

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 AR. 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 (0.41 ± 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

M25 Estimates of adaptability and stayability for postweaning weight gain in crossbred beef cattle raised in five environments in Brazil. J. C. d. C. Balieiro^{*1,2}, J. B. G. Barros², J. B. S. Ferraz¹, J. P. Eler¹, E. d. S. Balieiro^{*3}, L. G. G. Figueiredo¹, and E. C. Mattos¹, ¹University of São Paulo, Duqu de Caxias Norte, 225. Pirassununga/SP-Brazil, ²University Center of Av. Dr. Octavio da Silva Bastos, S/n. S. João da Boa Vista/SP-Brasil, ³Federal Rural University of Rio de Janeiro, Rodovia BR-465, km 47. Serpédica/RJ-Brasil.

This study was conducted to evaluate adaptability and stability parameters of nine genetic compositions of crossbred European-Zebu cattle raised in five different Brazilian environments. Data (n=16,546) from the present study refer to characteristic gain from weaning up to 160 days postweaning. The statistical model included the effects of genetic composition (G), environment (E), GxE interaction and contemporary group within E. Also included was a covariate adjustment for cow's age at calving (linear and quadratic). All sources of variation in the analysis were highly significant ($P < 0.01$). The decomposition of the GxE interaction was accomplished by regression method. Intercepts ($\beta_{0(i)}$) for genotypes 2, 3 and 5 showed the highest weight gains up to 160 days postweaning. On the other hand, the genotypes 7, 9, 8 and 6 showed the smallest postweaning gains. Based on t-tests for the angular coefficients ($\beta_{1(i)}$) adjusted for the environmental index from each environment, it was verified that only genotype 2 had general adaptability. In contrast, genotypes 1, 3, 4 and 5 were classified as having specific adaptability to favorable environments and genotypes 6, 7, 8 and 9 were classified as having specific adaptability for unfavorable environments. The variance components related to the deviations of the regression for the genotypes indicated that all genotypes had low stability. Genotypes 3 and 5 should not be considered completely undesirable since they had high weight gains and coefficients of determination from the regression. The adaptability analysis was efficient in discriminating among genetic types. However, the stability analysis was not effective in discriminating the variance components attributed to deviations from regression. In this case, it was necessary to use another approach (coefficient of determination) to aid in decision making.

Key Words: Adaptability, Crossbred Cattle, Beef Cattle

PSA-Genetics

M26 Interaction genotype and protein level on feed efficiency of Japanese quail in dry tropic weather. J. J. Portillo^{*1}, R. Barajas¹, M. A. Carmona², F. G. Rios¹, and G. Contreras¹, ¹FMVZ - Universidad Autónoma de Sinaloa (Mexico) Carr. Culiacan-Mazatlan km 3.5, ²FES Cuautitlan UNAM (Mexico) Cuautitlan 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 tropic weather. J. J. Portillo^{*1}, R. Barajas¹, M. A. Carmona², F. G. Rios¹, G. Contreras¹, and I. V. Ferrer¹, ¹FMVZ - Universidad Autonoma de Sinaloa (Mexico) Carr. Culiacán-Masatlan km 3.5, ²FES Cuautitlan - UNAM (Mexico) Cuautitlan Izcalli, Estado de Mexico.

To evaluate the interaction genotype and protein level on egg 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 leves 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 polinomial 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 lineal response ($P < 0.01$) and difference between 16-19-21 vs. 24-27 % of CP ($P < 0.01$) in SI to strain HH with

79.12 vs. 77.96; strain LH, the lineal tendency ($P < 0.01$) was by difference between 16-19 vs. 21-24-27 % ($P < 0.01$) with 76.90 vs. 78.35; egg SI of strain HL and LL, was similar between CP level ($P > 0.10$) with 78.16 and 77.36. YI and HU were similar between CP levels ($P > 0.10$) in four strain, with 45.50, 43.37, 44.62, and 43.68 to YI, and 93.16, 92.52, 92.06, and 89.98 to HU in HH, LL, LH, and HL, respectively. It is concluded, than exist interaction genotype-protein level to SI and YI, but not to HU, although CP levels to 16 at 27 % was not affected YI and HU.

Key Words: Protein Level, Egg Quality, Coturnix coturnix japonica

M28 Effect of genotype and protein level on hatchability of Japanese quail in dry tropic weather. J. J. Portillo*¹, R. Barajas¹, M. A. Carmona², F. G. Rios¹, G. Contreras¹, and S. Aza¹, ¹FMVZ - Universidad Autonoma de Sinaloa (Mexico) Carr. Culiacan-Mazatlan km 3.5, ²FES Cuautitlan - UNAM (Mexico) Cuautitlan Izcalli, Estado de Mexico.

To evaluate the interaction genotype and protein level (IGP) on hatchability of Japanese quail in dry tropic 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 two 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 lineal model to fixed effects by period, strain, protein, and interaction genotype-protein level, comparison means by orthogonal polynomials. ANOVA shown effect ($P < 0.01$) of period and protein, but not was strain ($P = 0.60$), and IGP ($P = 0.29$), with 71.35, 68.31, 64.79, 77.13, and 77.81 % for 16, 19, 21, 24 and 27 % respectively, with difference between control vs. others level ($P < 0.01$), the levels of 16-19 vs. 24-27 ($P < 0.01$), without difference between 16 and 19 ($P = 0.40$), and 24 and 27 % PC ($P = 0.86$). It is concluded that not exist interaction genotype-protein level on hatchability of fertile eggs, and 24 % is the better level.

Key Words: Protein level, Hatchability, Coturnix coturnix japonica

M29 Relationship between internal and external egg characteristics of Japanese quail. J. J. Portillo*, G. Contreras, F. G. Rios, and I. V. Ferrer, FMVZ-Universidad Autonoma de Sinaloa, Mexico Carr. Culiacan-Mazatlan km. 3.5.

With the objective of characterize the relationship between measuring internal and external egg of Japanese quail, were measured weight, length, width, height and width of yolk, and dense height of 1644 eggs. From this data were calculated: shape index (SI), yolk index (YI) and Haugh Units (HU). Data was conducted a descriptive analysis and correlation lineal simple (Pearson coefficients). Egg weight (13.89 ± 1.44) was related ($P < 0.01$) mainly with the width (26.93 ± 0.98 mm) with correlation coefficients of 0.82 to 0.90, length (37.01 ± 1.74 mm) 0.70 to 0.78 and width of yolk (25.99 ± 1.66 mm), 0.52 to 0.64. The width of the egg was related ($P < 0.01$) with the length, with coefficients of 0.44 to 0.51, as well as with the weight of yolk, 0.52 to 0.57. Length associates in negative form ($P < 0.01$) with SI (77.93 ± 3.39), -0.70 to -0.72, as well as width of yolk (0.48 to 0.53), and the height of yolk (11.40 ± 1.26 mm) 0.28 to 0.44. YI (44.24 ± 4.46) this determined ($P < 0.01$) for the height of the yolk (0.80 to 0.82) and in minor grade and negative form the width the yolk (0.17 to -0.41), while the measurements of yolk associate with values of 0.20 to 0.40. Haugh Units (91.85 ± 4.72) was determined ($P < 0.01$) for the dense albumin height (5.26 ± 0.90 mm) 0.98 to 0.99, and still when for their calculation the egg weight is employed, it has a null relationship ($P = 0.19$) whit is (0.01 to 0.05). The remainder of the correlations has a minor magnitud to 0.30. It is concluded that the most related positive measurements is weight and the width of the egg, length with the shape index, height of the yolk with the yolk with the yolk index, and the Haugh Units with dense albumin height, with negative relationship of the length of the egg with shape index.

Key Words: Egg Measures, Correlation, Coturnix Coturnix Japonica

M30 Interaction of Breed-by-Chitosan Supplementation on Growth and Feed Efficiency at Different Supplementing Ages in Broiler Chickens. Yoon O. Suk*¹ and Hyung C. Sung², ¹Sahmyook University, 26-21 Kongneung Dong, Nohwon-Ku, Seoul South Korea, ²EZ Life Science Co., Ltd., 335 Yangjae Dong, Seocho-Ku, Seoul, South Korea.

Three experiments were conducted to investigation the interaction of breed-by-chitosan supplementation on the major economic traits in broiler chickens. In experiment 1, one-day-old broiler chicks were fed ad libitum on a basal diet (CON-group) or basal diet containing chitosan at an inclusion level of 10.5 mg/bird/day (EXP-group). In experiments 2 and 3, the diets of 15-day-old broiler chicks were supplemented by the same amount of chitosan as used in experiment 1. In experiment 1, the mean body weight of the EXP-group chickens were significantly ($P < 0.05$) 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 breed-by-diet (chitosan) supplementation interactive effect on 35-day-old mean body weight and 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. Sapp*¹, R. Rekaya¹, I. Misztal¹, and T. Wing², ¹The University of Georgia, Athens, ²Cobb-Vantress, Inc., Siloam Sprints, 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-flock, 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 was 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 reranking of animals or service sires was expected between M2 and M3 for the three traits. However, greater reranking 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

M32 Growth parameters of live body weight, feather and protein weight of four commercial laying-type pullet strains. R. Neme¹, N. Sakomura^{*1}, F. Fialho², E. Carrilho¹, and F. Santos¹, ¹Faculdade de Ciências Agrárias e Veterinárias-Universidade Estadual Paulista Jaboticabal-SP Brazil, ²EMBRAPA Bento Gonçalves - RS.

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 Brown (HLB), Hy line White 36 (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 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 , g), 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 W_m than HLW. The brown pullets presented higher feathers weight at maturity (W_m) 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 W_m 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 HLW 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

Parameters	HLB	HLW	HSB	HSW
Live weight				
W _m	2060	1533	2064	1598
b	0.023	0.026	0.023	0.023
t*	59	52	59	55
Feather weight				
W _m	165	158	157	142
b	0.032	0.026	0.032	0.028
t*	55	58	56	55
Protein weight				
W _m	782	678	657	509
b	0.022	0.020	0.026	0.024
t*	71	71	63	60

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

M33 A comparison of carcass fat variables in different meat-type breeds of chickens. Z. Niu*, F. Liu, and S. Zhai, *College of Animal Science & Technology, Northwest Sci-Tech University of Agriculture & Forestry, Yangling, China.*

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

M34 Identification of virulence genes in Salmonella enteritidis required for survival in chicken infection. R. K. Gundelly* and Y. M. Kwon, *University of Arkansas, Fayetteville.*

Salmonella enteritidis (SE) is one of the most common serotypes of Salmonella causing food borne diseases in industrialized countries, which is frequently associated with chicken shell eggs. Persistent infection of SE in laying hens is an essential step for contamination of forming eggs. We have devised a genetic technique, termed transposon footprinting and demonstrated the utility of the technique in the rapid identification of SE genes that are required for survival during infection of 5-day-old chickens. The transposon-flanking sequences were amplified simultaneously from each pool of 24-30 random SE Tn5 mutants (input pool) and the mutants recovered from the spleen of infected chickens (output pool). Several mutants attenuated during infection were identified by the PCR bands that are present in the input pool but not in the corresponding output pool. We will continue the mutant screening, and the attenuated mutants identified in this screening will be tested for attenuation during infection of adult laying hens. We expect that the results of this study will contribute to the development of effective method to control egg contamination.

Key Words: Salmonella Enteritidis, Transposon Footprinting, Chicken

M35 Specific gene cloning and sequencing in pectoral muscle of Korean native chicken. S. Sun*, N. Kim, S. Kim, and D. Kim, *Chonnam National University, 300 Yongbong-dong, Buk-gu, Gwangju, 500-577, Korea.*

The objective of this study is to identify specific functional genes that related with growth in Korean native chicken (KNC). The KNC (12 months old, 2.4kg) and Cornish chickens (16 months old, 2.7kg) were obtained from Korean Livestock Research Institute. Pectoralis muscles were dissected and frozen immediately in liquid nitrogen. mRNA was subtracted by suppression hybridization method using PCR-select cDNA Subtraction Kit. Cloned cDNA were inserted in PCR4 Blunt-TOPO vector. The cloned vector was transformed in TOP 10 electro-competent cells. Cloned DNA was sequenced and the homology was compared with GEN-Bank in NCBI. The inserted DNA size was 0.5 - 1.0kb from agarose gel electrophoresis. Seven hundred cDNAs were sequenced and they were identified as triosephosphate isomerase, glyceraldehyde-3-phosphate dehydrogenase, 11-beta-hydroxysteroid dehydrogenase, carbamoyl phosphate synthase, endo-1,4-beta-D-glucanase, and makorin etc. Most genes were not specific in KNC. However, several candidates' genes were identified as a KNC specific DNA. We have been found eight (KNC-NDS-Clone 6, 8, 12, 13, 21, 22, 23, and 24) specific cDNA clones. These sequences were very low (less than 5%) homology in GEN-Bank. Three sequences were registered in GEN-Bank (Chicken, Korean native breast muscle cDNA clone KNC-NDS6, 8, and 21, Bankit 579658, 579768, 584343, respectively). The function was not confirmed yet, but they are related with pectoralis muscle development in chicken.

Key Words: Korean native Chicken, cDNA Clone, Gene Cloning

M36 Chicken and quail microsatellite primers are not efficient markers for guinea fowl. S. N. Nahashon*, N. Adefope, A. Amenyeu, and D. Wright, *Institute of Agricultural and Environmental Research, Tennessee State University, Nashville.*

Microsatellite markers are tandem repeats of short nucleotides which are abundant, evenly distributed and highly polymorphic in eukaryotic genomes. As such, they are a useful tool in poultry breeding. Microsatellite markers have been identified in genomes of poultry such as chickens and quail. Exchange of marker information between chickens, quail and other avian species such as guinea fowl would be an important step towards the construction of a high-resolution comparative genetic map of these poultry species of agricultural importance. Using the polymerase chain reaction, chicken and quail microsatellite markers were tested to see if they would be suitable as genetic linkage markers in guinea fowl. Eighty three percent (30/36) and 73 percent (19/26) of chicken and quail primers, respectively, amplified individual loci in guinea fowl. Fifty percent (15/30) and 42 percent (8/19) of the amplified loci using chicken and quail primers, respectively, were found to be polymorphic. These very few chicken and quail microsatellite markers that seem to work well in guinea fowl could be used as anchor points for comparative mapping.

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. Ramos³, D. Abi-Ghanem¹, M. H. Falahatpisheh³, and L. R. Berghman^{1,2}, ¹Department of Poultry Science, Texas A&M University, College Station, ²Department of Veterinary Pathobiology, Texas A&M University, College Station, ³Center 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

M41 Preparation and characteristics of spent hen meat enzymatic hydrolysate. O. Sangthrapitikul, 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 were 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 chickeny, meaty, mouth feeling, bitterness, and umami sensory

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. Ding^{*1}, Y. H. Ko¹, M. C. Huang², Y. P. Lee², and W. T. K. Cheng¹, ¹Dept. of Animal Science, National Taiwan University, Taipei 106, Taiwan, ²Dept. of Animal Science, National Chung Hsiung 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. . .

PSA-Processing and Products

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 treatments followed by P+A+B, A, and P+B. Considering enzyme efficacy, cost, and sensory attributes, P+A and P+A+B were recommended for spent hen meat hydrolysate preparation.

Key Words: Spent Hen Meat, Enzyme, Hydrolysate

M42 Spent hen meat enzymatic hydrolysate as a flavoring base. O. Sangthrapitikul, 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 hens. Proteins are the best sources of flavor because of their amino acids, peptide, 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