Carcass yield of Saudi chicken breeds raised under high ambient temperature. M. M. Fathi*, M. O. Fahmy, I. Al-Homidan, O. K. Abou-Emara, and A. Al-Homod, Department of Animal Production and Breeding, Qassim University, Al-Qassim, Saudi Arabia.

Key Words: Saudi chicken, carcass quality, high temperature

Genetics

Identifying polymorphism of single nucleotide polymorphisms located at NK-lysin in Saudi native chicken strains. M. M. Fathi*,1 H. A. Yacoub2, O. Fahmy1, and I. Al-Homidan1, 1Dept. of Animal Production and Breeding, Qassim University, Buraidah, Al-Qassim, Saudi Arabia, 2Department of Biological Sciences, King Abdul Aziz University, Jeddah, Saudi Arabia.

Key Words: chicken, NK-lysin, polymorphism

Withdrawn

Parent stocks (PS) of exotic hybrids have contributed immensely to commercial poultry production in Nigeria. The growth, reproductive performance, and seasonal sensitivity of Bovan Nera (BN) and ISA Brown (IB) hybrids were evaluated. Secondary data on 24 batches of PS of each of BN and IB kept over a period of 10 yr (1999–2008) in Ajanla Farms, Ibadan were used. Average batch population was 3,896 pullets and 600 cockerels at point-of-lay. Records on body weight (BW), age, hen-day-production (HDP), egg weight (EWt), egg fertility (EF), egg hatchability (EH), pullet day-old chicks produced (PDOC) and hatching rejects (HR) in 4 seasons: early-wet (EW, April–July); late-wet (LW, August–October); early-dry (ED, November–January) and late-dry (LD, February–March) were obtained. Data were standardized and analyzed for growth, age-at-first-egg (AFE), HDP characteristics, reproduction, seasonal sensitivity, genotype-season interaction using descriptive statistics, ANOVA, correlation and regression (P = 0.05). Effect of seasons on AFE was not significant in both hybrids, but ED and LD seasons delayed AFE. The HDP values (%) recorded for BN (63.2) and IB (72.9) in ED were significantly higher than in other seasons. There were significant differences in EF (80.8 and 88.7%), EH (69.1 and 73.6%), PDOC (32.6 and 36.1%) and EWt (56.2 and 59.9 g) for BN and IB respectively in EW season. EF (86.2 and 89.5%) and EH (73.1 and 73.9%) in LW were highest within hybrids respectively. Phenotypic correlation (r) between Age and Hen Weight, Age and EWt, Hen Weight and EWt, EF and EH, EF and PDOC, and EH and PDOC were 0.78, 0.74, 0.68, 0.73, 0.72 and 0.98 in BN; and 0.77, 0.52, 0.53, 0.69, 0.71, and 0.97 in IB respectively. The positive and significant correlation between HR and EWt (r = 0.14 and 0.13), for BN and IB respectively, indicated increase in HR as EWt increased. Predictions of BW by Age (R2 = 0.85, 0.84), EWt by Age in-production (R2 = 0.65, 0.65), and PDOC by EH (R2 = 0.99, 0.95) in both hybrids were significant at 25–75 weeks. HDP, EF, EH, PDOC were higher in IB than BN during the early-dry season.

Key Words: chicken growth, exotic, hatching indices, Nigeria, performance depression
Rapid growth has been associated with skeletal integrity and bone quality. We report herein the genetic relationship between growth and leg bone quality traits in a random mating broiler control population. The traits studied were shank length (SL), shank weight (SW), shank diameter (SD), tibia weight (TW), tibia length (TL), tibia diameter (TD), tibia breaking strength (TBS), tibia mineral density (TMD), tibia mineral content (TMC), tibia ash content (TAC) and growth rates from 0 to 4 wk (BWG 0–4) and from 5 to 6 wk of age (BWG 0–6) and residual feed intake from 5 to 6 wk (RFI 5–6). Genetic parameters were estimated by multiple-trait, restricted maximum likelihood (REML) using an animal model. Heritabilities of SW, SL, TD, TW, TL and TD were 0.45, 0.40, 0.14, 0.38, 0.60, and 0.40, respectively. On the other hand, TBS, TMD, TMC, and TAC had heritabilities of 0.22, 0.32, 0.34, and 0.11, respectively. Genetic relationship between growth and most of the bone traits ranged from 0.11 to 0.82. However, the additive genetic association between growth and TBS and TAC was unfavorable ranging from −0.11 to −0.26. Bone quality traits have an additive genetic background and they can be improved by genetic methods. It appears that selection for growth is negatively correlated with bone quality.

Key Words: bone quality, growth, genetics

**315P** Growth curve comparison of growth-selected and non-selected local chickens in Egypt. M. A. Helal* and E. A. El-Gendy, Department of Animal Production, Faculty of Agriculture, Cairo University, Giza, Egypt.

Growth patterns of local chicken strains are different from those of the commercial broiler strains as they differ in their genetic compositions. This study aimed to monitor the changes in the growth patterns of local chickens in Egypt due to selection for 6-week body weight. The chickens were of the normally feathered selected and control lines (CE1 and CE2) and the naked-neck selected and control lines (CE3 and CE4). The chicks of all lines have been raised together from hatch to 18 wk of age. The non-linear growth model of Gompertz was applied to fit the body weight measurements of the 8th selected generation. Growth functions were derived from the average of biweekly body weight from hatch to 18 wk of age. The coefficient of determination (R²) for the models was 0.9965. Lines CE1 and CE3 showed higher initial growth rates and lower ages at the inflection point compared with their corresponding control lines CE2 and CE4. The random-bred lines (CE2 and CE4) showed lower estimates of asymptotic body weights. It can be concluded that selection for high 6-wk body weight in local chickens modified the parameters of their growth curves.

Key Words: body weight, Gompertz model, growth curve, local chicken, selection.


In our previous studies, genomic integration in vitro was remarkably improved by the use of transposon vectors. In this study, we compared 2 types of transposon vectors: Tol2 and PiggyBac for genomic integration efficacy, using EGFP as a reporter. The Tol2 is derived from medaka fish genome and requires 2 plasmid vectors: a transposase expression vector and a cargo vector. The PiggyBac is derived from cabbage looper moth genome and its modified pmhyGENIE-3 is a transposase-cargo complex vector, requiring one plasmid vector for a task. In the study, 4 different methods to transfect plasmid vectors were also compared. These are lipofection, electroporation, lipofection plus electroporation, electroporation plus sonoporation. Chicken embryos at Stage X were transfected with a respective plasmid vector or vectors and by a respective transfection method and cultured through Day 6.5 ex ovo to excise embryonic gonads and mesonephros. Gonads and mesonephros were made into frozen sections with the thickness of 10 µm for immunohistochemical staining with SSEA-1 for primordial germ cells and EGFP for the reporter. Cell nuclei were detected with DAPI. With a confocal laser scanning microscope, primordial cells and primordial cells expressing EGFP were counted. Likewise, gonadal epithelial cells and epithelial cells expressing EGFP were counted. The number of primordial germ cells expressing the reporter gene per individual was, with Tol2, 6.33, 3.33, 5.00, and 4.33 cells by lipofection, electroporation, lipofection plus electroporation, and electroporation plus sonoporation, respectively, and was, with PiggyBac, 6.67, 4.67, 10.00 and 4.33 cells by lipofection, electroporation, lipofection plus electroporation, and electroporation plus sonoporation, respectively. In conclusion, transposon vectors are efficacious in chicken transgenesis and the use of pmhyGENIE-3 and transfection by lipofection with electroporation is the most appropriate.

Key Words: genomic integration, transposon, Tol2, PiggyBac, transgenic chicken.
Feather follicles in the dorsal, ventral and lateral tracts of naked neck, frizzled, and normally feathered birds were investigated. Nine birds, 3 from each genotype (nanaff, nanaff, and nanaff) were randomly slaughtered and the numbers of feather follicles in the dorsal, ventral and lateral regions were determined. Each experiment was repeated 3 times. ANOVA was performed using SAS (2012) and differences between separated by PDIF at P < 0.05. There was no significant difference in feather follicles in the dorsal ventral tracts between frizzled and normal feathered birds. However, naked neck genotype had no follicles in these tracts. The frizzled genotype had a significantly reduced number of follicles and the dorsal ventral region compared with the normal feathered. The frizzle genotype had a significantly higher follicles numbers in the dorsal ventral region compared with the naked neck. In the ventral region, the naked neck had a significant reduction in the number of follicles at ventral cervical tract, pectoral tract, sternal tract and the medial abdominal tract. There were no feather follicles in the ventral cervical aterium and the cloacal circllet. The frizzle had lower follicle numbers compared with the normal feathered counterpart at pectoral tract, medial abdominal tract and the cloacal circllet. In the lateral region, the naked neck genotype had a reduced number of follicles in the lateral body tracts compared with the frizzle and normal feathered genotypes. The naked neck and frizzled genotypes have their feather follicles reduced in the regions studied and this could form the basis for the enhanced heat dissipation in naked neck and frizzle birds under high ambient temperatures which results in increased productivity among these birds under tropical conditions as they do not become stressed under high ambient temperatures.

Key Words: pterylosis, feather follicles, feather tracts, genotype, dorsal

Estimation of genetic and phenotypic parameters for internal egg quality traits of Azerbaijan native chickens. M. Ranjar, S. Alijani*, S. A. Mirghelenj, and H. Daghighkia, Department of Animal Science, Faculty of Agriculture, University of Tabriz, Tabriz, Iran.

For the first time, an experiment was conducted to estimate of heritability, genetic and phenotypic correlations among internal egg quality traits of Azerbaijan native fowls. The data set that was used in this study included the records that collected in West Azerbaijan province’s native fowl breeding center and agriculture central laboratory complex of university of Tabriz. Statistical models for all traits were fitted using GLM procedure of SAS software. The probabilities of major genes segregation were separately studied in all investigated traits under a univariate animal model using Bayesian analysis and major gene index (MGI) procedure. The major gene index calculated using outputs from univariate animal model. Segregation of major genes was confirmed for internal egg quality traits including yolk width, yolk height, albumen pH, yolk weight to albumen weight ratio, yolk index, yolk and albumen percentages and finally for yolk and albumen dry matter values in Azerbaijan native fowls. Given that major gene segregation was confirmed for internal egg quality traits, it is concluded that molecular techniques can be successfully used to map the related major genes in Azerbaijan native fowl.

Key Words: major gene segregation, major gene index, Azerbaijan native fowl, molecular techniques

Genome resequencing for genetically selected chicken lines for progression and regression of Rous sarcoma virus induced tumors. B. W. Kong*, A. M. Hayden, G. F. Erf, and N. B. Anthony, University of Arkansas, Fayetteville, AR.

The Rous sarcoma Arkansas Progressor (AP) and Regressor (AR) lines, which are characterized by terminal progression or successful regression of Rous sarcoma virus induced tumors, were developed from White Leghorn and Giant Jungle Fowl strains. AP vs AR lines of chickens are important experimental models of disease susceptibility and resistance to pathogens in the commercial poultry industry. The identification of genome-wide genetic differences between AP and AR lines will provide insights into understanding the genetics of disease susceptible/resistant phenotypes. Whole-genome resequencing analysis was performed in AP and AR chickens with confirmed tumor progression and regression, respectively. Illumina sequencing technology and reference based assembly on Red Jungle Fowl genome sequences were used. Results of genome resequencing of pooled DNA of each 10 AP and AR chickens reached 4.9× and 4.4× coverage, respectively, of the Red Jungle Fowl reference chicken genome. Millions of SNPs were identified and only potentially causal genes containing non-synonymous mutations, which can induce amino acid changes, were focused on in this study. In total, 7,470 SNP including 4,256 for AP and 3,214 for AR showing >75% SNP rates could induce non-synonymous mutations. Of those, SNP showing over 10 read depths yielded 172 more reliable SNP including 140 for AP and 32 for AR. Bioinformatic analysis using Ingenuity Pathway Analysis for the 32 genes responsible for tumor regression in the AR line chickens revealed that 11 genes (ARHGA10, BANK1, BMX, CADM1, DNA2, LRP3, NUP210, PIK3R4, RPGR, SACS, SI)
contained amino acid changes associated with cancer. Gene network analysis revealed that genes including \textit{ITPR1P, THADA, PIK3R4, CADM1, NUP210, DNA2, SACS, BMX, and ARHGAP10} are associated with ubiquitinylation. In this study, various potential genetic biomarkers showing amino acid changes were identified in Rous sarcoma tumor development through genome resequencing. This work was supported by funds from the Arkansas Biosciences Institute-Agriculture and the Arkansas Agricultural Experimental Station.

**Key Words:** SNP, Rous sarcoma virus induced tumor, Arkansas Progressor, Arkansas Regressor, whole-genome sequencing

321P Genetic manipulation of neural crest cells using the PiggyBac transposon, Talen, and Crispr/Cas systems. J. A. Payne* and R. B. Beckstead, University of Georgia, Athens, GA.

Traditionally, the chicken has been a well-established model for the study of developmental biology with advantages such as a relatively small genome, a short generation interval, and the ability to easily access and manipulate the embryo in ovo. Studies in the chicken have led to advances in the understanding of neurogenesis, somite development and formation, and limb development. However, due to physiological differences from other species, the use of the chicken as a model organism has fallen behind in the areas of transgenic technology and molecular approaches. Consequently, the chicken has been replaced in basic research by other model organisms such as mice and zebrafish. There is a need to adapt molecular techniques for use in the chicken model system. Along with others, our laboratory has shown that transposable elements can be used to stably modify the chicken genome. Here we present the use of the PiggyBac transposon system in conjunction with electroporation to stably transfect and label neural crest cells with an expressed green fluorescent protein. Using this technique, we were able to follow the migration of those cells and to mark the tissues into which they differentiate. This demonstrates the ability to employ the PiggyBac system to express exogenous genes in these cells. To validate additional methods for genetic modification, we have adapted the Talen and Crispr/Cas systems to function within the neural crest cells. These molecular tools allow for targeted gene disruption. We have generated and are testing constructs that produce deletions within the tyrosinase gene, resulting in loss of pigmentation in the feather. This research will be advantageous to future studies for 2 reasons. First, through small changes to the PiggyBac system we will be able to stably label and follow specific gene expression in differentiated neural crest cells throughout the life of the chicken; and, second, new means by which gene knockouts can be produced in the chicken genome will enable further study of gene function and regulation.

**Key Words:** PiggyBac, transposon, electroporation, transgenic, gene disruption

322P Haplotype structure and variation of telomerase reverse transcriptase (turTERT) gene in turkeys (\textit{Meleagris gallopavo}). A. M. Adikari, T. Pleasant*, J. Xu, and E. Smith, Virginia Tech, Blacksburg, VA.

In humans and other animals, some mutations in the telomerase reverse transcriptase (TERT) gene cause a malfunction of the telomerase and telomere shortening. This often may result in age-related diseases. Here we investigated the distribution of SNPs and the resulting haplotypes identified in the turkey TERT gene. A total DNA sequence of 28 kb including the \textit{turTERT} gene was screened and the DNA variation was assessed using heritage, commercial and wild turkeys. Linkage disequilibrium among the SNP ranged from 0.46 to 1.00. A total of 15 haplotypes were identified and assembled into 4 haplogroups. The estimated frequencies of the haplogroups ranged from 0.10 to 0.38 in the turkeys. The most frequent haplogroup occurred at a frequency of 0.38. The Royal Palm had a unique haplogroup, turTERT Hap1, and was missing a haplogroup, turTERT Hap4, that was common to all the other populations. Most of wild turkeys were laid within the haplogroup of turTERT Hap3. The haplotype groupings suggest that the Royal Palm may have a unique genetic background distinct from other turkey varieties. Taken together with earlier studies, a case can be made that the Royal Palm is probably a breed while the others are varieties consistent with classic definitions.

**Key Words:** turkey, telomerase reverse transcriptase, haplogroup, diversity panel