

# Breeding and Genetics: Applications and Methods in Animal Breeding—Pigs, Poultry, Sheep, and Horses

**W195 Genetic analysis of the stayability for running of Thoroughbred horses.** J. A. V. Silva\*, L. H. Kato, A. M. Maiorano, R. A. Curi, and M. D. S. Mota, *Faculdade de Medicina Veterinaria e Zootecnia, UNESP, Botucatu, Sao Paulo, Brasil.*

Stayability is an economically relevant trait; it is directly associated with profitability of the production system by its relationship to specific costs or with efficiency. In this work, stayability is analyzed in racehorses and defined as stayability for running up to 4 years old (STAY4) and up to 6 years old (STAY6). Inclusion of this trait in genetic evaluation programs may permit selection of stallions that will have offspring with a greater probability of remaining productive (running) for a longer period of time. The objectives of the current study were to assess the feasibility of using stayability for running traits to improve the genetic potential of Thoroughbred horses and to examine the genetic relationship between STAY4 and STAY6. Stayability was considered to be a categorical trait and defined as whether a horse (male or female) that remained running up to the age of 4 (STAY4) and 6 (STAY6) yr of age, given that the opportunity to participate in races was provided. Data was gathered for 23,009 and 20,005 animals for STAY4 and STAY6, respectively, born from 1989 onward with performances between 1992 and 2010 analyzed using 2 trait animal threshold model based on Gibbs sampling algorithm. The matrix relationship included 35,422 animals until 6th generation. 60% and 17% were scored 1 for STAY4 and STAY6, respectively. Animals with stayability for running until evaluated ages were scored as 1, and those that failed were scored as 0. Analysis included fixed effects of breeder, breeding season, age at first competition and the linear covariate, the number of races to ages studied, in addition to the random animal effect. The sex and race distance effects were not include in the model because these were not significant. Heritability estimates for STAY4 and STAY6 were  $0.12 \pm 0.03$  and  $0.13 \pm 0.03$ , respectively. The genetic and residual correlation estimates between the 2 traits were  $0.48 \pm 0.18$  and  $0.92 \pm 0.03$ , respectively. Based on the results of this study, STAY can be used for selection of stallions for horse racing. Competition data provide a good tool for measuring the stayability for running in horses.

**Key Words:** heritability, genetic correlation, residual correlation

**W196 Population parameters in Quarter Horses in Brazil.** M. D. S. Mota, R. A. Curi, G. L. Pereira, A. C. Verdugo, and J. A. V. Silva\*, *Faculdade de Medicina Veterinaria e Zootecnia, UNESP, Botucatu, Sao Paulo, Brasil.*

The Quarter Horse was first bred in Brazil from horses imported from the King Ranch in Texas, United States. Since the founding of the Brazilian Association of Quarter Horse Breeders (ABQM) in 1969, there have been approximately 360,000 animals and just over 61,000 breeders, owners and associated in ABQM. In 2012, breeders conducted auctions involving 5,372 horses at an average price of US\$15,000. The objective of this study was to estimate population parameters of Quarter Horses registered by ABQM. We considered 122,355 animals born from 1950 to 2009. Of this total, 5,397 (4.41%) were inbred, with an average inbreeding coefficient of 8.56% and a maximum of 37.5%. To study the probability of origin of genes, we established a reference population of 56,329 animals born between 1980 and 2009. The number of founders (animals with unknown ancestors in the pedigree) was 5,479, while the effective number of founders reached 669.5. The difference between these 2 values indicates that not all horses' founders contributed

equivalently to the population. The evaluation of the effective number of ancestors indicates that the 100 main breed males account for 30.13% of the genetic diversity of the population reference, while the top 10 account for approximately 7.5%.

**Key Words:** genetic diversity, inbreeding, pedigree

**W197 Understanding the impact of frozen semen on swine production systems.** D. Gonzalez-Pena\*, N. V.L. Serão, R. Knox, and S. L. Rodriguez-Zas, *University of Illinois at Urbana-Champaign, Urbana.*

Frozen-thawed (FRO) boar semen preparation can intensify the dissemination of top genetics, reduce animal maintenance costs, enable genetics banking, and facilitate biosecurity compared with fresh-refrigerated (FRE) preparation. However, the freezing process can result in lower farrowing rate and litter size. The goal of this study was to compare the effect of FRO and FRE preparations on genetic improvement and profit. For a 3-tier system, average daily gain (ADG) was the trait studied. The cross of 2 nucleus breeds A and B (500 sows/breed) generated 200,000 AB sows at the multiplier level. The AB sows were mated to breed C boars (originated from 500 breed C nucleus sows) at the commercial level resulting in 4,500,000 weaned pigs/year. To understand the effect of preparation on genetics and profit, the simulation assumed 2.1 semen doses/estrus, 2.25 farrowings/year, 50 collections/boar/year, 6 FRO time spans (one to 6 semesters), 4 farrowing rates levels (60–90%), 9 litter sizes classes (7–15 pigs alive/litter), and 7 boar:sow ratios for FRE (1:172–1:258) and FRO (1:77–1:115) based on 27 and 12 doses/ejaculate for FRE and FRO, respectively. Sow stayability ranged from 1 year (nucleus) to 3 years (commercial) and the involuntary culling was approximately 32%. The 378 simulated scenarios were evaluated in ZPLAN. The average genetic gain for ADG was 19.33g/semester. Line C had the highest ADG of all lines (34% above the mean) and contributed 61% of the total ADG return. Per semester, the profit increased \$0.14 and \$0.33 per 5% increase in farrowing rate for FRE and FRO semen, respectively. The net profit increased \$0.37 and \$0.38 per additional piglet in the litter for FRE and FRO, respectively. The use of FRO for 6 semesters resulted in 6% higher genetic gain than the use of FRE from a boar for 2 semesters. Optimal profit was attained when FRO was used for 4 relative to one semester (16.6% difference). The use of FRO in swine production units for 4 semesters at a boar:sow ratio of 1:115 is profitable and accelerates the genetic improvement relative to FRE.

**Key Words:** frozen semen, fresh semen, simulation

**W198 Estimation of the additive and dominance Variances in South African Duroc pigs.** D. Norris\* and J. W. Ngambi, *University of Limpopo, Sovenga, South Africa.*

The objective of this study was to estimate dominance variance for number born alive (NBA), 21-d litter weight (LWT21) and interval between parities (FI) in South African Duroc pigs. A total of 10,703 NBA, 6883 LWT 21, and 6881 FI records were analyzed. Preliminary analysis showed low level of inbreeding and the elements of the dominance relationship matrix (D) were calculated using values of the additive relationship matrix, A. Bayesian analysis via Gibbs sampling was used to estimate variance components and genetic parameters. Estimates

of additive genetic variance were 0.554, 16.84, and 4.535 for NBA, FI, and LWT21, respectively. Corresponding estimates of dominance variance were 0.246, 9.572, and 0.661 respectively. Dominance effects were statistically not significant for all traits studied. Further research utilizing a larger data set is necessary to make concrete conclusions on the importance of dominance genetic effects for the traits studied.

**Key Words:** pig, additive, dominance

**W199 Accounting for population structure when predicting litter size in commercial pig lines.** L. Tusell\*<sup>1</sup>, S. Forni<sup>2</sup>, P. Pérez<sup>1</sup>, and D. Gianola<sup>1</sup>, <sup>1</sup>*Dept. of Animal Sciences, University of Wisconsin, Madison*, <sup>2</sup>*Genus Plc, Hendersonville, TN*.

Two pig lines (A and B) showed clusters of individuals in plots of the 2 largest principal components extracted from genomic and pedigree-based relationship matrices. This hidden population structure may be due to family aggregation. We assessed whether predictive ability of yet to be observed litter size phenotypes using genome-enabled models would be larger within clusters than within random samples of the whole population. Data from the A and B lines represented 2,598 and 1,604 sows that were assigned into 3 and 2 clusters (i.e., subpopulations), respectively, by visual separation of points observed in the principal component plots of the genomic relationship matrix. The target variable was the average number of piglets born per sow, pre-corrected for systematic environmental effects. Genotypes were obtained using the Illumina PorcineSNP60 BeadChip. Within subpopulations, a 10-fold cross-validation assessed predictive ability of genomic BLUP (GBLUP), reproducing Kernel Hilbert spaces with kernel averaging (RKHS), and a radial basis function neural network (RBFNN). Random samples with the same subpopulation size were used as benchmark, i.e., without accounting for population structure. Predictive ability, measured as the correlation between predicted and observed phenotypes in the testing set ( $r$ ), was very low in 2 subpopulations of the A line: with RBFNN (the model with the highest  $r$  in these subpopulations)  $r$  decreased  $-0.10$  and  $-0.05$  relative to their corresponding random samples using the same model. However,  $r$  (model with the highest  $r$  in each subpopulation shown in parentheses) was slightly better in all other subpopulations with an increase of  $+0.04$  in the remaining A subpopulation, and  $+0.06$  (GBLUP) and  $+0.04$  (RKHS) in the 2 B subpopulations with relative to those observed in the corresponding random samples. This approach could be exploited to potentially increase overall accuracy in predictions within purebred lines.

**Key Words:** genomic prediction, population structure, pig

**W200 Partitioning of within-litter birth weight variation and its distribution in piglets.** T. J. Zindove\*<sup>1</sup>, E. F. Dzomba<sup>1</sup>, A. T. Kanengoni<sup>2</sup>, and M. Chimonyo<sup>1</sup>, <sup>1</sup>*University of KwaZulu-Natal, Pietermaritzburg, KwaZulu-Natal, South Africa*, <sup>2</sup>*Agricultural Research Council, Pretoria, Gauteng, South Africa*.

Increasing within-litter birth weight variation in pigs affects litter performance. The objective of the study was to characterize within-litter birth weight variation in piglets. The study was conducted using 1 788 litters from 740 sow records collected between January 1998 and September 2010 from a Large White  $\times$  Landrace pig herd in South Africa. The factors affecting within-litter birth weight coefficient of variation (CVBWT) were analyzed using the General Linear Model procedure (SAS, 2008). The number of piglets born alive (NBA) ranged from 3 to 18. The mean CVBWT was 17.64% and CVBWT ranged from 0.47 to 50.65%. The distribution of CVBWT in the herd was positively

skewed. Year and month of farrowing did not affect CVBWT ( $P > 0.05$ ). Multiparous sows farrowed litters with higher ( $P < 0.05$ ) CVBWT than gilts. The litter weight (LWT) and NBA, fitted as covariates, also affected ( $P < 0.05$ ) CVBWT. The correlation between CVBWT and NBA was 0.299. Estimated phenotypic correlation between mean birth weight (MBWT) and CVBWT was relatively strong ( $-0.309$ ). The phenotypic correlation between LWT and CVBWT was low (0.058), but significantly different from zero ( $P < 0.05$ ). To enhance profitability of pig enterprises, the selection for NBA should, therefore, be accompanied by selection for CVBWT.

**Key Words:** parity, litter weight, coefficient of variation

**W201 Genetic analysis of longitudinal measurements of feed intake in Piétrain sire lines.** M. Dufrasne\*<sup>1,2</sup>, V. Jaspert<sup>3</sup>, J. Wavreille<sup>4</sup>, and N. Gengler<sup>1</sup>, <sup>1</sup>*Gembloux Agro-Bio Tech, University of Liege, Gembloux, Belgium*, <sup>2</sup>*FRIA, Brussels, Belgium*, <sup>3</sup>*Walloon Pig Breeding Association, Ciney, Belgium*, <sup>4</sup>*Walloon Agricultural Research Centre, Gembloux, Belgium*.

Feed efficiency (FE) is a very important trait in pig production because of the large part of feeding cost in production costs. Because FE involves feed intake (FI), it is useful to develop selection strategies that allow for a reduction of FI while keeping growth rate at least constant. The aim of this study was to estimate the genetic parameters for longitudinal measurements of feed intake (FI) in a crossbred population of pigs. An additional objective will be to develop a genetic evaluation model for the estimation of breeding values for FI of Piétrain boars. Data were collected on crossbred pigs in test station in the context of the genetic evaluation system of Piétrain boars in the Walloon Region of Belgium. Trait analyzed was the individual cumulated FI throughout the progeny-test. Because there were no facilities to record individual FI in the Walloon test station, individual FI were assumed to be averaged on the total pen FI. The edited data set consisted of 4,095 measurements of FI recorded on 2,127 crossbred pigs from 84 purebred Piétrain sires and 163 Landrace dams from the hyperprolific Landrace K+ line. A random regression animal model was used in this study to estimate variance components. Fixed effects were sex and batch. Random effects were additive genetic, permanent environment and residual. Random additive genetic and permanent environmental effects were modeled with quadratic Legendre polynomials. Estimated heritability for cumulated FI increased with age from 0.06 to 0.45 between 50 and 150 d of progeny-test. The average heritability over this period was 0.66. Estimated genetic correlations between adjacent ages were high and decreased when age interval increased. Negative genetic correlations were found between the very beginning and the very end of the testing period. Because heritability tended to increase with time, it seems that FI data at the end of the growing period is more informative. Moreover, a high FI at the beginning does not necessarily match a high FI at the end. Eventually, FI may be influenced by different genes during the growing period.

**Key Words:** feed intake, pig, random regression

**W202 General and specific combining abilities for reproductive and growth performance of three color variants of Nigerian indigenous turkeys.** M. A. Adeleke\*<sup>1</sup>, R. O. Ojo<sup>1</sup>, S. O. Peters<sup>2</sup>, and M. O. Ozoje<sup>1</sup>, <sup>1</sup>*Department of Animal Breeding and Genetics, Federal University of Agriculture, PMB 2240, Abeokuta, Ogun State, Nigeria*, <sup>2</sup>*Department of Animal Science, Berry College, Mount Berry, GA*.

This study was designed to estimate combining abilities for some reproductive and growth traits of 3 color variants of Nigerian indigenous

turkeys. Two hundred and fifty poultts consisting of 41 White × White (W×W), 40 Black × Black (B×B), 32 Lavender × Lavender (L×L) pure-breeds; 26 White × Black (W×B), 24 Black × White (B×W), 22 White × Lavender (W×L), 20 Lavender × White (L×W), 23 Black × Lavender (B×L) and 22 Lavender × Black (L×B) crossbreds were generated using artificial insemination. The poultts were raised from day-old to 20 wk of age. A 3 × 3 diallel design was set up to estimate general combining ability (GCA) and specific combining ability (SCA) for reproductive traits (fertility, hatchability, weak-in-shell, dead-in-shell, dead-in-germ) and growth parameters (body weight, breast girth, body length and thigh length) according to Hayman (1954) using Genstat (1996) and Dial 98 package. The highest GCA for fertility (4.44) and weak-in-shell (WIS) (0.32) were observed in B×B. The highest GCA for hatchability (5.39) and dead-in-germ (0.64) were recorded in L×L while W×W had the highest GCA for dead-in-shell (2.60). SCA for fertility was the highest in W×B (0.07). W×L had highest SCA (3.28) for hatchability. The highest GCA for body weight at week 20 was recorded for W×W (90.83). The highest SCA for body weight at wk 20 was 0.62 for W×L. B×B had highest GCA values for breast girth, body length and thigh length at wk 20 (1.46, 0.46 and 0.41 respectively). B×W had the highest SCA (0.94) for breast girth; W×L gave the highest SCA (2.34) for body length while the highest SCA (0.89) for thigh length was observed in B×L turkey genotype. The study showed that additive variance was more important for growth parameters, fertility and dead-in-germ while dominance variance was higher and more important in controlling hatchability, weak-in-shell and dead-in-shell. Dams from B×W crossbred indigenous turkeys could be used to improve growth performance while W×L could be used to achieve best combiners for improvement of reproductive traits in Nigerian indigenous turkeys.

**Key Words:** turkey, combining ability

**W203 Quail chick weight prediction using pre-hatch egg measurements and indices.** O. T. F. Abanikannda\*, A. O. Leigh, and A. M. Adeyeye, *Lagos State University, Ojo, Lagos, Nigeria.*

The weight of chicks at hatch is a good indicator of the future productivity of the bird and it is positively correlated to faster weight gain, increased final weight, reduced age at puberty, higher number of eggs laid and heavier eggs. This study was aimed at predicting the hatch weight of Quail chicks using pre-hatch egg parameters. An initial total of 987 hatching Quail eggs were sourced from a commercial farm in Jos in the Savannah region of Nigeria. Eggs were labeled and set in demarcated chambers covered with a net to prevent crossing at pip-out. Pre-hatch egg measurements include weight (Eggwt), length (Eggl), width (Eggwd), vertical circumference (VerCir), horizontal circumference (HorCir), egg weight at 14th day of incubation (14Dwt), while indices include shape index (ShpInd), egg volume (EggVol), egg surface area (EggSSA), egg density (EggDens), surface area to volume ratio (SSAVol) and percent weight difference (WtdiffP); chick weight (Chkwt) and shell thickness (Shltn) were taken at hatch (n = 612). All statistical analyses (exploratory, normality test, descriptive, correlation and modeling) were done using Minitab statistical software. Out of the 14 variables studied, only ShpInd and Shltn did not significantly ( $P > 0.05$ ) correlate with chick weight, while egg weight was significantly ( $P < 0.05$ ) correlated to all variables except ShpInd, and were thus eliminated from the final model, given as  $Y = \beta_0 + \beta_1X_1 + \beta_2X_2 + \beta_3X_3 + \dots + \beta_kX_k$ . All the regressors in the model significantly ( $P < 0.01$ ) affected chick weight, with egg density and d 14 incubation egg weight accounting for 30 and 26%, respectively. The model provides a veritable method for predicting chick weight based on pre-hatch egg parameters.

**Table 1.** Summary statistics and coefficients of variables

Variable	Mean ± SE	Correlation with chick weight
EggWt (g)	9.91 ± 0.04	0.54
EggLt (mm)	30.46 ± 0.05	0.40
EggWd (mm)	24.52 ± 0.04	0.38
VerCir (cm)	9.25 ± 0.02	0.30
HorCir (cm)	8.37 ± 0.01	0.30
ShpInd (%)	80.60 ± 0.16	-0.01
14Dwt (g)	8.89 ± 0.04	0.51
WtdiffP (%)	10.33 ± 0.20	-0.13
EggVol	10.32 ± 0.05	0.44
EggSSA	22.59 ± 0.07	0.46
EggDens	1.05 ± 0.001	0.54
SSAVol	2.20 ± 0.003	-0.44
ShlTkn (mm)	0.173 ± 0.001	0.05
ChkWt (g)	6.11 ± 0.03	1.00

**Key Words:** quail, Nigeria, chick weight

**W204 Genetic parameters of body weight at multiple ages in meat-type quails.** L. Silva\*<sup>1,2</sup>, D. González-Pena<sup>2</sup>, J. Ribeiro<sup>1</sup>, A. Crispim<sup>1</sup>, S. Rodriguez-Zas<sup>2</sup>, and R. Torres<sup>1</sup>, <sup>1</sup>*Departament of Animal Sciences, Federal University of Viçosa Universidade Federal de Viçosa, Viçosa, MG, Brazil,* <sup>2</sup>*Departament of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana.*

The domestic quail (*Coturnix coturnix*) is an accepted model to study the genetic parameters of meat production in domestic poultry due to the similar traits, low maintenance cost, and low generation interval. The estimation of the genetic variability and correlation associated with body weight (BW) at multiple ages can offer insights into effective selection strategies that maximize the genetic gain for BW at later ages while minimizing undesirable effects of higher BW at earlier ages. The aim of this study was to estimate the genetic variances and covariances of BW at multiple ages in meat-type quail. A total of 16,617 BWs from 4,777 quails across 13 generations of selection for higher body weight were measured at 0 (hatch), 14, 28, and 42 d of age. A multi-trait model including the fixed effects of generation and hatch (16 levels) and sex (2 levels), and the random additive genetic effect was used. The pedigree matrix included 8,755 quails, with an average inbreeding coefficient of 0.78 and REML parameter estimates were obtained using the software Wombat (Version 30/05/12). The mean (and standard deviation) phenotypic values were 9.62 g (1.09 g), 86.19 g (16.26 g), 210.24 g (29.76 g) and 274.30 g (36.71 g) for BW at 0, 14, 28, and 42 d, respectively. The heritability estimates (and standard errors) of BW at 0, 14, 28, and 42 d were 0.61 (0.02), 0.30 (0.03), 0.29 (0.03), and 0.27 (0.03), respectively. The higher heritability at 0 d may be due to the lower coefficient of phenotypic variation and similar genetic variation relative to the average of the reminder days. The genetic correlations (and standard errors) were 0.36 (0.06), 0.42 (0.05), 0.47 (0.06); 0.79 (0.06), 0.52 (0.07); and 0.65 (0.07) for 0 with 14, 28, and 42 d; 14 with 28 and 42 d; and 28 with 42 d, respectively. The higher correlations among BWs at later days suggest higher similarity on the genetic components of these BWs. The genetic correlation estimates indicate that it is possible to identify quails with high genetic potential for BW at older ages and low BW at earlier ages thus minimizing higher maintenance costs at earlier ages.

**Key Words:** coturnix, genetic correlation, heritability

**W205 Genetic relationships between cloacal gland area and fertility traits in meat quail.** L. Silva<sup>\*1,2</sup>, D. González-Pena<sup>2</sup>, G. Caetano<sup>1</sup>, R. Pacheco<sup>1</sup>, S. Rodriguez-Zas<sup>2</sup>, and R. Torres<sup>1</sup>, <sup>1</sup>*Department of Animal Sciences, Federal University of Viçosa Universidade Federal de Viçosa, Viçosa, MG, Brazil,* <sup>2</sup>*Department of Animal Sciences, University of Illinois at Urbana Champaign, Urbana.*

Quail production has experiencing substantial growth in world markets, constituting a considerable niche business. However, selection based on growth in quail may have a negative effect on reproduction. The cloacal gland area (CAREA) has been proposed as an indicator of fertility because can be measured earlier, and less expensively than hatchability and fertility. This work aimed to investigate the genetic correlation between CAREA and other indicators of reproductive fitness in meat quail. Data from 189 males, generated from 51 females and 48 males selected for higher BW. Males were allocated to individual cages and the width and height of the cloacal gland were measured using precision calipers (0.01mm) at 49 d of age. CAREA was estimated as the product between width and height. These males were mated to one fertile female each; the eggs were collected within 10 d, and placed on hatching trays. Eggs were candled after 9 d and after 17 d the number of chicks hatching alive was recorded. Fertility was computed as the proportion of fertile eggs among the incubated eggs, and hatchability was computed as the percentage of chicks that hatched among the incubated eggs. Multi-trait mixed models including the fixed effect of generation (2 levels) and a random additive genetic effect were used to estimate the genetic correlation between CAREA and fertility or hatchability. Pedigree matrix included 337 quails with an average inbreeding coefficient of 0.78 and REML parameter estimates were obtained using the software Wombat (Version 30/05/12). The mean (standard deviation) phenotypic values were 340.17mm<sup>2</sup> (106.52 mm<sup>2</sup>), 0.81 (0.23), and 0.80 (0.22) for CAREA, fertility, and hatchability, respectively. Heritability estimates (standard errors) were 0.36 (0.16), 0.02 (0.18), and 0.41 (0.27) for CAREA, fertility, and hatchability, respectively being consistent with the literature. Genetic correlations (and standard errors) were 0.51 (0.35) and 0.68 (0.17) between CAREA and hatchability or fertility respectively. Results suggest that correlated responses in reproductive performance can be achieved by selection based on CAREA.

**Key Words:** coturnix, fertility, hatchability

**W206 Genetic variation in Afec-Assaf ewes differing in their lamb survival rate at birth.** A. Lam, A. Rosov, E. Seroussi, and E. Gootwine\*, *Institute of Animal Science, The Volcani Center, Bet Dagan, Israel.*

High prolificacy is a desirable trait in sheep kept under intensive management. The prolificacy of Afec-Assaf ewes is high, being  $2.5 \pm 0.7$  lambs born/ewe lambing (LB/EL), with  $0.8 \pm 0.2$  lamb survival rate at birth (LSRAB). Investigating 419 lambing records (980 lambs) revealed lamb mortality rates of 0.0, 0.07, 0.24, 0.28, 0.21 and 0.72 for lambs born in litter sizes of 1, 2, 3, 4, 5 and 6, respectively. ANOVA that included crop, parity, sex, litter size and lamb viability in the model showed that average birth weight of liveborns ( $4.0 \pm 0.1$  kg) was significantly heavier ( $P < 0.0001$ ) than that of stillborns ( $3.5 \pm 0.1$  kg). However, the average crown rump length ( $0.51 \pm 0.01$  m) was similar among these groups, suggesting that fetal mortality occurred at the late stage of pregnancy following an intrauterine fetal growth restriction. To investigate the effect of the maternal genome on LSRAB, DNA was extracted from blood samples of 71 high prolific ewes with an average prolificacy of 3.04 LB/EL based on 4–8 lambing records and LSRAB varying from 0.00 to 0.95. Whole genome association analysis was performed utilizing a 50K single nucleotide polymorphism (SNP) beadchip (Illumina).

Association between 10-SNP haplotypes and LSRAB was carried out using PLINK package. Haplotypes located in altogether 14 regions of chromosomes: 1, 8, 10, 26 and X were found to be associated ( $P < 10^{-7}$ ) with LSRAB. Analysis by the EMMAX software that controls for genetic relatedness within the sample supported the existence of QTL for LSRAB on 10 of the chromosomal regions. Within the 10 regions, candidate genes associated with stillbirth and with fetal growth restriction were chosen from public genomic databases. We further characterized the SMOC2 gene on chromosome 8, for which increased expression has been previously associated with stillbirth in cattle. Deep and direct sequencing revealed copy number variation within the ovine SMOC2 gene in the Afec-Assaf sheep. Further study is needed to establish the link between this locus and LSRAB; and to investigate the effect of the fetal genome on perinatal lamb mortality.

**Key Words:** Afec-Assaf, lamb survival, GWAS

**W207 Factor analysis of biometric traits among the Djallonke sheep of Northern Ghana.** P. T. Birteeb<sup>1</sup>, S. O. Peters<sup>2</sup>, and M. O. Ozoje\*<sup>3</sup>, <sup>1</sup>*Department of Animal Sciences, University for Development Studies, Tamale, Ghana,* <sup>2</sup>*Department of Animal Science, Berry College, Mount Berry, GA,* <sup>3</sup>*Department of Animal Breeding and Genetics, Federal University of Agriculture, Abeokuta, Nigeria.*

This study aimed at using multivariate approach to describe the body structure of Djallonke sheep in Northern Ghana. Live weight (LW) and linear body measurements traits (heart girth (HG), neck girth (NG), chest depth (CD), height at withers (HW), rump height (RH), body length (BL) and pin-bone width (PBW)) were obtained from 172 sheep, between 2 and 3 years old. The fixed effects of sex and age were tested using the a generalized linear model, while the nearest neighbor method of hierarchical cluster analysis was used to group body traits into clusters. Principal component factor analysis was used to describe variation in body traits where extracted factors were Varimax rotated to enhance interpretability. The ANOVA revealed significant ( $P < 0.01$ ) differences in the morphological traits of the 2 sexes with higher values recorded for the male in all traits except PBW. Age had no effect ( $P > 0.05$ ) on all body traits. On the average these sheep weighed  $26.92 \pm 0.89$ kg and measured  $71.74 \pm 1.23$ ,  $40.52 \pm 0.79$ ,  $27.73 \pm 0.52$ ,  $60.72 \pm 0.86$ ,  $59.61 \pm 0.87$ ,  $58.87 \pm 1.06$  and  $12.81 \pm 0.23$  cm respectively for HG, NG, CD, HW, RH, BL and PBW. The product moments of correlation were positive and significant ( $P < 0.05$ ,  $0.01$ ;  $r = 0.18$ – $0.99$ ) for all pairs of traits. These traits were categorized mainly into 2 clusters. HG, HW, RH and BL formed the first cluster, while NG, CD and PBW formed the second cluster. The grouping of the traits was however different in Factor analysis, where 2 underlying principal components (PC) were extracted to discern the variance structure of the Djallonke. The first consisting of CD, HW, RH, BL and PBW explained 61.26%, while the second consisting of HG and NG explained 12.92%, giving a maximum of 74.17% generalized variance in body measurements. The traits loaded on the first PC are closely associated with bone growth; while the traits on the second PC described only the thoracic region. In conclusion, both hierarchical cluster analysis and factor analysis grouped body traits similarly. However, the later is recommended because of its additional ability to indicate the amount of variation explained by the developed factors.

**Key Words:** Djallonke, factor analysis, body structure

**W208 Evaluation of economic traits in Romanov × Iranian fat-tail sheep breed in the first generation (F<sub>1</sub>).** M. J. Najafpanah\*<sup>1,2</sup>, H. Mousapour<sup>2</sup>, N. Feiz<sup>1</sup>, M. H. Moradi<sup>2</sup>, and B. Ghorbani<sup>1</sup>, <sup>1</sup>*Center*

Governments all over the world have tried to provide healthy, sustainable, and cheap food for their people. Sheep are an important part of the agricultural economy and may be a medium of trade in barter economies. Besides, sheep are one of the most important livestock to meat supply and employment in Iran. Prominent features of Iranian breeds have a fat-tail and low lambing and/or litter size. The aim of this study was to compare some phenotypic traits of economic in purebred lambs (Afshari) and crossbred lambs (Romanov × Afshari in F<sub>1</sub>). The experimental broodstock was included of 40 Afshari pluriparous ewes. They were artificially inseminated with Canadian Romanov semen using laparoscopy. After the lambing, we observed all crossbred lambs were thin-tailed. The model that used for analysis contained the fixed effects of group (purebred and crossbred) and sex, the random effect of animal and a regression for dam's weight. The results proposed the dominance of the thin tail phenotype and suggesting that a few number of genes are associated with fat storage in the tail. We observed significant differences ( $P < 0.05$ ) between the 2 groups in terms of weaning weight, weight in 6 mo, Adg<sub>0-3</sub> and Adg<sub>3-6</sub> while the differences between male and female lambs were not significant. The characteristics of other phenotypic traits presented in the Table 1. Our results revealed that crossbred lambs in F<sub>1</sub> have better performance for other phenotypic traits comparing to purebred lambs. In conclusion, this study showed that the efficiency of meat production in Afshari breed can improve using crossbreeding with Romanov breed.

**Table 1.** The characteristics of economical important traits in Iranian fat-tail sheep breed and their crossbred lambs (raw means ± SD)

Item	Purebred		Crossbred	
	Male	Female	Male	Female
Birth weight (kg)	4.42 ± 1.29	4.17 ± 0.68	4.47 ± 0.41	4.38 ± 0.33
Weaning weight (kg)	29.5 ± 4.23	26.5 ± 2.88	30.7 ± 6.14	27.63 ± 3.40
Weight in 6 mo (kg)	41.24 ± 5.31	38.7 ± 2.03	44.33 ± 7.36	40.68 ± 2.57
Preweaning daily gain (kg)				
Adg <sub>0-3</sub>	0.327 ± 0.054	0.294 ± 0.03	0.307 ± 0.034	0.341 ± 0.061
Adg <sub>3-6</sub>	0.130 ± 0.011	0.135 ± 0.016	0.151 ± 0.020	0.149 ± 0.019
Adg <sub>0-6</sub>	0.229 ± 0.027	0.215 ± 0.028	0.246 ± 0.032	0.226 ± 0.021

**Key Words:** crossbred lamb, Romanov, fat-tail sheep

**W209 Phenotypic and genetic changes of ewe economic traits in the Makooei sheep.** H. M. Shahrabak\*<sup>1</sup>, H. Mohammadi<sup>2</sup>, and A. H. F. Khaltabadi<sup>3</sup>, <sup>1</sup>Department of Animal Science, Academic of Agronomy and Animal Science, University College of Agriculture & Natural Resources University of Tehran, Karaj, Alborz, Iran, <sup>2</sup>Department of Animal Sciences, Faculty of Agriculture, University of Tabriz, Tabriz, Iran, <sup>3</sup>Department of Animal Science, Faculty of Agriculture, University of Arak, Arak, Iran.

In this study 3418 records from the Makooei sheep stud were used to predict phenotypic, genetic and environmental change in ewe traits from 1996 to 2009. Best linear unbiased predictions (BLUP) of breeding values were estimated by restricted maximum likelihood (REML) procedure using single and multi-trait animal model with ASReml program. Phenotypic, genetic and environmental trends were calculated by regressing of the average phenotypic values, predicted breeding

values and environmental values in the year of ewe birth respectively. The estimated phenotypic trends were -0.1005 kg for ewe body weight, 0.447% for conception rate, 0.0002 for number of lambs born per ewe lambing, 0.0064 for number of lambs weaned per ewe lambing, 0.0270 kg for total birth weight per ewe exposed and 0.4522 kg for total weaning weight per ewe exposed. The estimated genetic trends were 0.0472 kg, -0.0004 kg, 0.0253%, 0.0015, 0.0005, 0.0040 kg and 0.0122 kg from single-trait analysis and 0.0365 kg, -0.0005 kg, 0.0074%, 0.0017, -0.0006, 0.0050 kg and 0.0157 kg respectively from multi-trait analysis. The estimated phenotypic and environmental trends were significant ( $P < 0.05$ ) but genetic trends were not significant ( $P > 0.05$ ) for all traits. Results from this study agree with those of the previous studies of the other sheep breeds that multi-trait analysis should be used rather than single-trait analysis when estimating genetic changes because of the effect that including correlated traits has on estimates of breeding values of other traits.

**Key Words:** phenotypic trend, genetic trend, ewe trait

**W210 Estimation of genetic trends for live weight traits in Raeini goats.** H. M. Shahrabak\*<sup>1</sup>, H. Mohammadi<sup>2</sup>, and A. H. F. Khaltabadi<sup>3</sup>, <sup>1</sup>Department of Animal Science, Academic of Agronomy and Animal Science, University College of Agriculture & Natural Resources, University of Tehran, Karaj, Alborz, Iran, <sup>2</sup>Department of Animal Science, Faculty of Agriculture, University of Tabriz, Tabriz, Iran, <sup>3</sup>Department of Animal Science, Faculty of Agriculture, University of Arak, Arak, Iran.

The aim of this study was to estimate genetic trends for live weight traits at different ages in Raeini goat. The data were collected from Baft city Breeding Research Station in southeastern Kerman province, Iran. Data were collected over the years 1982 to 2009, with records on total of 4,219 kids descended from 263 sires and 1653 dams. Major reasons for culling were old age, mastitis, and bad udder. Throughout the study replacement bucks and breeding does were selected on the basis of phenotypic characteristics such as visual conformation and WW. The investigated traits were birth weight (BW), weaning weight (WW), 6 mo weight (6W), 9 mo weight (9W) and yearling weight (YW). Number of observations for BW, WW, 6W, 9W and YW were 4219, 3473, 2692, 1641 and 1021, respectively. The (co)variance components and corresponding genetic parameters were estimated by restricted maximum likelihood method based on a single trait animal model, using ASReml program (Gilmour et al., 2006). The fixed effects of sex, birth year, dam age and birth type and the random effects of direct and maternal genetics were included in the model for all traits. Age of kid at weighing (in days) was fitted as a covariate. Genetic trends were estimated by regressing estimated breeding values on year of birth. The mean predicted breeding values of Goat kids generally show an increase over time for all studied traits. The additive direct genetic trends for BW, WW, 6W, 9W and YW were 2 ± 0.28, 95 ± 11.31, 65 ± 8.7, 18 ± 6.2 and 17 ± 4.9 g per year, respectively. Higher genetic trends for WW and 6W than other traits might be attributed to the relatively higher additive genetic variation in those traits. Results of this work showed, in general, low genetic improvement in the studied traits during the period of study. The main reason for this could be the absence of clear and focused selection criteria during the period of the study. The genetic trends estimates show that there has been a positive genetic improvement in all studied traits and indicate that selection would be effective.

**Key Words:** genetic trend, weight trait, goat

**W211 Linear models versus threshold models for predicting direct and maternal genetic effects on number of lambs weaned in Iranian Makooei sheep.** H. M. Shahrabak\*<sup>1</sup>, H. Mohammadi<sup>2</sup>, and A. H. F. Khaltabadi<sup>3</sup>, <sup>1</sup>Department of Animal Science, Academic of Agronomy and Animal Science, University College of Agriculture & Natural Resources, University of Tehran, Karaj, Alborz, Iran, <sup>2</sup>Department of Animal Science, Faculty of Agriculture, University of Tabriz, Tabriz, Iran, <sup>3</sup>Department of Animal Science, Faculty of Agriculture, University of Arak, Arak, Iran.

Meat quantity has traditionally contributed most of the net return in the sheep farmers of Iran. Recent high prices for sheep meat are likely to increase the interest in, and importance of the reproductive rate in sheep herds. The number of lambs weaned (NLW) can be a good criteria for reproductive performance in a sheep herd. This reproductive trait is recorded in discrete category but analyses as a continuous trait. The objective of this study was to compare the accuracy of a threshold animal model to a linear model for direct and maternal genetic evaluation of NLW in Iranian Makooei sheep. The information of NLW was extracted from data notebooks of Makooei sheep breeding station from 1996 to 2009. The number of lambs weaned was recorded in 2 categories (0 and 1) and a total of 3418 records were available. Most of the records categorized in class 1 (77.6%) and the average number of weaned lambs was 1.09. Analyses were performed using an animal model (linear and threshold) with a maternal effect. Year of birth and sex were considered as fixed effects and age of dam as a covariate in all models. A cross-validation method was used to assess the predictive ability of the models. The estimates of direct and maternal variances and also covariance between direct-maternal were obtained larger in threshold model comparing to the linear model. Larger estimates of heritabilities also were obtained when the threshold model was employed. For the direct additive genetic effect, the correlation from the threshold model was 10% higher than the linear model (0.53 vs. 0.48) and the maternal effects followed the same pattern with 6% increasing (0.57 vs. 0.52). The results confirmed the better performance of a threshold animal model compared with a linear animal model for genetic evaluation of NLW. However, the advantage of using a univariate threshold model instead of a linear model was small. Further investigation is needed for fully judge the predictive ability of the 2 models.

**Key Words:** threshold model, lambs weaned, prediction

**W212 Effect of egg weight on hatching weight and incubation period in Giant African land snail (*Archachatina marginata*).** J. A. Abiona\*, Y. F. Sokoya, A. O. Osinowo, A. O. Ladokun, and M. O. Abioja, Federal University of Agriculture, Abeokuta, Abeokuta, Ogun State, Nigeria.

An experiment was conducted to determine the effect of egg weight on hatching weight and incubation period in the Giant African land snail. A total of 30 *Archachatina marginata* eggs comprising of 4 weight range categories (1.24–1.55, 1.56–2.14, 2.15–2.83 and 2.84–3.20 g) were obtained from Dams of different body weight ranges (100g-150g, 151–200g, 201–250g) from the Snail Physiology Research Unit of the College of Animal Science and Livestock Production, Federal University of Agriculture, Abeokuta, Nigeria. Eggs were incubated, after which both incubation period and hatching weight after hatching were monitored. Results obtained showed that egg weight group had significant effect ( $P < 0.001$ ) on hatching weight. Egg weight with weight range of 2.84–3.20 had the highest hatching weight, followed by 2.15–2.14 while other 2 (1.24–1.55 and 1.56–2.14 g) were not significantly different from each other. Furthermore, egg weight had no significant effect ( $P > 0.05$ ) on incubation period. A positive significant correlation (Pearson) was obtained between egg weight and hatching weight, and also dam weight and hatching weight. It was concluded that egg weight had effect on hatching weight of eggs. It was also discovered that egg weight had no meaningful effect on incubation period.

**Table 1.**

Egg weight group	No. of observations	Hatching weight (g)	Incubation period (d)
1.24–1.55	6	0.947 ± 0.087 <sup>c</sup>	32.5 ± 2.325
1.56–2.14	6	1.100 ± 0.087 <sup>c</sup>	33.5 ± 2.325
2.15–2.83	6	1.555 ± 0.087 <sup>b</sup>	24.7 ± 2.325
2.84–3.20	5	2.118 ± 0.095 <sup>a</sup>	29.6 ± 2.546

**Key Words:** egg weight, incubation period, hatching weight