. Liyanage*[2], *and N. C. Rath*[3], [1]*Department of Poultry Science, University of Arkansas, Fayetteville, AR,* [2]*Department of Chemistry, University of Arkansas, Fayetteville, AR,* [3]*USDA-ARS Poultry Production and Product Safety Research Unit, Fayetteville, AR.*

5:00 pm – 5:30 pm Prevention of *Listeria monocytogenes* infection with bioengineered probiotic. (Abstract 131)
A. Bhunia, R. Drolia, S. Tenguria, V. Ryan, and T. Bailey, Purdue University, West Lafayette, IN.*

7:00 pm – 9:00 pm Reception: Arch View Ballroom
Sponsored by Elanco

Wednesday, November 15

7:00 am – 8:00 am Hot Breakfast Buffet: Arch View Ballroom

7:00 am – 12:00 pm Registration: Grand Foyer

SESSION 5

Chair: Mike Kogut, USDA-ARS
Salons A, B, and C

8:00 am – 8:30 am Characterization of cecal microbiome in broilers fed diets with tannins extracted from *Schinopsis lorentzii* (Argentine quebracho) and *Castanea sativa* (Italian chestnut). (Abstract 132)
J. D. Carrasco[2], E. Redondo[2], N. P. Viso[2], L. Eedondo[2], M. Farber[1,2], and M. F. Miyakawa[1,2], [1]National Institute of Agricultural Technology (INTA), Hurlingham, Buenos Aires, Argentina, [2]National Scientific and Technical Research Council (CONICET), Buenos Aires, Argentina.*

8:30 am – 9:00 am Effects of feed additives in alleviating enteric health challenges in broilers. (Abstract 133)
J. Chen, F. Yan, V. Kuttappan, and M. Vázquez-Añón, Novus International Inc, St. Charles, MO.*

9:00 am – 9:30 am In-depth analysis of mycotoxin contamination in US feed and feed ingredients from 2014 to 2017. (Abstract 134)
E. Hendel[1], T. Jenkins[2], P. Gott[1], and G. R. Murugesan[1], [1]Biomin America Inc, San Antonio, TX, [2]Biomin Holding GmbH, Getzersdorf, Austria.*

9:30 am – 10:00 am Feed efficiency phenotypes in lambs involve changes in ruminal, colonic, and small intestine-located microbiota. (Abstract 135)
K. Perea, K. Perz, S. K. Olivo, A. Williams, M. Lachman, S. Ishaq, J. Thomson, and C. J. Yeoman, Montana State University, Bozeman, MT.*

10:00 am – 10:30 am Coffee Break: Grand Foyer

10:30 am – 10:45 am Effects of chestnut wood extract (by water) or microencapsulated dry extract and blend of monoglycerides of butyric acid (in feed) on live performance and gut health of broiler chickens. (Abstract 136)
J. Ponebsek[1], P. Martin[2], and D. Hooge[3], [1]Tanin Sevnica, Sevnica, Slovenia, [2]Imogene Ingredients, Des Moines, IA, [3]Consulting poultry nutritionist, Eagle Mountain, UT.*

10:45 am – 11:00 am Evaluation of rye versus corn as a source of energy on the microbiome in different sections of the gastrointestinal track of broiler chickens. (Abstract 137)
M. F. A. Baxter[1], J. D. Latorre[1], S. H. Park[1,2], S. C. Ricke[1], X. Sun[1], B. M. Hargis[1], and G. Tellez[1], [1]University of Arkansas, Fayetteville, AR, [2]Oregon State University, Corvallis, OR.*

10:45 am – 11:00 am Effect of prebiotic supplementation on gut health and performance of heifer calves. (Abstract 138)
R. Gardinal[1], C. A. F. Oliveira[1], J. F. A. Koch[1], B. Mazzer[1], F. C. Horta[1], F. O. R. Filho[1], and V. Vetvicka[2], [1]Department of Research and Development, Biorigin Company, Lençóis Paulista, SP, Brazil, [2]Department of Pathology, University of Louisville, Louisville, KY.*

11:15 am – 11:30 am Effect of exogenous nucleotide supplementation on gut health and performance of newly weaned piglets. (Abstract 139)
R. Gardinal[1], C. A. F. Oliveira[1], J. F. A. Koch[1], B. Mazzer[1], F. C. Horta[1], F. O. R. Filho[1], and V. S. Cantarelli[2], [1]Department of Research and Development, Biorigin Company, Lençóis Paulista, SP, Brazil, [2]Department of Animal Sciences, University of Lavras, Lavras, MG, Brazil.*

11:30 am – 11:45 am The effects of phytase super dosing in combination with xylanase on jejunum and ileum mucosa morphology in market turkey hens. (Abstract 140)
M. Herchler, S. Black, R. Malheiros, and P. Ferket, North Carolina State University, Raleigh, NC.*

11:45 am – 12:00 pm Risks involved in the use of enrofloxacin for *Salmonella enteritidis* or *Salmonella Heidelberg* in commercial poultry. (Abstract 141)
G. Tellez[*1], *E. Morales*[2], *V. Luca*[3], *O. Prado*[4], *BM Hargis*[1], *and JD Latorre*[1], [1]*University of Arkansas, Fayetteville, AR,* [2]*Universidad Autonoma Metropolitana, Mexico City, Mexico,* [3]*Universidade Federal de Santa Maria, Santa Maria, RS, Brazil,* [4]*Universidad de Colima, Colima, Mexico.*

Poster Presentations

P100 Identification of the ileal, cecal, tracheal, and litter microbiomes in antibiotic-free commercial broilers and their correlations with performance.
B. Youmans[*1], *C. Cremers*[2], *T. Karnezos*[3], *N. Evans*[3], *and T. Johnson*[1], [1]*University of Minnesota, St Paul, MN,* [2]*Pilgrim's Pride, Sauk Rapids, MN,* [3]*PMI Nutritional Additives, Shoreview, MN.*

P101 Dietary supplementation of late pregnancy diet with yeast derivatives (mannan oligosaccharide) can influence the colostrum yield, colostrum composition and gut performances of sow.
S. Hasan[*1], *S. Junnikkala*[2], *O. Peltoniemi*[1], *and C. Oliviero*[1], [1]*Department of Production Animal Medicine, University of Helsinki, Helsinki, Finland,* [2]*Department of Veterinary Biosciences, University of Helsinki, Helsinki, Finland.*

P102 Effects of a malabsorptive rye diet on growth and adipose tissue in commercial broilers.
L. Reber[*1], *M. F. A. Baxter*[1], *B. M. Hargis*[1], *G. Tellez*[1], *and D. A. Koltes*[2], [1]*University of Arkansas, Fayetteville, AR,* [2]*Iowa State University, Ames, IA.*

P103 Effects of Noni-supplemented diet on tight junction protein expression in broiler chickens exposed to heat stress.
G. Tellez[*1], *E. Greene*[1], *J. Flees*[1], *A. Gupta*[2], *R. Narayan*[2], *W. Bottje*[1], *and S. Dridi*[1], [1]*University of Arkansas, Fayetteville, AR,* [2]*USDA-ARS, Fayetteville, AR.*

P104 Bovine colostrum increases the viability and the healing process of IPEC-J2 intestinal porcine epithelial cells while modulating the barrier function and *Escherichia coli*-mediated inflammatory responses.
M. Bouchard[*1,2], *M. Blais*[2], *K. Deschenes*[2], *G. Robitaille*[3], *Y. Arcand*[3], *C. Asselin*[1], *and M. Lessard*[2],
[1]*Département d'anatomie et de biologie cellulaire, Université de Sherbrooke, Sherbrooke, QC, Canada,* [2]*Sherbrooke Research and Development Centre, Agriculture and Agri-food Canada, Sherbrooke, QC, Canada,* [3]*St-Hyacinthe Research and Development Centre, Agriculture and Agri-food Canada, St-Hyacinthe, QC, Canada.*

P105 Effects of Original XPC Ultra and BMD on bacterial antibiotic resistance and litter microbial community composition in the commercial turkey litter environment.
*A. Wakil**, *B. Youmans, C. Flores-Figueroa, J. Munoz-Aguayo, and T. Johnson, University of Minnesota, St Paul, MN.*

P106 Development of swine enteroids: A novel tool for animal science research.
*M. P. Trudeau**, *P. E. Urriola, G. C. Shurson, and M. Saqui-Salces, University of Minnesota, St. Paul, MN.*

P107 *Bacillus subtilis* probiotic prevents heat-related complications in animals.
H.A.Giblot Ducray[*1], *L. Globa*[1], *O. Pustovyy*[1], *M. Roberts*[2], *D. Pascoe*[2], *V. Vodyanoy*[1], *and I. Sorokulova*[1],
[1]*Department of Anatomy, Physiology, and Pharmacology, Auburn University, Auburn, AL,* [2]*School of Kinesiology, Auburn University, Auburn, AL.*

P108 Evaluation of Actisaf and Safmannan effects on gastrointestinal microbiota in cecal and ileum contents of chicken broiler.
S. A. Kim[1], *P. Rubinelli*[1], *S. H. Park*[2], *T. Gaydos*[*3], *J. Corley*[3], *R. Raspoet*[3], *and S. C. Ricke*[1], [1]*Center for Food Safety and Department of Food Science, University of Arkansas, Fayetteville, AR,* [2]*Department of Food Science and Technology, Oregon State University, Corvallis, OR,* [3]*Phileo Lesaffre Animal Care, Milwaukee, WI.*

P109 Mode of caffeic acid phenyl ester (CAPE) inhibition of gut bacterial bile salt hydrolase: Implications for gut health and nutrient absorption in poultry.
A. Volland and J. M. Ridlon, University of Illinois at Urbana-Champaign, Urbana, IL.*

P110 Characterization of clostridia in beef cattle throughout production in natural and conventional settings.
J. S. Thompson, J. Schissel, M. N. Griffin, and T. G. Rehberger, Arm & Hammer Animal Nutrition, Waukesha, WI.*

P112 Systemic immunomodulatory effect of *Bacillus subtilis* and *Lactobacillus plantarum* probiotics compared with an antibiotic supplemented in milk replacer fed to dairy calves.
J. Christianson[1], J. O'Neill[1], H. Chester-Jones[2], D. Ziegler[2], and E. Davis[1], [1]Arm & Hammer Animal Nutrition, Waukesha, WI, [2]University of Minnesota, Southern Research and Outreach Center, Waseca, MN.*

P113 The protective effects of ButiPEARL Z during a porcine epidemic diarrhea viral infection in piglets.
V. Mani[1], J. Rubach[1], S. Curry[2], N. Gabler[2], and M. Poss[1], [1]Kemin Industries, Des Moines, IA, [2]Department of Animal Science, Iowa State University, Ames, IA.*

P114 Evaluation of performance and intestinal health of coccidiosis vaccinated broilers fed dietary tannic acid extract formulations.
R. Tonda[1], J. Rubach[1], B. Lumpkins[2], G. Mathis[2], and M. Poss[1], [1]Kemin Industries, Des Moines, IA, [2]Southern Poultry Research, Athens, GA.*

P115 Effect of quercetin on cecal microbiota in Arbor Acre broilers.
S. Wang, B. Zhou, J. Yao, M. Wang, F. Xiao, J. Yang, and Y. Li, Northeast Agricultural University, Harbin, Heilongjiang Province, China.*

P116 Mechanism of action quercetin improving apparent metabolic rate of dietary protein in Arbor Acre broilers.
B. Zhou, M. Wang, S. Wang, J. Yao, J. Yang, F. Xiao, and Y. Li, Institute of Animal Nutrition, Northeast Agricultural University, Harbin, Heilongjiang Province, China.*

P117 Effect of butyric acid glycerol esters on ileum and cecal microflora in chickens challenged with *Eimeria maxima*.
M. Proszkowiec-Weglarz[1], K. B. Miska[1], L. Schreier[1], T. Stout[2], R. Sygall[2], C. J. Grim[3], and K. G. Jarvis[3], [1]USDA-ARS, Beltsville, MD, [2]Perstorp, Waspik, the Netherlands, [3]Office of Applied Research and Safety Assessment, Center for Food Safety and Applied Nutrition, FDA, Laurel, MD.*

P118 Quercetin promoting protein absorption and synthesis in porcine intestinal epithelial cells.
J. Yao, B. Zhou, F. Xiao, M. Wang, and Y. Li, Northeast Agricultural University, Harbin, Heilongjiang Province, China.*

P119 Neonatal supplementation with bovine colostrum, vitamins A and D, and copper modulates piglets' immune system in the peri-weaning period.
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P120 Butter and cheddar decrease inflammatory markers and modulate gene expression in intestinal, hepatic, and adipose tissues of growing pigs fed a high fat diet.
M. Blais[1], J. L. M. Gonzalez[2], Y. Pouliot[2], S. Gauthier[2], Y. Boutin[3], D. Roy[2], A. Marette[2], C. Asselin[4], and M. Lessard[1,2], [1]Sherbrooke R&D Centre, Sherbrooke, QC, Canada, [2]INAF, Universite Laval, Quebec city, QC, Canada, [3]TransBioTech, Quebec city, QC, Canada, [4]Université de Sherbrooke, Sherbrooke, QC, Canada.*

P121 Do iodine and colistin in drinking water affect immune competence and growth performance of broiler?
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P122 The influence of using different sounds on feeding behavior of broiler chicken by using runway test.
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P123 Direct comparison of human microbiota-associated gnotobiotic piglet and mouse models for infant gut microbiota studies.
N. D. Aluthge[*1,3], W. Tom[1,4], S. Rohde[1], T. E. Burkey[1], K. D. Heath[2], C. Kreikemeier-Bower[2], H. Kittana[3], A. E. Ramer-Tait[3], and S. C. Fernando[1], [1]Department of Animal Science, University of Nebraska-Lincoln, Lincoln, NE, [2]Institutional Animal Care Program, University of Nebraska-Lincoln, Lincoln, NE, [3]Department of Food Science and Technology, University of Nebraska-Lincoln, Lincoln, NE, [4]School of Biological Sciences, University of Nebraska-Lincoln, Lincoln, NE.*

P124 Metazoan models and nutrigenomics: The new paradigm in human nutrition.
G. Tellez[*1], M. F. Baxter[1], D. A. Koltes[2], and S. Dridi[1], [1]University of Arkansas, Fayetteville, AR, [2]Iowa State University, Ames, IA.*

P125 Gastrointestinal tract weight and microbial composition of nursery pigs fed diets containing cold-pressed canola cake.
J. W. Lee, M. Thomas, J. Scaria, and T. W. Woyengo, South Dakota State University, Brookings, SD.*

P126 Differential expression of proteins in the duodenum of broilers fed diets rich in arginine or conjugated linoleic acid.
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Oral Abstracts
Session 1

100 Intracellular homeostasis and its impact in gut health and adaptation.

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Continuous improvements in gut health requires looking at new aspects of gut health. Currently, much research on the host aspect of gut health focuses on the epithelium as a tissue rather than as an assortment of cells. Maintenance of gut barrier function, a key aspect of gut health, requires epithelial cells to be anchored to other cells. Although this maintenance is important at the tissue level, the regulation of tight junction proteins and desmosomes happen at the cellular level. To maintain the tight junctions and intercellular anchors that form the gut barrier, epithelial intracellular pH must be regulated closely. Drops in intracellular pH lead to the cleaving of extracellular matrix proteins, which compromises barrier function. In the rumen, epithelial cells are known to recover rapidly from an acid challenge, maintaining barrier integrity. Intracellular pH homeostasis is disturbed during dietary transitions and during subacute ruminal acidosis (SARA), highlighting several opportunities for capitalizing on pH regulation to improve gut health. During weaning and parturition transitions, for example, rumen epithelial cells acidify as part of the cell division and differentiation needed to improve short chain fatty acid (SCFA) absorption. During these transitions, increased SCFA production is coupled with increased H^+ production, which can lead to SARA. Like dietary adaptation, SARA can lead to intracellular acidification that compromises barrier integrity. During SARA, dietary strategies must improve both SCFA uptake and H^+ uptake. Current dietary strategies require weeks of adaptation, which poses extended risks to gut health. During this adaptation period, ameliorating risks to gut health could make use of dietary strategies that improve H^+ uptake. Developing dietary strategies that capitalize on intracellular pH homeostasis to improve SCFA uptake and H^+ uptake holds much promise to augment barrier integrity and improve gut health.

101 The effect of coccidiosis and decreased feed intake on growth parameters of broilers as well as the expression of genes associated with nutrient uptake.

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Coccidiosis caused by *Eimeria* in poultry is a disease endemic to poultry operations and results in decreased feed intake, diarrhea, and decreased weight gain. Our goal was to determine the effect that *Eimeria maxima* causes on expression of genes that encode peptide and amino acid transporters (AATs). Because coccidiosis results in decreased feed consumption we wished to determine how much this factor contributes to the performance and change in gene expression, by adding a pair-fed group of broilers, which were not infected but fed the same amount as infected chickens. Male Ross broilers were used and the 3 experimental groups were (1) not infected, (2) infected, and (3) not infected pair-fed group. Chicks were infected with 1,000 oocysts of *E. maxima* or mock infected at 21 d of age. Feed consumption was obtained daily, and at d 0, 3, 5, 7, 10, and 14 post-infection (PI) 6 birds were euthanized, and a portion of the ileum was removed for qRT-PCR. Growth parameters reveal that infected birds had significantly decreased feed consumption between d 6 and 9 PI. At d 7 PI, infected birds had a 45% reduction in weight gain, and the pair-fed birds had a 32% reduction in weight gain. The feed conversion ratio at d 7 PI of infected birds was 2.2 whereas that of pair-fed birds was 1.7, compared with 1.5 in uninfected birds. We can conclude that growth parameters were more affected in infected birds than in pair-fed birds. By measuring gene expression levels of nutrient uptake and processing genes, we determined that genes encoding proteins located at the brush border of the ileal gut epithelium were most affected by infection and change in feed intake. The expression of AATs: BOAT, bO+AT, EAAT3, and di- and tripeptide transporter PepT1 in infected birds decreased sharply at the height of infected; however, in birds that were pair-fed, an increase in expression of bO+AT and PepT1 was observed, and little change was seen in expression of BOAT and EAAT3. We conclude that changes in expression of nutrient uptake are distinct between coccidia-infected birds that experience decreased feed intake compared with birds that experience limited feed intake but no infection.

Key Words: coccidia, nutrient transporter, broiler

102 Biogeographical differences in the influence of maternal microbial sources on the early successional development of the bovine neonatal gastrointestinal tract.

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The effect of maternal microbial influences on the early choreography of the neonatal calf microbiome were investigated. Luminal content and mucosal scraping samples were collected from 10 locations in the calf gastrointestinal tract (GIT) over the first 21 d of life, along with postpartum maternal colostrum, udder skin, and vaginal scrapings. Microbiota were found to vary by anatomical location, between the lumen and mucosa at each GIT location and differentially enriched for maternal vaginal, skin, and colostral microbiota. Most sample sites exhibited a gradual increase in a-diversity over the 21 d beginning the first few days after birth. The relative abundance of *Firmicutes* was greater in the proximal GIT, whereas *Bacteroidetes* were greater in the distal GIT. *Proteobacteria* exhibited greater relative abundances in mucosal scrapings relative to luminal content. Forty-six percent of calf luminal microbes and 41% of mucosal microbes were observed in at least one maternal source, with the majority being shared with microbes on the skin of the udder. The vaginal microbiota was found to harbor and uniquely share many common and well-described rumen bacteria, as well as methanogenic archaea, and appeared to have a major influence on the developing rumen and reticulum.

Key Words: ruminant, gastrointestinal tract, microbiota

103 Profiling the vaginal microbiome of sows of different parities.

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Litter performance of sows is lowest at the first parity (P), highest in P2 to P4, and reduces in older parities; however, the mechanism behind this fluctuation is unclear. The objectives of this study were to profile the vaginal microbial communities of sows of different parities and determine associations between bacterial taxa and sow litter performance. Fifty-eight sows (n = 25, 21, and 12 for P1, P2 to P4, and P5 to P6, respectively) from 4 farrowing groups were used. Vaginal swabs were taken on 2 to 7 d before farrowing and used for DNA extraction and subsequent multiplex sequencing of the V4 region of 16S rRNA. No differences ($P > 0.05$) in α diversity between parities was observed. However, β diversity was significantly different ($P < 0.05$) between parities when compared unweighted unifrac. The most dominant core phyla were *Proteobacteria* (P1: 32%, P2–4: 29%, P5–6: 43%), *Firmicutes* (P1: 29%, P2–4: 35%, and P5–6: 34%), *Bacteroidetes* (P1: 25%, P2–4: 20%, and P5–6: 11%), *Fusobacteria* (P1: 9%, P2–4: 13%, and P5–6: 11%), and *Actinobacteria* (P1: 5%, P2–4: 3%, and P5–6: 2%). Differentially abundant taxa ($P < 0.05$) among parities were observed at the order, class, family, genus, and OTUs levels. *Campylobacter*, *ph_2*, *Peptoniphilus*, *Collinsella*, and *Peptococcus* genera were more abundant in P1 and *Veillonella*, *Bacteroidales*, and *Aerococcus* were more abundant in P5–6 ($P < 0.05$). No differentially abundant genera were identified in P2–4; however, unclassified *Bacteroides* and *Prevotella* OTUs were more dominant in P2–4 compared with other parities. Several taxa were correlated to litter performance; in particular, negative correlations were observed between *Finegoldia*, *Peptoniphilus*, *Porphoryromonas*, *Dialister*, *Peptococcus*, and *Fackamia* genera and litter number born ($R = -0.31$ to -0.48; $P < 0.05$); *Porphoryromonas* and *Finegoldia* and litter number born alive (*(*$R = -0.32$, $P < 0.05$); and *Campylobacter* and *Peptoniphilus* and litter birth weight ($R = -0.35$ and -0.32; $P < 0.05$). In conclusion, vaginal microbial communities are shifted among parities and associated with litter performance at different taxonomic levels.

Key Words: parity, sow, vaginal microbiome

104 Interaction of beef calf health, performance and environmental impact by modifying the gut through natural feed additives.

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The objective of this study was to determine the effectiveness of bundling natural products to modify microbiota nutrition in the gut, enhance the immune system, improve performance, and reduce the effect of the waste products in the environment. The study bundled a pH modifier, saponins with physiologically active phyto-chemicals, microbial culture, yeast extract, trace minerals zinc, copper, manganese, and cobalt as free amino acid complexes and chromium. Two hundred fifty-six heifers were purchased from sale barns in eastern Canada. Heifers were transported to Advanced Agricultural Testing facility (Baden, ON, Canada). Cattle were fed 1.5% Biolite in all dietary treatments. There were 4 treatment groups with 8 replications of 8 cattle in each replication. Treatments were (1) Stress EZE 28 d, Dijaide and Rumensin-Tylan 140 d (2) Draxin injectable at arrival Rumensin-Tylan 140 d, (3) Rumensin-Tylan 140 d (4) Stress EZE 28 d Dijaide fed 140 d. Treatment 4 significantly($P = 0.00080$) reduced total antibiotic treatments from other treatments (28 d). Treatment 4 significantly $P \leq 0.18$ improved ADG, DMI, and FCR from the other treatments. The total feed cost per kg gain was significantly ($P = 0.001$) different from all other treatments also. Manure gases NO, CH_3, H_2S, and NH_3 were significantly ($P = 001$) reduced from treatment Rumensin Tylan. Animal stresses reduce immune function, DMI, and overall production. The Stress EZE bundle improved overall health, the gut, the immune system, and performance. The manure greenhouse gases were reduced significantly with feeding of the bundled natural products, thus reducing the environmental impact of greenhouse gases. Bundling the different mode of action products was successful and significantly reduced the cost of production. A healthy gut is important to reduce production losses and reduce the use of antibiotics.

Key Words: Stress EZE, immune system, gut health

105 Interrelationship between *Eimeria* species and *Clostridium perfringens* in the chicken intestine.

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Removal of growth promoters from poultry feed and a decrease in the use of anticoccidial drugs have caused spikes in the incidence of necrotic enteritis (NE) caused by *Clostridium perfringens* (CP). NE is a multifactorial disease and requires many predisposing factors to facilitate the development of the disease. It is known that *Eimeria* species have a proclivity to break down mucosa of the small intestine and promote mucin production, consequently enhancing the growth of CP in the intestines. Therefore, the objective of this study was to understand pathological processes of *Eimeria* species and its effect on the growth of CP in the jejunum, ileum, and cecum of chickens. Commercial broiler chicks were divided into 4 groups and challenged with *Eimeria*, *Eimeria*+CP, CP, or placebo. A commercial vaccine containing 5 *Eimeria species* was given orally at 10× the normal dose per bird at 10 d of age. CP was inoculated orally at 15 d of age using 3×10^8 cfu per day for 4 consecutive days. Typical lesions of *E. acervulina* and *E. maxima* were distinctly observed on d 11 to 12 post-*Eimeria* challenge and disappeared after 14 d. Bloody diarrhea and typical *E. tenella* cecum lesions were observed between13 and 15 d. Typical NE lesions were observed 1 to 3 d after the last CP challenge. Based on qPCR analysis, CP increased approximately 10^4 to 10^5 fold in the jejunum, ileum, and cecum in *Eimeria*+CP and CP challenge groups when compared with the negative control at 23 d of age. Interestingly, the number of CP also increased 10^3 to 10^4 fold in the *Eimeria* challenge group, compared with the control. At 23 d of age, the body weight of the *Eimeria* +CP and *Eimeria* challenge groups was significantly different ($P < 0.05$) from the CP challenge group and the control group. The results suggest that *Eimeria* challenge boosts CP

growth and decreases body weight gain with or without CP challenge.

Key Words: *Clostridium perfringens*, *Eimeria*, chicken

106 Transcriptome changes in neonatal calves treated with artificial dosing of rumen content from adult donor cow.

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In mammals, microbial colonization in digestive tract (GIT) occurs right after birth by the main bacteria groups. Numerous human and mouse studies have reported the importance of early gut microbial inhabitants on host health. However, few attempts were undertaken to understand the role of early gut/rumen microbial colonization on GIT development or host health in neonatal ruminants. Thus, the molecular changes associated with bacterial colonization are largely unknown in cattle. In this study, we aimed to study the host tissue transcriptome changes in response to dosing of exogenous rumen fluid in early life of calf, starting at birth, with repeated weekly dosing. Ruminal fluid from a donor adult cow was used for the experiment. A total of 10 calves were included in this study, with 5 of them treated with fresh rumen fluid from the donor cow, and 5 of them treated with sterilized rumen fluid. Several key organs vital to the calf nutrition were investigated using whole transcriptome sequencing. They included rumen along with 3 other stomach chambers, and liver. We observed significantly elevated expression in genes involved in immune and defense process in rumen tissues. Additionally, liver transcriptome changes suggested potential increased metabolism in sphingolipids, an essential molecular signal for bacteria survival in digestive tracts. Our study provided first-hand insights into host transcriptome changes associated with early colonization of microbial community in neonatal calves. Such knowledge laid a foundation for future probiotics-based research in microbial organism mediated rumen development and nutrition in ruminants.

Key Words: artificial dosing, neonatal calf, microbial colonization

107 A *Bacillus* direct-fed microbial, alone and with protease, improves barrier integrity in an in vitro porcine intestinal epithelial cell culture model.

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A novel combination feed additive for grower finisher pigs consisting of a protease and a 3-strain *Bacillus* direct-fed microbial (DFM) improves growth performance and nutrient digestibility, but the potential gut health benefits are unknown. This study investigated the effects on trans-epithelial resistance (TEER) of IPEC-J2 cells with an in vitro digestion. The 5 treatments included cell media, feed digesta (D), digesta+protease (DP), digesta+DFM (DD), digesta+DFM+protease (DDP). The *Bacillus* strains (1.5×10^5 to 10^6cfu/g feed) and/or the protease enzyme (5,000 U/kg feed) were added to a corn-soy-based feed before a swine digestion simulation. Porcine IPEC-J2 cells were polarized on Transwell permeable filters and a basal TEER measurement was taken. Digesta was applied to the cell apical side and TEER was measured after 3 and 6 h. Data were normalized to the initial TEER measurement and log-transformed to achieve normal distribution. In addition, human THP-1 cells were used to study the effects of the individual DFM strains on cytokine production. The strains were applied at 3 doses and cytokine production was measured after 24 h by ELISA. Data were analyzed in the fit model platform of JMP 11. The time × treatment interaction did not affect TEER ($P = 0.56$). The D and DP reduced TEER vs the media; however, TEER was restored to the media level by DD and DDP ($P < 0.01$). The TEER at 6 h was lower vs 3 h ($P < 0.01$). An interaction of dose × strain affected all cytokines. *Bacillus subtilis* had no effect on IL-10 production but increased IL-6 at the lowest and middle dose, and IL-1b at all 3 doses. One strain of amyloliquefaciens increased IL-10 production at the lowest and middle dose and increased IL-6 and IL-1b at all 3 doses. The second amyloliquefaciens strain had no effect on IL-10 or IL-6 but increased IL-1b production at the lowest and middle dose. In conclusion, the DFM and DFM+protease restored the barrier integrity of IPEC-J2 cells that was reduced by feed digesta. The 3 DFM strains had different effects on cytokine production and lower doses increased production of IL-10 and IL-6 more than higher doses.

Key Words: pig, direct-fed microbial, protease

108 Effect of *Bacillus* spp. direct-fed microbial on leaky gut, bone mineralization, serum peptide YY levels, and ammonia excretion in turkey poults fed a rye-based diet.

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Rye contains high concentrations of non-starch polysaccharides (NSP), leading to increments of intestinal viscosity and reduction of nutrient digestibility. Because poultry have little or no intrinsic enzymes capable of hydrolyzing NSP, exogenous carbohydrases are used in an attempt to reduce the anti-nutritional effects of these polysaccharides. Previously, an in vitro study conducted in our laboratory showed that inclusion of a certain *Bacillus* direct-fed microbial (DFM) candidate that produce exogenous enzymes in high NSP diets reduced both digesta viscosity and *Clostridium perfringens* proliferation ($P < 0.05$). In the present study, rye-based turkey starter diets with or without a *Bacillus*-DFM were administered ad libitum to day-of-hatch poults to evaluate the effect of the DFM on leaky gut, peptide YY, bone mineralization and ammonia excretion. Day-of-hatch turkey poults were assigned to either a control diet (CON) or a DFM treated diet (n = 25). At 10 d of age, poults were given an appropriate dose of fluorescein isothiocyanate-dextran (FITC-d) by oral gavage. Blood was collected to evaluate serum FITC-d and peptide YY concentrations. Liver samples were collected to evaluate bacterial translocation and tibias were removed for assessment of bone parameters. Poults fed the *Bacillus*-DFM candidate had

increased ($P < 0.05$) tibia diameter, breaking strength, and ash, calcium and phosphorus contents when compared with CON poults. Interestingly, poults fed the DFM showed a reduction in peptide YY. Furthermore, CON poults showed an increase in serum FITC-d and liver bacterial translocation, accompanied with higher ammonia excretion. However, these adverse effects were reduced by the inclusion of the DFM candidate. The results of this study suggest that the consumption of a selected *Bacillus*-DFM, producing a variable set of enzymes, could contribute to enhance performance in high NSP diets by reducing gut permeability, improving nutrient absorption and retention, resulting in decreased ammonia excretion.

Key Words: *Bacillus*-DFM, intestinal permeability, bone quality

Session 2

109 Why resist: Antibiotic alternatives in swine.
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Antimicrobial resistance (AMR) is a global health crisis, which has resulted in calls for more prudent antibiotic usage and development of antibiotic alternatives. Antibiotics have historically been administered to production animals to promote growth, and continue to be given to prevent or treat infection. To limit continued development of AMR, a multipronged approach is needed to meet the varied antibiotic needs of food producers. Dietary additives, such as prebiotics, are a promising approach to promote intestinal health and maximize growth potential. Dietary starch, including raw potato starch (RPS), promotes changes in intestinal T-cell populations, secretory IgA, and gene expression in pigs, skewing toward enhanced barrier function and regulatory status. In addition, dietary RPS can improve pig growth performance. Although some dietary additives may improve growth performance, they may not provide direct protection against infectious disease; thus, antibiotic usage is still a critical tool for humane treatment of food animals. Mass oral medication facilitates ease of administration in production systems, but the direct exposure of intestinal bacteria to antibiotics is selective pressure for AMR transmission. Targeted antibiotic administration via intramuscular injection, as opposed to in-feed administration, had minimal impact on intestinal bacterial communities compared with the in-feed antibiotic. The minimized disturbance to intestinal bacteria with injected antibiotic indicates less pressure for AMR mobility. In addition, injected antibiotic limited production loss associated with respiratory infection.

Key Words: swine, alternative, antibiotic

110 Comparison of multiple *Clostridium perfringens* strains and their influence on necrotic enteritis.
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Necrotic enteritis (NE), caused by *Clostridium perfringens* (CP), in broilers is often associated with a concurrent infection of *Eimeria maxima* (EM). However, breakouts of this disease have been reported to occur independent of EM, and to be related to CP strains that produce NE toxin B (NetB). Presently, multiple methods of inducing NE in broilers were compared with evaluate the role of various toxins in development of clinical disease. Six CP strains were evaluated by PCR for toxin-associated genes, including α-toxin and NetB, followed by inclusion of some strains, NetB+ and NetB−, for 2 in vivo experiments. Experiment 1 treatments consisted of non-challenged control (NC), EM + non-NetB CP (EMCP), non-NetB CP (nonNetB), NetB strain CP 1 (NetB1), NetB strain CP 2 (NetB2) or NetB strain CP 3 (NetB3). All groups, except NC, were challenged with 10^4 cfu of *Salmonella* Enteritidis on day of hatch. On d 16, EMCP birds were weighed and challenged with 2×10^4 EM oocysts. On d 20–22, nonNetB and NetB1–3 groups were challenged with 50 mL of 10^6 to 10^8 cfu/mL CP directly onto the feed once daily, all birds were weighed d 22. On d 17, EMCP birds were challenged with 10^8 cfu CP via oral gavage. On d 22, all birds were weighed for body weight gain (BWG) and lesion scores (LS). At D22, % change in BWG was significantly different ($P < 0.05$) between NC, EM, and EMCP, but not NetB1–3 treatments. Lesion scores were significantly higher ($P < 0.05$) than NC for only EMCP, with all others statistically similar to NC. The second experiment tested an increased dose of NetB1 CP, 1 L of 10^8 cfu/mL 2×/d on d 17–20, against NC, nonNetB, and EMCP. By d 22, EMCP had the greatest decrease ($P < 0.05$) in BWG and was lower than both NC and NetB1. NetB1 also had decreased BWG compared with NC ($P < 0.05$), but not EMCP. Lesion scores reflected BWG results. These studies suggest that Net-B positive strains of CP can induce NE, when administered in extremely high doses over a prolonged period, and that predisposing factors, such as *Salmonella* and EM play an important role in the pathogenesis of NE in nonNetB strains.

Key Words: necrotic enteritis, *Clostridium perfringens*, Net B

111 Genetically modified *Lactobacillus casei* could be a bio-therapeutic for enteric bacterial infections.
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As a major source of microbes and their numerous beneficial effects, the gut microflora/microbiome is intimately linked to human health, immunity, and diseases. The key intestinal microbial byproducts, commonly known as metabolites, are crucial to the maintenance of a balanced gut ecosystem and healthy gut microbial community. More specifically, the presence or absence of several genes and their expression levels, in the presence or absence of stimuli or stress, regulate the production and concentration/amount of various metabolites. These are essential for host defense and immunity and protecting from various diseases or pre-condition of diseases including inflammation, cancer, oxidation, atherosclerosis, and outcompetition of enteric bacterial pathogens. In a recent study, we found that in the presence of the prebiotic-like component peanut flour, *Lactobacillus casei* (LC) produced 100 times more linoleic acid (LA) than under normal conditions, and was able to outcompete several enteric bacterial pathogens. On the basis of this evidence, we have overexpressed the linoleate isomerase (myosin cross-reactive antigen, *mcra*) gene in a natural, sustainable, bacteriophage-resistant LC strain (LC^{+mcra}) in order to enhance the production of conjugated linoleic acids (CLA) and verify the ability of this genetically engineered strain LC^{+mcra} to inhibit growth, colonization, and infection of host cells by human enteric foodborne bacterial pathogens. We found that LC^{+mcra} excluded the *Salmonella* and EHEC in co-culture condition and altered the host cell-pathogens (both) interactions. The genetically modified mutant also altered the virulence properties of both bacterial pathogens significantly. This study showed that LC^{+mcra} could be a non-traditional bio-therapeutic for preventing the colonization of *Salmonella* and EHEC.

Key Words: linoleic acid, *Lactobacillus casei*, outcompete

112 Microbial modifying properties of reused litter and iodinated water in poultry production.

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The gut microbiota has been identified as an important driver of disease resistance in poultry. However, how environmental exposures affect the gut microbiota and the mechanisms through which microbes regulate host immunity remain poorly understood. Several studies have shown that exposing chicks to used litter results in greater resistance to *Salmonella* infection; however, these studies failed to characterize the effects on the composition of the intestinal microbiota and host responses. Iodinated water, which has antimicrobial properties, is another exposure associated with improved performance in poultry, but whether its effect on the gut microbiota contributes to improved growth is unknown. In this study, we investigated the effects of iodinated water and chicken litter exposure on early establishment of intestinal microbiota, *Salmonella* resistance, growth performance, and host intestinal transcriptome. We hypothesized that iodinated water and litter exposure would improve animal performance by altering the intestinal microbial community. Iodinated water increased average daily gain at 5 d, but effects were no longer significant at 10 d. Iodinated water also had an effect on the composition of the cecal microbiota ($P < 0.05$, Anosim); however, this effect was less pronounced when the chicks were reared on used litter and did not affect *Salmonella* colonization. Litter exposure substantially reduced the β-diversity of the cecal microbiome ($P < 0.01$, Anosim), suggesting a more stable microbial community. Chicken litter exposure significantly reduced *Salmonella* colonization by 1.2 log copy number/gram of ileal contents ($P < 0.05$) 7 d post-infection. Analysis of cecal gene expression is ongoing and will provide insights into the effects of the treatments on host physiology. This work will provide a greater understanding of the relationship between the environment, gut microbiota and poultry health outcomes. Defining how environmental exposures drive a healthy microbiota and support pathogen resistance will support the development of targeted microbiome based therapies.

Key Words: poultry, microbiota, infection resistance

113 Aqueous citrus extract supplementation affects gut microbiota and histological parameters of broiler chicken.

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Citrus aqueous extract (CAE) is a blend of complementary molecules, namely citroflavonoids and pectic oligosaccharides, obtained from natural extraction of citrus. Many studies have shown the effect of citrus extract on intestinal microbiota. Indeed, citroflavonoids modulate microbiota in favor of beneficial microorganisms (Unno et al., 2015). In contrast, microbiota, when well balanced, have a serious effect on gut health and morphology (Jandhyala et al., 2015). The aim of this trial was to assess the effect of supplementation with a commercial CAE, Nor-Spice AB, on histological parameters—intestinal length and villi volume—of the intestine of broiler chicken. The experiment took place at the Technical Institute of Livestock, Algeria (ITELV). Four hundred birds (Cobb 500) were divided in 2 groups (group 1: standard diet and group 2: standard diet + 250 ppm Nor-Spice AB). Two aspects of intestine were measured: the intestine length and the measurement of intestinal villi at different segment of the intestine. Birds that received CAE in their diet had a lower load of *E. coli* compared with negative control birds. No effect was observed on *Lactobacillus*, and *Salmonella* were not detected in both groups. Birds supplemented with commercial CAE Nor-Spice AB showed a greater intestinal length during the period of the trial. The group that received commercial CAE experienced an improvement of the villi volume. The greatest improvement took place in the jejunum compared with duodenum and ileum. We observed an improvement of the intestinal morphometry on the group supplemented with the CAE. Intestinal length was greater during the period of the trial and villi volume was increased. These improvements indicate stimulation of the intestinal absorption function and could explain the better zootechnical parameters obtained with the group supplemented with Nor Spice AB.

Key Words: citrus extract, gut, microbiota

114 Transcriptome changes in neonatal calves treated with artificial dosing of rumen content from adult donor cow.

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In mammals, microbial colonization in digestive tract (GIT) occurs right after birth by the main bacteria groups. Numerous human and mouse studies have reported the importance of early gut microbial inhabitants on host health. However, few attempts were undertaken to understand the role of early gut/rumen microbial colonization on GIT development or host health in neonatal ruminants. Thus, the molecular changes associated with bacterial colonization are largely unknown in cattle. In this study, we aimed to study the host tissue transcriptome changes in response to dosing of exogenous rumen fluid in early life of calf, starting at birth, with repeated dosing every other week. Ruminal fluid from a donor adult cow was used for the experiment. A total of 10 calves were included in this study, with 5 of them treated with fresh rumen fluid from the donor cow, and 5 of them treated with sterilized rumen fluid. Several key organs vital to calf nutrition were investigated using whole-transcriptome sequencing. They included rumen along with 3 other stomach chambers and liver. We observed significantly elevated expression in genes involved in immune and defense process in rumen tissues. Additionally, liver transcriptome changes suggested potential increased metabolism in sphingolipids, an essential molecular signal for bacteria survival in digestive tracts. Our study provided insights into host transcriptome changes associated with early colonization of microbial community in neonatal calves. This knowledge lays the foundation for future probiotics-based research in microbial organism–mediated rumen development and nutrition in ruminants.

Key Words: neonatal calf, artificial dosing of rumen content, host transcriptomics

Session 3

115 The poultry gut: Signals integrator, generator, and target for intervention.

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The poultry gut is the central organ of poultry health and production. The gut is the nutrient-absorptive organ, making it essential for efficient growth; it is also one of the main sites of pathogen entry, making a proper functioning gut important for maintaining disease-free production. Within the gut are the resident microorganisms, the gut microbiota. These microorganisms and their combined genetic material, the microbiome, are just as important to poultry health and production as any organ within the bird and are critical to the proper functioning of the gut. Much research has been done describing the taxonomy of the bacteria within the poultry gut. However, the relative bacterial species are highly variable, not just at the flock or bird level but within segments of the gut and over time. This variation has made identifying beneficial and harmful bacterial populations extremely difficult. The functional potential of the microbiome and its host interaction are critical to understanding poultry gut health. The microbiome and its functional shifts are only one signal that the gut receives and communicates to the rest of the bird. The poultry gut interacts with the rest of the body in several ways: it is the second most innervated organ, it is the major immunological organ, the hepatic portal vein drains directly into the liver, hormones influence gut activity, and so on. The gut sends signals to the rest of the body and to the gut microbiome, and it receives and integrates signals. It is these signals that should be considered targets for intervention. An intervention targeting the gut without a measurable positive effect on host response is wasted effort. In the age of restricted antibiotic use in poultry production, manipulation of the microbiome and gut activity via feed additives has become a promising alternative. Probiotics, prebiotics, postbiotics, synbiotics, and feed enzymes have been developed with the goal of enhancing poultry health, performance, and disease resistance. A comprehensive understanding using the latest molecular tools and a multi-omics approach from the host and microbe perspectives will be necessary to define this complex interaction.

Key Words: microbiome, poultry, signals

116 Evaluation of *Campylobacter jejuni* isolates to experimentally colonize and selective media to enumerate from poults.

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Consumption of contaminated poultry products is the main source of human campylobacteriosis, caused mainly by *Campylobacter jejuni*. Chickens, but not turkeys, have been experimentally colonized with different isolates of *C. jejuni*, and enumeration from intestinal samples can be challenging because routine *Campylobacter* selective media support the growth of non-*Campylobacter* organisms. We sought to identify (a) *C. jejuni* isolates that persistently colonize poults, and (b) selective media to enumerate their abundance in intestinal samples. For ease of isolation, mutants of *C. jejuni* strain NCTC 11168 were constructed resistant to chloramphenicol (CjCm) or kanamycin (CjK). Three-week-old poults were orally colonized with either CjCm, CjK or mock-colonized, and were euthanized up to 14 d post-colonization. Immunohistochemistry detected *Campylobacter* antigen in the cecum between the villi, and host-response was evaluated by qPCR on cecal tissue. Significant differences in IL-1β, IL-10, IL-13, IL-17A and IL-22 mRNA expression were detected 2 d after colonization. CjCm and CjK were enumerated on Campy-Line agar with sulfamethoxazole (CLA-S) supplemented with chloramphenicol or kanamycin, respectively. Cecal colonization by CjCm and CjK significantly dropped after challenge, and neither was isolated from ileal samples. Next, poults were colonized with wild-type isolates NCTC 11168, 81-176 and NADC 20827, and different *Campylobacter* selective media (Campy cefex, CLA-S and CampyChrome) were evaluated for enumeration. Isolates NCTC 11168 and NADC 20287 persistently colonized the cecum for up to 21 d, and were enumerated using CLA-S and CampyChrome agar. Enumeration from ileal and colon samples diminished throughout the study, indicating that the cecum was the primary site of *C. jejuni* colonization in turkeys. Data from this study demonstrated that wild-type isolates NCTC 11168 and NADC 20827 persistently colonized the cecum, and CLA-S or CampyChrome agar were the best selective media to enumerate *Campylobacter* from poults. These findings will be useful to evaluate the host-response by wild-type *C. jejuni* colonization in turkeys and evaluate strategies to reduce its colonization to promote food safety.

Key Words: *Campylobacter jejuni*, selective media, colonization

117 Enteric bacterial toxin neutralization by Calibrin-Z.

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Bacterial toxins are responsible for the clinical symptoms and tissue damage associated with enteric bacterial infections. This is true across multiple species, including *Vibrio parahemolyticus* (*Vp*) toxins that cause acute hepatopancreatic necrosis disease (AHPND) in shrimp, *Clostridium perfringens* (*Cp*) toxins cause costly necrotic enteritis in poultry and *Clostridium difficile* (*Cd*) toxins cause diarrhea in humans. Concern over antibiotic-resistant bacteria is growing and research is focused on finding alternatives. Many alternative solutions aim at reducing pathogenic bacteria but are not effective. Because bacterial toxins damage the gut, interest is growing in toxin neutralization as a means to combat enteric disease. Calibrin-Z, an activated mineral, has been proven to decrease the damage to intestinal tissue by toxins. This paper reviews research on the effects of Calibrin-Z on toxin neutralization as a means to control intestinal disease. In shrimp, AHPND is caused by bacterial toxins (PirA and PirB). In vitro tests prove mixing Calibrin-Z and toxins decreased their level in the supernatant, and shrimp had lower mortality when reverse-gavaged with this supernatant. Shrimp challenged with *Vp* had

lower mortality when fed Calibrin-Z. Calibrin-Z was proven to bind NetB and α-toxins from *Cp in vitro*. *Cp*-challenged broilers fed Calibrin-Z had improved villi height and performance. Calibrin-Z also neutralized other toxins affecting the gut: LPS, Shiga-like toxin II, heat-labile toxins from *E. coli*, and ToxA and ToxB from *Cd*. Killing or inhibiting pathogenic bacteria places pressure on the bacterium and increases the probability of resistance. Targeting enteric bacterial toxins prohibits the organism from disrupting host structural and immune homeostasis without threatening the bacteria. Toxin neutralization can be an important means to protect gut health and Calibrin-Z was proven to neutralize bacterial toxins. These findings offer an intriguing and promising alternative strategy for disease control.

Key Words: toxin neutralization, antibiotic resistance, gut health

118 A mixture of organic acids and botanicals ameliorates and prevents the damage induced by an inflammatory challenge in Caco-2 cell cultures.

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The aim of this study was to assess the potential of a mixture of organic acids and botanicals (1) in preventing an in vitro inflammatory challenge, and (2) in enhancing the barrier properties after the same challenge. Caco-2 cells were seeded on transwell inserts, cultured in DMEM+10% FBS (basal medium, BM) in 5% CO_2 at 37°C and allowed to grow until stable. Then (d 0), cells were cultured for 15 d in BM (control group, CTR) or BM added with a mixture of citric acid, sorbic acid, thymol, and vanillin at 88.8 (Mix1X) or 444 ppm (Mix5X). All the treatments were challenged with a mix of pro-inflammatory cytokines (IFNγ, IL1β, TNFα) and LPS (*E. coli* O55:B5) for 24 h either at d 0 (Experiment 1) or at d 14 (Experiment 2). Trans-epithelial electrical resistance (TER) was measured every other day and at d15 cells were harvested to assess mRNA expression of tight junctions (TJ) by qPCR. Data were analyzed with 1-way ANOVA (qPCR) or ANOVA repeated measures (TER) and each treatment had 6 independent replicates (n = 6). Experiment 1: Mix1X and Mix5X improved TER starting from d 5 and d 2, respectively, maintaining the improvement in TER throughout 15 d of treatments after the initial challenge ($P < 0.01$). At d 15, occludin (OCC) and zonula occludens-1 (ZO-1) mRNA were increased in a dose-dependent manner ($P < 0.01$). Experiment 2: Mix1X and Mix5X showed a higher TER in the 24 h immediately following the challenge (d 15) compared with CTR ($P < 0.01$). Compared with values at d 0, Mix5X maintained the same TER values despite the inflammatory insult and Mix1X prevented the decrease in TER by 50% compared with CTR. Moreover, Mix5X showed a higher expression of both ZO-1 and OCC ($P < 0.01$). In conclusion, the mixture of organic acids and botanicals was able to ameliorate (Experiment 1) and to prevent (Experiment 2) damages caused by a pro-inflammatory stimulus by reducing or preventing the drop in TER and by improving the TJ mRNA expression. These results highlight the barrier-improving potential of these additives in animal nutrition even during challenging conditions.

Key Words: organic acids and botanicals, intestinal barrier function, inflammation

119 Forskolin and butyrate act synergistically in protecting chickens from necrotic enteritis by inducing host defense peptide synthesis.

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Alternatives to antibiotics are needed to reduce antibiotic resistance and ensure animal health and productivity. Modulating the synthesis of endogenous host defense peptides is being explored as a novel antibiotic alternative approach to disease control and prevention. We previously demonstrated that forskolin, a natural labdane diterpene and an adenylate cyclase signaling agonist present in the Indian Coleus plant (*Coleus forskohlii*), synergizes with butyrate in promoting the expression of multiple chicken host defense peptide genes both in vitro and in vivo. Here, we further observed improvement in barrier function with no obvious induction of inflammatory response in chicken HD11 macrophages treated with butyrate and forskolin as revealed by RNA sequencing and kinome peptide array. Dietary supplementation of sodium butyrate and forskolin-containing *C. forskohlii* plant extract synergistically alleviated intestinal pathology and the *Clostridium perfringens* titer in a subclinical model of necrotic enteritis. Moreover, a 3-wk feeding of a combination of butyrate and the *C. forskohlii* plant extract has no negative influence on weight gain, feed intake, or feed efficiency of broiler chickens. Collectively, these results revealed the potential of feeding butyrate and forskolin as alternatives to antibiotics in enhancing gut immunity, barrier function, and disease resistance.

Key Words: host defense peptide, antimicrobial peptide, mucosal immunity

120 Effect of replacing antibiotic growth promoters with polyphenolic botanical extracts and essential oils in feed of laying hens on performance, health, Newcastle disease titer, and some blood parameters.

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Polyphenolic vegetative extracts and essential oils are very important replacement additives for the antibiotic growth promoters in layer feeds. The goal of this study was to investigate the effect of vegetative extracts and essential oils on egg producing layers' health, immunity against ND virus disease and other blood parameters. One hundred and twelve 9-mo-old, white Novagin egg-producing laying hens (1480 ± 50 g average live body weight each) were randomly distributed to 7 groups equally (n = 16). Each group/treatment was divided 4 times with 4 birds per replicate cage unit. Diets (rations) were prepared by adding vegetative polyphenolic extracts of black tea (c), seeds of black cumin (d), fenugreek seed (e) as well as oils from black cumin seeds (f) and fenugreek seeds (g) in the negative control (b; treatment with nil antibiotic and antioxidant added in the ration) and compared with positive control (a) having antibiotic (4.4%) lincomysin 120 mg/kg of feed, acetic acid (99.5%) 0.15 mL/kg of feed, antioxidant seldox (BHA, BHT, ethoxiquine, and citric acid) 120 mg/kg of feed. After end of the 5 weeks trial, weekly feed conversion ratio (FCR) of all treatments were significantly

good than negative control (b) ($P < 0.05$), however treatments a, b, d, e, f and g had non-significant differences among one another ($P > 0.05$). ND titer level remain same of all treatments and overall health performance was good and there was insignificant difference between all blood parameters except negative control ($P > 0.05$). These results clarify that polyphenolic vegetative extracts/oils have positive affect on the performance, health and there is no drastic change in blood parameters of the egg producing layers and thus can be replaced by antibiotic growth promoters.

Key Words: blood parameter, laying hen, Newcastle disease (ND)

Session 4

121 Favoring gastrointestinal health of pigs—Benefits of dietary concepts including rye as the main cereal?

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During the last decades, rye has lost its earlier role as food and feed in Europe. Due to diverse efforts in reducing intensity of fertilizer use (nitrogen, phosphorus) for ecological reasons and due to high yields of rye at lowered fertilizing levels and water availability—especially in regions with sandy soils—there are high perspectives for rye. The chemical composition of wheat and rye is quite similar regarding starch and crude fiber contents. When, estimating the chemical composition of the different cereals, there is one group of carbohydrates in rye that is unique—the fructans (~40–60 g/kg DM), which are rarely in the focus of animal nutrition so far. In comparison to what the fructan contents in rye are about 4 to 10 times higher. What are the main effects of a higher ingestion of fructans, which are degraded by the intestinal flora only? The predominant effect is markedly promoted microbial butyrate formation (Bach-Knudsen et al., 2005). Only a few intestinal products formed by microorganisms have garnered such a strong scientific interest in the last few years as butyrate, in the field of both human and animal nutrition. The local and systemic effects of forced intestinal butyrate formation are extremely diverse (Guilloteau et al., 2010), ranging from the control of important processes such as proliferation, differentiation, and apoptosis (delayed) in the epithelium of the gastrointestinal tract via the control of cytokine production (process of inflammation) and stimulation of certain immune cells (and their control), to the "signal effect" on certain bacteria in the intestinal tract (down-regulation of invasion genes in *Salmonella*). Finally, the butyrate flooding (liver) and concentrations in the peripheral blood are of interest in connection with "central" effects (satiety/behavior). Furthermore, interesting effects of stimulated intestinal butyrate formation (e.g., achieved by coarse grinding of cereals; Visscher et al., 2009); or by dietary inclusion of raw potato starch, inulin from topinambur, Jerusalem artichokes) concern reduced skatole formation, lowering the "boar taint" in fattening entire pigs (Vhile et al., 2012). Thus, there might be diverse benefits when rye is ingested by swine in higher amounts.

Key Words: rye, fructan content, butyrate formation

122 Inactivation of *Salmonella* and *Clostridium* by Alquermold Natural L, a fungicide/bactericide.

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Alquermold Natural L (AMN) is a natural bactericide and fungicide. We evaluated this compound for the inactivation of *Salmonella* Dublin and *Clostridium perfringens*. Different dilutions of AMN were prepared in sterile distilled water followed by the addition of an equal volume of a bacterial suspension. The mixtures were incubated at room temperature under aerobic (*Salmonella*) and anaerobic (*Clostridium*) conditions. At various time points, aliquots were removed followed by preparation and plating of serial 10-fold dilutions to determine the number of surviving bacteria after each time point. More than 5 logs of *Salmonella* were killed after 10, 20, and 60 min at 1:2 and 1:20 dilutions. At 1:50 and 1:100 dilutions, AMN was able to inactivate 5 logs of *Salmonella* after a contact time of 24 h. *Clostridium* was found to be more resistant; it took 60 min for inactivation of 4 logs at 1:2 and 1:20 dilutions. At 1:50 dilution, 24 h of contact were required for 4-log reduction in *Clostridium*. In summary, AMN is an effective compound that can kill both *Salmonella* and *Clostridium* at various dilutions and time points.

Key Words: *Salmonella*, *Clostridium*, Alquermold

123 Spray-dried plasma—A review of a unique functional protein ingredient on intestinal health.

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Normal gut barrier function is critical to the performance and productivity of livestock species. Supporting and maintaining intestinal integrity and reducing permeability is important for maintaining nutrient absorption, while reducing exposure of the animal to toxins or pathogens that may be present in the intestinal lumen. Spray-dried plasma (SDP) is a unique protein ingredient composed of a complex mixture of functional components with biological activity independent of their nutritional value. Several studies have demonstrated effects of functional proteins of spray-dried plasma on intestinal immune response and subsequent applications in livestock species. Research shows that functional proteins reduce the negative effects of inflammation by supporting and maintaining an efficient immune system. The functional proteins of spray-dried plasma are handled to retain their biological activity and contribute to both nutritional and functional properties of the diet. A series of mouse model, swine, and poultry experiments has been reviewed to provide insight into how these functional proteins benefit animal growth, affect intestinal integrity, and improve overall well-being. In rodents exposed to an inflammatory agent (i.p.-injected staphylococcal enterotoxin B), orally consumed functional proteins modulated subsequent stimulation of immune cell populations and modulated pro-inflammatory profile in the intestinal mucosa. By minimizing the inflammatory response, subsequent damage to mucosal surfaces was minimized. These effects were accompanied by increased anti-inflammatory cytokine production, reduced mucosal permeability, increased tight junction protein expression, and improved glucose absorption. Follow-up research in both swine and poultry has demonstrated the effect on gain and feed efficiency by orally feeding these proteins, which contributes to understanding the application of these proteins to improve animal well-being and aids in improving productivity. Collectively, these findings indicate that functional proteins of spray-dried plasma support and maintain the immune system, reduce inflammation, and improve barrier function.

Key Words: spray-dried plasma, immune system, livestock

124 Use of a novel methodology to validate that β-mannanase (Hemicell HT) reduces feed-induced inflammatory responses and alters metabolism in the avian gut.

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This presentation will discuss the development of a unique, species-specific tool for the study of immuno-metabolism in poultry. This tool is readily expandable to other species and of potential use to study a wide variety of biological, metabolic, immunological, and infectious questions. Biologically relevant data confirming that β-mannans induces feed-induced inflammatory responses (FIIR) and that Hemicell HT (Elanco Animal Health) can eliminate these responses are presented. Data from this study suggest that Hemicell HT has separate metabolic consequences besides its FIIR effects. We have shown that Hemicell may have positive effects in a normal diet formulation, as the kinotype of these birds is similar to those also fed β-mannans. Results from this study identified peptides that are differentially phosphorylated due to Hemicell HT at the 3 time points, showing Hemicell has age-specific effects on the jejunum of chickens. These age-specific effects can also be considered time-dependent biomarkers of Hemicell HT activity. The time-independent, dose-independent and β-mannan-independent markers of Hemicell activity generated in this study will be discussed in terms of how they can be used to monitor the activity and efficacy of Hemicell HT.

Key Words: kinome array, β-mannan, Hemicell HT

125 The effects of different feed additives on bird performance and the gastrointestinal microbiome of *Salmonella*-challenged broilers.

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A 42-d, 60-unit floor pen (10 pens per treatment, 25 birds per pen) *Salmonella* challenge study was conducted to determine the effects of supplementing broiler diets with virginiamycin (VM); medium-chain fatty acids (MCFA); MCFA plus lactic acid (MCFA+LA); and a phytogenic blend (PB). Effects were assessed on bird performance and ileal, cecal, and litter microbiomes in birds challenged with *Salmonella* Typhimurium. Treatments were compared with a non-inoculated control group (NIC) and a *Salmonella*-challenged group without feed additives (IC). At d 14, 28, and 42 of age, all bird weights and intake were measured, 20 birds from each treatment were euthanized, and the ceca and ilea of euthanized birds were collected along with grab litter samples from each pen. Bacterial profiling was performed using 16S rRNA amplicon sequencing. Subsequent analyses were performed for measurements of α and β bacterial community diversity, taxonomic classifications, and assessments of bacterial taxa that were shifted as a result of different treatments. At 42 d, body weights and mortality-adjusted feed conversions for the NIC were significantly better ($P < 0.1$) than the IC and VM whereas the MCFA, MCFA+LA, and PB treatments were similar to the negative NIC. The *Salmonella* challenge itself had significant ($P < 0.01$) effects on the bacterial microbiome of all sample types, with the greatest effects observed in the cecal microbiome of the bird. The VM treatment counteracted the effects of the *Salmonella* challenge on the overall bacterial communities of all sample types ($P < 0.05$). Although none of the antibiotic alternative treatments had significant effects on overall bacterial community structure consistent over time, specific bacterial taxa were affected by several treatments. These included Candidatus Arthromitus (segmented filamentous bacteria), *Peptostreptococcus*, and *Clostridium* species. Unique signature taxonomic effects were identified for each treatment type, demonstrating attributes of each feed additive type in contributing to unique effects on the bird microbiota. Overall, this work identifies microbiome modulations conferred by different antibiotic alternatives under a *Salmonella* challenge.

Key Words: poultry, microbiome, *Salmonella*

126 Microbial metabolite deoxycholic acid attenuates necrotic enteritis.

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Necrotic enteritis (NE) induced by coccidiosis and *Clostridium perfringens* is one of the refractory and prevalent broiler intestinal diseases in the era of antimicrobial free. Microbiota has been successfully used to treat human intestinal *Clostridium difficile* infection. It remains elusive if microbial metabolites prevent intestinal infection. Here we hypothesize that microbial metabolite secondary bile acid deoxycholic acid (DCA) attenuates NE. To examine this hypothesis, *C. perfringens* were cultured in various concentrations of bile acids. Broiler chicks were fed 0 and 1.5 g/kg cholic acid (CA, primary bile acid) or DCA. Birds were challenged with 20,000 oocysts/bird at d 18 and with 10^9 cfu/bird/day *C. perfringens* at d 23. Birds were weighed on d 0, 18, 23, and 26. Birds were killed at d 26 and ileal samples were collected for molecular and histopathological analysis. Real-time PCR was used to measure intestinal host response and *C. perfringens*. DCA at as low as 50 μ*M* inhibited 99.92% of *C. perfringens* growth in Tryptic Soy Broth, while CA and conjugated primary bile acid TCA failed to reduce the bacterial growth. Notably, DCA diet promoted bird growth performance on body weight gain before infection (d 0–18). NE by *C. perfringens* infection exacerbated *E. maxima*-induced growth performance loss. Importantly, DCA diet prevented against growth performance loss by coccidiosis and NE. CA diet attenuated body weight gain loss at NE but failed at coccidiosis compared with NE control birds. Upon examining molecular and cellular events, we found that DCA attenuated necrotic enteritis-induced severe intestinal inflammation. NE also induced strong inflammatory mRNA accumulation of *Infγ*, *Tnfα*, and *Mmp9*, effects attenuated by 51%, 82%, and 66% in DCA birds. In conclusion, dietary microbial metabolite DCA improves broiler growth performance and prevented *E. maxima*- and *C. perfringens*-induced NE and inflammatory response.

Key Words: antimicrobial free, microbiota metabolites, necrotic enteritis

127 Effect of synbiotic supplementation on intestinal development and integrity of broilers.

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Due to concerns of antibiotic resistance and changes in customer and regulatory demands, researchers and industry leaders are searching for alternatives to sub-therapeutic antibiotics. In

particular, probiotics have received increased attention for their ability to improve enteric health. The objective of this experiment was to evaluate the effects of synbiotic supplementation on broiler intestinal development and integrity. A total of 300, day-old, Cobb 500 broiler chicks were randomly assigned to either a non-treated control or a treated group supplemented with a synbiotic (PoultryStar me; 500 g/ton) with 3 replicate pens (50 birds/pen) for each group. On d 7, 14, 21, and 35, 8 birds per treatment were euthanized and duodenum, jejunum, and ileum samples were taken for histological analysis. Additionally, ileal samples were collected for epithelial integrity measurements (transepithelial electrical resistance (TER) before and after lipopolysaccharide (FITC-LPS) challenge). For all measurements, significance threshold was set at $P < 0.05$. Villus height was increased in all intestinal segments in the first week of life for the synbiotic group. Synbiotic-fed birds also had significant increases in duodenal villi height on d 14, while ileal villus height was increased through d 35. The TER for synbiotic-fed birds increased until d 35, while the TER for birds fed non-treated feed increased only until d 21. Challenging with FITC-LPS increased the TER in both groups on d 7, 14, 21, and 35 with synbiotic-fed birds having a significantly higher TER after FITC-LPS on d 35 compared with the controls. Additionally, the synbiotic group had a greater TER response to the FITC-LPS compared with control on d 21 and 35, suggesting synbiotic supplementation increased the resilience of intestinal tract in the face of a potential challenge. Overall, these results suggest that synbiotic used in this study may be an effective means of improving intestinal development and integrity and allow the intestinal tract to adapt to pathogenic stressors, thus helping to prevent bacterial translocation and enteric diseases.

Key Words: probiotic, barrier function, histology

128 Effects of Varium on expression of intestinal barrier, antioxidant and pro-inflammatory cytokine genes in young broiler chickens with experimental necrotic enteritis.

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In multiple trials, Varium, a formulated product, was proven to control enteric bacterial toxins and improve broiler performance. Meta-analysis revealed improvement in broiler chickens with and without a necrotic enteritis (NE) challenge, as well as with or without an in-feed antibiotic. Along with the improvements in performance parameters, Varium improved NE-induced intestinal lesion scores and reduced translocation of *Clostridium perfringens*-produced exotoxins across the intestine and into blood following NE challenge. This study investigated the effects of Varium on immune and antioxidant responses and intestinal barrier homeostasis during NE challenge. From hatch, chickens (8 pens/trt, 7 chicks/pen) were fed a diet with Varium, BMD (55 ppm), or with a non-supplemented control diet, and orally challenged with 1×10^4 sporulated oocysts of *Eimeria maxima* at 3 d and 1.0×10^9 cfu of *C perfringens* at 7 d of age. The group of uninfected chickens fed with a non-supplemented control diet was the negative control. At 2 d post *C perfringens* challenge, intestinal sections were scored for NE lesions and mRNA expression of intestinal tight junction proteins; pro-inflammatory cytokines and antioxidant enzymes were analyzed in intestinal tissues via qRT-PCR analysis. Feeding Varium decreased (vs. challenged controls, $P < 0.05$) the lesion scores of challenged chickens to a level like BMD. Feeding Varium increased intestinal mRNA expression of occludin and Zonula occludens-1, 2 key tight junction family members, relative to the challenged controls ($P < 0.05$). Reduced expression of catalase by NE challenge was completely reversed by feeding Varium. Further, Varium upregulated mRNA expression of IL-1β and Lipopolysaccharide-induced tumor necrosis factor-α factor (LITAF) ($P < 0.05$). In conclusion, Varium enhanced gut integrity and antioxidant defenses during an NE challenge. Additionally, Varium enhanced the host ability to mount adequate protective immunity against challenge by NE-causing pathogens. The benefits provided by using Varium can contribute to a better preserved immune homeostasis during NE challenge.

Key Words: necrotic enteritis, exotoxins, immune

129 Impact of exogenous carbohydrases on intestinal and peripheral inflammatory status in nursery pigs fed a higher fiber, lower energy diet.

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The objective of this experiment was to evaluate the effects of dietary xylanase (X; Hostazym X, Huvepharma Inc.) and an enzyme blend (EB: cellulase, β-glucanase, and xylanase; Hostazym DDGS, Huvepharma Inc.) on inflammatory responses in intestinal tissues and periphery of weaned piglets. A total of 460 pigs (6.43 ± 0.06 kg BW; F52 Gentaporc × 6.0 Gentaporc) were randomly blocked by weight and assigned to 4 treatments, in a 2 × 2 factorial arrangement: xylanase (0 or 0.01%) and EB (0 or 0.01%), There were 12 blocks and 48 pens. The diets were based on corn, soybean meal, corn DDGS, and wheat middlings. Blood samples were collected on d 0, 7, 14, and 28 to measure peripheral cytokine levels. Intestinal tissues were collected on d 28 to determine cytokines and tight junction mRNA abundance. Data were analyzed using PROC MIXED of SAS (9.4) with pen as the experimental unit. Plasma data were log-transformed and analyzed as repeated measurements. Treatment, day, and their interactions were considered fixed effects. Baseline cytokine level on d 0 was used as a covariate when there was a significant difference among treatments. Carbohydrase addition had no effect on ileal mRNA level of IL-1β, IL-6, IL-10, IL-17, and occludin ($P > 0.05$). However, EB increased claudin 3 and decreased IL-22 transcript abundance in the ileum ($P < 0.05$). More than half of the plasma samples were below the detection limit for IL-4, IL-6, IL-10, and IFN; thus no statistical analysis was performed. From d 0–28, X decreased plasma IL-1β ($P = 0.010$), but had no effect on IL-8 and TNFα ($P > 0.05$). Neither enzyme addition affected IFNα ($P > 0.05$). The EB reduced IL-8 in the blood ($P = 0.046$), suggesting a decreased immune activation status. Moreover, there was an X × EB interaction effect on TNFα, with the 2 enzymes added together, but not alone, decreasing TNFα ($P < 0.05$). These data suggest that the addition of X and EB may decrease peripheral inflammatory status, and EB treatment may also improve intestinal paracellular integrity.

Key Words: exogenous enzyme, immune status, swine

130 Development of a chicken enterocyte culture to study its functional physiology.

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We developed a method to culture chicken intestinal enterocytes, the cells that absorb and form protective barriers against enteric bacteria, to study their functional physiologies. Using intestinal villi, harvested from day old broiler chicks, the enterocytes were isolated by sequential digestion with streptococcal hyaluronidase and trypsin followed by a density gradient centrifugation over Histopaque. The isolated clusters of cells were plated in Dulbecco's modified Eagle's medium (DMEM) containing antibiotic/antimycotic, fetal bovine serum, epithelial cell growth factor, and insulin transferrin selenium (ITS) supplements, which allowed the epithelial-like cells to grow. These cells were subcultured for 2 passages upon which they were plated at a concentration of 10^5 cells/well in 6 well plates to semi-confluent. We tested the effect of butyrate, a short chain fatty acid, known to be beneficial for intestinal health using proteomic approach, to find its regulatory effects. Quadruplicate cultures of both control and butyrate treated cells were lysed and the soluble proteins in the lysates were subjected to electrophoresis on a 4–20% gradient gel, stained, and each lane was excised horizontally into 2 segments. The gel segments were then subjected to reduction/alkylation followed by digestion with trypsin. The tryptic peptides were then analyzed by liquid chromatography tandem-mass spectrometry (LC-MS/MS) to identify and quantify proteins in the sample. The differentially regulated proteins were identified using Scaffold software. We identified 487 proteins, out of which 16 were uniquely expressed in control enterocytes, 8 in Butyrate treated cells and 404 found in both. Of 487 proteins, 104 proteins were downregulated and 10 proteins are upregulated by butyrate. The proteins that are regulated by butyrate are Annexin, Cadherin13, Histone H_2A. Our study concluded that butyrate may affect cell motility, cytoskeleton changes, and energy metabolism.

Key Words: enterocyte, intestinal health, butyrate

131 Prevention of *Listeria monocytogenes* infection with bioengineered probiotic.

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Listeria monocytogenes is a foodborne pathogen that causes severe disease in immunocompromised hosts. Intestinal epithelial cells are the first line of defense against *L. monocytogenes*, however, the mechanism, the bacterium uses to overcome the epithelial barrier is not well understood. We show that *Listeria* adhesion protein (LAP) promotes translocation of *L. monocytogenes* across the intestinal barrier into the lamina propria and systemic dissemination in mice by disrupting epithelial barrier. LAP induces TNF-α and IL-6 expression, which correlates with increased paracellular permeability in mice challenged with WT or Δ*inlA*, but not the *lap*$^-$ strain. LAP binding to host receptor, Hsp60 directly activates NF-κB, which facilitates myosin light-chain kinase (MLCK)-mediated opening of the intestinal barrier via the cellular redistribution of the junctional proteins, claudin-1, occludin, and E-cadherin. Genetic knockout of MLCK in mice prevents mislocalization of junctional proteins and *L. monocytogenes* translocation. These data demonstrate that *L. monocytogenes* uses LAP to exploit epithelial innate defense to cross epithelial barrier in the gut, independent of other invasin proteins. Next, we investigated whether a probiotic strain expressing LAP could prevent listeriosis in mice and pregnant guinea pigs. The *lap* of *Listeria innocua*, a nonpathogen and the *lap* of *L. monocytogenes* was cloned and expressed on *Lactobacillus casei* (LbcWT). Both bioengineered probiotic (BP) supplied in drinking water for 10–15 d before *L. monocytogenes* challenge, reduced pathogen load by 3.5–5 log/organ after 48 h and protected >90% of mice. LbcWT and BP stimulated NF-κB, but only BP attenuated TNF-α and IL-6 levels, prevented mislocalization of the junctional proteins during *L. monocytogenes* infection and maintained epithelial integrity. Reduced *L. monocytogenes* load in organs and tissues of BP–fed pregnant guinea pigs and their fetuses was also observed. The study demonstrates that a probiotic expressing LAP from a nonpathogenic *Listeria* can protect mice and pregnant guinea pigs from listeriosis, by competitive exclusion, immunomodulation, and improving gut barrier function highlighting a novel approach in preventing an infectious disease.

Key Words: *Listeria monocytogenes*, infection, probiotic

Session 5

132 Characterization of cecal microbiome in broilers fed diets with tannins extracted from *Schinopsis lorentzii* (Argentine quebracho) and *Castanea sativa* (Italian chestnut).

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Low doses of tannins extracted from quebracho (Q) and chestnut (C) trees have been reported to improve animal health and productivity, ameliorate necrotic enteritis and other intestinal diseases when added in feed. It is believed that gastrointestinal microbiota play an essential role in maintaining intestinal health and performance, however, the effect of tannins on the gut microbiome is currently poorly understood. High-throughput 16S rRNA gene sequencing was used to characterize the chicken cecal microbiome during a 30-d experiment. A total of 120 Cobb mixed-sex broiler chickens were randomly divided into 3 groups of 40 birds each. Each of the groups was randomly assigned to 1 of 3 dietary treatments (additives): (1) Bacitracin (125 g/Mt level of BMD)-BA; (2) Q and C tannin blend (1 kg/Mt Silvafeed Nutri-P)-QC; (3) Negative control (NC) without additives. All birds were fed the same basal diet with the exception of the additive. On d 12, 19, 26, and 30, cecal samples were obtained from 5 birds of each treatment. Metagenomic DNA from cecal contents was isolated, and the V3-V4 region of the 16S rRNA gene was amplified, sequenced on an Illumina MiSeq and analyzed by bioinformatics. Alpha diversity varied significantly among dietary treatments ($P < 0.001$). Between d 12 and 26, cecal contents from animals fed diets with QC and BA showed no significant ($P > 0.05$) difference in richness and were significantly lower in richness than the NC. Day 30 richness of cecal contents from QC fed birds was not significantly different than that of the NC, while richness of BMD animals remained significantly lower than that of the NC. The addition of QC to diets of broiler chickens increased *Firmicutes*/*Bacteroidetes* ratio, mainly by favoring *Clostridiales* from the *Ruminococcaceae* and *Lachnospiraceae* families and a reduction in the *Bacteroides genus*. High-throughput 16S rRNA gene characterization was found to give insight into the dynamic nature of tannin-induced changes in the gut microbiome. This work may give a better understanding of the mechanism of action on health resulting from the addition of tannin extracts from Q and C in the diets of broiler chickens.

Key Words: feed additive, tannin, broiler

133 Effects of feed additives in alleviating enteric health challenges in broilers.

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Non-antibiotic feed additives are an integral part of maintaining a healthy gut and preventing enteric diseases in antibiotic growth promotor (AGP)-free poultry production. *Eimeria* infection is one of the major predisposing factors for necrotic enteritis. *Eimeria* challenge at 14 d of age in combination with corn-soy-DDGS/animal protein diet was used to create a mild gut health challenge model characterized by increased systemic (higher serum IL10) and intestinal (wider villus) inflammation, compromised nutrient absorption and immunity (serum decoloration), and reduced cecal bacterial a diversity in broilers. This model was used to test the efficacy of various Novus feed additives in alleviating gut health challenge in broilers. Data were analyzed using ANOVA and means were separated with Fisher's protected LSD test at $P < 0.05$. Probiotics, protease, organic acids (OA), and essential oils (EO) decreased jejunal villus width and serum IL-10 indicating less intestinal and systemic inflammation. Bacitracin methylene disalicylate (BMD), used as a positive control, reduced serum IL-10 but not jejunal villus width. Protease, EO, and BMD reduced serum endotoxin reflecting better gut barrier function. Protease and EO, but not BMD, also increased serum coloration possibly due to better carotenoid absorption, immunity, and less inflammation. In terms of gut microbiota, protease increased fecal bacteria a diversity and evenness, probiotics numerically increased cecal bacteria richness, and Mintrex Cu increased the abundance of beneficial bacteria such as *Lactobacillus* spp. and *Clostridium* Cluster XIVa, and reduced *E. coli* in ceca. In summary, supplementation of protease, EO, probiotics, OA, and Mintrex Cu were effective to different degrees in reducing local and systemic inflammation, improving nutrient absorption, gut barrier function, and gut microflora. With different modes of action, these AGP alternatives could complement each other and serve as effective nutritional tools to maintain a healthy gut, therefore improving growth performance during challenge phases of AGP free poultry production.

Key Words: probiotic, protease, organic acid

134 In-depth analysis of mycotoxin contamination in US feed and feed ingredients from 2014 to 2017.

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Mycotoxins are harmful fungal metabolites commonly found in commercial crops. The effects of mycotoxins on animal health include local *impacts* on the gastrointestinal tract and systemic impacts on organ systems. Although over 400 mycotoxins have been identified, diagnostic laboratories evaluate limited numbers of metabolites and at times analyze single mycotoxins to reduce costs. This presents an incomplete picture of mycotoxin risk, co-occurrence, and prevalence in feed and feed ingredients. The University of IFA-Tulln, Austria, has conducted multi-toxin analysis on feed materials and compound feeds from the United States since 2014. The purpose of this study was to evaluate these results for the prevalence of masked, emerging, and other mycotoxins not routinely tested for by diagnostic laboratories. Samples from the US were submitted from 2014 to 2017 (154 total) for analysis at the University of IFA-Tulln, Austria (Spectrum 380). Samples were analyzed utilizing liquid chromatography tandem mass spectrometry (LC-MS/MS). Most US commercial labs test for deoxynivalenol for type B trichothecenes (B-Trich), fumonisin B1, B2, and B3 (FUM), and zearalenone (ZEN). With Spectrum 380, contamination levels of 8 B-Trich, 8 FUM, and 4 ZEN metabolites were quantified. On average, 37 mycotoxins were detected per sample. The data from B-Trich, FUM, and

ZEN metabolites are presented. Of the 154 samples, 62% were positive for DON, with significant prevalence of 15-acetyl-DON, NIV, and DON-3-G (8%, 28%, and 50% respectively). Total B-Trich levels were on average 20% higher compared with DON alone. Of additional FUM metabolites, significant prevalence of FUM A1 precursor, A2, and B4 were detected (23, 14, and 46%, respectively). Overall, the total sum of FUM contamination was 10% higher compared with the summation of FUM B1, B2, and B3. The prevalence of ZEN was 84%, whereas α-ZEN, β-ZEN, and ZEN-sulfate were 16, 13, and 43%, respectively. The sum of ZEN metabolites was nearly double the contamination of zearalenone alone. Collectively, these results suggest an increased risk to animal health beyond that indicated by current detection methods in the United States.

Key Words: mycotoxin, *Fusarium*

135 Feed efficiency phenotypes in lambs involve changes in ruminal, colonic, and small intestine-located microbiota.

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Several studies have revealed differences in rumen-located microbes between greatly efficient and inefficient animals, however, how the microbiota vary in the hind gastrointestinal tract (GIT) has only been sparsely explored and how they vary in the small intestine remains to be determined. We therefore sampled the microbiota of the duodenum, jejunum, ileum, colon, and colorectally obtained feces, in addition to the rumen of 12 lambs that, in a residual feed intake trial were found to be at either extreme of feed efficiency phenotypes. The 16S rRNA gene (V3-V4 region) profiles of all samples were analyzed and revealed unique microbiota in all GIT locations except the jejunum and ileum (ANOSIM R > 0.2, $P < 0.001$). Measures of b-diversity revealed greater dissimilarity between more anatomically distant GIT locations (e.g., Rumen – Duodenum, ANOSIM R = 0.365, $P < 0.001$; Rumen – Colon, ANOSIM R = 1, $P < 0.001$) with the nearest distal region typically more similar than the nearest proximal location. The relative abundances of 13 operational taxonomic units (OTUs) from the duodenum, jejunum, colon, and feces, as well as the rumen, differed between efficient and inefficient animals (Bonferroni corrected $P < 0.05$), while another 2 OTUs trended toward significance. These OTUs were classified as taxa with known roles in fibrolysis (*Fibrobacteres*, *Ruminococcaceae*, and *Saccharofermentans*) and others who are commonly associated with health (*Bifidobacteriaceae*, and *Christensenellaceae*) and dysbiosis (*Proteobacteria*). Our findings show biospatial delineations of microbiota throughout the GIT and suggest that feed efficiency extends beyond the rumen, transcending these regions, and involves increases in both rumen-, and colon-located fibrolytic taxa, increases in bifidobacterial species in the small intestine, and reductions in small intestine and distal GIT-located *Proteobacteria*.

Key Words: feed efficiency, residual feed intake, gut biospatiality

136 Effects of chestnut wood extract (by water) or micro-encapsulated dry extract and blend of monoglycerides of butyric acid (in feed) on live performance and gut health of broiler chickens.

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Chestnut extract (Farmatan Liquid) or microencapsulated dry extract plus monoglycerides of butyric acid (Farmatan BCO) support gut mucosa and stabilize intestinal microflora. A field trial in Belgium compared results from 4 batches of broilers in 2 houses (changeover design) with ~27,000 per/house using tap water or water with chestnut extract (2 mL/1 L or 0.2% in water from 10 to 20 d). The 40-d BW were 2.660 kg for control *vs*. 2.710 kg for supplemented flocks ($P = 0.034$; 100 birds/house). No significant differences ($P > 0.05$) were found in feed conversion ratio (1.558 vs. 1.540, respectively) or mortality (2.58% vs. 2.21%, respectively). Bacterial enteritis lesion scores at 9, 19, 26, 33, and 40 d (5 birds/house) were not significantly different (1.94 for control *vs*. 2.04 for water treatment). Coccidiosis lesion scores were lower for chestnut extract treated group at 19 d (0.6 vs. 0.4; $P = 0.037$) but not overall (0.56 *vs*. 0.40, respectively). A 42-d pen trial on rice hulls in India compared mash diets with no supplement, BMD at 330 g/tonne, or combination product (500, 250, 150 g/tonne from 0 to 15, 15–30, and 30–42 d, respectively). The 35-d BW were improved ($P = 0.021$) by diets with combination product (1.724 kg) compared with control diets (1.663 kg), with BMD diets intermediate (1.705 kg). Differences at 42-d were approaching significance ($P = 0.088$). The 0–42 d feed conversion ratios, and 42-d ammonia emissions and litter moisture % differences were not significant. Foot pad lesion scores were significantly lower for diets with the combination product compared with control and BMD diets (2.2, 3.0, and 2.7, respectively; $P = 0.05$). In conclusion, chestnut extract via drinking water improved 19-d coccidiosis lesion scores and 40-d BW compared with control (tap water). Diets with chestnut extract and butyric acid blended product improved 35-d BW compared with control diets with BMD diets intermediate. The 42-d foot pad scores were lower with the combination additive.

Key Words: chestnut extract, butyric acid, coccidiosis

137 Evaluation of rye versus corn as a source of energy on the microbiome in different sections of the gastrointestinal track of broiler chickens.

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The purpose of this study was to evaluate the microbiome in different sections of the gastrointestinal tract of broilers consuming a rye or a corn-based diet from hatch to 10 d-of age. At 10 d of age birds were euthanized and samples of duodenum, upper and lower ileum and ceca were collected for microbiome analysis. Bacterial genomic DNA was extracted from the samples, and the V4 region of 16S rRNA gene was amplified. Amplicons were sequenced on Illumina MiSeq, and microbial communities were analyzed by using a QIIME pipeline. In the duodenum there was no difference between the 2 treatments at phylum, family

and genus levels. In the upper ileum corn fed chicks had a higher abundance of Cyanobacteria at the phylum level ($P < 0.05$) however there were no differences between treatments at the family and genus levels. In the lower ileum, rye fed chicks had a significantly higher amount of *Firmicutes* while corn fed birds had significantly higher amounts of *Bacteroidetes*. In the lower ileum at the family level, corn fed chicks had higher amounts of *Bacteroidaceae*, *Ruminococcaceae*, and *Lachnospiraceae* than rye fed chicks. At the genus level in the lower ileum corn fed birds had a higher abundance of *Ruminococcus* and *Oscillospira*. In the ceca at the phylum level, corn-fed birds had significantly higher *Bacteroidetes* while rye-fed chicks had a higher abundance of *Proteobacteria* and *Firmicutes*. At the family level, rye-fed chicks had significantly greater proportions of *Enterobacteriaceae*, *Clostridiaceae*, *Bifidobacteriaceae*, and *Lactobacillaceae* while corn fed chicks had a higher abundance of *Ruminococcaceae* and *Bacteroidaceae*. Similar trends were observed at the genus level in the ceca where rye fed chicks had significantly high abundance of *Clostridium*, *Lactobacillus*, *Bifidobacterium*, *Proteus*, and *Ruminococcus*. The corn fed chicks had a significantly higher abundance of *Ruminococcus*, *Oscillospira*, *Fecalibacterium*, *Dorea, Blautia*, and *Bacteroides*. The results of this study confirm that diet ingredients have a profound impact on the microbiome in the lower ileum and ceca.

Key Words: rye, microbiome, chickens

138 Effect of prebiotic supplementation on gut health and performance of heifer calves.

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The commensal gut microbiota plays an important role for the host. Many carbohydrates from yeast cell wall, such as mannanoligosaccharides are used in livestock as prebiotics, acting as substrates for beneficial bacteria in the gut and as a binding agent for pathogenic bacteria by inhibiting binding of it on the gut wall. This study aimed to evaluate if Hypergen (Biorigin, Brazil), a new generation of functional carbohydrates from yeast cell wall, is able to modulate the gut environment. The study was performed at University of Louisville, Kentucky. A total of 30 heifer calves with 20 d of age were randomly and equally assigned to 2 treatments: (1) Control (C; n = 15), no supplementation; (2) Hypergen (n = 15), fed 100 mg of Hypergen kg^{-1} of body weight during 28 d. The body weights were recorded weekly to quantify the average daily gain (ADG). At d 14 of feed, the calves were orally challenged with hemolytic *E. coli*. During 10 consecutive days after the challenge, hemolytic *E. coli* and Ig-A were measured in fecal samples. Short-chain fatty acids (SCFA) in feces were measured by PCR at d 28. Data were analyzed by ANOVA using the PROC MIXED of SAS 9.1 with fixed dietary effect, time effect, interaction between diet and time. The calves supplemented with Hypergen demonstrated lower ($P < 0.05$) average concentration of *E. coli* cfu/g of feces (4,757.5 *vs*. 6,796.8), higher ($P < 0.05$) Ig-A titers (132.6 *vs*. 161.4 µg/mL) and higher ($P < 0.05$) SCFA concentration (105.5 *vs*. 125.2 mmol/L) in feces compared with control animals, demonstrating prebiotic effect and an more efficient immune response against hemolytic *E.coli* challenge. Moreover, calves supplemented with Hypergen showed higher ($P < 0.05$) ADG and final body weight compared with control animals, demonstrating that modulation of the intestinal environment can result in higher absorption of nutrients. In conclusion, Hypergen can improve gut health and performance of supplemented heifer calves.

Key Words: gut health, prebiotic, dairy calves

139 Effect of exogenous nucleotide supplementation on gut health and performance of newly weaned piglets.

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Weaning is often characterized as a critical phase during piglets development due transition from liquid to solid diets, where some inputs from the nursery diets can induce severe intestinal inflammation on gut wall due to dietary antigens with consequent gastrointestinal damage and lower performance. Nucleotides are essential for cell division and when provided in the diet can be used to enhance growth and repair of tissues with fast cell turnover such as the intestine. The aim of this study was to evaluate the effect of nucleotides supplementation in performance and on gut health in weaned piglets. The study was performed at University of Lavras, Minas Gerais, Brazil. In total, 72 piglets weaned at 24 d of age with an average weight of 6.1 ± 0.7 kg were randomly assigned to 1 of 2 diets: (1) Control (n = 36), without yeast extract; (2) Yeast extract (YE; n = 32; Biorigin, Brazil), inclusion 0.2% of yeast extract in the diet (500 ppm of nucleotides). Each of the 2 treatments was fed 9 replicates (pens), with 4 piglets/pen, during 42 d. At d 7 of feed, the piglets were orally challenged with 1 mL of a solution containing $K88^{+}$ *E. coli*. Animal performance and diarrhea incidence were evaluated weekly and short-chain fatty acids (SCFA) in cecum were measured after slaughter in the last of the experiment. Data were analyzed by ANOVA using the PROC MIXED of SAS 9.1 with fixed dietary effect, time effect, interaction between diet and time. The piglets of YE group had lower incidence of diarrhea ($P < 0.05$) compared with control group (12.6 *vs*. 17.6%, respectively) with greatest difference observed in the first week (17.6 vs. 25.5%, respectively), suggesting lower deleterious effect on gut mucosa. YE group had higher ($P < 0.05$) SCFA concentration (1,581.7 *vs*. 1,450.4 m*M*/g, respectively) and final body weight (23.0 *vs*. 22.4 kg, respectively) compared with the control group, suggesting a better use of the nutrients by the animals. In conclusion, the inclusion of yeast extract in the diets for weaned piglets can minimize deleterious effect of the first solid diet or transitional diet and *E.coli* on gut mucosa besides improving animal performance.

Key Words: weaning, pig, microbiota

140 The effects of phytase super dosing in combination with xylanase on jejunum and ileum mucosa morphology in market turkey hens.

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Supplementation of xylanase and phytase is commonly used to minimize formula costs, risks of formulation, and animal performance variation, and improve nutrient utilization, but little

is known on their effects within the gut. A market turkey trial was conducted to evaluate the effects of super dosing phytase (Phy) in combination with xylanase (Xyl) on enteric mucosal morphology and microbial profile. Nicholas Super Select turkey hen poults were randomly assigned among 16 litter floor pens containing 36 poults, and 4 dietary treatments were assigned according to a randomized complete block design. The treatment consisted as a positive control (POS) and a negative control (NEG) basal diet, which differed by 0.145% aP, 0.125% Ca, and 100 kcal of ME/kg. The 2 enzyme treatment diets were made from NEG basal diet to contain the same level of xylanase (Huvepharma Inc., Sofia, Bulgaria) but differing phytase (Huvepharma, Inc.) levels: standard enzyme levels (REG; 250 FTU Phy/kg, 1500 EPU Xyl/kg) or the super dosed phytase levels (SUP; 1500 FTU Phy/kg, 1500 EPU Xyl/kg). Birds were sampled for morphometric analysis of jejunum and ileum mucosa at wk 1 and wk 5, and microbial profile at wk 14. At wk 1, jejunal villi surface area was greater (P = 0.018) due to increased villus width among REG and SUP than POS (94,039.0 and 90,754.8 vs. 58,345.5 μm^2, respectively), but was not different from NEG (74,832.8 μm^2). There were no treatment effects on ileal gut morphology in wk 1. At wk 5, jejunal villi surface area was greater (P = 0.014) due to increased villus height among POS and REG than NEG (264,433 and 273,873 vs 188,036 μm^2), but was not different than SUP (254,730 μm^2). In contrast, there were no treatment effects on ileal villi surface area at wk 5, but ileal villus width and crypt depth were decreased (P = 0.02 and P = 0.008, respectively) by SUP. This study confirms that jejunal villi surface area has a compensatory response to dietary nutrient density or enzyme-enhanced bioavailability. However, super dosing of phytase may reduce ileal mucosal inflammation due to a change in ileal microflora profile.

Key Words: phytase, xylanase, turkey hen

141 Risks involved in the use of enrofloxacin for *Salmonella* Enteritidis or *Salmonella* Heidelberg in commercial poultry.

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The objectives of the present study were to evaluate the risks involved in the use of enrofloxacin for *Salmonella* Enteritidis (SE) or *Salmonella* Heidelberg (SH) in commercial poultry and determine the effects of a probiotic as an antibiotic alternative. Two experiments were conducted. Experiment 1 consisted of 2 trials. In each trial, chickens were assigned to 1 of 3 groups; control + SE challenged; enrofloxacin 25 mg/kg + SE; enrofloxacin 50 mg/kg + SE. Chickens received enrofloxacin in the drinking water from d 1 to 5 of age. On d 6, all groups received fresh water without any treatment. All chickens were orally gavaged with 10^7 cfu/chick of SE at 7 d of age and euthanized on 8 d of age. In Experiment 2, turkey poults were assigned to 1 of the 3 groups; control + SH; probiotic + SH; enrofloxacin 50 mg/kg + SH. Poults received probiotic or enrofloxacin in the drinking water from d 1 to 5 of age. On d 6, poults received fresh water without any treatment. Poults were orally gavaged with 10^7 cfu/poult of SH at 7 d of age. Poults were weighed and humanely killed 24 h post-SH challenge to evaluate serum concentration of FITC-D to evaluate intestinal permeability, metagenomics and SH infection. In both trials of Exp 1, chickens treated with enrofloxacin were more susceptible to SE organ invasion and intestinal colonization when compared with control non-treated chickens ($P < 0.05$). In Exp 2, poults treated with 50 mg/kg of enrofloxacin showed an increase in body weight, however, this group also showed an increase in SH susceptibility, intestinal permeability and lower proportion of *Firmicutes* and *Bacteroidetes*, but with control group had the highest proportion of *Proteobacteria*. In contrast, poults that received the probiotic had the highest proportion of *Firmicutes* and *Bacteroidetes*, but lowest *Proteobacteria*. The results of the present study suggest that prophylactic utilization of enrofloxacin at 5 times the recommended dose in poultry, increases the susceptibility to salmonellae infections, and confirms probiotics may be an effective tool in salmonellae infections.

Key Words: enrofloxacin, *Salmonella*, poultry

Poster Abstracts

P100 Identification of the ileal, cecal, tracheal, and litter microbiomes in antibiotic-free commercial broilers and their correlations with performance.

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The microbiome is increasingly being recognized for its importance in the establishment of gut health in commercial poultry. Critical to the understanding of the microbiome's role in health and disease is defining the core microbiome of different anatomical sites. In this study, a commercial broiler operation was sampled to identify the core bacterial microbiomes of the broiler ileum, cecum, trachea, and litter. Four commercial flocks were sampled weekly (10 birds per flock and time point) and sampled again in a successive growout. Additionally, random sampling was performed on birds from multiple flocks and ages in 3 successive months during routine monthly postings. DNA was extracted from each of the 2,309 samples, followed by amplification and sequencing of the V4 region of the 16S rRNA gene. Sequences were quality filtered and then assessed using QIIME. The ileal and cecal microbiomes demonstrated considerable consistency across the flocks examined. There was a predictable pattern of species succession over time, and this pattern closely resembled that of commercial turkeys assessed in a separate study using the same approach. The litter microbiome was also predictable and was more variable between flocks than gut samples. In contrast, the tracheal microbiome had considerable variability between birds of the same flock and between flocks sampled. Still, there was a longitudinal pattern of species succession in the trachea. Unexpectedly, the tracheal microbiome was dominated by *Lactobacillus*, with other expected genera following, including *Staphylococcus*, *Streptococcus*, *Corynebacterium*, and *Escherichia*/*Shigella*. Correlations were sought between bacterial community composition and individual bird weight as well as flock performance parameters. Some bacterial taxa were identified as positively or negatively correlated with performance. Overall, this study demonstrates that a core bacterial microbiome exists in sample types examined, and correlations exist between the bacterial microbiome and broiler performance. This suggests that modulating the microbiome may confer benefits in poultry production.

P101 Dietary supplementation of late pregnancy diet with yeast derivatives (mannan oligosaccharide) can influence the colostrum yield, colostrum composition and gut performances of sow.

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The aim of this study was to examine whether yeast derivative (YD) based on brewery yeast hydrolysate added to a late pregnancy diet affected colostrum composition, yield (CY) and gut microbiota in sows. Thirty-seven sows were randomly allocated to 2 groups as follows: a negative control diet (n = 19) and the same diet supplemented with 2 g of YD/kg (n = 18) during the last 3 weeks of pregnancy. The YD used was Progut (Hankkija Oy/Suomen Rehu, Hyvinkää, Finland). Within the first 2 h from the beginning of farrowing, a 10 mL colostrum sample was obtained to check for nutritional composition (protein, fat, lactose, dry matter, with FITR analysis), and immunoglobulin content (IgA, IgM and IgG with ELISA analysis). All piglets were individually weighted at birth and 24 h later to calculate CY. Fecal samples were collected from sow at the beginning of farrowing. Extracted DNA samples were analyzed by 16S rRNA gene sequence analysis. Colostrum content of protein, lactose, and dry matter did not significantly differ between the 2 groups, whereas YD fed sows had higher level of fat in colostrum ($P < 0.05$). Immunoglobulin A, IgM, and IgG levels in colostrum did not significantly differ between the 2 groups. CY was 3701 g in the control group and 4581 g in the YD fed group ($P < 0.05$). Gut abundance of *Roseburia*, *Paraprevotella*, *Eubacterium* were significantly increased in YD supplemented sows. On the other hand, feeding sow YD significantly reduces the abundance of *Proteobacteria*, especially *Desulfovibrio*, *Escherichia/Shigella* and *Helicobacter*. In conclusion, adding YD to late pregnancy diet in sows did not affect immunoglobulin level, protein and lactose content in colostrum, but contributed to higher fat content and increase the CY. The treatment group was characterized by more hind gut digestion bacteria but fewer opportunistic pathogens. Therefore, YD added to sow diet seems to increase colostrum availability and its energy content for neonate piglets and promote better maternal microbial sources.

Key Words: sow, colostrum, gut microbiota

P102 Effects of a malabsorptive rye diet on growth and adipose tissue in commercial broilers.

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Diets high in non-starch polysaccharides such as rye are known to reduce nutrient absorption, resulting in decreased performance. Upon refeeding, birds increase weight gain to rates similar to non-restricted cohorts. Historically, this weight gain would be expected to be partitioned toward adipose tissue. However, with modern selection strategies it is unclear if this traditional view still holds true. To determine if adipose tissue accretion was similar following a 10 d malabsorptive diet modern broilers (n = 36) were assigned to 1 of 4 dietary treatments which consisted of a control corn based diet (CD); an early phase malabsorptive diet where birds were on a rye diet from d 0 to 10 then switched to a corn diet until d 20 (EMD); a late phase malabsorptive diet where birds were on a corn diet from d 0 to 10 and then a rye diet until d 20 (LMD); and a malabsorptive (rye) diet throughout (MD). Birds were weighed on d 9 and 19 and sampled on either d 10 or 20. From d 0 until d 10, only the CD or MD diets were applied. At d 9, body weight was not reduced with the rye diet ($P = 0.25$); however, birds on the MD diet were numerically lighter. At d 10, the CD fed birds had greater percentage of adipose tissue per amount of body weight compared with MD ($P < 0.01$). This was accompanied by an increase in adipocyte area ($P < 0.01$)

indicating increased lipid fill. By d 19, body weight, percent of adipose tissue per unit of body weight, and adipocytes area were significantly different across the 4 dietary treatments ($P < 0.01$). Birds fed CD or EMD were the heaviest and had the highest percent of adipose tissue; with birds on a rye diet during the late phase (LMD) an intermediate to the MD and CD or EMD ($P < 0.05$). Adipocytes area was greatest in CD birds compared with MD ($P < 0.01$) with the EMD and CD being similar and EMD and LMD being similar ($P > 0.5$). In conclusion, recovery from a malabsorptive diet did not significantly increase the amount of adipose or lipid fill of adipocytes compared with standard diets; however, those birds that underwent nutrient restriction had a 7% increase in adipose tissue compared with those that did not undergo nutrient restriction, suggesting that extra nutrients may be diverted to adipose accretion.

Key Words: compensatory gain, fat, undernutrition

P103 Effects of Noni-supplemented diet on tight junction protein expression in broiler chickens exposed to heat stress.

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Heat stress hampers gut health by impeding its ability to absorb nutrients which leads to a lower feed efficiency and sicker birds. Therefore, there is a critical need to identify mechanism-based strategies to alleviate these effects. The purpose of the present study was to evaluate the effect of *Morinda citrifolia* (Noni)-supplementation on the expression of tight junction proteins. Male Broilers (Cobb 500, 3 wks, n = 480) were subjected to 2 environmental conditions (TN, 24°C *vs*. HS, 35°C), and fed 2 diets (control *vs*. 0.2% Noni) in a 2 × 2 factorial design. Chickens received water and feed ad libitum. Functional in vitro studies were conducted using primary chicken gut epithelial cells, and IPEC-J2 cell lines. At 80% confluence, cells were exposed to HS (45°C) for 2 h and 30 min. Control cells were maintained at 37°C. The expression of target genes and proteins were determined by quantitative real-time PCR using $2^{-\Delta\Delta CT}$ method and Western blot, respectively. A significant increase ($P < 0.05$) in the expression of heat-shock protein (HSP70 and HSP90) were observed in the gut of control and noni feed chickens that were exposed to HS, as well as in cell cultures indicating a stress status. Furthermore, in primary chicken gut epithelial cells, no changes were observed in gene or protein expression for claudin 1 or Calprotectin. However, ZO-2 genes were downregulated and occludin protein expression had no change. In IPEC-J2 cells, claudin 5, and claudin 1 had no change in protein expression. However, occludin and TAZ expression seemed to be altered. In the 1 week HS chicken gut, HSP 70 was uprgeulated whereas claudin 5 and claudin 1 did not change. In Noni-fed chickens, ZO-1 was downregulated in both control and heat-stressed birds whereas claudin 5 was upregulated. Together, our results indicate that HS dysregulates the expression of certain tight junction proteins which may explain the alteration of intestinal barrier integrity and leaky gut. Further research is necessary to help define mechanism to develop future nutritional strategies to combat HS.

Key Words: Noni, heat stress, tight junction proteins

P104 Bovine colostrum increases the viability and the healing process of IPEC-J2 intestinal porcine epithelial cells while modulating the barrier function and *Escherichia coli*-mediated inflammatory responses.

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Piglet gut response to weaning results in impaired intestinal barrier function and increased inflammatory response and susceptibility to enteric diseases. Because the use of antibiotics as growth promoters will be restricted in the swine industry, novel feeding strategies to improve gut health are needed. This study aims to determine the potential of defatted bovine colostrum (BC) and its fractions, the serocolostrum (SC) and caseins (CAS), to promote viability and the healing process and to modulate barrier integrity and the inflammatory response induced by enterotoxigenic *E. coli* (ETEC) in IPEC-J2 intestinal epithelial porcine cells. To evaluate cell viability and wound healing, XTT cell proliferation and migration scratch assays were performed on IPEC-J2 cells incubated with BC, SC, or CAS. Monolayer permeability of ETEC infected IPEC-J2 cells incubated with BC, SC or CAS was monitored by transepithelial electrical resistance measurements. Inflammatory and oxidative responses were assessed by gene expression analysis of several cytokines and chemokines by qPCR. Incubation with BC derivatives led to 8 to 14% increases in undifferentiated IPEC-J2 cell viability, in comparison to untreated cells ($P \leq 0.05$). Differentiated IPEC-J2 cell migration was increased by 42% after SC addition, as opposed to non-treated cells ($P \leq 0.05$). BC and SC treatments significantly reduced ETEC-mediated increases in *IL-8* and *CCL20* expression ($P \leq 0.05$). BC treatment also significantly reduced IPEC-J2 cell monolayer permeability induction after ETEC infection. These results show that BC and SC fractions improve intestinal epithelial cell integrity and decrease ETEC-mediated inflammatory responses. Therefore, the use of bovine colostrum to improve epithelial barrier function and innate immunity of weaning piglets should be considered as an alternative to antibiotics.

Key Words: intestinal barrier function, inflammation, bovine colostrum

P105 Effects of Original XPC Ultra and BMD on bacterial antibiotic resistance and litter microbial community composition in the commercial turkey litter environment.

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With increasing pressures to reduce antibiotic use in commercial poultry, there is a need to identify alternative products that confer beneficial effects on the gut and the poultry environment. However, simply reducing antibiotic use will not eliminate antibiotic resistance. Therefore, other strategies are needed to reduce the reservoir of antibiotic resistance genes in the poultry environment. One product targeting gut health is Original XPC Ultra. In addition to reducing the prevalence of *Salmonella* in

broiler production, this product has also demonstrated reduction of multidrug resistant *Salmonella*. The purpose of the present study was to determine if XPC Ultra exerted similar effects within the litter environment of commercially raised turkeys. Litter samples from 64 flocks were sampled at d 140 of each growout, which was the second or third successive growout using the product combinations. Each sampling consisted of 3 barns from the same farm: a control feed barn with BMD at 50 g/ton fed continuously, a barn with BMD plus XPC Ultra, and a barn with XPC Ultra alone. Samples were cultured to determine the proportions of drug resistant bacteria. Additionally, shotgun metagenomic sequencing was used to assess effects on the microbiome and resistome. For cultured bacteria, no statistically significant differences were found between any of the groups examined. Similarly, no statistically significant differences in resistance gene abundance were observed in any treatment group. Some unique taxonomic differences were observed and attributed to BMD or XPC treatment. The results of this study suggest that XPC Ultra was not effective at reducing bacterial resistance in commercial turkey production. However, many possibilities exist to explain why this contrasts previous results, including differences in methodology, differences in organisms sought, and differences in turkey versus broiler production. More studies are needed to determine how and where products such as XPC Ultra exert their beneficial effects on the bacterial resistome.

P106 Development of swine enteroids: A novel tool for animal science research.

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Enteroids are 3-dimensional structures grown in vitro that contain all of the differentiated cells of the small intestine. Enteroids provide the opportunity to evaluate biological responses resulting from nutritional interventions and pathogen challenges. Although enteroid culture techniques are well established for mice, there is limited information on methods to culture enteroids from other species, such as swine. Physiological differences between species make swine enteroids a valuable tool in animal science research. The objective of our study was to determine the optimal protocol for sustaining swine enteroids. Intestinal crypts were isolated from sections of jejunum collected from 120-kg pig by dissociation using EDTA. Crypt suspension was pelleted by centrifugation, and re-suspended in culture media. The suspension was mixed with Matrigel, and plated in 24-well plates forming firm Matrigel beads, covered with 500 µL of media (Table 1) once jellified. Enteroids were passaged once a week. As pieces of the Matrigel bead began to break off around 4 d, loose Matrigel containing enteroids were moved to a separate well where they remained suspended in media. Wells with firm Matrigel were mixed with fresh Matrigel and cultured as firm beads covered with media. Enteroids remained viable for up to 28 d in firm Matrigel and 50 d in loose Matrigel. In addition, by 36 d, a subset of cells grew as a monolayer attached to the bottom of the well surrounding the enteroids cultured in loose Matrigel. Future research is needed to characterize these cells and their effect on enteroid viability. In summary, porcine enteroids grown under this protocol survived 50 d. Future experiments will be conducted to validate their use to study biological responses in swine.

Table 1. Media composition

Compound	Concentration[1]
Wnt3a conditioned media	10%
R-spondin conditioned media	20%
Antibiotic/antimycotic	1%
B-27 supplement w/o vit A	2×
HEPES	1×
N-2 supplement	1×
Penicillin Streptomycin	1×
Glutamax	1×
Epithelial growth factor	50 ng/mL
Noggin	100 ng/mL
Acetyl-cysteine	1 mM
Y-27632	10 µM
SB202190	10 µM
LY 2157299	500 nM
Porcine insulin	10 ng/mL

[1]Concentrations were balanced with Dulbecco's modified Eagle medium/Nutrient Mixture F-12.

Key Words: organoids, in vitro, porcine

P107 *Bacillus subtilis* probiotic prevents heat-related complications in animals.

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It has become increasingly recognized that various types of stress have a major effect on gastrointestinal physiology, thereby causing dysfunction and diseases. Thus, exposure to heat results in significant economic losses in livestock production: $897 million, $369 million, $299 million, and $128 million for dairy, beef, swine, and poultry industries, respectively. Heat stress can damage the gastrointestinal mucosa, which protects the internal environment of the body from bacteria and bacterial endotoxins (lipopolysaccharides, LPS). Dysfunction of this protective barrier results in increased intestinal permeability and diffusion of toxic bacterial components from the gut lumen into the circulation. The gut microbiota is key in maintaining the mucosal barrier function and, as a result, the ability of the host to tolerate stress. The main objective of this study was to evaluate the effect of *Bacillus subtilis* probiotic strain (BS) on gut health during heat stress. Adult rats were treated by oral gavage with *B. subtilis* in PBS or with PBS twice a day for 2 d. On d 3, all rats were forced to run on a treadmill for 30 min. Control rats received the same treatment, but received no exercise. The body temperature of rats significantly increased after exercise. The level of LPS in the serum of rats pre-treated with PBS before treadmill exercise significantly increased, but not the in rats, which were administered BS before exercise. Elevated body temperature in exercised rats pre-treated with PBS resulted in significant changes in the gut structure: decreased number of Paneth and goblet cells. No changes were found in the rats treated with BS before treadmill exercise. Analysis of the gut microbiota revealed significant disruption of microbial composition in the exercised rats pre-treated with PBS. Our results demonstrated efficacy of

BS treatment in protecting the integrity of the intestinal barrier by protecting the gut microbiota.

Key Words: gut barrier integrity, *Bacillus subtilis*, heat stress

P108 Evaluation of Actisaf and Safmannan effects on gastrointestinal microbiota in cecal and ileum contents of chicken broiler.

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Biological supplements in poultry feed have been developed and utilized to increase feed efficiency, protect from pathogenic bacteria, and maintain a healthy immune system. This study identified gastrointestinal microbiota changes in ceca and ileum by adding biological supplements such as Actisaf and Safmannan to feed using next generation sequencing. The 40 d-of-hatch broiler chicks were placed into 4 treatment groups (total 160 chicks) and fed by control (group A), 0.2% Actisaf (group B), 0.2% Safmannan (group C), and 0.2% Actisaf + 0.2% Safmannan (group D). Cecal and ileal samples from the feeding trial chickens after 42 d were employed to microbiome sequencing with Illumina MiSeq platform and analyzed via the quantitative insights into microbial ecology (QIIME). In α diversity analysis to estimate species richness, ceca samples exhibited greater diversity than ileal samples. The increased diversity is apparent in both organs of chickens receiving a combination of Actisaf and Safmannan (group D). Sequenced microbiota from ceca and ileum exhibited proportionally different bacterial community compositions. At the phylum level, cecal microbiota were dominated by *Firmicutes* (79.3%) and *Bacteroidetes* (15.3%) while the ileum sections were dominated by *Firmicutes* (83.0%) and *Proteobacteria* (11.3%). At the genus level, relatively higher abundances of *Lactobacillus* were observed in group B to D (6.65, 8.79, and 8.89%, respectively) compared with group A (3.41%) in cecal contents. In conclusion, biological supplements inclusion leads to changes in cecal and ileal microbiological community compositional profiles.

Key Words: microbiota, chicken, feed supplement

P109 Mode of caffeic acid phenyl ester (CAPE) inhibition of gut bacterial bile salt hydrolase: Implications for gut health and nutrient absorption in poultry.

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Bile acids are nutrient signaling molecules synthesized in the vertebrate liver from cholesterol. Bile acids are conjugated to amino acids taurine or glycine before being secreted into the gallbladder and stored during the interdigestive period. Bile salts are released into the small bowel during a meal where they solubilize dietary lipids allowing efficient absorption of lipid-soluble vitamins, cholesterol, and fatty acids. At the terminal ileum, conjugated bile salts are actively transported from the intestinal lumen and transported back to the liver through the portal circulation in a recycling process known as enterohepatic circulation (EHC), which is ~95% efficient. Conjugated bile salts are toxic to gut bacteria, and function in part to decrease the microbial burden at the site of nutrient absorption. Gut bacteria have evolved an enzyme known as bile salt hydrolase (BSH) which removes the amino acid, resulting in free bile acids, and decreased toxicity to bacteria. BSH can be thought of as a "gateway reaction" allowing further metabolism of bile salts by bacteria. BSH activity decreases lipid absorption and decreases the efficiency of EHC, resulting in more bile acids in the cecum. In poultry, the predominant bile salt is taurochenodeoxycholic acid (TCDCA; 5β-cholanic acid-3α, 7α-diol-*N*-2-sulphoethyl-amide). BSH is a widespread feature of the gut microbiota. In feces, the predominant metabolite is lithocholic acid (LCA; 5β-cholanic acid-3α-ol), a product of gut microbial remove of the 7-hydroxy group from CDCA, through a process known as 7α-dehydroxylation. LCA is toxic to poultry, resulting in liver damage and intestinal turnover, and has a growth depressing effect. We predict that inhibition of BSH activity will diminish LCA formation, resulting in intestinal health and growth promotion. Here, we cloned and overexpressed a BSH from *Lactobacillus salivarius* and determined the mode of inhibition with a previously identified BSH inhibitor, caffeic acid phenyl ester (CAPE). We report the efficacy of CAPE to inhibit LCA formation in defined culture and in chicken excreta suspensions.

Key Words: bile salt hydrolase, caffeic acid phenyl ester, *Lactobacillus salivarius*

P110 Characterization of clostridia in beef cattle throughout production in natural and conventional settings.

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Clostridium perfringens has been associated with digestive deaths such as hemorrhagic bowel syndrome (HBS) in ruminants, while other *Clostridium* species have been correlated with poor performance. The removal of growth-promoting antibiotics from feedlot diets, due to policies such as the Veterinary Feed Directive and consumer-demand for antibiotic free meat production, may affect clostridia in the gastrointestinal tract. The objective of this experiment was to determine the effect of diets with and without growth-promoting antibiotics on the clostridial populations of the gastrointestinal tract of feedlot cattle. Fecal samples from a single Texas feedlot, feeding both conventional and natural; that is, antibiotic-free diets, were collected from different stages of production (starter, intermediate 1, intermediate 2, and finisher). Clostridia were enumerated and isolates were collected for further analysis. Clostridia were significantly higher in animals on the natural diet ($P = 0.02$) especially during the finisher phase ($P = 0.03$). A higher ratio of *C. perfringens* isolates were present in the animals on the natural diet. Representatives from the isolates that were not *C. perfringens* were identified based on sequencing the 16S rRNA gene. The majority of the isolates from animals on conventional diets were identified as *Clostridium beijerinckii,* while there was more diversity in the animals on the natural diets. The absence of growth-promoting antibiotics resulted in higher levels of *C. perfringens* and increased diversity of other clostridial species. Alternatives to antibiotic growth promoters such as probiotics may be useful to reduce clostridia levels, optimize efficiency, and reduce subclinical challenge of *C. perfringens*.

Table 1.

Item	Natural	Conventional
No. of samples	68	52
Total clostridia (cfu/g)	1.9×10^5	1.6×10^4
C. perfringens (cfu/g)	1.2×10^5	4.1×10^3
C. beijerinckii (% of total)	0	70
C. bifermentans (% of total)	25	0
C. sordellii (% of total)	25	0
C. paraputrificum (% of total)	17	15
C. tertium (% of total)	8	5
C. colicanis (% of total)	17	5
Other (% of total)	8	5

Key Words: ruminant, *Clostridium perfringens*, clostridia

P112 Systemic immunomodulatory effect of *Bacillus subtilis* and *Lactobacillus plantarum* probiotics compared with an antibiotic supplemented in milk replacer fed to dairy calves.

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The intestinal microbiota plays an important role in the intestinal innate and adaptive immune system, affecting many different aspects of its function and development. Furthermore, immune responses in the intestinal environment may translate to systemic immune function changes as well. This study was conducted to determine the effect of administering *Bacillus* and *Lactobacillus* probiotic strains on the systemic immune health of dairy calves. One hundred thirty-five individually fed Holstein heifer calves were randomly assigned to 1 of 5 treatment groups: (1) a non-medicated milk replacer (control); (2) control supplemented with neomycin sulfate and oxytetracycline (antibiotic); (3) control supplemented with *Bacillus subtilis* strain 747; (4) control supplemented with a combination of 2 *B. subtilis* strains, 747+1781; and (5) control supplemented with the 2 *B. subtilis* strains 747+1781 and *Lactobacillus plantarum* strain 1037. Milk replacer fed in this study contained 20% CP, 20% fat and was fed at 0.28 kg in 2 L of water 2 × daily from d 1 to d 35 and 1 × daily from d 36 to weaning at d 42. Blood samples were obtained from a subset of 45 calves (9/treatment) 14 d after treatment administration and preserved in RNA Later. Blood RNA was extracted from the samples and synthesized into cDNA for qPCR analysis to assess gene expression of immune cytokines, chemokines, and toll-like receptors, including inflammatory cytokines, interleukin (IL)-6 and IL-18, the chemokines, CCL2 and CCL8, and toll-like receptor (TLR)-2 and TLR-4. Gene expression of IL-6 was greater ($P < 0.05$) in calves fed antibiotics and those fed *B. subtilis* 747+1781 compared with control calves. When *L. plantarum* 1037 was combined with *B. subtilis* 747+1781 and when calves were administered the antibiotic treatment, CCL8 gene expression was lower ($P < 0.05$) compared with control calves. These data demonstrate that probiotics supplemented to calf milk replacer elicits similar immune factor changes in the systemic circulation as antibiotic administration, and the addition of *L. plantarum* to the *Bacillus* probiotic diverges the immunomodulatory functionality to the regulate systemic inflammation.

Key Words: calf, direct-fed microbial, immune

P113 The protective effects of ButiPEARL Z during a porcine epidemic diarrhea viral infection in piglets.

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Porcine epidemic diarrhea virus (PEDV) infection has a huge economic potential on the swine industry. PEDV primarily affects the intestine, which leads to compromised intestinal integrity and poor gut health. There are few treatment options effective against this virus. Zinc is an essential trace mineral involved in tight junction formation and intestinal health, as is butyric acid. Both molecules have shown consistent beneficial effects toward gut health. It was hypothesized that combining zinc and butyric acid together would harvest the synergistic benefits of both molecules. A novel formulation that encapsulates zinc oxide and butyric acid was developed with a controlled release mechanism and is marketed as ButiPEARL Z (BPZ). To test the efficacy of BPZ mitigating PEDV associated intestinal damage, a swine trial was conducted with 32 weanling piglets (n = 16 pigs/trt, 2 pigs/pen). There was a total of 2 treatments, PEDV and PEDV+BPZ. Piglets were given a control diet or diet supplemented with BPZ (5 kg/ton of feed) and gastric gavaged with 5 mL of 10^3 $TCID_{50}$ of the PEDV plaque-cloned isolate from Iowa (18984/2013) 7 d after allocation to pens. At 5 and 20 d post-infection (dpi), 8 pigs per treatment (1 pig per pen) were weighed, euthanized, and necropsied. Lowest viral cycle threshold (Ct) was at 5 dpi and increased thereafter. Overall, ADG was not different, but BPZ had a greater ADG on d 10 (0.53 vs 0.47 kg, $P < 0.05$) and d 20 (0.66 vs 0.53 kg, $P < 0.05$). BPZ had a greater ADFI on d 20 (1.21 vs 1.04 kg, $P < 0.05$) and overall (0.82 vs 0.77 kg, $P < 0.05$). There was no difference in body weight. Gain:feed was not different overall but BPZ gain:feed was lower on d 5 and greater on d 10. Lesion score in the jejunum was significantly lower on d 5 in jejunum (1.4 vs 2.1, $P < 0.05$). Villus height to crypt depth ratio was greater in d 5 jejunum in BPZ group (1.1 vs 0.9, $P < 0.05$). There was no difference in the intestinal stem cell marker ki67 nuclei count. The data provides evidence that BPZ may have the potential to mitigate some of the negative effects associated with PEDV infection.

Key Words: swine, butyric acid, porcine epidemic diarrhea virus (PEDV)

P114 Evaluation of performance and intestinal health of coccidiosis vaccinated broilers fed dietary tannic acid extract formulations.

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Phytogenic molecules have been identified as promising alternative feed ingredients due to their reported positive influence on the intestinal microbial balance of production animals. Combinations of plant bioactive feed additives with vaccination is one potential strategy to control enteric diseases such as coccidiosis, through the modulation of poultry gut heath and immune development. The aim of the present study was to investigate the effects of tannic acid extract (TAE) formulations on performance and intestinal health of male Cobb × Cobb 500 broilers vaccinated for coccidiosis. Broiler chicks (n = 3,000) were vaccinated on day of hatch with live coccidial oocysts

then randomly assigned to 5 treatments (75 pens; 40 birds/pen). Treatments included non-medicated (CON), salinomycin (Bio-Cox 60 g/t), Robenidine (Robenz, 30 g/t), TAE (1 lb/t), and TAE combined with *Bacillus coagulans* (TAE+BC, 1 lb/t). On d29, a subset of pens (n = 20) were orally challenged with a mixture of *Eimeria* spp. oocysts. During the challenge period, pens were divided into 2 subgroups, one of which was reissued commercial grower feed containing supplemented additives and the other, which additives were withdrawn from the reissued feed. On d 35 (6 d post-challenge) performance, intestinal lesions, and oocysts in feces were evaluated in the challenged pans. For the non-challenged pens (n = 55) performance was measured up to d 49. Of both challenged bird groups, TAE+BC tended ($P = 0.0574$) to have fewer lesions. Withdrawal of Bio-Cox or Robenz during the challenge resulted in FCR similar to the challenged-CON group ($P > 0.05$) whereas withdrawal of TAE or TAE+BC from feed resulted in improved FCR compared with challenged-CON birds ($P < 0.05$). All treatments improved performance ($P < 0.05$) of non-challenged vaccinated-CON birds at d21 and d49. Based on these studies, concomitant use of TAE products in poultry diets along with vaccination provides a possible alternative coccidiosis management practice that may help mitigate the adverse effects of vaccination on broiler performance.

Key Words: tannic acid extract, coccidiosis, vaccination

P115 Effect of quercetin on cecal microbiota in Arbor Acre broilers.

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To investigate the effect of quercetin on cecal microbiota of broilers, 2 hundred and 40 of Arbor Acre (AA) broilers (1 d old) were randomly allotted to 4 treatments (negative control, 0.2, 0.4, and 0.6 g of quercetin/kg of diet) for 42 d. Distribution and population of cecal microbiota were determined at the end of the experiment. Results showed that the main microflora in cecum of AA broilers included *Proteobacteria* (*gamma-proteobacterales*, *Helicobacter* and *Campylobacter jejuni*), *Firmicutes* (*Clostridium*), *Bacteroidetes* (*Bacteroides*), and *Deferribacteres* (*Deferribacterales*). Compared with the negative control, 0.2 g/kg quercetin significantly decreased copies of *Pseudomonas aeruginosa* and *Helicobacter pylori* ($P < 0.05$), *Salmonella*, *Staphylococcus aureus*, *Escherichia coli*, *Clostridium perfringens* and *Campylobacter jejuni* ($P < 0.01$), but significantly increased copies of *Lactobacillus* and *Enterococcus faecalis* ($P < 0.01$); 0.4 g/kg quercetin significantly decreased copies of *Pseudomonas aeruginosa* and *Salmonella* ($P < 0.05$), *Staphylococcus aureus*, *Clostridium perfringens*, *Campylobacter jejuni* and *Helicobacter pylori* ($P < 0.01$), but significantly increased copies of *Bifidobacterium* ($P < 0.01$); 0.6 g/kg quercetin significantly decreased copies of *Staphylococcus aureus* and *Helicobacter pylori* ($P < 0.05$), and *Clostridium perfringens* ($P < 0.01$), but significantly increased copies of *Bifidobacterium* and total bacteria ($P < 0.05$, $P < 0.01$). Our findings indicated that dietary supplementation of quercetin promoted the growth of beneficial bacteria and inhibited the growth of harmful bacteria. The optimum supplementation of quercetin was 0.2 g/kg diet.

Key Words: broiler, cecal microbiota, quercetin

P116 Mechanism of action quercetin improving apparent metabolic rate of dietary protein in Arbor Acre broilers.

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This trial was conducted to evaluate mechanism of action quercetin improving apparent metabolic rate of dietary protein in Arbor Acre (AA) broilers by measuring apparent metabolic rate of dietary protein, activity of pepsin and proteinase in small intestinal, content of serum and muscle protein, and intestinal structure. 240 healthy AA broilers (1-d old) with similar body weight were randomly divided into 4 groups with 6 replicates of 10 each replicate, respectively. The broilers were fed with corn-soybean basal diet supplemented with 0, 0.02, 0.04 and 0.06 g quercetin/kg diet for 6 weeks. The results showed that compared with control, protein apparent metabolic rate and pepsin activity were increased ($P < 0.05$) at 0.02 g/kg quercetin. The content of serum albumin and thigh muscle protein were increased ($P < 0.05$) at 0.02 g/kg quercetin. Villus height and crypt depth in the duodenal and ileum were increased ($P < 0.05$) at 0.02 g/kg quercetin. The content of serum albumin and thigh muscle protein were increased ($P < 0.05$) at 0.04 g/kg quercetin. The activity of small intestinal chymotrypsin and ileum villus height were increased ($P < 0.05$) at 0.0 4g/kg quercetin. The ileal villus height was increased ($P < 0.05$) and the content of serum albumin, thigh muscle protein were increased ($P < 0.05$) at 0.06 g/kg quercetin. In conclusion, a certain dose of quercetin promoted the growth of small intestinal villi and the digestion and absorption of dietary protein in AA broilers. The optimum level of quercetin for increasing apparent metabolic rate of dietary protein was 0.2 g/kg in the basal diet.

Key Words: quercetin, Arbor Acre broiler, protein apparent metabolic rate

P117 Effect of butyric acid glycerol esters on ileum and cecal microflora in chickens challenged with *Eimeria maxima*.

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Coccidiosis is one of the most prevalent diseases seen in the poultry industry leading to excessive economic losses. Butyric acid is being considered as an alternative to antibiotics. The aim of this study was to investigate the effect of butyric acid glycerol esters (BE) on ileal and cecal microbiota in birds challenged with *Eimeria maxima* (EM). Ross 708 male broilers were fed starter diet supplemented with 0 (C) or 0.25% BE (ProPhorce SR 130, Perstorp) from day (d) 1. On d 21, half of the birds were infected with 10^3 EM oocysts. Ileal and cecal contents as well as epithelial scrapings were collected at 7 and 10 d post infection (PI) for bacterial DNA isolation. Microbiota was determined by sequencing bacterial 16S rRNA gene V1-V3 region (Illumina). Regardless of BE treatment (trt), EM had a significant ($P < 0.05$) effect on microbiota composition on phylum, class, order, and family level in all tissues on d 7 PI. Most changes in microbiota were observed in cecal content and scrapings. Ileum contents and scrapings were characterized by minimal changes in microbiota

due to EM infection. No significant ($P > 0.05$) interaction between BE and EM was observed for bacterial populations at any taxonomic level. However, differences ($P < 0.05$) in bacterial populations were observed between d 7 and d 10 regardless of trt. The PERMANOVA analysis showed no significant changes between trt groups (C, C+EM, BE and BE+ME) at both sampling times in every tissue. No significant differences in microbial biodiversity (Shannon index) were observed in cecal and ileal content, and cecal scrapings in all trt groups. In contrast, microbial richness was significantly affected in ileal scrapings by trt (Shannon index, $P = 0.043$) and time (d7 vs. d10, $P = 0.0003$). Beta-diversity analysis (principal coordinates (PCoA) and principal component (PCA) analysis) showed separation of bacterial communities in cecal content (due to time and EM) and scrapings (due to EM), and in ileal content and scrapings (due to time). In conclusion, our results show that EM infection disturbs microbiota balance in chicken but BE had no effect on microbiota changes elicited by EM.

Key Words: 16S, coccidia, gut

P118 Quercetin promoting protein absorption and synthesis in porcine intestinal epithelial cells.

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In vitro and some animal models have shown that quercetin improved production performance of livestock and poultry, promoted digestive absorption and synthesis of proteins, as feed additives. However, the underlying mechanisms are largely unknown. This trial was conducted to study the effect of quercetin and mechanism of protein absorption on porcine intestinal epithelial cells. Preliminary tests showed that quercetin (0.01 to 1 mg/L) promoted cell proliferation by MTT and CCK8 method compared with solvent control in 7 d growth test. To determine effects and mechanism of quercetin, porcine intestinal epithelial cells were cultured for 24, 48, and 72 h in DMEM/F12 medium containing 0.1, 0.2, 0.4, 0.8, 1.6 mg/L quercetin and solvent control (DMSO). Protein absorption, synthesis and amino acid transporters mRNA expression of cells was determined using BCA and real-time PCR method. Compared with control, 0.4 mg/L quercetin promoted protein absorption and protein synthesis in cells at 48 h and 72 h, the content of total cellular protein was significantly increased ($P < 0.05$). The expression of amino acid transporters mRNA, including ASCT2, CAT-1, Y+LAT1 were significantly increased at 72 h and the expression of rBAT mRNA was significantly increased at 24, 48, and 72 h with extracellular 1.6 mg/L quercetin concentrations ($P < 0.01$) compared with control. In conclusion, these results suggested that 0.01–1 mg/L quercetin promoted cell proliferation in 7 d growth test; 0.4–1.6 mg/L quercetin regulated protein turnover protein absorption and synthesis in intestinal epithelial cells via upregulating expression of amino acid transporters.

Key Words: quercetin, intestinal epithelial cells, porcine

P119 Neonatal supplementation with bovine colostrum, vitamins A and D, and copper modulates piglets' immune system in the peri-weaning period.

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Gut response to weaning results in intestinal morphology changes, intestinal barrier function impairment and increased inflammatory response. This study aims to evaluate the potential of a neonatal supplementation with bovine colostrum (BC), vitamins A and D and copper to improve piglet immune functions during the peri-weaning period and to mitigate the post-weaning inflammatory status. A total of 47 litters were assigned to one of the following 4 treatments: (1) control (C); (2) oral administration at 2 and 8 d of age of retinol-acetate (8 and 16 mg respectively), 25-OH-D3 (100 and 200 µg respectively) and $CuSO_4$ (4 and 8 mg respectively) and exposure to UVB lights (15 min/d) every second day from d 5 to weaning at d 21 (ADCu); (3) oral administration of BC (4g/d) from 5 to 10 d of age (BC); (4) ADCu + BC. Within each litter, 2 piglets were killed at 16 or 23 d of age to characterize the mononuclear immune cell subsets in mesenteric lymph nodes (MLN) and blood by flow cytometry and to measure the gene expression in the MLN and jejunal mucosa by qPCR. Time effect showed that the expression of pro-inflammatory cytokines and chemokines such as *IFNγ, IL8, CCL4, CXCL9, CXCL10*, and *CXCL11* was increased after weaning compared with d 16 in the jejunum and MLN ($P < 0.05$), and the percentage of monocyte/macrophage lineage was reduced in the blood and increased in the MLN ($P < 0.05$). After weaning, *IL5* jejunal expression was reduced in BC treated piglets compared with ADCu ($P = 0.03$) and C groups ($P = 0.09$), whereas *TNFSF13B* expression was increased in ADCu+BC compared with C ($P = 0.03$). Before weaning, BC piglets showed a reduction of blood T cells ($P = 0.06$) and γδT cells ($P = 0.09$) and an increase of $CD3^{-}CD16^{+}$ leukocytes ($P = 0.02$) compared with C and a reduced *IL15* expression in the MLN compared with C and ADCu ($P = 0.03$). Osteopontin expression was also increased in BC ($P = 0.08$) and ADCu+BC ($P = 0.03$) compared with C. In conclusion, early dietary supplementations had the potential to influence responses related to immune function and inflammation in the peri-weaning period. The effect on weaned piglet robustness and health remains to be elucidated.

Key Words: piglet, vitamin, colostrum

P120 Butter and cheddar decrease inflammatory markers and modulate gene expression in intestinal, hepatic, and adipose tissues of growing pigs fed a high fat diet.

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Although high fat diets have been associated with increased level of inflammation and metabolic health impairment, new evidences show that the source of fat plays an important role

on these outcomes. To investigate the specific role of dairy fats on metabolic health, a model of growing pigs fed high fat diet (17.5% lard) was used. Dairy fats from either butter or cheddar were incorporated in experimental diets to provide 4.5% of fats and to replace part of the lard. Forty pigs of 6 weeks of age were randomly allocated to 4 different treatments, including a low fat diet and the high fat diets supplemented or not with dairy products. Pigs were fed the experimental diets for 10 wk. After 5 and 10 wk, blood samples were collected to determine hyperlipidemia and inflammatory markers level by ELISA. After 10 wk, pigs were euthanized to collect intestinal, hepatic and adipose tissues to measure the expression of a selection of genes involved in inflammation, oxidative stress, and energy metabolism by qPCR. Finally, 16S Microbial Sequencing was performed from the fecal samples to analyze gut microbiota, and OTUs were obtained using Qiime and Picrust software. Blood levels of IL-1β and TNF-α were decreased in pigs fed either butter or cheddar compared with control lard high fat diet ($P < 0.05$), while no changes were observed in the level of blood lipids. To visualize the effect of dairy fats on gene expression, a Heatmap of gene expression was drawn and showed that both butter and cheddar affected gene expression in jejunum, whereas butter specifically modulated the gene expression in liver and fat tissues, and cheddar specifically changed gene expression in colon. Fecal microbiota analysis showed there were no significant differences between dietary treatments. However, discrete association between the genera *Bifidobacterium* (4%) and *Desulfovibrio* (0.2%) in the high fat diets supplemented with butter and cheddar suggest an association to homeostatic levels. In conclusion, replacement of lard for dairy fats in a high fat diet protects from systemic inflammation and changes gene expression in pig intestinal, hepatic and adipose tissues.

P121 Do iodine and colistin in drinking water affect immune competence and growth performance of broiler?

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A total of 150 unsexed chicks (Ross 308) at 1 d of age were used in a completely randomized design to study the immune responses against Newcastle disease vaccine (NDV), infectious bronchitis vaccine (IBD), and growth performance of broiler with iodine and colistin. The chicks were divided into 6 treated groups with 5 replicated pens (5 birds per pen). The treatments were as follows: G1: received iodine (1 ppm) in drinking water during all week days of experimental period (35 d); G2: received iodine (1ppm) in drinking water, added 3 d a week; G3: received colistin (colistin sulfate, 0.5 mg/L) in drinking water during all week days; G4: received colistin sulfate (0.5 mg/L) in drinking water, added 3 d a week; G5: vaccinated with NDV+IBD but did not receive iodine or colistin (positive control); and G6: neither vaccination nor iodine or antibiotic (negative control). Oral administration of colistin enhanced the antibody titers against NDV and IBD ($P < 0.05$), growth performance (body weight gain, feed intake feed conversion ratio), and reduced the intestinal bacterial counts ($P < 0.05$) during all the experimental periods (35 d). Iodine also caused a marked increase ($P < 0.05$) in the Ab titers against NDV and IBD during the maternal, primary, and secondary response and showed a moderate effect in reducing the intestinal bacteria counts ($P < 0.05$). In the present study, both colistin and iodine could improve the immune response and health status of broiler at all the experimental period. We can use colistin and iodine during outbreak periods of NDV and IBD at neighboring farms.

Key Words: broiler, colistin, iodine

P122 The influence of using different sounds on feeding behavior of broiler chicken by using runway test.

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This study was conducted from August 24 to October 4, 2015, the chicks brought from hatchery Kasha in the area Taslojh, the sounds treatment as follow: Movement of Chicken Feet (1), Regular Soft Timid Hens (2), Chicks Care (3) and Control (T4 without sound). Hatched, straight run chicks (n = 160), were randomly distributed among 4 treatments, which had 4 replicates (2 replicates male and 2 replicates female) per treatment and 40 chicks per replicate (10 chicks/treatment), the sound hearing to the bird for 14 d from 1 to 14 d of ag. The sound began from 8 a.m. to 12 p.m., for 15 min per hour, at a sound level of frequency 20 to 30 dB, and birds were reared to the end of experiment (42 d). Productivity traits were measured as live body weight cumulative, weight gain cumulative, relative growth rate cumulative, and total feed conversion ratio, as well as measured behavioral traits by using run way test, as measured the number of times to approach and move away from the sound, the stay of chicks and the percentage of the stay near the sound. The production results showed a significant increase ($P < 0.01$) in live body weight cumulative, weight gain cumulative, relative growth rate cumulative, and total feed conversion ratio to the broiler from 22 to 42 d and 0 to 42 d to the Movement of Chicken Feet (1), and Chicks Care (3). The behavioral results showed a significant increase ($P < 0.01$) in the number of times to approach and move away from the sound to the Chicks Care (3) and Movement of Chicken Feet (1) and Regular Soft Timid Hens (2), in the first and second weeks (14 d) in runway test. Significant increase ($P < 0.01$) in the stay of chicks and the percentage of the stay near the sound to the Chicks Care (3) and Movement of Chicken Feet (1) and Regular Soft Timid Hens (2), in the first and second weeks (14 d) in runway test.

Key Words: sound, feeding behavior, broiler chicken

P123 Direct comparison of human microbiota-associated gnotobiotic piglet and mouse models for infant gut microbiota studies.

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Animal models are used extensively for investigating the influence of the gut microbiota on host health and disease. Germ-

free mice in particular are often colonized with human fecal microbiota to create human microbiota-associated (HMA) mouse models. Similarly, HMA piglet models have also been developed, although they have not been utilized to the same extent as their rodent counterparts. Because pigs are more similar to humans in terms of anatomy, physiology, and especially the immune system, it has been suggested that HMA pigs are a more relevant model for human gut microbiota research than mouse models. However, no study to date has directly compared these 2 animal models to determine which model more faithfully recapitulates a transplanted human microbiota. The objective of the present study was to determine which animal model establishes a transplanted human microbiota more closely to the original human donor. Specifically, both gnotobiotic piglets (*Sus scrofa*) and gnotobiotic mice (C3H/HeN) were transplanted with a fecal microbiota from a 5-mo-old human infant and were maintained on the same solid diet. To monitor the establishment of the transplanted microbiota, fecal samples were collected weekly for 5 consecutive weeks from both the piglets and the mice. All fecal samples were subjected to 16S rRNA gene-based amplicon sequencing using the Illumina MiSeq platform to characterize bacterial community composition. Beta diversity analysis using weighted unifrac distances suggested that the abundances of major taxa were more similar between mice and the human infant donor than they were between the piglets and the human infant. However, β diversity analysis using unweighted unifrac distances, as well as α diversity analysis, suggested that more of the infant bacterial diversity was captured in the HMA piglets compared with the HMA mice. A follow-up study is planned to further corroborate these findings.

Key Words: human microbiota-associated, piglet, mice

P124 Metazoan models and nutrigenomics: The new paradigm in human nutrition.

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In recent years, nutrition research has moved from classical epidemiology and physiology to molecular biology and genetics. Modern nutritional research is aimed at health promotion, at disease prevention, and on performance improvement. Hence, nutritional sciences are discovering the application of the so-called 'omics' sciences. Nutritional genomics is a recent offshoot of this genetic revolution. Because of these ambitious objectives, the disciplines "nutrigenetics" and "nutrigenomics" have evolved. Although nutrigenetics focuses on the effect of single gene/single food compound relationships, nutrigenomics studies the junction between health, diet, and genomics; it can be seen as the combination of molecular nutrition and genomics, addressing the inverse relationship, which is how diet influences gene transcription, protein expression, and metabolism. To carry out these studies transcriptomics, proteomics and metabolomics approaches are used together with an adequate integration of the information that they provide. Even though, murine knockout models have become major sources of genomic-based data as a holistic approach to evaluate the effect of nutrients and diet on gene expression and metabolic pathway, current knowledge in nutrition is based largely on the use of appropriate animal models together with defined diets. Numerous examples are cited where animal models have been used to solve nutrient-nutrient interactions, to evaluate bioavailability of nutrients and nutrient precursors, and to test for nutrient deficiencies, tolerances, and toxicities. However, more recently, animal nutrigenomic models have contributed to important breakthroughs in other diseases related to diet such as undernutrition, inflammatory disorders, autoimmune diseases, diabetes, obesity, and cancer. While undernutrition and compensatory growth have been extensively study in animal models, obesity is also one of the most widely studied topics in nutrigenomics by exploring the interaction between dietary pattern and genetic factors.

Key Words: nutrigenomics, animal model, human nutrition

P125 Gastrointestinal tract weight and microbial composition of nursery pigs fed diets containing cold-pressed canola cake.

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A study was conducted to determine effects of including cold-pressed canola cake (CPCC) in diets for nursery pigs on gastrointestinal tract (GIT) weight and microbial communities. A total of 160 nursery pigs (initial BW: 6.8 ± 0.8 kg) fed a commercial diet for 1 week postweaning were housed in 40 pens (4 pigs per pen) and fed 4 diets in a randomized complete block design (10 pens per diet). The 4 diets included a corn-soybean meal-based basal diet containing 0, 20, 30, or 40% CPCC. Pigs were fed the diets in 2 phases, phase 1 for 14 d and phase 2 for 21 d. One pig from each pen was euthanized for determining empty weights of various sections of GIT relative to live BW, and microbial communities in ileal digesta and feces. Microbial genomic DNA was extracted from ileal digesta and feces, followed by PCR-amplification of V1-V3 region of 16S rRNA gene and sequencing of gel-purified amplicons using Illumina Miseq platform. Empty weights of small intestine and cecum were unaffected by dietary CPCC. However, dietary CPCC tended to linearly reduce ($P = 0.08$) colon weight. At the phylum-level, *Firmicutes* predominated in both ileal digesta and feces regardless of dietary level of CPCC. *Proteobacteria* were more abundant in ileal digesta than in feces, whereas *Bacteroidetes* were more abundant in feces than in ileal digesta. Dietary CPCC decreased abundance of *Bacteroidetes* and increased abundance of *Firmicutes* in feces. Among *Firmicutes*, predominant family members in ileal digesta were *Clostridiaceae*, *Lactobacillaceae*, and *Streptococcaceae*, whereas *Ruminococcaceae* and *Lachnospiraceae* were predominant in feces. Among *Bacteroidetes*, predominant family member in feces were *Prevotellaceae*, whereas *Enterobacteriaceae* were predominant in ileal digesta. In conclusion, increasing dietary CPCC inclusion increased abundance of *Firmicutes* and decreased abundance of *Bacteroidetes* in feces, implying that it can affect BW gain partly through its effects on gut microbial composition because the BW gain is partly dependent on the ratio of *Bacteroidetes* to *Firmicutes*. Also, dietary CPCC reduced colon weight, implying dietary CPCC reduced energy expenditure in colon relative to live BW.

Key Words: canola meal, microbial compositions, pig

P126 Differential expression of proteins in the duodenum of broilers fed diets rich in arginine or conjugated linoleic acid.

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The primary objective of this study was to determine the effects of diets high in arginine and conjugated linoleic acid (CLA) on expression of small intestinal proteins. Day old broiler chicks were randomly allocated into 3 dietary treatments with 7 pens each and 14 chicks per pen. The birds were provided for 5 wk with 1 of 3 diets: control, arginine-, or CLA-rich diet. At the end of experimentation, 6 birds from each treatment were euthanized to collect blood and small intestine. The duodenum, jejunum, and ileum were cut out to measure their length and weight after being longitudinally cut open, gently wished with saline, and softly soaked up with paper towels. The intestines were then folded at the midpoint, from which they were cut out so that their proximal half (3 cm length) were frozen on dry ice and stored at −80°C whereas the distal half were placed in a PBS-buffered formalin solution. Two-dimensional electrophoresis (2DE) was performed with protein extracted from each treatment. Image analysis showed that dietary Arg or CLA affected intestinal protein expression ($P < 0.05$) although no significant changes were observed in body weight, length and weight of the intestines, and their relative length and weight, when compared with control.

Key Words: protein expression, duodenum, dietary effect

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