

DL-methionine. The methionine activity of each methionine source was 45.9, 52, 88, and 98% respectively. Starter and grower diets were formulated to contain 0.5%, and 0.38% methionine activity, respectively (except control group, 0.35% methionine activity). No significant differences were observed in body weights, feed consumption or feed conversion among the treatments. Broiler excreta were collected at week 4, 5, and 6 for 24 hours to be analyzed by the trained sensory panel (7 people). Each panelist was given 25 g of manure heated at 27C for 5 minutes for sensory analysis. The thirteen odor attributes utilized to determine differences in broiler excreta by the trained sensory panel were ammonia, dirty socks, wet poultry, fermented, rotten fruit, hay, musty wet, sharp, sour, urinous, rotten eggs, irritating, pungent, and nauseating. Panelist marked intensities for each attribute ranging from 0=none and 15=extremely intense. Each panelist was given 2 replications of each treatment group in a random order each week (total of 10 samples per week). All data were evaluated by analysis of variance using the GLM procedure of SAS. The data indicated that ammonia, wet poultry, rotten fruit, musty-wet, sharp, and pungent differed ($P < 0.05$) across treatment groups. These findings demonstrate that supplemental methionine sources significantly influences odor related compounds in broiler excreta.

Key Words: Sensory, Odor, Methionine, Broilers, Excreta

89 In-house composting of catastrophic poultry mortalities: An educational opportunity. G. W. Malone*¹, N. T. Tablante², and L. E. Carr², ¹University of Delaware, ²University of Maryland.

Composting of poultry mortalities is a widely accepted method of carcass disposal. Various configurations of bin systems have been used for

disposal of routine mortalities. Outside, windrow composting has also been used for disposal of catastrophic events such as major heat losses. However, economical, biosecure, and acceptable methods for disposal of catastrophic poultry mortalities due to highly pathogenic diseases are limited. With support from the US Poultry and Egg Association, a demonstration was implemented to evaluate, demonstrate and perfect in-house composting as an option for disposal of catastrophic mortality events. Processing plant dead-on-arrival were used to simulate a whole-house depopulation of market age birds with a highly infectious disease. The following combinations of composting variables were studied; bird size (broiler vs. roaster), carbon source (litter vs. sawdust) water (added vs. no water), and carcass type (whole vs. shredded). During the first 2-week primary heat, all treatments achieved temperatures conducive to virus inactivation and only one treatment produced marginally acceptable compost. The poultry industry and select agencies personnel were invited to observe the construction of the in-house windrows and turning of the piles within the house. All procedures, labor, time, equipment, material requirements and estimated cost were documented. Photographs and documentation of the in-house process are being compiled for production and distribution of an educational compact disk. The educational value of conducting this demonstration will be discussed. Additional technical details of the composting treatments will be reported in subsequent presentations.

Key Words: Carcass disposal, Catastrophic mortalities, Carcass composting

Genetics

90 Effects of selection for increased breast yield on growth and performance of female Japanese quail. J. M. Reddish*, K. E. Nestor, and M. S. Lilburn, *The Ohio State University/OARDC.*

The objective of this study was to determine the effect of selection for increased breast yield on growth and performance of female Japanese quail in a short term selection experiment. The hypothesis is that selection for increased breast yield in female quail will be of low heritability and will negatively affect characteristics of reproduction. Quail used in this experiment originated from a random bred control (RBC) population of Japanese quail. For each generation, three separate hatches were raised and at 4 weeks of age measurements of body weight were recorded. Body weight and *Pectoralis major* muscle data from female quail in hatch three were used for selection. Selection scheme was maternal family selection based on *Pectoralis major* weight with adjustment for BW differences by covariance analysis. Selected female quail were then paired with RBC male quail to reproduce the next generations. Selection for *Pectoralis major* muscle in maternal Japanese quail lines made slight increases in the absolute weight of the *Pectoralis major* muscle without subsequent increases in BW. Comparisons were made between the selected line (SEL) and the RBC for days to first egg, BW at first egg, first egg wt. There were no significant differences between the SEL and RBC lines for any of the measured traits. Average *Pectoralis major* weight in the SEL line in generation 1 was 11.6 g and 12.9 g in generation 5. The maternal selection scheme for breast yield in female Japanese quail did appear to increase the weight of the *Pectoralis major* muscle.

Key Words: Japanese quail, Selection, Yield, Muscle, Reproduction

91 Effect of hypobaric hypoxia on ascites resistant and susceptible lines and their reciprocal F1 crosses. 1. Production parameters and ascites mortality. H. O. Pavlidis*¹, J. M. Balog², L. Stamps¹, G. R. Huff², W. E. Huff², N. C. Rath², C. R. Cisar², G. Tellez¹, and N. B. Anthony¹, ¹University of Arkansas, Fayetteville, AR, ²PP&PSR/ARS/USDA, Fayetteville, AR.

Tremendous advances in genetic selection, nutrition and management have allowed poultry producers to grow market broilers in record time. However, it is believed that the rapid growth rate, better feed conversion and heavy body weight of the modern broiler has led to a predisposition of the birds to develop injurious metabolic diseases. While the etiology of ascites syndrome is multi-factorial, there appears to be a strong genetic

component. Over the past 7 years, our laboratories have used sire-family selection on a commercial elite line base population to produce an ascites resistant (RES) and an ascites susceptible (SUS) line of broilers. After seven generations of selection, the RES line exhibits < 22% ascites mortality while the SUS line has > 86% ascites mortality. To determine the genetic factors involved in ascites susceptibility, reciprocal F1 crosses of the RES and SUS lines were produced. The objective of this trial was to determine the effects of hypobaric exposure on pure-lines RES and SUS, and their reciprocal F1 crosses (RS, SR). Four hundred and eighty vaccinated, pedigreed broiler chickens (40 groups of 12 birds) were randomly assigned to cages in either a hypobaric chamber (simulated 2900 m above sea level) or a matching local altitude chamber (390 m above sea level). Individual bird weights were collected on Day 0, 14, 28 and 42. Mortalities were necropsied daily to determine cause of death. On Day 42, birds were sacrificed, scored for ascites, and BW, liver, spleen, and split heart weights were obtained. Ascites mortality differed between lines, with the SUS line having the highest, the RES line having the least, and the RS and SR lines having intermediate ascites incidence. The number of days to death were highest for the RES (37 ± 1), with the RS (32 ± 1) and the SR (32 ± 1) intermediate and the SUS survived the shortest number of days (19 ± 1) ($P = 0.0001$). Significant positive heterosis for BW was observed in the F1 crosses at 14, 28, and 42 days of age, and there were no BW differences between RS and SR. No pure line differences were observed for BW at these same ages. Supported in part by U.S. Poultry & Egg. (# 285) and Cobb-Vantress, Inc.

Key Words: Ascites susceptibility, Genetic selection, Hypobaric, Reciprocal crosses, Broilers

92 Effect of hypobaric hypoxia on ascites resistant and susceptible lines and their reciprocal F1 crosses. 2. Gut development. G. Tellez*¹, J. M. Balog², H. O. Pavlidis¹, W. E. Huff², G. R. Huff², N. C. Rath², L. Stamps¹, A. M. Donoghue², B. M. Hargis¹, and N. B. Anthony¹, ¹Department of Poultry Science, University of Arkansas, Fayetteville, Arkansas, 72701, ²USDA-ARS-PPPSRU University of Arkansas, Fayetteville, Arkansas, 72701.

Genetic selection based on rapid growth rates, better feed conversion and heavy body weight for broilers has led to a predisposition to ascites in broiler populations. Sire-family selection was applied to a commercial elite line to produce divergent lines of ascites resistant (< 22% ascites mortality, RES) and ascites susceptible (> 86% ascites mortality, SUS) broilers. In a continuing effort to determine the genetic factors associated

with ascites syndrome, reciprocal F1 crosses of the RES and SUS lines were produced. One objective of this multidisciplinary trial was to determine the effects of hypobaric hypoxia on gut development in the pure-line RES, pure-line SUS, and the reciprocal F1 crosses (RS, SR). Four hundred and eighty vaccinated, pedigreed broiler chickens (40 groups of 12 birds) were randomly assigned to cages in either a hypobaric chamber (simulated 2900 m above sea level) or a matching local altitude chamber (390 m above sea level). On Day 42, specimens of duodenum and distal ileum were collected from five chickens in each line at each altitude. Each sample of intestine was cut open longitudinally at the antimesenteric attachment. Sections were fixed, cut (5 μ m) and stained with hematoxylin and eosin. From these stained sections, 10 measurements of villus height were made at random from different parts of each tissue slide using a reticle (100 mm divisions) placed in the eyepiece of the microscope. There were significant effects on gut development due to both altitude and genetic line. Villus height (mm) of the duodenum and ileum were greater across all lines at local altitude compared to the hypobaric chamber ($P = 0.0001$). Similar morphometric increases were observed in pure-line RES and F1 crosses when compared with pure-line SUS at local altitude ($P = 0.0001$). This study suggests that birds selected for ascites resistance also exhibit improved gut development and this improvement is maintained in their reciprocal crosses. Additionally, hypobaric hypoxia alone results in a significant reduction in gut development across all lines. This work was supported in part by the U.S. Poultry & Egg Association Project # 285 and Cobb-Vantress, Inc.

Key Words: Hypoxia, Gut development, Villus height, Ascites susceptibility, Broilers

93 Differential expression of vascular endothelial growth factor gene between broilers susceptible and resistant to tibial dyschondroplasia. S. Shen^{*1}, W. Berry², S. Pillai¹, J. Totten¹, and J. Zhu¹, ¹Dept. of Poultry Science, Texas A & M University, ²Dept. of Poultry Science, Auburn University.

Tibial dyschondroplasia (TD) is a genetic leg defect with a lesion of avascular, non-mineralized cartilage below the growth plate of the proximal tibia-tarsus in rapid growing broilers. It is believed that TD is a consequence of the inability of chondrocytes of the growth plate to undergo terminal differentiation. Thyroid hormones, Indian hedgehog (Ihh), and parathyroid hormone related protein (PTHrP) regulate the pace of chondrocyte differentiation, and vascular invasion of hypertrophic cartilage is a crucial step for bone formation. No differences were found in the plasma concentration of total triiodothyronine and the expression levels of Ihh and PTHrP in the growth plate between chickens with and without TD from a high and low TD incidence line, respectively. However, the expression level of vascular endothelial growth factor (VEGF) was one fold higher in the growth plate without TD than that with TD based on a real-time PCR assay. The results indicate that the inadequate production of VEGF in the growth plate contributes to the pathogenesis of TD in broilers.

Key Words: Broiler, Tibial dyschondroplasia, Vascular endothelial growth factor

94 Associations of BMP genes with skeletal integrity traits in chickens. H. Zhou^{*1}, N. Deeb¹, A. Mitchell², C. Ashwell², and S. Lamont¹, ¹Iowa State University, ²U.S. Department of Agriculture.

Bone problems in both meat-type and egg-type poultry can impair bird health, productivity and processing quality. The bone morphogenetic protein (BMP) gene family is reported to have important roles in formation of demineralized matrix for bone. Four BMP genes (BMP 2, 4, 5 and 7) were selected as candidate genes to investigate for associations with skeletal integrity in chickens of the Iowa Growth and Composition Resource Population (IGCRP). The IGCRP was established by crossing broiler breeder sires with dams from two unrelated, highly inbred lines (White Leghorn and Fayoumi). The F₁ birds were intercrossed to produce F₂ populations, maintained separately by granddam line. At 8 wk, F₂ birds (n = 720) were euthanized and shank length, shank weight, tibia length, and tibia weight were measured and calculated as percentage of BW. The bone mineral content of the tibia was estimated by DEXA. No polymorphism was detected within BMP2 (1000 bp) or BMP4 (1800 bp) genes in the founder lines of the resource population. Single nucleotide polymorphisms (SNP) between two founder lines (broiler and Fayoumi) were detected by DNA sequencing in BMP5 and BMP7; then PCR-RFLP

methods were developed to screen the F₂ progeny of the broiler by Fayoumi cross. The general linear model was used to analyze associations between BMP genes and skeletal integrity traits. The evaluated SNP of BMP5 had no significant effect on bone-related traits. There were significant associations of the BMP7 with % shank weight to length ratio and with % shank weight. The results suggest that one gene of the BMP family is associated with traits of skeletal integrity, and may therefore be of use in altering leg bone traits by genetic selection.

Key Words: Skeletal integrity, Bone morphogenetic protein, Single nucleotide polymorphism

95 Association of variant alleles of the uncoupling protein with feed efficiency in broiler chickens. P. M. Sharma^{*}, W. G. Bottje, and R. Okimoto, University of Arkansas, Fayetteville, AR.

A broiler population was screened by direct PCR DNA sequencing for variant alleles of the chicken uncoupling protein gene (avUCP, GenBank AF433170). Multiple polymorphism were detected representing, at least, 6 distinct allele haplotypes in the population. All polymorphisms were in introns or silent substitutions in the coding sequence except for one exon substitution. This single nucleotide substitution was found to change an Ala residue at position 118 to a Val. A PCR-RFLP test was designed to identify this polymorphism. A population of 44 individuals from a pedigreed commercial broiler line that had been typed for feed efficiency was genotyped. The individuals with the UCP Val118 allele were found to be more feed efficient ($P=0.04$). The difference between the means for the feed conversion ratio (FCR: feed consumed/weight gain) was 0.09. Only 9 of the birds had the Val118 allele and all were heterozygous, but the total range of the difference in phenotypic variation within this group of 44 animals for the FCR was 0.44. The mean difference between genotypes was 20.5% of the range of FCR values. The allele frequency of Val118 was 0.10. 111 bird samples collected from the same pedigreed line three years previously were typed and the Val118 allele was found to be at a frequency of 0.11. The similar frequency could indicate stabilizing selection in the population for this allele. No Val118 homozygotes have been identified in the 155 birds typed from this line.

Key Words: UCP, Broiler, Allele, Feed conversion ratio

96 Genetic penetrance of embryonic chick edema. W. A. Phillips^{*1}, T. F. Savage¹, J. C. Hermes¹, and A. I. Gitelman², ¹OR State University, Dept. of Animal Sciences, ² Dept. of Statistics.

The concept of genetic penetrance, "the frequency of manifestation of a genetic factor," was introduced by Timofeeff Ressovsky (Naturwissenschaften 19:493,1931). Incomplete penetrance has been used to explain the absence of phenotypic expression when anticipated. Investigational studies of Embryonic Chick Edema, ECE (Poultry Sci. 77(Suppl.1):69, 1998) have been conducted in order to determine the origins for incomplete penetrance of this disorder. ECE was originally reported as the expression of two autosomal recessive loci with incomplete penetrance. Pedigreed *inter se* mating of ECE individuals have resulted in familial incidences ranging from 0 to 100 % with a mean of 48.2% in the most recent generation selected. ANOVA of the penetrance data indicated no significant sire effect ($P>.16$) while the dam component was significant ($P<.01$). The statistical analysis of this trait suggests that ECE is not a qualitative trait as first thought but rather a quantitative trait.

Key Words: Penetrance, Embryonic edema, Mutation, Quantitative trait

97 Ring Lethal-2, an autosomal and recessive early embryonic failure in Coturnix quail. T. F. Savage, W. R. Colvin^{*}, and J. C. Hermes, OR State University, Corvallis, OR.

An early embryonic disorder affecting blastoderm development in Coturnix quail embryos (Poultry Sci 80[Suppl.1]:35,2002) has been observed and studied. Ring Lethal-two (RL-2) describes an embryonic failure that was initially observed at 7 days of incubation and can be detected by 72 h. The disorder is characterized by the presence of an irregular shaped ring of blastoderm cells with a central mass of additional undifferentiated cells. The diameter of the ring and central cell mass have ranged from 3 to 13 mm and 1 to 4 mm, respectively. Expressivity of the disorder has varied from the presence of a blastoderm visible as a central cell mass to its presence encircled by a ring of dense cells approximately 1mm in dia. Macroscopic studies have revealed that the disorder can be detected as

early as 19 h of incubation. This condition, RL-2, has a resemblance to a previously described early embryonic failure in turkey embryos, Ring lethal (J Hered 76:474,1985). This new disorder is not influenced by the length of pre-incubation storage, incubation temperature and duration. The mode of genetic transmission determined by select matings indicated the disorder was the expression of an autosomal and recessive gene. The gene locus and allele symbol, RL-2 is proposed for this embryonic developmental mutation.

Key Words: Coturnix quail, Embryo, Lethal mutation, Autosome, Recessive

98 Comparison of myosin heavy chain isoform transitions in poultry lines selected for breast yield, an unimproved line and White Leghorns. J. M. Reddish*, M. Wick, J. C. Sawdy, and M. S. Lilburn, *The Ohio State University/OARDC*.

The temporal expression of the developmental fast myosin heavy chain (MHC) isoforms in commercial broiler lines selected for breast yield (A and B) and an unimproved line (C), were compared with a White Leghorn line in a semi-quantitative immunoassay. The hypothesis was that accelerated growth is accompanied by changes in the temporal expression of the developmental chicken fast MHC isoforms. Randomly selected male chicks from all lines were sampled at hatch, 7 d, 14 d, and 21 d post-hatch. Myosin was extracted from the *Pectoralis major* muscle from 3 birds per line per day. Myosin purity and total protein concentration were determined by SDS-PAGE and BCA protein analyses. Microtiter plate wells were incubated with 500 ng of total protein and the relative concentration of MHC isoforms evaluated by semi-quantitative ELISA employing three monoclonal antibodies specific for chicken fast embryonic (EB165), neonatal (2E9) and adult (AB8) MHC. The temporal expression of the embryonic MHC was similar in lines A, B, and Leghorn, with expression being maximal at hatch and declining through 14 d and increasing again by 21 d. In contrast, expression of the embryonic MHC isoform in line C was similar, except no increase in the isoform was observed at 21 d. The temporal expression of the neonatal MHC isoform in the Leghorn and line C was similar with expression beginning at 7 d and decreasing through 21 d. In contrast, the expression of the neonatal MHC in lines A and B began at hatch and then decreased through 21 d. Expression of the adult MHC isoform in the Leghorn began at 14 d and increased through 21 d, as expected. However, lines A, B and C exhibited expression of the adult MHC isoform at 7 d and increased through 21 d. These results support the hypothesis that the accelerated muscle growth is accompanied by changes in the temporal expression of the developmental MHC isoforms. The association of MHC isoform transitions during embryonic development with rapid growth is being further investigated.

Key Words: Myosin, Muscle, Broiler, ELISA

99 Markers associated with Marek's Disease survival in commercial layers. J. P. McElroy*¹, H. H. Cheng², J. Fulton³, M. Soller⁴, E. Lipkin⁴, J. C. M. Dekkers¹, and S. J. Lamont¹, ¹Iowa State University, ²USDA-ARS-ADOL, ³Hy-Line International, ⁴Hebrew University of Jerusalem.

The objective of this study was to locate genomic regions affecting resistance to Marek's disease (MD), a major disease affecting the poultry industry, for use in marker-assisted selection or candidate gene analyses. The experimental population was a backcross (BC) of two partially inbred commercial lines that were fixed for different serologically typed B blood group alleles and that differed in mortality, tumor development, and other disease-related parameters when MD virus challenged. Pair mating of susceptible-line males to resistant-line females produced 5 full-sib F1 families. BC chicks were produced by mating 7 F1 males per family each to 15 susceptible-line females, vaccinated with HVT/SB1 MD vaccine at 0 d, and subcutaneously inoculated with MD virus 648A at 6 d. Of survivors past 33 d (n = 692), 134 individuals with tumor(s) and short survival times (33 to 48 d) and 133 individuals with long survival (76 to 140 d = test end) were selectively genotyped for 56 out of 117 microsatellites that were chosen based on selective DNA pooling analysis. Markers associated with MD were identified within each B genotype by regressing survival on line allele inheritance probabilities, which were calculated based on marker genotypes and BC dam line allele frequencies (BC dams were unknown and not genotyped). A total of 17 marker by B genotype effects, on chromosomes 1, 2, 5, 8, and Z, were significant at the 10% comparison-wise level, of which 9 were significant at 5%. Two markers were significant for both B genotypes. Significant QTL were confirmed on chromosomes 2, 5 and Z by least-squares interval mapping at the 5% chromosome-wise level. B genotype was not significant; however, several markers had significant interactions with B genotype. Within-grandsire family analysis revealed differential marker effects among families. The results suggest that non-B blood group QTL for MD survival segregate between and within the parental lines.

Key Words: Marek's disease, QTL, Chicken

100 Integrating the chicken classical linkage group II and the new consensus molecular map. D.M. Karcher* and J.J. Bitgood, *University of Wisconsin - Madison*.

The chicken classical linkage group II includes dominant white (I), crest (CR), and frizzled feathers (F). The current consensus linkage map for E22C19W28 includes I and MCW 0317, a microsatellite. The objective of this study was to determine the order of CR, I, F, and MCW 0317. Heterozygous males carrying all three phenotypic traits were backcrossed to Light Brown Leghorns recessive for all three traits. The males were polymorphic for the marker while the females were not. The progeny were raised to six weeks of age where blood was collected and traits recorded. After PCR and gel electrophoresis of the progeny DNA, segregation of the microsatellite was recorded. The results of the study indicated the order was MCW 0317 (12.5 ± 3.3) CR (14.2 ± 3.3) I (14.7 ± 3.3) F; map distances agreed with both the published classical and molecular maps.

Key Words: Linkage map, Chicken, Linkage Group II

Nutrition - Feed Ingredient and Broiler Nutrition

101 Protein quality of poultry byproduct meal from whole fowl co-extruded with corn or wheat. O. C. Aimiuwu* and M. S. Lilburn, *The Ohio State University, Columbus, Ohio*.

The disposition of mortality and fowl are two critical issues facing the commercial egg industry. In a series of experiments, a test protein source resulting from the co-extrusion of whole fowl with either corn (CHM) or wheat (WHM) was compared with soybean meal or meat and bone meal. In a preliminary experiment, semi-purified diets were formulated to contain 12%, 15% or 18% CP with the only source of protein being either CHM or WHM. Each diet was fed to 4 replicate pens of turkey poults for a 7 d experimental period. There were positive, incremental increases in BW with each level of protein so these diets were utilized for subsequent experiments. In Experiment 2, a nitrogen-free dietary treatment was included in the study. In the 12% and 15% CP treatments, there was considerable variation between protein sources in intake, gain, protein efficiency ratio (PER), and net protein ratio (NPR). The values for all variables were consistent, however, between the CHM and WHM diets for

poults fed the 18% CP diet. In Experiment 3, diets containing commercial meat and bone meal (MBM) and soybean meal (SBM) were included in the comparisons. The four sources of protein were again incorporated into diets containing 12%, 15%, or 18% CP. Over all levels of dietary CP, PER and NPR values for SBM, CHM, and WHM were similar and all were significantly higher (P < 0.05) than for diets containing MBM. This was supported by amino acid digestibility comparisons among the three animal protein sources. The methionine and lysine digestibility values for MBM were 63% and 58%, respectively, compared with values greater than 80% for the two extruded hen meals. In summary, the CHM and WHM protein sources compare favorably with soybean meal as a source of protein for turkey poults and was significantly better than a commercial source of meat and bone meal.

Key Words: Turkey poults, CHM, WHM, SBM, MBM