Major histocompatibility complex variability in Finnish Landrace chickens. Janet E. Fulton*,1, Mark E. Berres2, Juha Kantanen3,4, and Mervi Honkaukia1, 1Hy-Line International, Dallas Center, IA, 2University of Wisconsin, Madison, WI, 3Natural Resources Institute Finland, Jokioinen, Finland, 4Department of Environmental and Biological Sciences, University of Eastern Finland, Kuopio, Finland.

The major histocompatibility complex (MHC) is a cluster of genes involved with immune responses. The chicken MHC has been shown to influence resistance to viruses, bacteria and both internal and external parasitic infections. The highly variable chicken MHC haplotypes were initially identified by the use of haplotype-specific serological reagents. A SNP-based panel encompassing 210,000 bp of the MHC was developed to enable in-depth genetic analysis plus rapid identification of novel haplotypes for which serological reagents are not available. The Finnish Landrace breed of chickens traces its origins to almost 1,000 years, with multiple lineages maintained as small populations in isolated villages. The breed is well adapted to the Finnish climate and is considered a light egg layer. Conservation efforts for this endangered breed were initiated in the 1960s and 12 different lineages are currently maintained by a network of volunteer hobbyist breeders. The MHC variability within this breed was examined using the MHC SNP panel. A total of 195 samples from 12 distinct populations (average of 15 samples per population) were genotyped with the 90-SNP MHC panel. There were 36 haplotypes found, 16 of which had been previously identified in either commercially utilized or heritage breeds from North America, with the remaining 20 haplotypes being novel. The average number of MHC haplotypes found within each Finnish Landrace population was 5.9 and ranged from one to 13. While common haplotypes were found in multiple populations, population-specific haplotypes were also found. This study shows that substantial MHC diversity occurs within the Finnish Landrace breed and exemplifies the significance tied to conserving multiple lineages of rare breeds.

Key Words: Finnish Landrace breed, major histocompatibility complex variability, SNP genotype, haplotype

SNP identification of major histocompatibility complex haplotypes in Lakenvelder and Golden Sebright chickens. Robert L. Taylor Jr.*,1, Mark E. Berres2, and Janet E. Fulton3, 1West Virginia University, Morgantown, WV, 2University of Wisconsin, Madison, WI, 3Hy-Line International, Dallas Center, IA.

High genetic polymorphism is a hallmark of the chicken major histocompatibility complex (MHC). First described as the B blood group alloantigen, that system’s influence on skin graft rejection identified it as the chicken MHC. Later studies showed that resistance to bacterial, parasitic and viral pathogens was also affected by MHC genes. Many MHC types were identified within populations using specific alloantisera. Comparison tests using antisera and cell samples submitted by multiple laboratories enabled a unified nomenclature for 27 distinct MHC types. Most these standard haplotypes originated in White Leghorn chickens. Recently, a high-density SNP-based panel encompassing 210,000 bp across the chicken MHC was used to describe MHC haplotypes in heritage chicken populations, which revealed many additional and non-serologically defined haplotypes. In the present study, DNA from the Lakenvelder and Golden Sebright chicken breeds were tested on this SNP panel. The MHC haplotypes found were compared with those types that were identified previously. Relationships between these haplotypes and those types described previously were determined using computational phylogenetic methods, which identify similarity based on SNP identity across the MHC region and establish clusters of related haplotypes. The Lakenvelder population (n = 21) was homozygous for a novel MHC type, whose closest relative was BSNP-C02 which was found in a broiler population. This unique Lakenvelder haplotype (subsequently named BSNP-C06) differed from BSNP-C02 by 3 of the first 10 SNPs (encompassing 11,000 bp of the MHC). The Golden Sebright population (n = 14) was found to be segregating for 3 haplotypes. BSNP-Q02 was novel and varied from BSNP-Q01 in 4 of the initial 10 SNPs (encompassing 20,000 bp). BSNP-K02 which was previously reported in Barred Plymouth Rock, and broiler lines (BRL), and the third type, BSNP-A09, was identical to BSNP-A09 (serotype BQ) previously found in BRL, and Red Jungle Fowl. These results add to the array of MHC haplotypes described in various chicken breeds and show that rare breeds can contain novel MHC haplotypes.

Key Words: haplotype, genetic distance, diversity

Withdrawn

Determination of the capacity of Bacillus amyloliquefaciens CECT 5940 to inhibit quorum sensing. Alvaro Ortiz*, Pilar Honrubia, and Juan J. Mallo, Norel, Madrid, Spain.

Quorum sensing (QS) is a bacterial communication system based on the production and secretion of autoinducers (Fuqua et al., 1994). Once activated, QS triggers the synchronized expression of multiple genes in the population, thus regulating important biological functions and the transfer of plasmids, motility, aggregation, luminescence, antibiotic biosynthesis, virulence, etc. (Swift et al., 2001; Waters and Bassler, 2005; Williams et al., 2007). So QS inhibition is being investigated as a promising technique to prevent disease. The best-characterized QS system involves the autoinducers N-acylhomoserin lactones (AHLs). Due to its capacity to produce violacein (a violet pigment) when QS is activated, Chromobacterium violaceum CECT 5999 (CV026) is used in QS assays. QS is activated by applying in the culture medium AHLs with acyl chains of 4 to 8 carbons resulting in the apparition of violacein. In the detection assay (based in the methodology described by Romero et al., 2011) the apparition (+) or absence (-) of violet color was controlled in C. violaceum seeded plates when adding the following test compounds: sterile distilled water(-), AHL(+), probiotic sterile culture medium(-), probiotic sterile culture medium + AHL(+), sterile medium + probiotic culture supernatant(-), AHL + probiotic culture supernatant(-). The violet pigment was detected in the plates whenever AHL was applied. The combination of AHL with B. amyloliquefaciens CECT 5940 culture supernatant resulted in an inhibition of the production of the pigment violacein, indicating that quorum sensing has been blocked by the probiotic culture supernatant.

Key Words: probiotic, quorum sensing, Bacillus amyloliquefaciens, quorum quenching
Newcastle disease (ND) results in an increased morbidity and mortality to commercial and backyard poultry. The disease occurs in many domestic and wild avian species; nevertheless, the clinical outcomes are often devastating in commercial poultry flocks resulting in incurable economic losses. Despite following strict vaccination plans for commercial flocks in Pakistan, large-scale outbreaks have occurred in the last few years, even in the vaccinated flock and wild birds. In this regard, the role of wild-birds either as a reservoir or source of spread in the environment cannot be ignored. Here, we characterized an isolate recovered from ND-suspected outbreak in peacock through complete F and HN gene based sequence and residue analysis. With characteristic F$_{\text{pro}}$ proteolytic cleavage site ($^{117}$RRQKR$\downarrow$F$^{117}$), the whole F and HN gene based sequence analysis of the ND-isolate demonstrated evolutionary relationship to genotype VII. Subsequent in depth analysis of F-gene hyper-variable region revealed clustering of the study isolate close to genotype VII. Further, the deduced residue analysis for both F and HN protein showed several substitution mutations in the functional domains distinct from representative strains of each genotype including the vaccine strains. Perhaps some of reported mutations were found exclusive to the present study isolate. Though the present study presents limited and preliminary data, yet the findings can enhance our knowledge toward circulating strains of APMVs in Pakistan. Future studies are much needed to determine ND potential for transmission in commercial and backyard poultry and subsequent shedding into the environment.

**Key Words:** avian paramyxovirus type 1 (APMV-1), fusion protein, hemagglutinin gene, peacock

**295 Genetic and pathobiologic characterization of pigeon-originated Newcastle disease virus.** Muhammad Z. Shabbir$^1$, Sameera Akhtar$^1$, Yi Tang$^2$, Tahir Yaqub$^1$, Arfan Ahmad$^1$, Gulham Mustafa$^1$, Muhammad A. Alam$^1$, and Muhammad Munir$^1$, 1University of Veterinary and Animal Sciences, Lahore, Pakistan, 2The Pennsylvania State University, State College, PA, 3The Pirbright Institute, Woking, United Kingdom.

Newcastle disease (ND) causes significant economic losses to the poultry industry worldwide. The disease is enzootic in Pakistan and recurrent outbreaks are being reported in multiple avian species even with the use of classic vaccine. Several virulent Newcastle disease viruses (vNDVs) have been isolated and genetically characterized in the recent years from species other than chicken. However, there exist an absolute paucity for genetic and pathotypic characterization of pigeon-originated NDVs. Here we determined the complete genetic and clinicopathologic characterization of virulent pigeon-originated NDV's in vaccinated and non-vaccinated chickens following the commonly practiced vaccine schedule in Pakistan. The complete genome length of isolates was found to be 15,189 nt with gene order of 3-NP-P-M-F-HN-L. The complete genome and the hypervariable region of F gene based phylogeny revealed clustering of pigeon isolate to genotype VIIb. Several substitutions were observed in the functional domains of F and HN protein including fusion peptide, hydrophobic regions, transmembrane region and neutralization epitope. Given the polybasic residue ($^{112}$RRQKR$\downarrow$F$^{117}$) at the cleavage motif of F protein, trans-species transmission, clinical symptoms and gross necropsy lesions observed, tissue tropism, viral shedding and histopathology, the isolate was found to be velogenic to chicken. Beside expected genetic distance between vaccine strains and study isolate, vaccine efficacy study revealed that commonly practiced vaccine schedule may be the potential reason of vaccine failure.

**Key Words:** Newcastle disease, pigeon-originated NDV, vaccine, vaccine failure

**296 Staphylococcus agnetis involvement in bacterial chondronecrosis with osteomyelitis in broilers.** Adnan A. Al-Rubaye, Sura Zaki, Nnamdi S. Ekesi, Abdulkarim Shwani, Robert F. Wide- man, Young Min Kwon, and Douglas D. Rhoads*, University of Arkansas, Fayetteville, AR.

Lameness is a significant problem in the poultry industry resulting in millions of dollars in lost revenue annually. In broilers, a common cause of lameness is bacterial chondronecrosis with osteomyelitis (BCO). Using a wire flooring model to induce lameness we identified *Staphylococcus agnetis* as the principle species isolated from BCO lesions on our research farm. Administration of *S. agnetis* isolates in drinking water at 20 d of age can induce high incidence of BCO in birds on wire flooring. Our data supports a model that rearing chicks on wire flooring leads to bacterial translocation across the intestinal epithelium into the blood. *S. agnetis* appears to colonize the susceptible proximal femoral and tibial growth plates inducing necrosis and lameness by 40 to 56 d. As this species has previously not been associated with BCO in poultry, it may have emerged as a result of our protracted experiments inducing high levels of lameness. We have sequenced, assembled, and annotated the *S. agnetis* genome from chicken isolates. Current work is aimed at understanding the relationships between our poultry isolates and isolates from other sources. In addition, we are investigating how the bacterium is transferred between birds and what management methods can reduce colonization. Defining the likely route of transmission to broilers, and genomic analyses should contribute substantially to the development of measures for mitigating BCO losses in poultry.

**Key Words:** broiler, lameness, bacteria, pathogen, genome, leg

**297 Reduced Escherichia coli burdens and virulence in US commercial flocks fed multi-strain *Bacillus*.** Alexandra L. Weal-leans*$^*$, Kirsty A. Gibbs$^1$, Jodi Benson$^2$, Firmin Delago$^2$, Jennifer Lambrecht$^2$, Elizabeth Galbraith$^2$, and Marion Bernardeau$^1$, 1Danisco Animal Nutrition, DuPont Industrial Biosciences, Marlborough, United Kingdom, 2DuPont Nutrition and Health, Waukesha, WI.

Avian pathogenic *Escherichia coli* (APEC) causes colibacillosis in poultry and is a significant economic production burden. This study investigated *E. coli* burdens and virulence in broiler complexes following the introduction of multi-strain *Bacillus* direct-fed microbials (DFMs). Sampling occurred pre-DFM supplementation in 4 complexes (C1–4) from different producers in Georgia, United States, and again after a minimum of 3 flock cycles. Whole intestinal tracts were extracted from 760 birds; sections were collected from the duodenum, jejunum and ileum and used to isolate and quantify *E. coli* using selective CHRO-Magar media. Five *E. coli* were selected per bird for genetic analysis. A previously defined pentaplex PCR assay screened all *E. coli* for virulence-associated genes (VAG; *cvaA*, *ipr2*, *iss*, *iuC*, *tsh*); isolates with ≥2 VAG were identified as APEC. APEC prevalence was based...
on a % of total plate count proportional to the number of APEC from each bird. E. coli count was reduced by 0.29 log₁₀ cfu/g and APEC prevalence by 20.8% (P < 0.0001; Table 1). The proportion of E. coli with ≥2 VAG dropped from 58.8 to 40.8% (P < 0.0001) post DFM. The proportion of isolates with 5 VAG was 4.3% pre-DFM and 1.3% post-DFM while isolates with no VAG increased from 14.2 to 17.2% (P < 0.0001). This data suggests Bacillus DSM positively affect resident microbial populations and may form part of a multipronged approach to improving bird performance in an era without antibiotics or APEC specific targeted therapies.

Table 1. Escherichia coli burdens and virulence-associated genes (VAG) pre/post DFM supplementation

<table>
<thead>
<tr>
<th>Complex</th>
<th>E. coli count, log₁₀ cfu/g</th>
<th>APEC prevalence, %</th>
<th>VAG/E. coli</th>
</tr>
</thead>
<tbody>
<tr>
<td>C1</td>
<td>Pre 5.06</td>
<td>83.77</td>
<td>1.86</td>
</tr>
<tr>
<td></td>
<td>Post 4.85</td>
<td>82.76</td>
<td>1.97</td>
</tr>
<tr>
<td></td>
<td>P-value 0.013</td>
<td>0.632</td>
<td>0.198</td>
</tr>
<tr>
<td>C2</td>
<td>Pre 4.50</td>
<td>74.76</td>
<td>1.80</td>
</tr>
<tr>
<td></td>
<td>Post 3.96</td>
<td>79.60</td>
<td>1.67</td>
</tr>
<tr>
<td></td>
<td>P-value &lt;0.0001</td>
<td>0.224</td>
<td>0.330</td>
</tr>
<tr>
<td>C3</td>
<td>Pre 4.71</td>
<td>89.37</td>
<td>2.14</td>
</tr>
<tr>
<td></td>
<td>Post 4.39</td>
<td>53.05</td>
<td>1.14</td>
</tr>
<tr>
<td></td>
<td>P-value 0.0002</td>
<td>&lt;0.0001</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>C4</td>
<td>Pre 4.29</td>
<td>93.25</td>
<td>2.57</td>
</tr>
<tr>
<td></td>
<td>Post 4.36</td>
<td>46.54</td>
<td>3.32</td>
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<tr>
<td></td>
<td>P-value 0.462</td>
<td>&lt;0.0001</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Pooled</td>
<td>Pre 4.74</td>
<td>83.37</td>
<td>1.99</td>
</tr>
<tr>
<td></td>
<td>Post 4.45</td>
<td>62.56</td>
<td>1.49</td>
</tr>
<tr>
<td></td>
<td>P-value &lt;0.0001</td>
<td>&lt;0.0001</td>
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</tr>
</tbody>
</table>

Key Words: Bacillus, broiler, direct-fed microbial, Escherichia coli

298 A preliminary study on carrier potential of Salmonella enterica serotype Gallinarum biotypes pullorum and gallinarum in common wild bird species in Pakistan. A. Aslam*1, M. Ali1, I. Ahmad1, M. Ijaz2, Habib Rehman2, N. Ahmad2, K. Ashraf2, Raheela Akhtar1, and G. Mustafa1, 1Department of Pathology, University of Veterinary and Animal Sciences, Lahore, Pakistan, 2Department of CMS, University of Veterinary and Animal Sciences, Lahore, Pakistan.

Many wild and game birds are reported to harbor pullorum disease and fowl typhoid, and are believed to play an important factor in transmission of diseases. The present study investigated the carrier potential of selected wild birds (Indian Myna, crows, sparrows and pigeons) for Salmonella enterica serotype Gallinarum biotypes pullorum and gallinarum. A total of 100 wild birds, 25 each of Indian Myna (Acridotheres tristis), house crows (Corvus splendens), house sparrows (Passer domesticus indicus), and pigeons (Columbia livia domestica) were procured from local markets of Lahore. Bird selection was random and independent of age and sex. To avoid the transfer of salmonella infection from poultry, only recently captured birds were selected. Birds were autopsied to collect spleen, which was processed for DNA extraction.

Specific primers TGTTGATGACGGTAATGGT (fliC F: 866–885) and CAGAAAGTTTCGCACTCTCG (fliC R: 1063–1044), were used for amplification of flagellin gene phase against above-mentioned organisms. Data were analyzed using Pearson’s Chi-squared. Results revealed that carrier potential of salmonella infection in selected wild birds in Lahore was 08%. The occurrence of salmonella infection was similar (P > 0.05) in all wild birds as carrier potential of Salmonella enterica serotype Gallinarum biotypes pullorum and gallinarum was 8, 4, 12, and 8% in myna, crows, sparrows and pigeons respectively. In conclusion, all 4 wild birds were infected with salmonella and may act as reservoir of the organism. As carriers, these birds may act as potential source of transmission of salmonella infection to healthy birds in open-house poultry farms or indigenous backyard poultry in Pakistan.

Key Words: Salmonella, wild birds, carrier potential, broiler

299 Antibiotics: New use policies won’t change the outcome. Hector M. Cervantes*1,2, 1Phibro Animal Health, Atlanta, GA, 2University of Georgia, Athens, GA.

Changes on antibiotic use policies in food-producing animals published on FDA-CVM Guidance for Industry #209 and 213 are scheduled to start on January 1, 2017. The main changes include elimination of use of medically important antimicrobials (MIAs) for growth promotion and feed efficiency, use of MIAs only to ensure animal health and under veterinary supervision. This means that MIAs administered to food producing animals will require a prescription (if administered via the drinking water) or a Veterinary Feed Directive (VFD) order (if administered via the feed). Although the proposed policy changes are good and embraced by the veterinary profession they are not likely to improve the antimicrobial resistance (AMR) problem confronted by the medical profession because antimicrobial use in food-producing animals is not a significant contributor to AMR in humans. In the poultry industry the antibiotic growth promoters (AGPs) used have a gram-positive spectrum of activity whereas in human medicine the bacteria of concern in regards to foodborne diseases (Salmonella, E. coli and Campylobacter) are gram-negative so it can be safely predicted that the banning of AGPs will have no effect on AMR on the main food pathogens of concern in human medicine. Other examples from European human and animal databases on AMR will be used to illustrate that the likelihood of a measurable positive effect on human health from the new policy on antimicrobial use in food-producing animals is likely very small to nil.

Key Words: antibiotic growth promoters (AGP), antimicrobial resistance, GFI-209, GFI-213

300 The effects of coccidiosis and Clostridium perfringens challenge on immune cell dynamic and nutrient digestibility in broiler chickens: Combination of antibiotic growth promoter and protected organic acid plus essential oils. Antonio Leonardo Kraieski1, Paula Gabriela Santin1, Carolina Oliva Pinto1, Mariana Lemos Moraes2, Duarte Almeida Neves2, and Elizabeth Santin*1, 1Federal University of Parana, Curitiba, PR, Brazil, 2Jefo Nutrition Inc., St-Hyacinthe, QC, Canada.

We investigated the dietary supplementation of protected organic acids and essential oils [P(OA+EEO)] with an antibiotic growth promoter (AGP) in challenged broilers. Cobb chicks (192; 1–28d) were allocated in a completely randomized design with 4 treatments: negative control (NC), positive control (PC), AGP (10 ppm) and AGP + P(OA+EEO).
301 Focal duodenal necrosis is evident in end-of-lay table egg flocks in Saskatchewan. Tennille D. Knezacek¹, Jenny A. Fricke², and Henry L. Classen¹, ¹Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada, ²Department of Veterinary Pathology, Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, SK, Canada.

Focal duodenal necrosis (FDN) has been diagnosed sporadically in Saskatchewan table egg flocks. A survey was conducted to investigate the incidence of FDN in 5 70-week-old laying hen flocks in Saskatchewan, Canada. From each flock, 100 birds were euthanized and the presence or absence of FDN lesions in the duodenal loop was recorded. On a sub-set of the euthanized birds from each flock (n = 40), body weight, as well as full and empty gizzard weights were documented to determine if hen size and gizzard function affected FDN occurrence. Chi-squared analysis compared FDN prevalence between flocks. Hen and gizzard weight data were analyzed using Proc CORR of SAS 9.4. Despite a lack of reported clinical signs, all flocks had birds exhibiting FDN lesions. The average incidence of FDN from all birds examined was 25.7% (n = 498), with significant differences between flocks (range: 6 to 49% FDN positive). Pale-colored depressions in the duodenal wall were observed in an average of 8.4% of the birds (flock range: 1 to 19%) and recorded as focal depressions. Hen weight did not affect the prevalence of FDN. With the exception of one flock, relative full and empty gizzard weights were not related to FDN. A comprehensive field study of laying hen flocks at different stages of production is required to monitor and better understand the effect of FDN on laying hen performance in Saskatchewan.

Key Words: laying hen, small intestine, enteric disease, gray gut

302 Factors influencing coccidiosis as a disease challenge model for broiler chickens housed in cages. Rachel K. Savary*, Timothy A. Fiss, Dawn A. Abbott, Jenny A. Fricke, Andrew G. Van Kessel, and Henry L. Classen, University of Saskatchewan, Saskatoon, SK, Canada.

Reduced use of medication in animal feeding has led to increased investigation of dietary factors that enhance bird health. Disease models are required for this research and this study used 3 trials to evaluate coccidial vaccination for this purpose. Trials 1 and 2 were randomized complete block designs with 4 doses (0, 10, 20, or 30 x label dose) of Coccivac-B (Merck Animal Health) administered to 12 replicate cages of 6 birds by repeater pipette (Trial 1) or gavaging needle (Trial 2). Trial 3 used a completely randomized design with 0 and 30 x label dose of Coccivac-B52 (Merck Animal Health) administered by gavaging needle to 6 replicate cages of 6 birds. Gavaging occurred at 15 d and response criteria were evaluated 7 d later in all trials and again at 10 d in Trials 1 and 2. All means are reported in order of increasing vaccine dose with significance at P ≤ 0.05. Broiler performance was not affected by vaccination in Trials 1 and 3, but declined linearly in Trial 2 (body weight gain: 445, 421, 388, 365 g; feed to gain: 0.72, 0.68, 0.66, 0.63). As vaccine dose increased, AMEn decreased (Trial 1: 3387, 3318, 3267, 3170 kcal kg⁻¹; Trial 2: 3358, 2535, 2422, 2309 kcal kg⁻¹), while relative weight, length and content for intestinal sections increased (Trials 1–3). Gross lesion (duodenum, jejunum/ileum, ceca) and microscopic oocyst scores (jejunum/ileum, ceca) increased with dose, however gross scoring did not distinguish differences satisfactorily in the jejunum/ileum. Gavaging needle more accurately delivered vaccine to the crop than the repeater pipette and larger differences in response were seen at 7 than 10 d. Intestinal weight and AMEn were more reliable response criteria of vaccine dose than performance. While lesion and oocyst scores were useful in confirming infection, high variability and limited accuracy suggest scoring may be unreliable for evaluating subtle nutritional influences. Careful attention to protocol development will be crucial for the effective application of a coccidial vaccination model to assess dietary factors affecting bird health.

Key Words: coccidiosis vaccination, gavaging technique, dose response, vaccine formulation, sampling day

303 Ileal and cecal microbiota in early onset of necrotic enteritis in chickens. Rosemary L. Walzem¹, Thomas Gaydos², Omar Gutierrez², Katie Burchfield³, and Audrey P. McElroy¹, ¹Texas A&M University, College Station, TX, ²HuvePharma, Peachtree City, GA.

Necrotic enteritis, NE, causes significant morbidity and economic loss within the poultry industry. Detailed analyses of early changes in microbiota during NE are scarce. Birds studied were drawn from 90 pens (n = 28 male broilers/pen, 15 pens/diet) that were fed one of 2 basal diets differing in Ca content (0.95% or 0.75%) and either no, or one of 2 supplemental products. The first observed incidence of NE identified 19 birds on d 18. A healthy pen-mate was taken to compare with each NE bird. Birds were euthanized by CO2 asphyxia immediately before collection of distal ileum and cecum. Tissues were transferred to sterile tubes and sent to MrDNA Lab (Lubbock, TX) for microbiota characterization using Illumina sequencing with >12.5K reads follow-
ing rarefaction. NE incidence varied by diet, but microbiota outcomes varied significantly by health status only and were pooled across diet to give healthy (n = 19) and NE (n = 19) bird groups for ileum and cecum. Alpha diversity, species richness, was greater in cecum than ileum in both healthy and NE birds (P < 2.5 × 10−19, Chao1) with similar values for healthy and NE birds within each sampling location. Beta diversity assesses whether differences exist between populations and is most valid when α diversity is equivalent. PCoA found no difference in ileal populations of healthy and NE birds, albeit at the genus level streptococcus was reduced (P < 0.016) in NE ileum. Cecal populations separated but did not fully diverge. NE birds had reduced Firmicutes (P < 0.0042) and increased proteobacteria (P < 0.055). Reductions within the eubacteria and Lachnospiraceae families were most responsible for Firmicutes loss, while Enterobacteriaceae family members were most responsible for increases in proteobacteria. Changes to metabolic processes of ileal bacterial may amplify changes seen in cecal populations.

Key Words: broiler, necrotic enteritis, microbiota, ileum, cecum