an open pen. Scores were rated from 1 to 5: higher scores indicated more nervous or aggressive behavior. Calves (n = 657) were from diallel matings of Angus (A), Brahman (B), and Romosinuano (R; tropically adapted Colombian breed). Fixed effects included breed (n = 9), calf sex, year (n = 2), farm (n = 3), day of record (n = 3; 0, 24, or 72 h post-weaning). Order through the chute and calf age at weaning were covariates. Random effects were calf and sire. BB (sire and dam breed, respectively) calves had the highest values for exit velocity, chute score, and pen score (2.41 ± 0.1 m/s, 2.42 ± 0.06, 3.31 ± 0.09); all were higher (P < 0.05) than all other breed groups for chute and pen score, and had higher (P < 0.05) exit velocity than all but BA and AB. RR calves had the lowest exit velocity (1.66 ± 0.07 m/s), lower (P < 0.05) than all but AA, RA, and AB. AA calves had the lowest values for chute and pen score, lower (P < 0.05) chute score than all but RR, and lower (P < 0.05) pen score than all but RR and RA. Estimates of direct breed effects for exit velocity (P < 0.001) were 0.68 ± 0.16 m/s for B and 0.49 ± 0.14 m/s for Romosinuano. Estimates of direct effects for chute and pen score were highly significant for B (0.91 ± 0.1 and 1.13 ± 0.15), A (0.5 ± 0.1, 0.6 ± 0.14), and R (0.4 ± 0.09, 0.52 ± 0.13). Estimates of heterosis (P < 0.05) were 0.21 ± 0.09 m/s (7.4%) for exit velocity for B with A, 0.12 ± 0.05 (3.1%) for chute score for A with R, and 0.18 ± 0.08 (3.2%) for pen score for R with B. Results suggest that R may be included in similar breeding programs without detrimental temperament changes.

**Key Words:** Brahman, Romosinuano, Temperament

### PSA-Genetics

**M26 Interaction genotype and protein level on feed efficiency of Japanese quail in dry tropic weather. J. J. Portillo1, R. Barajas1, M. A. Carmona2, F. G. Rios1, and G. Contreras1. 1FMVZ - Universidad Autónoma de Sinaloa (Mexico) Carr. Culiacan-Mazatlan km 3.5, 2FES Cuautitlán UNAM (Mexico) Cuautitlán Izcalli, Estado de México.

This study was conducted to evaluate the interaction genotype and protein level and protein level on egg production of Japanese quail, were used 515 females and 200 males of four strains: 1) HH, quails selected for high mature weight; 2) LL, quails selected for low mature weight; 3) HL, reciprocal crosses from males HH with females LL; and 4) LH, reciprocal crosses from males LL with females HH. At 52 days old, the quails was contained in batteries with five levels and four cage by level. In each cage, was allocated six females and two males. With base at arrangement combinatory, five cages of each strain was designated a 16, 19, 21, 24, and 27 % of crude protein (CP) level. During eight weeks, was registered egg production and egg weight from strain and protein level. Each week was measurement the feed intake (FI) only by three days consecutives. To evaluate the interaction genotype-protein level, was utilized a general lineal model of fixed effects by week, strain, protein, and interaction strain-protein level, the tendency on the response was determinate by orthogonal polynomials, a simple lineal regression was used to estimate protein level with better feed efficiency (FE). ANOVA shown effect (P<0.01) in FE by week production, strain, protein level, than as interaction by week x strain, and strain x protein, the tendency by FE was lineal (P<0.01) to strain HH, and quadratic (P<0.03) to strain HL, LH and LL, with CP levels and FE estimated of 26, 20.5, 16, 16 %, and 0.246, 0.248, 0.219, 0.264, to strain HH, HL, LH and LL, respectively. It is concluded, that exist interaction genotype protein in FE to egg production in Japanese quail, and better FE in low mature weight strain with 16 % CP, than high mature weight strain require 26 % CP.

**Key Words:** Protein Level, Feed Efficiency, Coturnix coturnix japonica

### M27 Interaction genotype - protein level on egg quality of Japanese quail in dry quality of Japanese quail, were used 639 eggs from four strain: 1) HH, quails selected for high mature weight; 2) LL, quails selected for low mature weight; 3) HL, reciprocal crosses from males HH with females LL; and 4) LH, reciprocal crosses from males LL with females HH. At 52 d old, the quails was contained in batteries with five levels and four cage by level. In each cage, was allocated six females and two males. With base at arrangement combinatory, five cages of each strain was designated a 16, 19, 21, 24, and 27 % of crude protein (CP) level. From two weeks start hatching and every 14 d, during egg was collected by strain - CP level combination. The next measurement weight, length, width of eggs, dense albumin height, yolk height, and width. From these data, shape index (SI), yolk index (YI), and Haugh Units (HU) were calculated. To evaluate the interaction genotype-protein level, was utilized a general lineal model of fixed effect by week, strain, protein, and interaction strain-protein level, the tendency of the response determinate by polynomial and the means comparison was used contrasts. ANOVA shown effect (P<0.03) in SI, YI, and HU; by week, strain, protein level, and strain x protein level, except to genotype-protein interaction in HU (P<0.20). Was observed linear response (P<0.01) and difference between 16-19-21 vs. 24-27 % of CP (P<0.01) in SI to strain HH with

**Key Words:** Adaptability, Crossbred Cattle, Beef Cattle
To evaluate the interaction genotype and protein level (IGP) on hatchability of Japanese quail in dry tropical weather, were incubated 5176 egg four strains, 1) HH, quails selected for high mature weight; 2) LL, quails selected for low mature weight; 3) HL, reciprocal crosses from males HH with females LL; 4) LH, reciprocal crosses from males LL with females HH. At 52 days old, the quails were contained in batteries with five levels, and four cage by level. In each cage was allocated six females and six males. With a base at arrangement combinatory, five cages of each strain was designated to consume 16, 19, 21 (control), 24 and 27 % PC. After two weeks of adaptation, each 21 days, egg hatch was selected and incubated with four repetitions by treatment. To evaluate the interaction genotype-protein level, was used a general linear model to fixed effects by period, strain, protein, and interaction genotype-protein level, comparison means by orthogonal polynomials. ANOVA shown effect (P < 0.05) heavier in comparison with those of CON-group birds on day 21 of the experiment in two of three breeds. Furthermore, the EXP-group birds showed to be significantly (P < 0.05) heavier than the CON-group birds in all of the three breeds on day 28 and 35 of the experiment. Especially in the 35-day-old mean body weight, the EXP-group birds of Arbor Acres, Peterson, and Ross were significantly (P < 0.05) heavier by 121.8 g, 118.5 g, and 242.8 g than the CON-group birds, respectively. However, the body weights in experiments 2 and 3 did not significantly differ between the CON-group birds and the EXP-group birds fed with chitosan supplementation from day 15 post birth. The mean 15 35 d FCR of the EXP-group birds were generally lower (P < 0.05) than that of the CON-group birds in experiment 1 only. By the results of the analysis of variance, the best strategy (chitosan) supplementation interactive effect 15-35 day-old mean body weight of 1.35 or 15 35 day-old mean weight gains showed significant (P < 0.05) in experiment 1 only; however, these traits in both experiment 2 and 3 were not shown significant interaction of breed-by-diet supplementation. The interactive effects of breed-by-diet supplementation on the mean 15 35 d FCR. Results of these experiments indicate that dietary supplementation with chitosan for the improvement of growth or feed conversion ratio has an efficacy when the supplementation begins from one-day-old broiler chickens.

Key Words: Breed, Chitosan, Broiler

M31 Male and female fertility and hatchability in chickens: A longitudinal mixed model approach. R. L. Sapp1, R. Rekaya1, I. Misztal2, and T. Wing3, 1 The University of Georgia, Athens, 2 Cobb-Vantress, Inc., Siloam Springs, AR.

The objective was to investigate different approaches for handling missing records and to develop and implement a multivariate longitudinal mixed model for the genetic evaluation of male and female fertility and hatchability in chickens. Traits recorded on a weekly basis were eggs set (E), fertility percentage (F), and percentage hatched of fertile eggs (H). Three approaches for handling missing records were investigated: 1) records with zero weekly laid eggs were removed and remaining records with missing F and H were predicted (M1); 2) missing records, including zero weekly laid eggs, were assumed known and equal to zero (M2); and 3) zero weekly laid eggs were assumed as a valid record and missing F and H were predicted (M3). A longitudinal mixed model was employed for the multiple trait analysis of E, F, and H. Fixed effects included week, age of service sire, and age of hen; unrelated service sire, additive hen, permanent environment, and residual were included as random effects. Heritability estimates of E, F, and H ranged from 0.104 to 0.127, 0.055 to 0.074, and 0.059 to 0.074, respectively, using the three methods. Heritability estimate of E using M1 was significantly higher than estimates obtained from M2 or M3 suggesting that removing records of E that were zero was not the best approach. Heritability estimates of F and H using M2 were significantly larger than estimates obtained from M1 or M3 indicating that predicting missing F and H with a better approach than assuming missing F and H were zero. Correlations among the three traits were highest using M2 and lowest using M1. Pearson correlations indicate that virtually no re-ranking of animals or service sires was expected between M2 and M3 for the three traits. However, greater re-ranking could occur when using M1. Therefore, M1 should not be used for the analysis of longitudinal fertility and hatchability data in chickens. Furthermore, M3 seems to be the most ideal method for handling missing records.

Key Words: Eggs Set, Fertility, Percentage Hatched of Fertile Eggs
A study was conducted to evaluate the growth curves of four commercial laying-type pullet lines, from 1 to 18 weeks. 300 birds of each line, Hy line Black (HLB), Hy line White (HLW), Hisex Brown (HSB), and Hisex White (HSW) were distributed into 4 groups of 75 birds. Eight birds of each group were slaughtered weekly to determine the chemical composition and to measure feathers weight. The data were used to fit the Gompertz growth equation in order to estimate the growth parameters \( W_t = W_m \exp(-\exp(-b(t-t^*))) \). The weights of body, feather, protein and fat contents at time \( t \) (\( W_t \)) were described in terms of the mature weight (\( W_m \)), their rates of maturing (b), and the time to reach the maximum rate of growth of each component (\( t^* \), day ). According to the growth parameters for live weight, the HLB, HSB and HSW showed lower b than HLW, consequently, those lines showed higher t and Wm than HLB. The brown pullets presented higher feathers weight at maturity (Wm) and b compare to the white pullets. The HLW took more time (58 days) to reach the maximum rate of feathers growth. In contrast to the results of live BW, this strain exhibited the lowest t, indicating that it was precocious to BW. The Wm and t for body protein weight for Hy line were higher than those of Hisex, however the b for Hy line were inferior to Hisex. The b for protein deposition showed that the pullets are near to the maximum development of lean and visceral tissue. The rates of protein deposition at maturity were higher for HLB than HSW and for HSB than HSW, which could modify the protein requirements, and show that the genetic provides differences in body composition.

### Growth curve parameters for the pullet strains studied

<table>
<thead>
<tr>
<th>Parameters</th>
<th>HLB</th>
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<th>HSB</th>
<th>HSW</th>
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<tr>
<td>Wm</td>
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<td>1533</td>
<td>2064</td>
<td>1598</td>
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<td>0.023</td>
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<tr>
<td>( t^* )</td>
<td>59</td>
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<td>59</td>
<td>55</td>
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<tr>
<td>Wm</td>
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<td>158</td>
<td>157</td>
<td>142</td>
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<tr>
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<td>0.026</td>
<td>0.032</td>
<td>0.028</td>
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<tr>
<td>( t^* )</td>
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<td>58</td>
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<td>55</td>
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<td>Protein weight</td>
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<td>0.024</td>
</tr>
<tr>
<td>( t^* )</td>
<td>71</td>
<td>71</td>
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</tbody>
</table>

**Key Words:** Growth Parameters, Body Composition, Laying-Type Pullet Lineages

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The genetic characteristics of carcass and the cellularity of the adipose tissue were analyzed and compared when a Chinese local breed(White-feather Lueyang, WL), a modern commercial broiler strain(Arber Acres, AA), and their F1 achieved a common physiological age. The result demonstrated that, compared with AA and F1 broilers at a body weight of 1800 g, WL broilers had lower breast meat yield, higher leg meat yield, and lower abdominal fat weight (p<0.05 or p<0.01), and the slaughtering age of WL was 132 d, which is 3 times more than that of AA (43 d). The number of adipose cells of WL in the abdominal fat pad was significantly greater, but the size of adipose cells was smaller (p<0.01). F1 broilers had a greater positive heterosis in growth rate and abdominal fat deposition. High-protein diet can significantly reduce fat deposition of broilers, and there is a greater interaction between genotypes and diets.

**Key Words:** Meat Performance, Physiological Age, Meat-Type Chicken
However, more effort should be committed to developing guinea fowl-specific markers since those of chickens and quail may not be sufficient for studies in guinea fowl.

Key Words: Guinea Fowl, Microsatellite Markers, Polymorphisms

M37 Withdrawn by author.

M38 Dioxin-induced changes in chicken macrophage (HD11) gene expression. N. Puebla-Osorio*,1, K. S. Ramos1, D. Abi-Ghanem1, M. H. Falahatpisheh3, and L. R. Berghman1,2,1 Department of Poultry Science, Texas A&M University, College Station, 2 Department of Veterinary Pathobiology, Texas A&M University, College Station, 1Center for Genetics and Molecular Medicine, University of Louisville Health Sciences Center, Louisville, KY.

In this study, we used specific chicken immune cDNA arrays (constructed at the Fred Hutchinson Cancer Research Center) to identify the transcriptional profile induced by 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD) in chicken macrophages (HD11). The complete array contained 3,011 chicken lymphocyte cDNA spots representing 2,200 genes. Cultures of the chicken myelomonocytic line HD11, transformed by the myc-encoding MC29 virus, were exposed to two doses of TCDD (1 and 10 nM) for 6 and 12 h. Cells exposed to a similar amount of DMSO were used as the negative controls. Total RNAs were extracted using the Trizol method. The labeled cDNA samples (Cy3 and Cy5) were co-hybridized to an individual array. Scanning and image processing involved a GenePix 4000 scanner. The resulting images were analyzed using GenePix Pro 3.0. The Log2 values of the median of ratios were used. Upon filtering, a total of 217 genes showed significant up- or down regulation, and were further analyzed using hierarchical clustering (HCL) and tree formation, k-means clustering, and self-organizing maps (SOM). Nine clusters were formed using tree average linkage of genes with similar expression. Seven clusters were selected from the SOMs. K-means clustering produced 6 clusters. At least a 2-fold up-regulation after 6 h of exposure to TCDD (regardless of the dose) and subsequent down-regulation after 12 h of exposure, was observed in the following genes: mitochondrial cytochrome C, M phase inducer phosphatase 2, lysosomal transmembrane protein, alpha enolase, and HSP70 and HSP90. Consistently down-regulated genes included: inflammatory response-related MTMMP2 (matrix metalloproteinase 2), AKT1 (involved in TNF-related activation of NFκB), and oxidative-stress related neuronal NOS, among others. Specific primers will be designed for each of these genes and real-time PCR will be used for validation of the microarray data.

Key Words: Dioxin, Microarray, Macrophages

M39 The expression of genes related to egg production performance in the liver of Taiwanese country chickens. S. T. Ding1, Y. H. Ko1, M. C. Huang2, Y. P. Lee2, and W. T. K. Cheng1,1 Dept. of Animal Science, National Taiwan University, Taipei 106, Taiwan, 2 Dept. of Animal Science, National Chung Hsing University, Taichung, Taiwan.

The purpose of this study was to detect expression of genes related to egg production performance in Taiwanese country chickens by suppression subtraction hybridization (SSH). Liver samples from two Taiwanese country chicken breeds (L2 and B lines) with very distinct egg production rates were taken for mRNA extraction. The SSH procedure utilized a kit from Clontech (PCR Select). Two-way subtraction was performed and the differentially expressed gene fragments were cloned into pGEM-T Easy TA cloning vector (Promega). cDNA from the high egg production line (L2) was subtracted by the cDNA from the low egg production chickens (B). The resulted clones were selected for sequence analysis by a genetic analyzer (ABI 3730). We have select 288 clones for forward subtraction and 96 clones for the reverse subtraction. These genes were subjected to further differential screening to confirm the differential expression of genes between the two genetic breeds of chickens. We found that at least eight genes expressed greatly in the liver of L2. Among the genes were chicken apoVLDLII, liver basic fatty acid-binding protein, and two novel genes. We have also found that a glucose-regulated protein and chaperonin T-complex protein 1 were highly related to the poor egg production trait. The chicken apoVLDLII and liver basic fatty acid-binding protein in the liver involved in the egg yolk ingredient deposition. Greater expression of these genes assures more egg forming capacity in order to generate greater egg production rate. Specific functions of the other genes for egg production need to be further investigated.

Key Words: Chicken, SSH, ApoVLDLII

M40 Withdrawn by author.

M41 Preparation and characteristics of spent hen meat enzymatic hydrolysate. O. Sangthcrapitikul, Y.C. Chen*, and T.C. Chen*, Mississippi State University, Mississippi State.

Excessive expansion of egg industry resulted in abundant availability of spent hen. Meat from spent hens is generally tough and poor in functional properties. Due to the inherent qualitative differences between broiler and spent hen meat, the spent hen meat has created a difficulty in its effective disposal.

Spent layer carcasses were obtained from a commercial spent hen processing plant and breast meat was hand-deboned. Bromelain (B), trypsin (T), papain (P), and Aspergillus oryzae protease (A) were purchased from Sigma Chemical Co. (St. Louis, MO). Fine ground breast meat, water, and enzyme were mixed and hydrolyzed in a water bath at 50°C for four hours. For optimal hydrolyzing pH selection, the pH of the meat suspension was adjusted by adding either 1N HCl or 1N NaOH. The enzyme activity was terminated by placing the reaction bottles in boiling water for 15 min. Optimal hydrolyzing pH and concentration were determined for each enzyme and enzyme combinations. The sensory characteristics of enzymatic hydrolysates were also investigated.

Data indicated that the optimal pH values for enzyme hydrolysis of spent hen breast meat suspension were: 5.0-7.0 for B, 6.0 for T, 5.0-7.0 for P, and 5.0-7.0 for A. One percent (w/w) of P and A based on raw meat weight showed the highest (P<0.05) hydrolysis efficacy, followed by 0.5% (w/w) and 0.1% (w/w). Considering the enzyme cost factor, the hydrolysates from A, P+A, P+B, and P+A+B were selected for sensory study. Undiluted enzymatic hydrolysates showed higher (P<0.05) scores in chicken, meaty, mouth feeling, bitterness, and umami sensory attributes compared with the controls but there were no (p>0.05) difference on all sensory attributes among those enzyme hydrolysates. Generally, P+A showed the highest acceptability in sensory attributes among those enzyme hydrolysates. Generically, P+A showed the highest acceptability in sensory attributes among those enzyme hydrolysates. Generally, P+A showed the highest acceptability in sensory attributes among those enzyme hydrolysates.

Key Words: Spent Hen Meat, Enzyme, Hydrolysate

M42 Spent hen meat enzymatic hydrolysate as a flavoring base. O. Sangthcrapitikul, Y. C. Chen*, and T. C. Chen*, Mississippi State University, Mississippi State.

Due to the inherent qualitative differences between broiler and spent hen meat, the spent hen meat has created a difficulty in its effective disposal. The industry is actively seeking new and alternative uses for spent hen meats. Proteins are the best sources of flavor because of their amino acids, peptides, and nucleotide components. Protein hydrolysates are the main products derived from protein hydrolysis and have been used specially for flavoring purposes, as savory flavors or taste enhancers.

Fine ground spent hen breast meat and water (1:10 or 1:2) were blended and hydrolyzed with either Papain + Protease (P+A, 0.5% (w/w) of raw meat weight for each enzyme) or Papain + Protease + Bromelain (P+A+B, 0.33% (w/w) of raw meat weight for each enzyme) at their optimal hydrolyzing conditions in the water bath at 50°C for four hours. The enzyme activity was terminated by placing the reaction bottles in boiling water for 15 min. After cooling, either whole hydrolysates or