

Breeding and Genetics: Applications and Methods in Animal Breeding

T38 Effect of diet and sex on growth of cattle evaluated with non-linear mixed effects models. A. Dufek^{*1,2} and E. Vacatko^{1,2}, ¹Research Institute for Cattle Breeding, Ltd., Rapotín, Czech Republic, ²AgriResearch Rapotín Ltd., Vlkov, Czech Republic.

Accurate statistical model is a reliable basis for testing hypothesis especially in cases of non-linear relationship between variables. The aim of this study was to analyze mass growth pattern in beef cattle in the R software. We used the Gompertz and logistic function to describe the mass vs. age relationship and to test differences in growth patterns among groups of 2x2 experimental design (heifers, bulls vs. intensive fattening system: IF = maize silage in feedlot, extensive fattening system: EF = grazing, finishing on brewer's grains). Repeated measures growth data (8 measures per animal, n = 76) were evaluated in the package *nlme* (3.1-92) in the R (2.9.1). The Gompertz [$y = A * \exp(-\exp(-K * (x - T_i)))$] and logistic [$y = A / (1 + \exp(-K * (x - T_i)))$] functions were parameterized in the R where A = a response (body mass [kg]) that approaches a horizontal asymptote as $x \rightarrow \infty$, \exp = exponential function, K = a rate constant, x = age, T_i = the inflection point representing age with the highest growth rate. The values of the parameters for the basic models including all animals were A = 613, K = 0.004, T_i = 240 for Gompertz and A = 565, K = 0.006, T_i = 299 for logistic function. Based on the lower residual sum of square, the logistic function was selected to build the mixed model with one random effect: animal, 2 fixed effects: sex, fattening system and one covariate: the day of birth of an animal in a suckler herd representing the effect of season. Significance of the effects was determined using likelihood ratio test. The effects of sex, diet and interaction on the A and T_i were significant on the level $P < 0.001$; the A-values were 897, 470, 703, 372 and the T_i were 348, 278, 345, 205 for IF bulls, EF bulls, IF heifers, EF heifers, respectively. The date of birth had no effect on the A ($P = 0.67$) or T_i ($P = 0.12$). Analysis of residual variability showed differences between groups of sex ($P < 0.001$) and diet ($P < 0.001$): the standard error for the heifers was 49% of that for the bulls and for the IF group was 68% of that for the EF group. The results revealed that fattening system and sex affected both growing pattern and its variability. The *nlme* in the R is very effective tool for non-linear analyses.

Key Words: growth, nonlinear, mixed

T39 The effect of the ancestor on inbreeding depression in milk yield during the first lactation. J. Bezdicek^{*1}, L. Stadnik², F. Louda³, and O. Latal¹, ¹Agrovýzkum Rapotín Ltd., Vlkov, Czech Republic, ²Czech University of Life Sciences Prague, Prague, Czech Republic, ³Research Institute for Cattle Breeding, Ltd., Vlkov, Czech Republic.

The objective of this study was to examine the effect of ancestor on inbreeding depression in milk yield (in kg) in Holstein cows. In total we evaluated differences in 9 ancestors. The database included Holstein cows (215,000) calved in the Czech Republic in the years 1995–2006. For proper comparison, each inbred cow was assigned an outbred equal. Inbred cows were matched with their outbred equals on characteristics such as identical sire, first calving on the same farm, in the same year and period (± 2 mo) and dam reaching the same breeding value of milk production ($\pm 5\%$). In each group of ancestors, the goal to create pairs of inbred and outbred cows equivalent in terms of origin (the same sire, dam with similar breeding value) and which would also produce in the same environment. The PROC GLM of SAS[®] with fixed effects (F_X ,

ancestor, age at first calving, year of birth, milk production, breeding values of the sire and dam) was applied to all data. For evaluation of F_X level we used the software B-calc. The level of inbreeding was between $F_X = 3.125$ –6.25%. Differences in the inbreeding depression of the 9 ancestors with the following number of inbred daughters (144; 107; 24; 48; 40; 25; 21; 20; 20) were evaluated. The total group of inbred cows (n = 449 cows) showed a significant decrease in milk production (-269 kg; $P < 0.001$) compared with their outbred equals (n = 449). A decrease in milk production was also found after dividing the studied group according to the 9 ancestors. The decrease was in the range -151 to -466 kg. These differences were significant within groups 1 and 9 ($P < 0.05$) and non significant within other groups. An effect of ancestor and breeding value of dam and sire as well was found to be highly significant ($P < 0.001$). Coefficients of determination varied within different groups of ancestors rating from 0.1552 to 0.5601 (total group 0.3514). The correlation coefficient (negative) between milk production and calculated coefficient F_X was significant ($r = -0.09$; $P < 0.01$). This study showed an inbreeding level $F_X = 3.125$ –6.25% depression effect on milk production. There was also a significant effect of ancestor found.

Key Words: ancestor, inbreeding, milk production

T40 Association between milk production and Holstein fraction of upgraded dairy cattle in the Thai tropics. S. Koonawootrittriron¹, P. Yodklaew¹, M. A. Elzo^{*2}, and T. Suwanasopee¹, ¹Kasetsart University, Bangkok, Thailand, ²University of Florida, Gainesville.

Upgrading local dairy cattle to Holstein (H) has been used as a strategy to increase milk production in many tropical countries. The expectation is that milk production will increase alongside increments in H fraction of upgraded animals. However, lack of adaptation of high percent H cattle to tropical conditions may prevent them from achieving their expected production potential. The aim of this study was to evaluate the association between milk production and H fraction of high percent upgraded cattle in Central Thailand using 305-d milk production (MY) of 3,222 first lactation cows from 304 farms. Data were gathered between 1990 and 2011. Eight high H fraction groups were defined: BG1 (H < 0.625), BG2 (0.625 ≤ H < 0.6875), BG3 (0.6875 ≤ H < 0.75), BG4 (0.75 ≤ H < 0.8125), BG5 (0.8125 ≤ H < 0.875), BG6 (0.875 ≤ H < 0.9375), BG7 (0.9375 ≤ H < 1) and BG8 (H). The model included herd-year-season subclass, calving age (month) and breed group as fixed effects, and residual as a random effect. Least squares means (LSM) of MY were estimated for each breed group and then used to fit a second degree polynomial function to explain the change in MY for every 0.0625 H fraction in cows 62.5% H and above. The average milk production of all cows in this study was 4,145 kg (SD = 1,115 kg). Milk production differed across herd-year-seasons, calving ages, and breed group subclasses ($P < 0.01$). Cows with H fraction from 0.8125 to less than 0.875 had the highest MY of all breed groups. The LSM of MY tended to increase as H fraction increased from BG1 (4,075 ± 109 kg) to BG5 (4,285 ± 47 kg) and then it decreased toward BG8 (4,120 ± 76 kg). This association between MY and H fraction can be explained with a second degree polynomial equation: $MY = 2,055 + 5,082(H \text{ fraction}) - 2,957(H \text{ fraction})^2$ ($R^2 = 0.61$). The quadratic association between MY and H fraction found in Central Thailand stressed the limitations of upgrading adapted local dairy cattle to H as a means of increasing milk production under tropical conditions.

Key Words: milk production, tropics, upgrading

T41 Genetic analysis of longevity traits in a Holstein cattle population near Benghazi, Libya. E. Abdalla*¹, S. A. M. Bozrayda², and I. A. S. Al-Drussi², ¹*Department of Animal Sciences, University of Wisconsin-Madison, Madison*, ²*Department of Animal Production, University of Benghazi, Benghazi, Libya*.

The aim of this study was to estimate the longevity of 2196 German Holstein Frisian cows under Libyan conditions. Three different longevity measurements were used to estimate the effect of inbreeding and management on the survival of those cows. True herd life (THL), which is the period in days from birth of an animal until culling, productive life (PL), which is the period in days from birth of an animal until culling and number of lactations were used as measurements of longevity. Cows were distributed in 6 generations in the period from 1989 to 2004. In 1996, Libyan dairy cattle producers faced some difficulties in importing semen from foreign countries so they started using local sires. The analysis was performed using linear animal model. Origin of sire, generation, age at first calving, level of milk production, year and month of calving were considered as fixed effects. Additive animal effect was the only random effect in the model and days open was included as a covariate. All factors included in the model showed a highly significant effect ($P < 0.001$) on THL, PL, number of lactations and 305-d milk yield with the exception of true herd life, which was independent of age at first calving and month of calving. Daughters of local sires compared with daughters of North American and European sires, had a shorter THL and PL ($P < 0.01$). They also had less number of lactations and lower 305-d milk yield at the same significant level. Heritability estimates of longevity traits and 305-d milk yield were low because the effect of inbreeding in the last 3 generations. Effect of inbreeding was also clear on longevity traits. Very high genetic and phenotypic correlations were found between longevity traits. Genetically, 305-d milk yield was moderately correlated with longevity traits.

Key Words: longevity, heritability, genetic correlations

T42 Ranking of Brown Swiss cattle based on genetic evaluation and grades in judgment at the show ring. R. Ramírez-Valverde,* R. Núñez-Domínguez, M. Hernández-León, and M. A. Pablo-Altunár, *Universidad Autónoma Chapingo, Chapingo, Mexico, Mexico*.

The objective was to determine the association between ranking of animals based on grades of conformation in judgment of cattle (JUD) at the show ring and their predicted transmitting abilities (PTA), for registered Brown Swiss cattle in Mexico. Ranking values obtained in JUD were transformed using the rankit transformation, assigning the highest rankit to the first place. Correlation analyses were performed between JUD and PTA. Records of JUD were used for the total of 735 animals; by sex (454 males and 194 females), in 6 years of livestock national show ring competitions (2003, 2004, 2005, 2006, 2009 and 2010) and 3 categories (adult, youth and calf). PTA values came from the most recent national genetic evaluation (2009) for milk yield adjusted to 210 d. Additionally, averages of the PTA and percentage of animals with positive PTA from those used in JUD were estimated. Using the complete data set, correlation between JUD and PTA was different from zero (0.17, $P < 0.05$). This result suggests a low association between both ways to evaluate animals. The correlation between JUD and PTA of adult animals was higher than using those of young animals and calves, which indicates a better association for adults. Correlations by sex and category varied throughout the years; this could indicate differences in the ability to judge animals by evaluators. Averages of the animals' PTA were positive and the percentages of animals with positive PTA

fluctuated between 67 and 86%, indicating just a tendency of Brown Swiss breeders to use animals genetically superior in the JUD.

Key Words: breeding value, judgment of cattle, Brown Swiss

T43 Genetic evaluation of mobility for Brown Swiss dairy cattle. G. R. Wiggans¹, J. R. Wright*¹, C. J. Muenzenberger², and R. R. Neitzel², ¹*Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD*, ²*Brown Swiss Cattle Breeders Association of the USA, Beloit, WI*.

Genetic parameters were estimated for mobility score and 16 current linear type traits for Brown Swiss dairy cattle. Mobility is defined as a composite trait measuring the cow's ability to move as well as the structure of her feet, pasterns, and legs. Scores from 50 to 99 were assigned by appraisers for the Brown Swiss Cattle Breeders Association beginning in June 2007. Only scores made before 69 mo of age were used. After edits, 32,710 records were available for 19,472 cows in 819 herds. The model included fixed effects for the interaction of herd and appraisal date (2109 groups); appraisal age within parity (46 groups); lactation stage within parity (21 groups), as well as random effects for animal, permanent environment and residual error. A multitrait analysis was run using canonical transformation, multiple diagonalization, and a decelerated expectation-maximization REML algorithm. Resulting heritability was 0.21 for mobility, and ranged from 0.06 to 0.37 for the other 16 type traits. The traits with the highest genetic correlation with mobility were final score (0.78), rear legs rear view (0.74), rear udder width (0.52) and foot angle (0.51). Predicted transmitting ability (PTA) for mobility was calculated using the current Brown Swiss multitrait type evaluation system, but using only appraisals where all traits were scored. For 1868 bulls evaluated, PTA mobility ranged from 1.6 to -1.8, standard deviation 0.5, and was most highly correlated with the PTA for final score (0.88), rear legs rear view (0.77), rear udder height (0.70) and rear udder width (0.69), similar to the trait correlations as was expected. When matched with official evaluations from August 2011, PTA mobility had moderately high correlations with PTA of milk, fat, protein, and productive life (0.31 to 0.41). The mobility trait may increase accuracy and timeliness of predictions of productive life by increasing the accuracy of the foot and leg composite.

Key Words: mobility, type trait, genetic evaluation

T405 Covariance functions, genetic parameters and breeding values for longitudinal ultrasound measures of ribeye area in a Colombian multibreed cattle population. C. A. Martínez¹, M. A. Elzo*², A. Jiménez³, C. Manrique¹, and G. Hu², ¹*Universidad Nacional de Colombia, Bogota, Colombia*, ²*University of Florida, Gainesville*, ³*Colombian Association of Zebu Cattle Breeders, Bogota, Colombia*.

The objective of this research was to obtain restricted maximum likelihood estimates of covariance functions and predictions of breeding values for longitudinal records of ribeye area measured by ultrasound in a Colombian multibreed cattle population. The data set contained 708 records from 340 calves progeny of 37 sires from 9 breeds (Gray Brahman, Red Brahman, Guzerat, Blanco Orejinegro, Romosinuano, Braunvieh, Normand, Limousine and Simmental) mated to Gray Brahman Cows. The model was a random regression model that used Legendre polynomials (LP) of order 1 to 3. Fixed effects were age of animal, dam parity, contemporary group (herd-year-season-sex), breed additive genetic and heterosis, whereas direct and maternal additive genetic and maternal permanent environment were random effects.

Residual variances were modeled as constant or changing across the growth trajectory. Models were compared with the corrected Akaike's information criterion and the Schwarz's Bayesian information criterion. The best model had first order LP and constant residual variance. This model was used to obtain genetic parameters and breeding values. Direct additive genetic variance decreased until 156 d of age and increased afterward. Maternal additive genetic and maternal permanent environment variances increased with age. Direct heritability estimates for REA at 4 mo, weaning, 12 and 15 mo (taken as target ages) were 0.004, 0.01, 0.03 and 0.06, respectively. Maternal heritabilities for the same ages were 0.32, 0.35, 0.37 and 0.38. Direct additive correlations ranged from -0.7 to 1. Maternal additive genetic and permanent environmental correlations were close to unity across the entire range of ages. According to these results selection for maternal ability appeared to be feasible in this multibreed population and maternal effects showed an important influence on REA pre and postweaning. Validation of these results with larger multigenerational multibreed populations is required.

Key Words: carcass composition, covariance functions, crossbred cattle

T44 Considerations in using residual feed intake to define feed efficiency in dairy cattle. M. VandeHaar*¹, D. M. Spurlock², L. Armentano³, R. Tempelman¹, K. Weigel³, and R. Veerkamp⁴, ¹Michigan State University, East Lansing, ²Iowa State University, Ames, ³University of Wisconsin, Madison, ⁴Wageningen UR, Wageningen, the Netherlands.

With the advent of genomic selection, the dairy industry will soon be able to focus more directly on selection for feed efficiency. Thus, it is important that geneticists and nutritionists agree on how best to define and measure feed efficiency. The objective of this study is to quantify relationships among factors that affect feed efficiency in dairy cattle. Residual feed intake (RFI) is a measure of actual versus predicted intake for an individual. Predicted intake can be determined from nutritional models, or it can be determined statistically as the deviation from average intake of cohorts, after adjustment for differences in production, body weight (BW), and/or BW changes. A cow with negative RFI is more efficient than her cohorts because she has lower maintenance requirements, digests feed more efficiently, or uses digested feed more efficiently for maintenance, gain, or milk. Decisions about whether and how to adjust for differences in BW or BW change are critical to selection strategies focused on improving feed efficiency. Inappropriate adjustment for BW and body energy change may cause inadvertent bias toward cows that are larger, lose body condition to support milk output, or gain body condition when fed a high energy diet. Moreover, adjustment for BW change requires accurate measures of BW that are not unduly influenced by gut fill. Daily feed intake and milk production, and weekly body weight and milk composition data were recorded on 500 cows for 8 wk starting at approximately 70 DIM. RFI was calculated as the deviation from average intake of cohorts, after appropriate adjustments. Metabolic BW was a significant contributor to variation in intake. However, it accounted for only 10% of the variation whereas milk energy output accounted for 60%. BW change accounted for even less variation in intake, but its consideration likely is essential to ensure improvement in feed efficiency does not occur at the expense of health and fertility. Careful consideration of all factors affecting feed efficiency, including RFI, maintenance requirements, and production, will be necessary to achieve continued improvement of feed efficiency.

Key Words: genomic selection, feed efficiency, residual feed intake

T45 Contribution of heredity, nutrition and management to milk yield improvement in Shanghai from 1998 to 2010. G. L. Liu*^{1,2}, L. M. Huang², C. G. Zhang¹, X. L. Tang², and F. S. Fu², ¹State Key Laboratory of Dairy Biotechnology, Shanghai Bright Holstan Co. Ltd., Shanghai, China, ²Shanghai Dairy Breeding Center Co. Ltd., Shanghai, China.

Milk yield of Chinese Holstein cow is influenced by a variety of factors, including management, genetic effect, nutritional status, disease and environment. The purpose of this work was to establish the contribution of heredity, nutrition and management to milk yield improvement in Shanghai area. Milk yield changes were analyzed with total 68,138 milk yield records of 17,034 cows in 10 dairy farms from Shanghai Dairy Herd Improvement Project (from 1998 to 2010). The nutritional statuses of the 10 dairy farms were evaluated through 120 TMR diet samples assays. The management statuses were quantified through Brightdairy Thousand Points Evaluation. The hereditary effects were analyzed with breeding value of sires and maternal grandsires of the 17,034 cows. Hereditary effect, nutritional status and management status were defined as independent variables, and milk yield change as dependent variable. The results indicated that average 305-d milk yield increased from 7,418 kg in 1998 to 8,356 kg in 2010. Hereditary effect, nutritional status and management status were the significant factors ($P < 0.05$) affecting milk yield improvement. The results of path analysis revealed that management status (cumulative effect was 0.3324) had the highest positive relationship with milk yield improvement followed by hereditary effect (0.2816) and nutritional status (0.2086).

Key Words: heredity, nutrition, management

T46 Multiple trait analysis for milk yield and milking time of Holstein Cows. L. El Faro*¹, J. P. Pereira², C. C. P. Paz¹, D. A. C. Cruz³, V. L. Cardoso¹, and A. B. Bignardi⁴, ¹APTA/SAA, Ribeirao Preto, Sao Paulo, Brazil, ²UNESP, Jaboticabal, Sao Paulo, Brazil, ³Instituto de Zootecnia, Nova Odessa, Sao Paulo, Brazil, ⁴Federal University of Mato Grosso, Rondonopolis, Mato Grosso, Brazil.

Test-day milk yields and milking time of 2,175 first lactation Holstein cows of one herd of southeast region of Brazil, calving from 1997 to 2005 were analyzed by standard multiple trait model (MT), principal components (PC) and by random regression models (RRM). Cows were milked 3 times a day, by electronic machines, totalizing 18,666 records. The reduced rank analysis adjusted the first 2, 3, or 4 genetic principal components. RRM fitted Legendre polynomials (LP) for random additive genetic and permanent environmental trends, respectively with 4 and 5 coefficients. For all models, fixed effects included contemporary groups (year-month of test), linear and quadratic effects of age of cow at calving, and management group. For RRM only, the average trend of milk yield and milking time were fitted by a third order LP and residual variances by step functions considering 4 heterogeneous classes. Comparing MT and PC models, a PC with 2 genetic principal components (PC2), with 220 parameters, was enough to fit the data. Heritability estimates for milk yields ranged from 0.10 to 0.32 and from 0.07 to 0.29 for milking time, considering PC2. For RRM the estimates ranged from 0.17 to 0.35 for milk and from 0.23 to 0.33 for milking time. Both models estimated higher heritability at the end of lactation. The RRM was less parameterized (105 parameters) and produced higher heritability estimates than PC2, but unexpected negative genetic correlation between some milk yields were estimated by RRM, differently from those estimated by PC2 model. Genetic correlation for PC2 were all positive and higher estimates were found among closer test-days, ranging from 0.38 to 0.99 for milk yields and from 0.33 to 0.99 for milking time. The genetic correlations of milk yields and milking time at the same test-days were negative

between records of the first half of lactation (-0.38 to 0.99) and positive on the second half (0.06 to 0.61), but the association was stronger for the first 5 mo. The negative genetic correlation at the first half of lactation is in desirable direction, suggesting that greater production is associated with smaller milking time or higher milk flow. This could be related to a scaling factor because the milk yield is higher during early lactation

Key Words: dairy cattle, functional traits, longitudinal data

T47 Milk fat:protein ratio in lactating dairy cows: Effects on conception at first postpartum AI. A. H. Souza*¹, L. F. Ferraretto¹, P. D. Carvalho¹, A. R. Dresch¹, L. M. Vieira^{1,2}, R. A. Cerri³, M. C. Wiltbank¹, and R. D. Shaver¹, ¹University of Wisconsin-Madison, Madison, ²University of Sao Paulo-VRA, SP 05508, Brazil, ³University of British Columbia, BC, Canada.

Objectives of this retrospective study were to use information of milk composition from the first 5 DHIA milk test results to predict conception at 1st postpartum AI (CRAI1) in lactating Holstein cows. Specific interest was to study if milk fat:protein ratio (FPR) was associated with CRAI1. Edits in the data set were: Holstein herds only, herd size ≥ 100 lactating cows only, herds with CRAI1 between 20 to 60% only, DIM at 1st AI between 30 to 200d, only confirmed pregnancy outcomes included, lactation number 1 to 6 only, 305ME $\geq 20,000$, %protein between 2.0 to 4.5, and %fat between 1 to 8. After edits, data from 207,506 1st postpartum breedings performed in 648 herds in Midwest-USA from July/2009 to July/2010 were included in the analysis. A scoring system based on FPR in a scale from 0 to 5 was as follows: FPRS0, cows with zero milk tests with FPR within 1 to 1.4 included; FPRS1, cows with only 1 out of first 5 milk tests with FPR within 1 to 1.4 included; FPRS2, cows with 2 out of 5 milk tests with FPR within 1 to 1.4; so forth. The procedure Glimmix of SAS using cow within herd and herd as random effects was used. The software Weka was used to find thresholds of milk composition and CRAI1. At first test, only about 50% of the cows had their FPR within 1 to 1.4, but this percentage increased to $\sim 70\%$ at 2nd through 5th tests. Most cows not 1–1.4 FPR were above ($\sim 45\%$ of the cows at 1st test), and only minority ($\sim 5\%$ at 1st test) below these thresholds. At 5th test % of cows above 1.4 FPR decreased to only $\sim 10\%$; but, % of cows below 1.0 FPR increased to $\sim 18\%$. This pattern did not ($P > 0.10$) seem to change throughout different seasons. In addition, FPRS5 cows presented significantly ($P < 0.01$) greater CRAI1, followed by FPRS4, and cows with FPRS0 to 3 did not differ in terms of conception at 1st AI (FPRS5 = 38.8%a, FPRS4 = 36.8%b; FPRS3 = 35.2%c; FPRS2 = 34.4%c, FPRS1 = 34.7c; FPRS0 = 34.2%c). Interestingly, an interaction between FPRS and season was found in which cows with FPRS5 had essentially same CRAI1 across all seasons; however, FPRS ≤ 3 had considerably lower CRAI1 in warmer months compared with cooler months of the year. In conclusion, cows presenting 4 or more out of the first 5 postpartum milk tests within FPR range of 1 to 1.4 seem to have improved fertility after 1st postpartum AI. Possible underlying reasons for this lower fertility in cows deviating from 1 to 1.4 FPR at beginning of lactation need to be further investigated through manipulative studies. Supported by AgSource Cooperative Services, USDA Grant 2010–85122–20612.

Key Words: milk composition, fertility, dairy cow

T48 Prediction of milk and fat production and estimation of breeding values in Holstein dairy cows using neuro-fuzzy and artificial neural networks. S. Shahinfar*¹, H. Mehrabani-Yeganeh¹, C. Lucas², A. Kalhor², A. Kazemian², and K. A. Weigel³, ¹Department of Animal Science, University of Tehran, Karaj, Tehran, Iran, ²Center of Excellence: Control and Intelligent Processing, Faculty of Electrical and Computer Engineering, Tehran, Iran, ³Department of Dairy Science, University of Wisconsin-Madison, Madison.

New computational techniques enable for rapid data analysis and fast decision making on dairy farms. The goals of such techniques are to detect short-term management changes and adjust the breeding strategies in real time. The objective of this study was to investigate the potential of 2 types of intelligent learning methods, artificial neural networks (ANN) and neuro-fuzzy systems (NFS), for computing the estimating breeding values (EBV) and production potential of Iranian dairy cattle. The back propagation algorithm was used to build ANN that could predict breeding values from the performance data of selection candidates. Subsequently, fuzzy logic was incorporated into the ANN to form a NFS that was also used to predict the breeding values and performance records. Explanatory variables included age at first calving, days in milk, ambient temperature, ambient humidity, length of the photoperiod, raw and adjusted (ME) milk and fat production and average production of contemporaries, and milk and fat EBV of parents. Correlations of 0.7 and 0.8 were achieved between predicted and actual values for milk and fat production, respectively. Correlations between EBV for milk yield and predictions from the ANN and NFS learning method were 0.917 and 0.926, respectively, whereas for fat yield correlation were 0.926 and 0.932, respectively. Finally, correlations between multi-trait predictions of BLUP EBV for milk and fat yield and corresponding predictions from a multi-trait implementation of ANN were 0.925 and 0.930, respectively; correlations with predictions from a multi-trait implementation of NFS were 0.935 and 0.949, respectively for milk and fat yield.

Key Words: artificial neural networks, neuro-fuzzy systems, machine learning

T49 New software for sparse matrix factorization and inversion using the supernodal techniques. Y. Masuda* and M. Suzuki, *Obihiro University of A & VM, Obihiro, Japan.*

We developed a set of subroutines for various sparse matrix operations including symbolic and numerical factorization, solution, and sparse inversion by using some modern sparse algorithms. Some programs for ordering or symbolic operations were imported from public domain packages. Ordering routines (AMD, QAMD, and AMF) were extracted from the MUMPS package. Symbolic factorization was performed by SMBFCT from the public domain version of SPARSPAK with some modifications. Supernodal left-looking approach for factorization and inverse-multifrontal method for sparse inversion were implemented. They relied on Basic Linear Algebra Subprograms (BLAS). When a highly optimized BLAS library was used, supernodal algorithms for factorization and inversion were 5 and 10 times faster than traditional approaches for a coefficient matrix of order 1 million or more from an animal model with random regressions. The time-efficiency was more improved as increasing the order. For solution of mixed model equations, estimation of genetic parameters by restricted maximum likelihood, and calculation of reliabilities, computing time would be greatly reduced. All programs were written in standard Fortran 95 and packaged into several modules. The source codes are available by requests to the first author for the academic and noncommercial purposes.

Key Words: computation, algorithms, mixed model equations

T50 Genotype × climate interaction in the genetic evaluation for growing traits in Braunvieh cattle. L. A. Saavedra-Jiménez¹, R. Ramírez-Valverde¹, R. Núñez-Domínguez*¹, N. López-Villalobos², A. Ruiz-Flores¹, and J. G. García-Muñiz¹, ¹Universidad Autónoma Chapingo, Chapingo, México, ²Massey University, Palmerston North, New Zealand.

The presence of genotype × environment interaction causes changes in ranking of breeding values (BV) of sires from one environment to another, which affects genetic progress. The objective was to determine the magnitude of genotype × climate interaction (G×C) for growth traits in the genetic evaluation of Braunvieh cattle. Traits studied were weaning weight (WW) and yearling weight (YW). Records provided by the Asociación Mexicana de Criadores de Ganado Suizo de Registro, were grouped based on the meteorological variables recorded nearest to the herd by the National Weather System. The CLUSTER procedure in SAS was used to classify herds into 3 climates: dry tropic (DT), wet tropic (WT) and temperate (TE). Records of WW were 5348, 4501 and 2515 in DT, WT and TE, respectively, with 25173 animals in the pedigree. For YW, there were 3811, 2652 and 1528 records in DT, WT and TE, respectively, with 18072 animals in the pedigree. An animal model with ASReml software was used to estimate genetic parameters and to predict BVs. Bivariate analyses were carried out for pairwise combinations of climates for each growth trait. The criteria to evaluate G×C were: 1) genetic correlations (r_g) in bivariate analyses, and 2) frequencies of coincidence (FC) in the ranking of top 25 sires. Estimates of r_g between DT and WT, DT and TE, and WT and TE were -0.36, 0.84 and 0.72 for WW, and 0.23, 0.99 and 0.23 for YW, respectively. The FC between DT and WT, DT and TE, and WT and TE were 0.16, 0.92 and 0.76 for WW, and 0.60, 1.00 and 0.64 for YW, respectively. The size of r_g and FC imply the presence of G×C when compared WT with DT or TE, suggesting that genetic evaluations should be carried out separately for animals performing under wet tropical conditions.

Key Words: genotype by environment, weaning weight, Braunvieh cattle

T51 Relationships among visual scores with feedlot performance and feed efficiency in *Bos indicus* cattle. P. H. Cancian*¹, S. L. Silva¹, A. C. Ianni¹, F. R. Manicardi¹, R. C. Gomes², and J. B. S. Ferraz¹, ¹Faculdade de Zootecnia e Engenharia de Alimentos / Universidade de São Paulo (FZEA/USP), Pirassununga, São Paulo, Brazil, ²Departamento de Zootecnia / Universidade Estadual de Londrina (UEL), Londrina, Paraná, Brazil.

Visual evaluation of live beef cattle have been largely used to identify more adequate animals for meat production and, in Brazil, even as selection criteria in breeding programs. However, the relationship of these evaluations with feed efficiency traits in feedlot are unknown. The objective of this work was to evaluate phenotypic correlations of visual scores of conformation (C), precocity (P) and muscularity (M) with feedlot performance. Forty 3 bulls and 43 steers of Nellore were visually evaluated by an experienced technician twice. In the first evaluation (VS16), cattle (16-mo old, 313 ± 25 kg BW) was grazing in *Brachiaria* spp. pastures. At 22-mo of age, they were fed ad libitum for 84 d for individual dry matter intake (DMI) and average daily gain (ADG) records. A second evaluation of visual scores (VS22) were carried out on d 21 of the 84-d period. The body weight (BW) was measured each 28 d to calculate average daily gain (ADG) and gain to feed ratio (G:F). The visual were assigned to each animal in a within-gender comparison and the relationship among traits was evaluated by Pearson correlation. Visual scores showed moderate to high correlations with BW in both

evaluations. The correlations between BW and C were 0.75 and 0.35 in VS16 and VS22, whereas with P the correlations coefficients were 0.46 and 0.29, respectively. For muscularity, the correlation with BW was 0.5 in both evaluations. Conformation score was positively correlated with DMI and ADG in both VS16 (0.47 and 0.27) and VS22 (0.33 and 0.13) and negatively with G:F in both evaluations (-0.15 and -0.19). Correlation of P with DMI was low and positive (0.25) in VS16 and nonsignificant ($P > 0.05$) with the rest of traits in both evaluations. Visual evaluation of M had nonsignificant correlations with all efficiency traits in both evaluations, except with DMI in VS22 (0.25; $P < 0.05$). The visual score of conformation may be an indication that animals with larger frame sizes, can ingest more food than the others. Visual assessments for precocity and musculature appeared as features of low accuracy to select efficient cattle.

Key Words: conformation, precocity, muscularity

T52 Genetic parameters for carcass traits and weaning weight of composite beef cattle in Brazil. J. Ramírez-Díaz¹, T. A. Oliveira¹, A. Zampar¹, S. F. N. Pertile¹, M. A. Elzo³, J. B. S. Ferraz², and G. B. Mourão*¹, ¹University of São Paulo - ESALQ, Piracicaba, São Paulo, Brazil, ²University of São Paulo - FZEA, Pirassununga, São Paulo, Brazil, ³University of Florida, Gainesville.

Heritability and genetic correlations for weaning weight (WW; n = 328,326) and real-time ultrasound measurements of ribeye area (REA), subcutaneous fat thickness (BF) and rump fat (RF) from 863 calves were estimated using data from the Montana Tropical composite beef cattle population in Brazil. Images of carcass traits were obtained for ultrasound scanning (Aloka, SSD 500, with linear transducer of 3.5 megahertz and 172 mm long and acoustic guide attached) and analyzed using LINCE software. Calves were weaned at 6 m (205 d) of age, and ultrasounds were collected at 21 m (639 d) of age. Single-trait and multi-trait analyses with direct additive effects only were considered. The maternal additive effects was considered only for WW. Models included contemporary group (herd of birth-herd of weaning-herd of measurement-year of birth-season of birth-sex of animal) as a fixed effect, and age of dam, individual and maternal heterozygosity, and age at measurement as covariates for single trait analyses. Two-trait analyses excluded the covariate for age of dam. Random effects were animal and residual. The A^{-1} matrix contained 536,120 animals. Variance and covariance components were estimated using REML methodology and ASREML software. Heritabilities (h^2) and standard error (in parenthesis) for WW, BF and RF were 0.31(0.0104), 0.13(0.1320), 0.10(0.1278) respectively. The h^2 for REA was close to zero. Maternal (h^2) was 0.1940(0.0066) for WW. The genetic correlation between WW and BF was near zero (0.038), low and negative between WW and RF (-0.26), and positive between WW and REA (0.20) with standard errors of 0.23, 0.27 and 0.24. The low heritability estimates for ultrasound traits indicated that selection for these traits at this age would be rather ineffective. Selection for WW may reduce RF. In the 2-trait analysis, the h^2 were 0.36 (0.0047) and 0.14 (0.1322) for WW and BF, 0.36 (0.0047) and 0.12 (0.1322) for WW and RF and 0.36 (0.0047) and 0.01 (0.0829) for WW and REA. These results should be considered with caution because of the small number of observations for ultrasound carcass traits.

Key Words: beef cattle, tropical composite, ultrasound traits

T53 Influence of maternal genetic effect on the estimation of genetic parameters in post-weaning traits. G. A. Oliveira Júnior^{*1}, F. M. Rezende¹, J. B. S. Ferraz¹, J. P. Eler¹, and G. B. Mourão², ¹Faculdade de Zootecnia e Engenharia de Alimentos - Universidade de São Paulo, Pirassununga, São Paulo, Brazil, ²Escola Superior de Agricultura Luiz de Queiroz - Universidade de São Paulo, Piracicaba, São Paulo, Brazil.

The maternal genetic effect may interfere with the performance of the animal's post-weaning traits in beef cattle. The aim of this study was to estimate the importance of maternal effects on genetic analyses of post-weaning traits in Nelore cattle. The database used for estimation of (co)variance components contained information from 115,922 animals corresponding to 176,679 animals in the pedigree, with 80,581 different dams. The traits analyzed were scrotal circumference (SC), visual score of muscling (MUSC) and post weaning weight gain (PWGAIN), measured around 18 mo of age. (Co)variance components and direct breeding value estimates were predicted using restricted maximum likelihood and univariate animal model analyses as implemented in the MTDFREML software. Two models were evaluated for each trait: one including only the direct animal effect, and the other including a maternal effect. Contemporary group, the age of animals at the measurement and the age of dam at delivery (AOD), considered as a covariate with quadratic effects, were considered as fixed effects. The AOD was not used for MUSC. The management group at weaning was fitted as a random effect for all analyzed traits. Basic edits involved the exclusion of all information out of the interval between -3.5 and 3.5 standard deviations for each trait, data from contemporary groups including fewer than 20 animals, and data from progeny of sires or dams with only one offspring in the data set. Likelihood ratio tests and Pearson and Spearman correlations were used to compare models. The likelihood ratio test showed that the inclusion of the maternal genetic effect was statistically significant ($P < 0.01$) in the prediction of (co)variance components for all post weaning traits analyzed. However, the rank of the animals did not change, indicating that there is no gain from including genetic maternal effects in the model. The results of the estimates of direct additive heritabilities with no maternal effect were 0.23, 0.21, and 0.55 for PWGAIN, MUSC and SC respectively. When we added the maternal additive effect in the analyses, these results didn't vary significantly (PWGAIN = 0.22, MUSC = 0.23), except for SC, with 0.44 for heritability. The maternal additive heritabilities were lower than the direct additive heritabilities for all traits considered, that was expected. The estimates for maternal additive heritabilities were 0.05 for PWGAIN, 0.01 for MUSC and 0.10 for SC. The prediction of maternal additive genetic merit can be an indicator of maternal effect, mainly on the post weaning weight gain and scrotal circumference traits. However, due to the low value of maternal heritability of these traits, the value of accuracy of these predictions might be low as well and they must be used carefully.

Key Words: *Bos indicus* cattle, genetic parameters, variance components

T54 Selection for resistance to *Haemonchus contortus* in Santa Ines hair sheep: Comparisons of methods of animal evaluation at countryside and in the laboratory. P. S. Oliveira, * J. B. S. Ferraz, J. P. Eler, L. S. Oliveira, C. T. Moncau, M. D. Poleti, B. Silva, F. M. Rezende, G. A. Oliveira Júnior, J. Daniel, and E. C. Mattos, Faculdade de Zootecnia e Engenharia de Alimentos - Universidade de São Paulo, Pirassununga, São Paulo, Brazil.

The use of new tools to assist selection resistant or susceptible animals to gastrointestinal parasites, associated with the fecal egg counts (FEC), have been developed and applied to Santa Ines hair sheep to

distinguish between resistant and susceptible individuals, without the need for laboratory tests. Distinguishment is needed to identify animals to be used in a DNA marker association study that is being developed. Thus, this study aimed to evaluate possible correlations between traits evaluated at countryside in the animals (Conjunctival Mucous Color (FAMACHA) and body score (BS) and in the laboratory (the Fecal Egg Counts (FEC), Hemoglobin (HGB) and Packed Cell volume (PCV)) in 503 sheep from Santa Ines, from 4 herds located in 3 different states of Brazil. For the laboratory analysis were collected individual samples of blood for the determination of HGB and PCV, and feces for FEC. FAMACHA test consisted in the visual evaluation of the color the ocular mucosa (scale from 1 to 5), where the higher value meant more anemic animals. The assessment of BS was performed by palpation in the lumbar region, where 0 meant cachectic animals and 5 meant obese animals. Subsequently, simple correlation coefficients between all variables were obtained by SAS PROC CORR. The correlations of greater magnitude ($P < 0.0001$) were found for FAMACHA with HGB and PCV ($r = -0.63$ and -0.64 respectively) and BS with HGB and PCV ($r = 0.68$ and 0.65 respectively). Lower magnitude correlations were found for FEC with FAMACHA, BS, HGB and PCV ($r = 0.21, 0.25, -0.30$ and -0.29 respectively) and between BS and FAMACHA ($r = -0.44$). Analyzing the study it can be concluded that the association of the method FAMACHA with BS can be considered an efficient method to diagnosis of anemia in Santa Ines sheep at countryside. Furthermore, increase in FEC also reduces levels HGB and PCV, however, this can't be considered as the only cause of anemia in sheep.

Key Words: FAMACHA, body score, packed cell volume

T55 Test-day model for milk yield of dairy buffaloes in Colombia. N. Hurtado Lugo^{*1,2}, G. M. F. de Camargo¹, R. Aspilcuenta¹, S. Gutiérrez², E. Taccari¹, F. M. M. Gil¹, L. G. Albuquerque¹, M. Cerón², and H. Tonhati¹, ¹State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, São Paulo, Brazil, ²University of Antioquia, Medellín, Ant, Colombia.

The test-day model is the preferred method for genetic evaluations in dairy cattle. The aim of this study was to estimate the genetic parameters for the milk yield at the Test-Day (TD) in dairy buffalo in Colombia. Test-day records were collected from 7 dairy herds, members of the Colombian Buffalo Breeders Association (ACB). The TDs were separated in 9 classes of 30 d each, for total of 9 test-day controls (TD, 1 to 9). For this study, 28372 TDs records of 1220 lactations from 1997 to 2009 were used. Single and multiple trait analyses were used and variance components were estimated by Restricted Maximum Likelihood. The (co)variance components were estimated with the MTDFREML software. The model used in the TDs analysis included the additive genetic, permanent environment and residual as random effects; and the contemporary group (herd, year, and season of calving) as fixed effect. The buffalo age at calving was considered as covariate (linear and quadratic). The calving seasons were January–April, May–July, August–October, and November–December. The TDs varied from 4.84 to 3.2 kg/day. The heritability estimations for TD varied from 0.07 ± 0.087 to 0.16 ± 0.11 for single-trait analyses and from 0.31 ± 0.098 to 0.45 ± 0.198 for the multiple-trait analyses. The genetic correlations for single and tetra-trait TD models were high, bigger and varied from 0.36 to 0.96 and from 0.41 to 0.99, respectively. Correlations among TD increased as time between observations decreased for single- and multiple-trait models. In conclusion, the results of this study suggest that selection of buffaloes in Colombia should use breeding values obtained in a multi-trait test-day model, because of their high heritability.

Key Words: buffalo, genetic correlation, yield

T56 Random regression models for test-day milk production for first lactation in Colombian buffaloes. N. Hurtado-Lugo^{*1,2}, M. Cerón², R. Aspilcuelta¹, S. Gutierrez², L. Albuquerque¹, F. R. Araujo Neto¹, G. M. F. de Camargo¹, and H. Tonhati¹, ¹Faculty of Agriculture and Veterinary Sciences, State University of São Paulo, Jaboticabal, São Paulo, Brazil, ²Faculty of Agriculture Sciences, University of Antioquia, Medellín, Colombia.

The Random regression models for genetic evaluation in dairy cattle consider individual lactation curves using ordinary polynomials of linear functions. Alternative models to understand the genetic variability for milk yield along the lactation curve are required for genetic evaluations of the buffalo population in Colombia. The knowledge of the lactation curve may be of interest for production and management requirements of this specie. This study has the aim to estimate the genetic parameters using RRM for the milk yield at the Test-Day in Colombian buffalo dairy. A total of 9432 milk yield records were analyzed, corresponding to 1,746 first lactations of crossbred buffalo cows. The fixed effects were: contemporary group that was composed by farm, month and station of parity and milking days and age of the cow at calving (linear effect) as fixed effects and the random effects were the direct genetic and the permanent environment. The variance components were estimated using the statistical package WOMBAT. The residual variances were heterogeneous, modeled by a step function (LRT), containing 4 classes of variances. Results from different models of analyses were compared by the Restricted Maximum Likelihood (REML) form of the Akaike information criterion (AIC), the Schwarz Bayesian information criterion (BIC) and by inspecting the variance component and genetic parameter estimates. The most appropriate model was the one using a Legendre's polynomial function of 4rd order for the genetic effect and 5th order for the permanent environmental effect (4,5,4). The phenotypic mean for test-day was $3,6 \pm 1,42$ kg. The heritabilities for all models test ranged from 0.38 to 0.01. For the best model (4,5,4) the heritabilities ranged from 0.38 to 0.12. The highest values were observed between the 2 and 5 test day. For genetic and phenotypic correlation estimates ranged from 0.39 to 0.96 and from 0.42 to 0.91, respectively. Genetic correlations were higher than phenotypic ones. The results of this study indicate the necessity to consider the heterogeneity of residual variances to model changes in the variations for days in milk.

Key Words: animal model, Legendre polynomial, heritability

T57 Genetic parameters for growth curves in free range chickens. G. A. Rovadoski, F. L. Silva, T. A. Oliveira, A. Zampar, V. J. M. Savino, A. A. D. Coelho, J. Ramírez-Díaz, G. B. Mourão, R. S. Bueno, and G. A. Oliveira Junior,* University of São Paulo, Piracicaba, São Paulo, Brazil.

Nonlinear models have been used to describe growth in different species. These models feature parameters of biological meaning, and they have proven quite effective, especially in research related to animal breeding programs. The estimation of genetic parameters for growth curves fitted by nonlinear models provides the identification of animals that were more suitable for certain purposes of selection, for example, the optimum age of slaughter. Growth models usually have 2 parameters with biological meaning. The asymptotic weight (A) estimates the adult weight, whereas mature rate (k) is an indicator of the rate at which the animal approaches the adult body weight. The objective of this study was to estimate the genetic variance for the parameters A and k of the growth curves in free-range chickens by univariate and bivariate models. For this experiment we used an experimental lineage called 7P. Data from 11 weights of 934 chickens, being 470 males and 464

females, collected from birth to 84 d of age, totaling 5183 observations. The growth curve was estimated by nonlinear logistic model by OLS. The (co) variances were estimated using the methodology REML by ASREML® software. The coefficients of heritability (h^2) for A were 0.1816(0.0618) and 0.1888(0.630) and for k were 0.1571(0.0569) and 0.1567(0.0568), for the univariate and bivariate, respectively, with little difference between the values obtained for the models. The correlation between A and k, found for the bivariate model was -0.77 , indicating that animals that grow faster have lower adult weight.

Key Words: variance components, heritability, performance

T58 Comparative analyses of proximate and chemical characteristics of eggs from six indigenous bird species. O. T. F. Abanikannda,* A. O. Leigh, and H. Y. Ogungbo, Lagos State University, Ojo, Lagos, Nigeria.

Birds are raised mainly for their meat, eggs or feathers. Egg is a common food and the cheapest per unit source of animal protein and serves as a good source of vitamins and minerals. However, despite its nutritional value some health issues may arise as a result of its consumption. This study was aimed at assessing the inter specie differences in the physical characteristic, proximate composition and chemical constituents of eggs from 6 species (Chicken, Duck, Guinea Fowl, Pigeon, Quail and Turkey) of extensively managed indigenous birds. A total of 240 eggs comprising 40 eggs from each of the 6 species were sampled. The eggs were cleaned, labeled and measured with digital weighing scale and vernier calipers for its physical characteristics (egg weight, length, width, vertical, and horizontal circumferences). Proximate composition (moisture content, dry matter, total ash, crude protein, crude fat and carbohydrate) of the eggs along with mineral analyses (calcium, magnesium, manganese, iron, zinc and cobalt) were conducted using standard laboratory procedures for proximate and mineral assay procedures. All statistical analyses (descriptive and model fitting) were conducted using the JMP software. The one way ANOVA procedure for each of the response variable investigated was fitted by the model $Y_{ij} = \mu + a_i + e_{ij}$, while species was the sole predictor variable. Further comparison of the means was done after a significant ANOVA using the Tukey's post-hoc method. Specie was a significant ($P < 0.001$) source of variation in all the 5 physical characteristics accounting for over 90% of the variation, while its effect was significant ($P < 0.001$) and moderate to high on proximate composition with the exception of crude fat ($P > 0.05$). In the same vein species was a significant ($P < 0.001$) source of variation on mineral content except ($P > 0.05$) for magnesium and zinc. The nutritive value of Quail eggs are quite promising considering its proximate and mineral content mix which makes it a safer and healthier dietary source of nutrients and minerals when compared with Pigeon eggs.

Table 1. Means of proximate composition and mineral content of eggs

Species	N	Crude		Carbo- hydrate (%)	Ca (%)	Fe (ppm)	Co (ppm)	Mn (%)	
		DM (%)	ash (%)						
Chicken	40	26.59 ^b	5.50 ^{ab}	6.51 ^c	33.12 ^c	0.050 ^b	25.71 ^b	0.375 ^b	21.67 ^b
Duck	40	34.40 ^a	4.00 ^{bc}	8.14 ^b	42.35 ^{abc}	0.049 ^b	30.00 ^{ab}	0.350 ^b	27.50 ^b
Guinea Fowl	40	29.93 ^{ab}	6.00 ^a	6.15 ^c	34.78 ^{bc}	0.053 ^b	22.50 ^b	0.400 ^b	18.75 ^b
Pigeon	40	20.25 ^c	3.14 ^c	13.01 ^a	46.50 ^a	0.053 ^b	41.43 ^a	0.543 ^a	68.57 ^a
Quail	40	30.00 ^{ab}	3.25 ^c	8.72 ^b	48.35 ^a	0.120 ^a	20.00 ^b	0.400 ^b	24.00 ^b
Turkey	40	33.87 ^a	3.88 ^c	7.04 ^c	45.40 ^{ab}	0.048 ^b	30.00 ^{ab}	0.400 ^b	23.75 ^b

Key Words: species, proximate composition, mineral content

T59 Statistical classification of six indigenous bird species based on external and internal qualities of their eggs. O. T. F. Aban-ikannnda,* A. O. Leigh, and O. I. Adekanbi, *Lagos State University, Ojo - Lagos, Nigeria.*

Classification is a method of categorizing organism into different groups based on their biological similarities and differences, and it is a systematic grouping of organisms into categories on the basis of evolutionary or structural relationships between them. Conventionally, such classifications could be traditional, phenetic or cladistic but the objective of this study is to employ statistical techniques to discriminate among the different species based on the external and internal measurements of the birds' eggs. A total of 210 eggs comprising 35 each from 6 free ranging indigenous species (chicken, duck, guinea fowl, pigeon, quail and turkey) were sampled. Five external characteristics (egg weight, egg length, egg width, vertical and horizontal circumference), 3 internal qualities (yolk, albumen and shell weights) were measured and 6 indices (shape index, egg surface area, egg volume, surface area to volume ratio, yolk to albumen ratio and egg density) were computed. All weights were measured with a digital scale sensitive up to 0.00g and linear measures were with digital vernier caliper (0.00mm) and flex tape for the circumferences. The distribution and fit model procedures of JMP statistical software were used to analyze the data and further mean separation after a significant effect was done using the Tukey's method. The model for each of the 14 variables studied is given by Y_{ij}

$= \mu + \alpha_i + e_{ij}$. Complete method of hierarchical clustering of JMP was used for classification of the species. Specie was a highly significant ($P < 0.001$) and the largest source of variation in all the parameters studied, accounting mostly for over 95 percent of variation observed except in shape index (31%) and yolk to albumen ratio (36%). Three primary clusters of 2 species each were formed comprising chicken and guinea fowl, duck and turkey, and pigeon and quail, respectively, with the duck and turkey cluster been intermediate in distance between the other 2 clusters. The dendrogram from this clustering is similar to the classification from traditional methods which are used in taxonomy to classify the birds. The result revealed that statistical classification is a reliable and veritable method for specie identification and constellation.

Table 1. Hierarchical clustering history of the 6 species of birds¹

Number of Clusters	Distance	Leader	Joiner
5	2.081991550	Pigeon	Quail
4	2.765695694	Duck	Turkey
3	3.539278540	Chicken	Guinea Fowl
2	5.216181164	Chicken	Duck
1	9.632125371	Chicken	Pigeon

¹Complete method of hierarchical clustering.

Key Words: species, cladistic, cluster analysis