

week study period. Necropsy of birds alive at the end of the 4-week study confirmed the ECH measurements that identified birds as DCM. Our data suggest that ECH may be a reliable and consistent tool for identifying birds suffering

from DCM. This will help us and others now begin to investigate the genetic factors that influence DCM.

**Monday, January 24**  
**SCAD (Avian Diseases)**  
**Room: B312**

**Key Words:** Echocardiography, Dilated cardiomyopathy, Furazolidone, *Meleagris gallopavo*

**S53 Effects of probiotics on the development on the ileal bacterial community of the broiler chicken.** M. Lee\*, J. Lu, *The University of Georgia.*

The intestinal microbiota is part of a complex ecosystem that affects a bird's resistance to colonization with enteropathogens. Probiotic bacterial formulations are commonly fed to animals to augment formation of a mature intestine. In order to study the effects of probiotic administration on the development of the small intestinal bacterial community, we used two 16S ribosomal DNA community analysis protocols to profile the changes in composition of the ileal microbiota over the growout. Significant differences were found between the control and probiotic-treated groups by pairwise-analysis of the abundance of certain bacteria and diversity profiles of the bacterial communities. *Enterococcus* and *Clostridium* species were more likely to be detected as dominant bacteria in the ileum of young birds fed the probiotic while *Streptococcus* species were prevalent in the control group. The ilea of both groups contained an abundance of *Lactobacillus* although the dominant species varied between the groups. Probiotics were found to stabilize the development of the bacterial community although the composition of the community was different from that of the control birds.

**Key Words:** Probiotic, Intestine, Microflora

**S54 The microbial composition of poultry litter and potential as a reservoir of antibiotic resistance.** J. Maurer\*, G. Avellaneda, J. Lu, M. Lee, C. Hofacre, *The University of Georgia.*

As the US population has grown, so has our food production system grown and evolved to mass-produce meats, eggs, and produce. Food animal production systems have become more consolidated and integrated, producing large, concentrated animal populations and their unwanted waste by-product. However, animal wastes, cattle manure and poultry litter in particular, serve as an inexpensive means to supplement soils of pasture and crop lands with nitrogen. At issue is the impact animal waste has on the environment, especially with regards to water quality and safety. Using a molecular approach, we set out to define microbial composition of poultry litter, stability of this population in response to antibiotic usage, and diversity of antibiotic resistance genes present within this microbial community. The microbial community of litter consisted primarily of gram-positive bacteria, some of whom were representative of fecal microflora present in litter as well as group that appeared to be unique to this environment. PCR screens failed to detect specific veterinary and foodborne pathogens. If these pathogens were present, they were at cell density far below the limit of PCR detection. Usage of growth-promoting antibiotics did seem to have a significant affect on microbial community structure. Streptogramin, macrolide and other antibiotic resistance genes and associate, mobile genetic elements were present within microbial community of poultry litter, regardless antibiotic usage. What remains to be determined is the fate of these microorganisms and their resident, antibiotic resistance genes once applied to soils.

**Key Words:** Litter, Microflora, Antibiotic, Resistance, Environment

**S55 Novel clostridia that colonize the small intestine of young broilers.** M. Lee\*, J. Lu, X. Qin, C. Hofacre, *The University of Georgia.*

The intestinal microbiota is part of a complex ecosystem that is involved in the health of animals. Our microbial ecology studies, using the chicken intestine as a model of intestinal ecology, indicate that some diets result in small intestinal communities rich with clostridia of unknown virulence. While the cytotoxic activities of pathogenic clostridia have been well studied, similar activity associated with commensal isolates has not been investigated. The toxins of pathogenic clostridia often exhibit enzymatic activity on host macromolecules as substrates. However, some of the mucinase activities of clostridia, including neuraminidase, glycosylhydrolase, protease, and sulfatase, are very similar to those produced beneficial commensal organisms. Therefore, some bacterial enzymatic activities are involved in promoting normal host intestinal development while others produce damage to host cells. In order to study the effects of these novel clostridia on the host, we produced a metagenomic library of intestinal bacterial community DNA and screened it for hydrolytic enzymatic clones. We did not detect phospholipase-producing clones indicating that these bacteria were unlikely to produce a-toxin activity. However, we have identified two novel neuraminidase genes among the genomes of the intestinal bacterial community. The findings of these studies and their implications for broiler intestinal health will be discussed.

**Key Words:** Clostridium, Toxin, Intestine

**S56 Detection of specific antibody responses to *Salmonella enteritidis* in lung wash samples from infected hens.** P. Holt\*, H. Stone, R. Gast, R. Moore, *USDA/ARS Southeast Poultry Research Laboratory.*

We have developed a simplified method for collecting lung lavage samples from adult chickens. Adult white leghorn hens previously infected with *Salmonella enteritidis* (SE) were euthanized using carbon dioxide inhalation and the tracheas were exteriorized. Narrow gauge tygon tubing (6/32 inch) was inserted down the trachea near the bronchi. Using a 30 ml syringe, containing 10 ml of glycine buffer and attached to the tubing, a vacuum was applied to remove all air from the lung through the buffer. The buffer was slowly introduced into and then slowly aspirated from the lung. Samples contaminated with blood were discarded. Antibody responses in the lung were determined via an ELISA using SE lipopolysaccharide as the solid phase antigen. A detectable IgA anti-SE response was observed in the lung lavage fluids one week post infection and these increased substantially over the next several weeks. These results indicate that a detectable immune response will develop in the lung of individuals intestinally infected with an enteric pathogen.

**Key Words:** Mucosal immunity, Food safety, Lung antibody, *Salmonella enteritidis*, Enteric pathogen

**S57 Distribution of Fimbrial, Phage and Plasmid Associated Virulence Genes among Poultry *Salmonella enterica*. Serovars.** R. Whitaker\*, C. Hofacre, M. Lee, M. Maier, J. Maurer, *The University of Georgia.*

Taxonomic relatedness does not define the pathogenicity of a microbe, biological properties do. Microbes that are designated "pathogens" possess virulence

factors, which enable them to cause disease. Virulence genes are frequently found on large "pathogenicity islands" or they are part of mobile genetic elements, such as bacteriophages or plasmids. A species can be pathogenic or non pathogenic depending on the virulence gene(s) it harbors. *Salmonella* is of interest given its ability to colonize and cause disease in a variety of animal species including man. There is considerable genetic variability among *S. enterica* as evident with its multitude of serovars, and yet only a handful cause disease in man. Several of *Salmonella* serovars prevalent in poultry, ex. Kentucky, are minor serovars associated with foodborne outbreaks in the US, compared to the other serovars like Enteritidis and Typhimurium. Are these differences attributed to variability in virulence gene distribution among serovars? In this study, we examined the distribution of several virulence genes among 470 *S. enterica* isolates representing 15 serovars, from poultry isolated in the southeastern US. *Salmonella* isolates were screened by DNA: DNA hybridization using DNA probes to several virulence genes associated with prophages. (*sopE*, *sseI*, *sodCI* and *grvA*), pathogenicity islands (*avrA*, *sugR*, and *pagJ*, *K*), virulence plasmid (*spv*, *pef*) and fimbrial operons (*sef*, *stf*, and *stj*). One of the major genetic differences among poultry *Salmonella* serovars was in the distribution of the virulence plasmids, with serovars most commonly associated with foodborne outbreaks, possessing this 90 kb plasmid. While it is important for the poultry industry to reduce *Salmonella* contamination, aggressive eradication/control programs might be better directed towards pathogenic serovars Typhimurium and Enteritidis.

**Key Words:** *Salmonella*, Phages, Plasmid, Virulence, Serovar

**S58 Hematological changes reflect stress response differences and disease susceptibility in lines of turkeys selected for increased body weight.** G. R. Huff<sup>\*1</sup>, W. E. Huff<sup>\*1</sup>, J. M. Balog<sup>1</sup>, N. C. Rath<sup>1</sup>, N. B. Anthony<sup>2</sup>, K. E. Nestor<sup>3</sup>, <sup>1</sup>USDA/ARS/PPSRU, <sup>2</sup>Dept. of Poultry Science, University of Arkansas, <sup>3</sup>Dept. of Animal Sciences, The Ohio State University.

Three genetic lines of turkeys were compared for their hematological responses to *Escherichia coli* challenge following dexamethasone injection (Dex) or *E. coli* challenge preceding transport stress (Stress). The turkey lines were a slow growing line selected for egg production (Egg), a fast growing line selected for increased 16 wk BW (F-line), and a commercial line (Comm). At 14 wks of age, the Dex group was treated with 3 injections of 2mg Dex/kg BW followed by airsac challenge with 100 cfu of *E. coli*. The Stress group was given the same *E. coli* challenge without Dex treatment, and was subjected to transport stress, which included 12 hours of holding time in a transport vehicle, eight days after the challenge. All treated birds and untreated control birds were bled at the same time, which was 1 day after transport and 9 days after challenge with *E. coli*. The overall average total leukocyte counts (WBC) and the percentages of eosinophils (Eos) and basophils (Baso) were the same for all 3 lines, however the percentages of heterophils (Het) and monocytes (Mono) and the heterophil/lymphocyte ratio (H/L) were lower and the percentage of lymphocytes (Lym) was higher in the Egg line as compared to the two fast-growing lines. Both DEX and Stress increased WBC, Het, and H/L and decreased Lym in all three lines, however these effects were significantly greater in both fast growing lines as compared to the Egg line and were greater in the Comm line as compared to the F-line. Mortality was significantly higher in the Comm line as compared to the Egg line and was intermediate in the F-line. Sixteen week BW was unaffected by either treatment in the Egg line and was decreased by both treatments in the Comm line and by the Dex treatment in the F-line. The differences between these lines in their physiological response to stress in two stress models suggests that increasing selection for body weight of turkeys is accompanied by changes in the stress response resulting in increased susceptibility to opportunistic bacterial infection.

**Key Words:** Turkeys, Transport stress, Genetics, Heterophil/lymphocyte ratio, *Escherichia coli*

**S59 The performance and anticoccidial efficacy of clopidol fed to broiler chickens.** G. Mathis<sup>\*1</sup>, M. Cope<sup>2</sup>, <sup>1</sup>Southern Poultry Research, Inc., <sup>2</sup>Merial Select, Inc.

A floor pen study was conducted with broiler chickens to compare performance and the anticoccidial efficacy of Clopidol to various commercial in feed anticoccidials. The study consisted of 72 pens starting with 50 broiler chickens. The treatments were replicated in eight blocks, randomized within blocks. The treatments were: Unmedicated, noninfected, Unmedicated, infected, Clopidol 125 ppm starter to Monensin 99 ppm grower, infected, Clopidol 125 ppm starter to Salinomycin 55 ppm grower, infected, Nicarb 125 ppm starter to Monensin 99 ppm grower, infected, Nicarb 125 ppm starter to Salinomycin 55 ppm grower, infected, Diclazuril 1 ppm starter to Monensin 99 ppm grower, infected, Diclazuril 1 ppm starter to Salinomycin 55 ppm grower, infected, and Salinomycin 44 ppm starter to Salinomycin 55 ppm grower, infected. On Day 15 all birds, except Treatment 1, were exposed to field strains of *E. acervulina*, *E. maxima*, and *E. tenella*. Bird weights kg by pen were recorded at Day 0, Day 15, Day 21, Day 35 and 42. On Days 21 and 42, five pre-selected birds from each pen were examined for the degree of coccidial lesions. A significant weight reduction and increased feed conversion was observed on Days 21, 35, and 42, with an average of 2.4 coccidial lesion score in the Unmedicated, infected birds. As observed by the average lesion score of 1.4, the coccidial field isolates were slightly resistant to Diclazuril. Performance and coccidiosis control were significantly improved by feeding Clopidol, Nicarbazine, or Diclazuril in the starter feed versus a straight Salinomycin program. The Clopidol and Nicarbazine shuttle programs had very similar results and had equal performance compared to the Noninfected birds. No significant difference in performance was observed feeding either Salinomycin or Monensin in the grower feeds. This study shows that Clopidol is a highly effective anticoccidial. A Clopidol starter feed shuttle program should provide equal anticoccidial protection and similar performance to a Nicarb shuttle program.

**Key Words:** Clopidol, Monensin, Salinomycin, Nicarb, Coccidiosis

**S60 Commercial field trials testing a live coccidiosis vaccine administered in ovo.** R. M. Poston<sup>\*</sup>, A. P. Avakian, J. L. Schaeffer, J. E. Hutchins, A. G. Martin, V. W. Doelling, Embrex, Inc.

Paired house field trials were conducted at a commercial broiler rearing facility to evaluate the safety and efficacy of an *in ovo* administered live coccidiosis vaccine consisting of *Eimeria acervulina*, *E. maxima*, *E. tenella* and *E. mitis*. All broiler embryos were vaccinated *in ovo* with Marek's disease vaccine HVT/SB1 and infectious bursal disease vaccine on day 18 of incubation. Control house feed had 60 g/ton salinomycin and 35-45 g/ton 3-nitro-4-hydroxyphenylarsonic acid in both the starter and grower feeds. Anticoccidial drugs were not present in withdrawal feeds. Bacitracin methylene disalicylate at 25-50 g/ton was in the starter and grower feeds in coccidiosis vaccinated and control house. Within each paired house trial, flocks were matched, placement in control and coccidiosis vaccinated houses occurred at the same time, house conditions were equal and processing occurred on the same day. At approximately three weeks of age, a sample of birds from each treatment house was removed and tested for vaccine efficacy at an animal research laboratory. Intestinal lesion scores and body weight gains were determined 6 days after a multi-species challenge by oral gavage with *Eimeria acervulina*, *E. maxima*, *E. tenella* and *E. mitis*. The vaccine was found to be efficacious for both body weight gain and a reduction in intestinal lesion scores post challenge. Four necropsies were conducted in the field during each trial and intestinal lesions assessed. Necropsies, including intestinal lesion and microscopic mucosal scraping evaluations, indicated that a successful uniform vaccination occurred in each trial. Standard production measurements including percent hatch, percent mortality, feed conversion, average body weight, and settlement costs were collected for each trial. Overall, coccidiosis vaccinated birds performed similarly to medicated controls for all performance parameters. Additionally, the *in ovo* administered coccidiosis vaccine was shown to be both safe and effective in commercial broiler chickens.

**Key Words:** Coccidiosis, Vaccine, Performance, *In ovo*, Broilers