

days, 193-293 days, 283-383 days, 376-476 days, 467-567 days, 551-651 days and 633-733 days, respectively. Two sample data sets with all known ancestors with genetic ties were created. The number of animals from all herds was 18,889 and 16,161 from herds with no missing traits. Records preadjusted to fixed age were analyzed by a multiple trait model, which included the effects of contemporary group, class of age of dam, and direct, maternal and permanent environmental effects. Analyses by REML were conducted five traits at a time, and analyses by the Bayesian method using block Gibbs sampling involved all nine traits. For REML and the first data set, the range of estimated direct genetic correlations for each pair of traits was 0.43 to 0.99, with higher values between weights at higher ages. Direct heritability varied from 0.17 to 0.33, and was highest for weight at 551-651 days; however, ma-

ternal and permanent environmental variance decreased after an age of 193-293 days. Additive and residual estimated variance increased from birth weight through weight at 551-651 days, however maternal and permanent environmental variance decreased after age of 193-293 days. Heritabilities with the complete data set were slightly lower. With the Bayesian method, chain length of 50,000 was insufficient to obtain consistent maternal and permanent environment estimates, especially for weights over 476 days. This is most likely due to extreme correlations between these traits. The parameter estimates will be used to validate parameter estimates obtained from random regression models.

Key Words: Beef cattle , Covariance components, Longitudinal data

PSA Genetics

1423 Influence of genetics on phytate phosphorus utilization by chickens. T. N. Smith, S. E. Aggrey*, R. I. Bakalli, and G. M. Pesti, *University of Georgia*.

An experiment was conducted to determine whether there is a genetic basis for selection for phytate phosphorus (P) utilization in chickens. Fifty-eight Athens-Canadian random bred chickens were fed a phosphorus deficient diet and the phytate P levels in their excreta was determined by Near Infra-red Spectrophotometry. Five roosters categorized as High sire excreta phytate P (SEPP) (1.17 ± 0.002) and Low SEPP (1.09 ± 0.002) were selected to sire progeny. The SEPP values were significantly different ($P < 0.0001$) between the two sire groups. One hundred and seventy chicks from Low SEPP and 180 chicks from the High SEPP were hatched and fed a P deficient diet (.53% P). The chicks were sacrificed at 16 d by carbon dioxide asphyxiation and body weight (BWT) was recorded. The left tibia were collected for ash determination on a fat-free basis. There was a negative correlation ($r = -0.15$; $P = 0.0053$) between sire excreta phytate P and 16 d BWT. The correlation between SEPP and tibia ash was also negative but not significant ($r = -0.01$; $P > 0.05$). Progeny from Low SEPP had higher BWT (152.7 ± 1.5 g) than progeny from High SEPP (146.8 ± 1.4 g) ($P = 0.0042$). Similarly, progeny from Low SEPP had higher tibia ash ($36.57 \pm 0.31\%$) than progeny from High SEPP ($35.55 \pm 0.03\%$) ($P = 0.0187$). This implies that sires that excrete low phytate P, that is, those that are better able to utilize phytate P, produced progeny that were significantly heavier at d 16 and had better bone mineralization than progeny sired by poor phytate P utilizers.

Key Words: Broilers, Phytase, Phosphorus

1424 Inheritance of Alkaline Phosphates in Local Iraqi Chicken and its association with Production. Ali Al-Hillali¹ and Khalid Al-Soudi*², ¹*Iraqi Atomic Energy Commission, Baghdad, Iraq*, ²*Animal Production Department, Agriculture College, Baghdad University, Baghdad, Iraq*.

Ninety eight dams and twenty one sires representing the parent stock of local Iraqi chickens, and their progeny (305 pullets) were typed for alkaline phosphates isozymes and activity in order to assess the effect of sex, age and genotype. Genetic analysis revealed three types of electrophoretic isozymes, namely fast, slow and a mixture of a fast and slow band. Gene frequencies of the fast band were 0.41 and 0.39 and that for the slow band were 0.59 and 0.61 for dams and progeny flocks, respectively. Furthermore, age, sex and type of enzyme were found to have significant effects on enzyme activity, and birds of fast isozyme type had higher egg weight, lower age at sexual maturity and higher body weight at sexual maturity. Heritabilities of plasma alkaline phosphatase at different ages and economic traits ranged from moderate to high. Phenotypic, genotypic and environmental correlations between level of plasma alkaline phosphatase and growth rate and production characters indicated that the high activity of alkaline phosphatase was associated with higher growth rate at early stages, earlier sexual maturity and production of heavier but fewer eggs. Genetic and phenotypic correlations among enzyme activities at three ages were positive and high and expected genetic response after one generation of individual selection for alkaline phosphatase activity leads to improved production characters.

Key Words: Alkaline phosphates, Electrophoresis, Enzymes

1425 Multisource Multitrait Selection Indices For Genetic Improvement In Poultry Breeding Programs For Laying Hens. 2. Construction And Evaluation Of Various Indices. A. A. Enab¹, N. Kolstad², and F.H. Abdou¹, ¹*Fac. Of Agric., Minufyia Univ., Shebin El-Kom, EGYPT*, ²*Agricultural Univ. Of Norway*.

Records on 11689 pullets progeny of 326 sires and 1546 dams produced in two hatches of four strains of White Leghorn hens raised under Norwegian conditions were utilized to construct and evaluate general, reduced and restricted selection indices. Eight indices were constructed using five traits and three sources of information for each trait in different combinations. The studied traits were age at sexual maturity (SM); egg number up to 260 days of age (EN); egg weight (EW); body weight (BW) and egg specific gravity (SG). The sources of information used in different combinations for each trait were individual's own phenotypic value (OP) and its full (FS) and half sister's (HS) average. It was noticed that the female general index which included all of the five traits and all of the three sources of information was found to be the most efficient index ($r_{TI} = 0.76, 0.65, 0.69$ and 0.61) in the four lines, respectively. The general index for males which included only two sources of information (FS&HS) for each of the five traits was found to be less efficient ($r_{TI} = 0.60, 0.54, 0.55$ and 0.51) in the four lines, respectively. The restricted index for both EW&BW in line 1 was the lowest efficient index ($r_{TI} = 0.50$). Expected and actual genetic progress (G) achieved in each trait was also maximum for female general index, for most traits in the four lines. It was noticed that the multisource index considering all of the five traits was superior to the multisource index involving only three or four traits. It was concluded that an index based on five traits and three sources of information could be applied to improve egg production and specific gravity traits.

Key Words: Genetic improvement, Multisource selection indices, Layers.

1426 A comparative genomic approach to identify-QTL's for growth in chickens. J. Funk-Keenan and G. F. Barbato, *The Pennsylvania State University, University Park, PA*.

It has long been surmised that different genes must influence different aspects of the growth curve. Unsurprisingly, different sets of QTLs influencing either early or late growth have been identified in mice and pigs. Using data from Vaughn et al (2000), we performed a modified candidate gene approach to identify QTLs influencing early growth in an F2 cross of chickens divergently selected for 14-day exponential growth rate (EGR). By aligning the mouse QTL's with the murine physical map; we targeted QTL's having syntenous genes in both the mouse and chicken genome. We selected the three to five microsatellite markers from the chicken linkage map based on their proximity to the locations of the murine syntenous genes in the chicken genome. Twenty-four microsatellite markers corresponding to six murine QTL's on six chicken chromosomes (1,3,4,5,6 and Z) were targeted for investigation. We chose the top and bottom 3% of chicks from the 14-day EGR distribution from the F2 cross. We then tested whether the microsatellite marker allele frequencies differed between the two tails of the distribution. Of the twenty-four microsatellite markers genotyped, eight markers (representing 5 putative QTL's) exhibited significantly different marker allele frequencies between birds having high or low 14-day EGR. The significant markers were located on chicken chromosomes 3,4,5,6 and Z. Notably, the putative QTL located on chromosome 4 is located at 148cM,

corresponding to a previously identified QTL for feed intake in chickens! These data support our hypothesis that the genetic architecture of growth is highly conserved across species and provides us with an opportunity to pursue QTL's that may have common mechanisms among most domestic animal species.

Key Words: Genetics, Growth, QTL

1427 Preliminary mapping of a gene affecting male fertility in the chicken. K Song*¹, F.G. Sizemore III², J.D. Kirby¹, and D.D. Rhoads¹, ¹University of Arkansas, Fayetteville, AR, ²USDA-Avian Disease and Oncology Lab, East Lansing, MI.

SDD is a dominant gene effecting degeneration of the ductules leading from the testis which results in defects in excurrent sperm maturation and thus production of degenerate, immotile sperm in a line of Delaware chickens (Froman, and Bernier. Biol. Reprod. 37:969-977, 1987; Kirby, Bernier, and Froman. Jr. Androl. 11:49, 1990). We used RAPD and bulked segregant analysis to identify a 1500 bp PCR product which appears linked to SDD. This PCR product was used to isolate a single BAC comprising approximately 100 kbp from a Jungle Fowl library (Dodgson). A single, polymorphic, simple sequence repeat was characterized from this BAC clone and was used to screen the East Lansing backcross mapping population. The repeat maps this BAC, and thus the 1500 bp product, to linkage group E41 on the East Lansing map. Based on gene order this linkage group appears syntenic with a region on the long arm of human chromosome 9. We are currently using additional microsatellites from this linkage group to more accurately position SDD on the chicken genomic map. Since most, if not all, of the genes in this region can be identified from the human sequence this should greatly speed isolation of the gene and molecular characterization of the defects responsible for the SDD phenotype. Although SDD was identified in the Delaware line it is likely that other alleles of the SDD gene affect male fertility in commercial poultry lines. Characterization of the SDD gene is of great importance in improving male fertility in the poultry breeding industry and the SDD gene should have homologs which affect testis development and fertility in humans and other species.

Key Words: fertility, male, sperm, gene mapping

1428 Zona pellucida 3 protein (ZP3) and gene (ZPC) expression in the turkey, *Meleagris gallopavo*. M. L. Block*¹, K. E. Nestor², and G. F. Barbato, ¹The Pennsylvania State University, University Park, PA, ²The Ohio State University, Wooster, OH.

The purpose of the following study was to characterize the protein expression of the turkey zona pellucida 3 protein (tZP3) and establish the cDNA sequence for tZP3 (tZPC). Six female turkeys from 2 genetic lines: F line and RBC line were used in this experiment. Using antibodies developed to specific amino acid sequences from chicken ZP3 (chZP3), western blot analysis of the perivitelline membranes (PVM) of laid turkey eggs revealed an immunoreactive band with the molecular mass of approximately 45 kD – which is larger than the 42kD chZP3 protein. Western blots of turkey tissue (liver, ovary, infundibulum, granulosa cells, and uterus) confirmed the presence of the tZP3 protein in granulosa cells, ovary and, unexpectedly, in the infundibulum. Further, not all subjects tested showed ZPC protein expression in the ovary and infundibulum. Turkey ZPC cDNA sequences were obtained by rtPCR using primers sets designed from chZPC. Sequence analysis of tZPC revealed high homology of the carboxy-terminus and the mid-portion of tZPC with both chZPC and qZPC (Japanese quail). Results from rt-PCR analysis in turkey tissues (liver, ovary, infundibulum, granulosa cells, and uterus) revealed tZPC mRNA expression in both granulosa cells and the ovary, but not the infundibulum. Together, these data suggest that expression of tZP3 may be temporally regulated in different tissues, perhaps related to hormonal cycling.

Key Words: Genetics, Turkey, Zona pellucida

1429 Molecular characterization of a partial inverted repetitive (PIR) DNA family in the chicken genome. Juan Li, Xiaofei Wang, and Frederick Leung*, University of Hong Kong.

Tandem array repetitive sequences constitute a major component of the eukaryotic genome. Although the general characteristics of the tandem

repeats have been well characterized, the process involved in their origin and maintenance remain unknown. Chicken Partially Inverted Repetitive (PIR) DNA is a novel repetitive DNA family first characterized by our laboratory. With the basic repeat unit of 1.43Kb, it is characterized as tandem array pattern and located on chromosome 8. The central core of the repeat unit consists of 814bp showing 65% homology with w chromosome XhoI/EcoRI repeats. Sequence analyses show that they share the similar characteristics: (A)₃₋₄ and (T)₃₋₅ clusters are separated by 6-7 nucleotides. Such arrangement enables the A and T clusters to appear alternatively at every pitch of the DNA double helix. Hence, they behave as bent molecules in solution affecting the mobility of the repeat unit in the PAGE running slower as compared to its mobility in the agarose gel. Tandem array pattern of repetitive family in the genome is largely due to the unequal exchange happening within homologue chromosomes and sister chromatids. From sequence analyses, we have characterized an 86bp fragment unit flanking the central core in the inverted direction. Detailed sequence analyses further show high frequency of this inverted structure within this repetitive family. Our results indicate that other forces may be involved in the formation of higher organization region of the PIR family. Junction region analyses show that this inverted fragment often associated tandem array repetitive sequence with the non-tandem array repetitive sequence. Such arrangement indicates that the inverted structure may function as the recognition site during the evolution of this repetitive DNA family in the chicken genome. In addition, we observed polymorphism within different populations of domestic gallus gallus species indicating that PIR family is evolving fast. In conclusion, chicken genome may serve as an experimental model for the study of the origin and dynamics of repetitive DNA.

Key Words: Chicken, Repetitive sequence, Inverted structure

1430 The temporal expression of the Myogenic Regulatory Factor genes during proliferation and differentiation of satellite cells derived from chicken *Biceps femoris* and *Pectoralis major* muscles. A Sarver, J Richter*, H Kocamis, S Gahr, and J Killefer, ¹West Virginia University, Morgantown, WV, 26506.

Satellite cells are responsible for postnatal skeletal muscle growth and repair. In the adult muscle, these mononucleate cells are mitotically quiescent until activated by an external stimuli, such as weight bearing or injury. Once activated, they undergo proliferation, differentiation and fusion into new or existing muscle fibers. Skeletal muscle myogenesis in vertebrates is largely managed by the myogenic regulatory factor gene family (MRF): Myo D, Myf-5, Myogenin, and MRF-4. We investigated the expression pattern of MRFs in chicken satellite cells isolated from *Biceps femoris*(BF) and *Pectoralis major*(PM) from the time of quiescence to the fusion of muscle fibers using reverse-transcription polymerase chain reaction (RT-PCR). There was little expression of any MRFs in the quiescent cell of both BF and PM satellite cells. Myo D was first expressed in both muscle types at 24 hr, corresponding with proliferation. Expression level then increased at 48 hr, remained constant to 96 hr, and began to decrease at 120 hr in both BF and PM cell cultures. Myf-5 displayed a similar expression pattern to Myo D in both BF and PM cell cultures. Myogenin was first expressed at 24 hr in both BF and PM. In BF satellite cells, expression remained relatively constant to 72 hr, and increased at 96 hr, corresponding to differentiation. Expression then decreased during late myotube formation (144 hr). In PM satellite cells, myogenin expression gradually increased from 24-96 hr, and then decreased at 120-144 hr. MRF-4 mRNA was at its highest at 72 hr in PM cell cultures and 144 hr in BF cultures. In PM, MRF-4 expression remained low during proliferation and gradually increased through differentiation (72-144 hr). This correlates with its role as a late differentiating gene. Predicted activities and patterns in the expression of members of the myogenic gene family correlate with satellite cell activation in the chicken.

Key Words: satellite cells, myogenic regulatory factor genes, muscle

1431 Social stress induced different alterations of dopamine concentrations and adrenal function in genetically selected chicken lines. P. Singleton*¹, Y. Chen¹, M.W. Muir², and H.W. Cheng¹, ¹USDA-ARS, Livestock Behavior Research Unit, ²Dept of Animal Science, Purdue University.

Dopamine (DA) and corticosterone (CORT) are involved in regulating animals' response to stress. The objective of this study was to examine whether alterations of DA concentrations and adrenal function are associated with behavioral response to social stress in two strains of White leghorns hens that were selected for high (HGPS) and low (LGPS) group productivity and survivability resulting from cannibalism and flightiness in multiple-hen cages. At 17-wk of age, hens were randomly assigned into single and 2-hen cages. The 2-hen cages contained one hen from HGPS or LGPS line and one from a commercial Dekalb XL line that was used as standardized genetic competitors. At 24-wk of age, seventy hens were bled (10 hens from 3 genetic line, 2 replicates, plus 10 extra testers). Plasma concentrations of DA were measured using HPLC. Changes of the adrenal function were indicated by plasma concentrations of CORT, and hypertrophy of the adrenal gland indicated as a percentage of adrenal gland weight/body weight (AW/BW). In single-hen cages, HGPS hens had heavier adrenal glands indicated as a greater AW/BW ratio ($P < 0.05$). However, LGPS hens tended to have greater plasma concentrations of DA ($P = 0.07$). In 2-hen cages, there were no difference in AW/BW ratio between HGPS and LGPS hens ($P > 0.1$). However, both plasma concentrations of CORT and DA were greater in LGPS hens ($P < 0.05$ and $P < 0.01$, respectively). The results suggest that social stress induced an up regulation of DA and adrenal function in LGPS hens but not in HGPS hens. The data was consistent with the previously findings that HGPS hens adapted better to social competition. Some of the parameters, such as concentrations of DA and CORT, could be used as an indicator of chicken well-being.

Key Words: Social stress, Dopamine and corticosterone, Genetic selection, chickens

ASAS/ADSA Forages and Pastures: Silages, Forage Quality, and Digestion

1433 Effect of wilting and molasses on silage quality of *Leucaena leucocephala*. T. Clavero*¹ and Rosa Razz¹, ¹La Universidad del Zulia.

An experiment was conducted in the dryland farming area of northwest, Venezuela in order to evaluate the ensiling properties of *Leucaena leucocephala* through microsilage techniques. Factors studied were two levels of molasses (0 and 5%) added during ensiling and wilting for 0 and 3h. Statistical analysis was made using a 2x2 factorial arrangement and mean values were compared by Fisher's least significant difference test. Response variables considered were: crude protein (CP), content, ammonia nitrogen as percent of total nitrogen, pH, acetic and lactic acid contents. Addition of molasses increasing ($P < 0.05$) lactic acid content (2.01 vs 7.15%), the crude protein content was about the same (21.8 vs 21.6) whatever the molasses treatment, while reducing ammonia products (2.8 vs 1.9%), pH, (4.7 vs 4.1) and acetic acid (4.8 vs 3.6%). Silages prepared from non-dehydrated forage had higher ($P < 0.05$) CP contents (21.5 vs 20.8%), ammonia products (4.1 vs 2.2%) and acetic acid (5.3 vs 2.6%) and lower pH (4.4 vs 4.7) with less lactic acid (3.5 vs 6.5%). This suggests that combination of molasses and wilting can improve the fermentation quality of *Leucaena leucocephala* silage more than each of them being as a single treatment.

Key Words: *Leucaena leucocephala*, molasses, silage

1434 Prediction of reed canarygrass quality as influenced by N fertilization and maturity. D.J.R. Cherney*, D.R. Dewing, and J.H. Cherney, Cornell University, Ithaca, NY.

The need for more control over forage quality will increase with expanding herd size and increasing individual cow production. Our objective was to develop equations for predicting NDF and CP of first cutting reed canarygrass (*Phalaris arundinacea* L.) using growing degree days base 32°F (GDD32) and Julian date. Previous research has indicated a base temperature of 32°F resulted in better predictions than the 41°F base typically used for forage crops. Pure stands of established reed canarygrass in replicated field plots were fertilized with 0, 56, or 112 Kg of N/ha at the onset of spring growth at four locations in central

1432 MHC and Family Effects of Cellulitis on Lymphocyte proliferation in MHC defined broiler chickens. K. S. Macklin*, R. A. Norton, and S. J. Ewald, Auburn University, Auburn, AL.

Previous work, using avian cellulitis origin *E. coli* isolate (EC-AR1) in broilers demonstrated that the MHC (B type) effects lesion development, specifically that B¹³ was resistant, while B²¹ was susceptible. Other researchers have reported that B¹³ in leghorn chickens has a stronger response than B²¹, when tested with a lymphocyte proliferation assay. The purpose of this study was to use a lymphocyte proliferation assay to: 1. Investigate previously reported leghorn MHC responses in broiler chickens. 2. Use pedigreed matings to determine family effects. 3. Determine proliferation responses in MHC family defined (pre-challenged and challenged) birds to 2.5ug ConA, 1:100 Pokeweed and 1x10⁶ killed *E. coli* (EC-AR1). *E. coli* isolate EC-AR1 has been extensively characterized by this lab in developing two cellulitis models. Matings for the following experiments were designed using B¹³/B²¹ birds (1 male: 10 females). Four experiments were conducted with serological MHC typing at three weeks of age. At week four nine birds of the appropriate MHC (B¹³/B¹³ and B²¹/B²¹) and family types (A-D) were bled and a lymphocyte proliferation assay performed. The following day birds were challenged with a subcutaneous injection of *E. coli* (EC-AR1). Eighteen days post challenge these birds were bled for the proliferation assay, sacrificed and assessed for the presence of cellulitis lesions. Results of lymphocyte proliferation assays closely mimic previously reported results for leghorn type chickens in that B¹³/B¹³ birds produce a stronger response than do B²¹/B²¹ birds. A significant sire family difference was also noted in both proliferative response and development of cellulitis lesions. Results support the hypothesis that MHC plays an important role in influencing lymphocyte response and cellulitis development, while also implying that other yet to be identified genes play a role in these responses.

Key Words: MHC, broiler chicken, lymphocyte proliferation

and western New York over two growing seasons. Plots were sampled beginning Mid-May and continued until the end of May or early June. Regression analysis indicated that GDD32 was the best single predictor of NDF ($R^2=0.608$ and $MSE=31.8$) across all locations, years, and N rates. At each individual location and N rate, however, prediction equations generally had R^2 above 0.90 and MSE generally was below 6. The harvest window, when forage NDF was between 50 and 60% NDF, was predicted using regression analysis. Harvest window ranged from 6 to 11 days. Julian date was the best single predictor of CP, but maturity explained only 50% of CP variation. Data suggest that development and use of prediction equations at individual locations would assist producers in developing harvest strategies to optimize forage quality.

Key Words: Forage quality, Grass, Reed canarygrass

1435 A survey of phytoestrogen activity in Kansas Flint Hills native grass pastures. D.A. Blasi*¹, S.I. Paisley¹, W.V. Welshons², and G.E. Rottinghaus², ¹Kansas State University, ²University of Missouri, Columbia.

Plant-derived estrogens have been implicated as a contributing factor to observed increases in bulling activity and/or reduced efficiency to growth-promoting implants. In an effort to characterize Kansas Flint Hills native grass pastures, the botanical composition and basal cover in three pastures were surveyed using a modified step-point procedure to estimate the incidence of individual plant species. In order to better characterize estrogenic activity, one hundred individual plant species were collected from the three pastures over three sampling periods and frozen. Using estrogen-stimulated growth of MCF-7 cells in tissue culture, all plant samples were subjected to a bioassay screening procedure designed specifically for feed/forage samples. Results are expressed on a zearalenone equivalent (ZE) ppm basis, which reflects the level of zearalenone required to elicit a comparable response. Approximately 85% of the plant species counted were warm season perennial grasses.