148 RNASeq analysis of the liver transcriptome of heat-stressed broilers. D. J. Coble1, D. Fleming1, C. J. Schmidt2, M. F. Rothschild3, M. E. Persia1, C. M. Ashwell1, and S. J. Lamont1, 1Iowa State University, Ames, 2University of Delaware, Newark, 3North Carolina State University, Raleigh.

In broilers, heat stress results in reduced feed intake, digestion inefficiency, impaired metabolism, and death. Our objective was to initiate a study on the effects of heat stress by profiling the transcriptome of a metabolically active organ, the liver, from heat-stressed and non-heat-stressed broilers. From 21 to 28 d of age, heat-stressed broilers were exposed to daily 7-h cycles of 35°C, while a control group was kept at 25°C throughout this time. Body weight, body temperature, and several blood parameters were measured before the first heat episode began and at the midpoint of the last heat cycle on d 28. Then, liver samples were harvested from 5 sets of full-sibs, with one bird of each pair from the heat-stress treatment and one from the control group. As expected from the small sample size and standard error of the traits, the phenotypes of the birds did not differ significantly (P > 0.05) between the 2 heat treatments. However, 3 traits associated with respiration (HCO3, pCO2, tCO2) differed between heat treatments at 0.08 < P < 0.12, strongly suggesting different physiological responses to heat. This observation was in agreement with the marked panting observed only in the heat-stressed birds during the heat episodes. Ribonucleic acid (mRNA) isolated from the liver samples was used for Illumina Hi-Seq 2000 sequencing. Over 130,000,000 reads, averaging 100 base pairs each, were generated, yielding an average of 1.6 billion bp sequenced per individual bird’s transcriptome. We conclude that the heat-stress treatment was an effective experimental model to generate heat-induced physiological changes, and that high-quality transcriptomic data have been generated to initiate the process of identifying the impact of heat on the liver’s metabolic function. Continuation of this research will help clarify the effects of heat stress on broiler metabolism and thus provide a platform for future investigations into the application of breeding strategies for production of commercial broilers resilient to heat stress.

Key Words: broiler, heat stress, metabolism, transcriptome, liver

149 Establish overexpressed and knock-down IRF7 chicken HD11 cell line using PiggyBac transposon system. T. H. Kim* and H. Zhou, Department of Animal Science, University of California, Davis.

Interferon regulatory factor 7 (IRF7), a member of the interferon regulatory transcription factor family, is a crucial regulator of type I interferons (IFN) against pathogenic infections in the Toll-like receptor signaling pathway. The qRT-PCR results revealed that IRF7 was only expressed in immune-related tissues including spleen, bursa and intestine. A better understanding of host immune response to pathogen infection in chickens will generate new insights in enhancing animal health and food safety using marker assisted selection in disease resistance. Stable overexpression or knock-down cell line provides a powerful tool in elucidating the role of IRF7 in the host-pathogen interaction. The objective of this study was to generate IRF7 overexpressed DF-1 and HD11 cell lines and IRF7 knock-down chicken HD11 cell line using PiggyBac transposon system. IRF7 full-length coding sequence obtained from cDNA and 3 miR RNAi constructs targeting IRF7 used for overexpression and knock-down, respectively, were cloned into PiggyBac transposon expression vector that has GFP and Puro dual selection markers. Overexpression or knock-down vector were co-transfected with transient PiggyBac transposase expression vector into HD11 cells using Lipofectamine 2000 reagent followed by one-week puromycin selection, stably integrated GFP positive and Puromycin resistant cell lines were established. As a result of IRF7 overexpression, mRNA expression of type I IFN (IFNa, IFNb) were restored in the overexpressed DF-1 cell line, whereas they were not expressed in the control DF-1 cell line. Establishment of stable overexpressed cell line has laid a solid foundation in further determining the role of IRF7 in the toll-like signaling pathway and host immune response to pathogen infection in the chicken.

Key Words: IRF7, PiggyBac, overexpression, HD11 cell line, immune response

150 Genetic polymorphism among Cairo B-2 and random bred control lines as detected by protein, RAPD, and SSR analyses. R. E. A. Moghaieb*2, F. S. Nassar1, A. M. Abdou1, and F. K. R. Stino1, 1Department of Animal Production, Cairo University, Giza, Egypt, 2Department of Genetics, Faculty of Agriculture, Cairo University, Giza, Egypt.

RAPD, Microsatellite (MS), and protein markers were used to characterize the genetic diversity among the local broiler breeder female line (Cairo B-2 line) that has been selected for increasing 6 week live body weight (LBW) and the Random Bred Control (RBC) line. DNA samples, collected from individuals of both lines, were subjected to PCR analysis using 10 RAPD random primers and 7 microsatellites markers associated with meat production for both lines. All primers used in the present study resulted in the appearance of PCR products with a variable number of bands. Protein was extracted from breast meat of each line and subjected to SDS-PAGE electrophoresis. The genetic similarities between the 2 lines tested were estimated by calculating band sharing. According to our results, it was possible to distinguish between Cairo B-2 and RBC lines. The results indicated that a total of 200 and 196 RAPD markers were detected for Cairo B-2 and the RBC lines respectively. The genetic polymorphism detected from this study was 79% and 88.7% for Cairo B-2 and the RBC lines respectively. Also, the results indicated that Cairo B-2 line had more alleles than the RBC line for the MS: MWC0018, ADL0328 and ROS0025. Also, concentrations and numbers of protein bands in Cairo B-2 line were the highest in comparison to the RBC line. The genotype specific RAPD, MS, and protein marker for Cairo B-2 and RBC lines were detected and can be used as a useful genetic markers that can be used in future breeding program aiming to improve the performance of Cairo B-2 line.

Key Words: broiler, breeder, microsatellite, genetic diversity, genetic marker

151 Re-annotation of chicken genome using RNA-seq data. H. I. Zhou*, Y. Wang1, S. J. Lamont2, and P. Ross1, 1University of California, Davis, 2Iowa State University, Ames.

Genome annotation is critical for conducting animal genetic research. The current chicken gene annotations are primarily based on computationally predicted models and, therefore, contain inaccuracies and omissions. One billion uniquely mapped reads from RNA-Seq experiments from 26 chicken lung and trachea tissues from Leghorn and Fayoumi chicken lines were used to re-annotate the current Ensembl version of the chicken genome. These data sets were from 100bp pair-end reads generated using Illumina HiSeq2000 sequencer. We used the CLC...
Bio Genomic Workbench Large Gap Mapping and Transcript Discovery algorithms to generate an annotation that combines the Gallus WASHUC_2 annotation with that derived from the RNA-seq sequences. Using this approach, we found 2,737 novel genes that were not included in the Ensembl annotation, for which the average of 945 chicken reads per gene substantiated these potentially new transcribed regions of the chicken genome. Also, 40,505 alternative transcripts were identified for already annotated genes, adding on average 2.3 new transcripts per gene. The 3′ and 5′ sequences were extended for 12,820 and 13,954 genes, already annotated genes, adding on average 2.3 new transcripts per gene.

In the RBC lines, differences in BWSM, EN, and EW in comparison to the RBC line for all generations. Heritabilities, genetic and phenotypic correlations between all of these economic traits were also calculated. Our results indicated that the average 6 week LBW of Cairo B-2 and RBC lines were 1085 g vs. 700 g in the 7th generation. Also, females of Cairo-B-2 line had significantly higher BWSM, EN, and EW in comparison to the RBC line for all generations. Also, Cairo-B-2 line showed higher heritabilities for 6 week LBW in comparison to the RBC line for all generations. Heritabilities for 6 week LBW, using dam plus sire components, for Cairo-B-2 line and the RBC line, were 0.44 vs. 0.29 in the 7th generation. Also, Cairo-B-2 line had higher heritabilities for BWSM, EN, and EW in comparison to the RBC line for all generations studied. The genetic correlations between LBW at 6 weeks of age and BWSM ranged from 0.27 to 0.33 for Cairo-B-2 and from 0.22 to 0.23 for the RBC lines. If these improvements, in LBW, of Cairo-B-2 line will continue at the same rate, we can expect that after several generations of selection, Cairo-B-2 line can be a very good commercial local female broiler line.

**Key Words:** chicken genome, RNA-SEQ, re-annotation, bioinformatics

**152 Effects of selection on body weight, productive performance, and genetic measurements in Cairo B-2 line.** F. S. Nassar*,†, R. E. A. Moghaieb‡, A. M. Abdou‡, and F. K. R. Stimo‡, †Department of Animal Production, Cairo University, Giza, Egypt; ‡Department of Genetics, Cairo University, Giza, Egypt.

An experiment was conducted to evaluate the effect of selection on production performance of the Cairo B-2 line, at the 4th, 5th, 6th, and 7th generations of selection. A Random Bred Control (RBC) line was used as control for all generations. The performance during the 4th, 5th, 6th, and 7th generation was evaluated in the Cairo B-2 and RBC lines for live body weight (LBW), body weight at sexual maturity (BWSM), age at sexual maturity (ASM), egg number (EN), and egg weight (EW) over the first 36-weeks of age. Heritabilities, genetic and phenotypic correlations between all of these economic traits were also calculated. Our results indicated that the average 6 week LBW of Cairo-B-2 and RBC lines were 1085 g vs. 700 g in the 7th generation. Also, females of Cairo-B-2 line had significantly higher BWSM, EN, and EW in comparison to the RBC line for all generations. Also, Cairo-B-2 line showed higher heritabilities for 6 week LBW in comparison to the RBC line for all generations. Heritabilities for 6 week LBW, using dam plus sire components, for Cairo-B-2 line and the RBC line, were 0.44 vs. 0.29 in the 7th generation. Also, Cairo-B-2 line had higher heritabilities for BWSM, EN, and EW in comparison to the RBC line for all generations studied. The genetic correlations between LBW at 6 weeks of age and BWSM ranged from 0.27 to 0.33 for Cairo-B-2 and from 0.22 to 0.23 for the RBC lines. If these improvements, in LBW, of Cairo-B-2 line will continue at the same rate, we can expect that after several generations of selection, Cairo-B-2 line can be a very good commercial local female broiler line.

**Key Words:** broiler, breeder, productive, heritability, genetic correlation

**153 Genetic analysis of production and feed efficiency traits in an Orloff turkey line (Meleagris gallopavo).** O. W. Willems*,†, S. P. Miller‡, N. J. H. Buddiger‡, and B. J. Wood†,‡, †University of Guelph, Guelph, ON, Canada; ‡Hybrid Turkeys, Kitchener, ON, Canada.

Assessing production and feed efficiency traits in each line of turkeys at the pedigree level is an important step in determining the breeding goals and future potential of the line in a long-term development plan. In female lines, the focus is on mixture of body weight, feed efficiency traits, such as feed conversion ratio (FCR), egg production and fertility traits. Means and heritabilities for body weight at 10 and 18 weeks of age (BW10, BW18), breast conformation score, average egg weight, fertility, hatch of fertile and total egg production were determined and shown in Table 1. Feed efficiency information was available on 271 toms, where each individual bird was measured for feed intake and body weight gain over a 4-week period, from 16 to 20 weeks of age, during which they had ad libitum access to feed and water. Moderate heritabilities were found for feed intake and body weight gain (0.25 to 0.31) with standard errors (SE) also shown in Table 1. Average feed conversion ratio was 3.14, with heritability of 0.10. Body weight, breast conformation score and egg production traits showed moderate heritabilities (0.22 to 0.52), while fertility traits were low (0.04 and 0.09). Genetic correlations between breast conformation score, BW10 and BW18 were moderate, 0.50 and 0.45, respectively. Average egg weight also showed moderate genetic correlations with BW10 and BW18 (0.59 and 0.42).

**Key Words:** turkey, feed efficiency, egg production, fertility trait

**154 Whole-genome sequencing of ascites resistant and susceptible lines of broilers.** K. Rowland*, A. Alban, N. B. Anthony, and B. W. Kong, University of Arkansas, Fayetteville.

Poultry is a key organism in genetic research due to breeding feasibility, relatively short generation period, and distinct phenotypes. It is estimated that 8% of broiler deaths annually can be attributed to ascites, an economically important disease that has been challenging the industry for the past 2 decades. Genetically selected ascites resistant (RES) and susceptible (SUS) chicken lines have been established and maintained by the University of Arkansas, Fayetteville. Intensive research efforts have been made to reveal physiological and biochemical characteristics for the incidence of ascites. Since the whole genome of the major ancestral chicken, the Red Jungle Fowl, has been sequenced, genome-wide genetic study is now possible in chickens to identify genetic variations throughout the entire genome. To identify genetic biomarkers responsible for ascites resistance or susceptibility, whole genome sequences of genetically selected chicken lines (RES and SUS) in addition to the unselected parental Relaxed line (REL) were analyzed using the Illumina platform of next generation sequencing techniques and bioinformatics tools. Over 4 million SNPs were identified in each line and over 95% of SNPs were found in the intergenic regions. In the protein coding regions (CDS), SNPs that generated synonymous, non-synonymous, frameshift, non-sense, no start, and no stop mutations were 69.3%, 29.3%, 1%, 0.3%, 0.07% and 0.03%, respectively. Eight of the most reliable SNPs were chosen by the following parameters: over 75% SNP rate, over 10 depth (read counts of contig), and verified in the larger number (96) of birds for each line using PCR and Sanger sequencing. Hence, most reliable SNPs identified in this study can be utilized as genetic biomarkers to detect ascites resistance or susceptibility.

**Key Words:** whole-genome sequencing, ascites, SNP