

Breeding and Genetics: Quantitative Animal Breeding

476 Cooperation under directional selection with kinship-based groups. F. Siewerdt^{*1}, A. D. Franklin¹, J. A. Carrillo¹, A. K. Sasikala-Appukuttan¹, A. S. Schierholt², T. E. Callicrate¹, M. A. Campbell¹, and H. L. M. Moreira³, ¹University of Maryland, College Park, MD, ²Universidade Federal Rural da Amazônia, Belém, PA, Brazil, ³Universidade Federal de Pelotas, Pelotas, RS, Brazil.

The goal of this selection experiment was to determine if the accumulation and expression of genes with associative genetic effects is dependent on selection being performed in the presence of closely related individuals. Laboratory colonies of *Tribolium castaneum* were assigned to 3 selection lines and 3 replications. A selection line consisted of 64 demes of 16 adults, placed in small glass jars with a small amount of medium (95% flour and 5% yeast) in a walk-in incubator with controlled temperature and humidity. The medium was a limiting factor for census growth of the deme, creating competition between individuals and the opportunity for reduction in reproductive activity and manifestation of cannibalism. Two lines were group selected for increased number of adults at 35 d after establishment of the demes. The best demes were used to place as many demes in the following generation as possible. In one selection line kinship structure was preserved in consecutive generations by placing new demes only with beetles from the same original deme. In the other selection line the deme structure was disrupted at each generation by placing the new demes with beetles coming from 16 different demes in the previous generation. A randomly selected control was kept; adult counts were expressed as deviations from this line. Each selected line was split into 2 lines at generation 11. One newly formed line was kept on the original selection strategy and the other was placed on the competing selection strategy. After 16 generations of selection, genetic gains suggest that accumulation and expression of associative genetic effects may be dependent on the presence of kin. Average cumulative genetic gains in the selected lines with intact deme structure and with disrupted deme structure were, respectively, 49.8 ± 10.1 and 28.9 ± 2.7 adults. Between-deme variability was 5.5 times higher in the lines with intact deme structure. Swapping selection strategies at generation 11 had no effect on genetic progress measured at generation 16. There may be latency in the expression of accumulated associative genetic effects, which could only occur in the presence of close kin.

Key words: *Tribolium castaneum*, Associative genetic effect

477 A recursive binomial model for piglet mortality. L. Varona^{*1} and D. Sorensen², ¹Unidad de Genética Cuantitativa y Mejora Animal, Universidad de Zaragoza, Zaragoza, Spain, ²Department of Genetics and Biotechnology, University of Aarhus, Tjele, Denmark.

Several interesting traits in animal production do not follow a Gaussian distribution. Statistical procedures based on Bayesian analysis allows to model successfully unconventional distributions of data. However, sometimes is not clear how to model environmental correlation between traits. Structural models may provide a useful alternative to model this relationship. In this study, we have developed a recursive procedure between a linear (litter size) and a binomial trait (number of piglets born dead) and we have tested the procedure with data from 2 Danish pig breeds: Landrace and Yorkshire. The Landrace data set included 5178 litter size records and a pedigree file of 8800 individuals, whereas the Yorkshire data set consisted of 3938 litter size records and a pedigree file of 7143 individuals. The posterior mean (and standard deviation) estimates of the recursive parameter of litter

size on the logit-transformation of the probability of born dead were 0.094 (0.005) and 0.121 (0.007) for Landrace and Yorkshire, respectively. These results indicate that as litter size increase, the probability of a piglet to born dead also does. Moreover, the procedure provides a useful alternative to model non genetic relationship between traits. The adequacy of the model was tested by the logarithm of the conditional predictive ordinate of data, showing that the proposed model improves the predictive ability over the one that does not include the recursive relationship with litter size.

Key words: recursive models, pig, Bayesian analysis

478 Genetic correlation between purebred piglet birth weight and crossbred performance. C. Y. Chen^{*1,2}, I. Misztal¹, S. Tsuruta¹, J. Holl³, W. O. Herring³, and M. Culbertson³, ¹Department of Animal and Dairy Science, University of Georgia, Athens, ²Newsham Choice Genetics, Chesterfield, MO, ³Smithfield Premium Genetics Group, Rose Hill, NC.

The objective was to estimate the genetic correlation between purebreds and crossbreds for several weight traits. Data consisted of 157,600 purebreds (Durocs) and 94,185 crossbreds (Duroc x (Large White x Landrace)). Traits were purebred birth weight (PBWT), crossbred birth weight (CBWT), crossbred carcass weight per day of age (CWDA), and binary crossbred hot carcass weight (CHCW) with cut-point at 75 kg. Two linear 3-trait models (PBWT, CBWT, and CWDA) and one linear-threshold 3-trait model (PBWT, CBWT, and CHCW) were used. Fixed effects included sex, parity, and litter size for all models with age at slaughter for CHCW. Contemporary groups were fitted differently for linear traits (fixed) and CHCW (random). Random effects of litter and residual were included for all models. Genetic effects were fit differently for purebreds (animal additive) and crossbreds (animal or sire additive). A dam effect (composed of genetic and environmental) was also evaluated for crossbreds. Heritability was 0.18 for PBWT with all models. For CBWT, estimates of heritability were 0.07 with the animal model and from 0.03 to 0.05 with the sire models. For CWDA, same estimates were 0.17 and 0.12 for animal additive and sire genetic effects, respectively. Heritability was 0.08 for CHCW. Estimates of genetic correlations ranged from 0.77 to 0.89 for PBWT-CBWT, 0.16 to 0.30 for PBWT-CWDA, 0.13 to 0.56 for CBWT-CWDA, 0.45 for PBWT-CHCW, and 0.13 for CBWT-CHCW. The selection for birth weight in purebreds is efficient for selection of birth weight in crossbreds. Such a selection is also useful in achieving market weight in crossbreds.

Key words: birth weight, crossbreds,, genetic correlation, pigs

479 Construction of individual breeding values for feed intake of Piétrain boars based on mean pen feed intake, weight and weight gain test station records. M. Dufresne^{*1}, V. Jaspert², J. Wavreille³, and N. Gengler^{1,4}, ¹Animal Science Unit, University of Liege, GxABT, Gembloux, Belgium, ²Walloon Pig Breeders Association, Ciney, Belgium, ³Walloon Agricultural Research Centre, Gembloux, Belgium, ⁴National Fund for Scientific Research, Brussels, Belgium.

The aim of this study was to predict genetic merit of Piétrain boars for feed intake by constructing an index combining individual residual feed intake (RFI), average daily gain (ADG) and live weight (LW) of their progeny. Reliabilities of estimated breeding values (EBV) of 50

recently tested boars for individual Estimated Feed Intake (EFI) and for Index Feed Intake (IFI) were compared. Data were collected on pigs in test station in context of the genetic evaluation system of Piétrain boars for crossbred performances in the Walloon Region of Belgium. Because there were no facilities to record individual feed intake, individual EFI was computed as the total pen feed intake divided by number of individuals per pen. Data file contained 1 397 records of individual EFI. Model developed was an animal model with sex and pen as fixed effects. EBV for ADG between 100 and 210 d and for LW at 100 d were defined as linear covariables, therefore EBV are expressing RFI. Mean EFI was 1 876.8 g/d with a SD of 177.5 g/d. Heritability for EFI considered without regressions on ADG and LW was 0.08 and mean reliability of EBV was 0.16 which was low to base selection decision. Coefficients of linear regression estimated were used to estimate IFI as followed: $IFI, g/d = RFI, g/d + 2.61 LW, kg + 214.37 ADG, kg/d$. Heritability for RFI was 0.06 and was low compared with literature. Heritability for IFI was 0.09 which was more consistent with literature values. Mean reliability for RFI was 0.13 and mean reliability for IFI was 0.35. Therefore, thanks to combining RFI with EBV for ADG and LW which have high mean reliabilities (0.71 for ADG and 0.72 for LW) accuracy of EBV for individual feed intake was increased. These results show that with index combining genetic values of growth and live weight with RFI, genetic potential for individual feed intake of boars could be estimated more accurately than with only individual EFI.

Key words: feed intake, index, reliability

480 Genetic correlations between purebred Limousin and F1 Limousin*Angus. R. Davis^{*1}, I. Misztal¹, M. Lukaszewicz^{1,2}, S. Tsurut¹, and J. K. Bertrand¹, ¹University of Georgia, Athens, ²² Polish Academy of Sciences, Institute of Genetics and Animal Breeding, Jastrzębiec, Poland.

The purpose of this study was to estimate correlations between purebred and crossbred animals to verify efficiency of current models used in crossbreeding selection. Records on 3 weight traits: birth weight (BW), weaning weight (WW) and post-weaning gain (PW) from a purebred Limousin line (L) and a crossbred line made of Limousin*Angus F1 progeny (F1), were used to estimate correlations between crossbred and purebred animals as well as other genetic parameters using single trait models (ST; weights are the same traits in both populations) and a multiple trait crossbred model (MT; weights are different traits). For BW there were 148,647 records for L and 17,981 for F1, for WW 81,585 for L and 21,778 for F1, and for PW 37,687 for L and 11,021 for F1. Fixed effects in all models for L and F1 animals were contemporary group and month. Random effects for L animals in both models were direct genetic, maternal genetic and maternal permanent environment. Random effects for F1 were sire genetic and dam environmental. The pedigree for Angus dams was unavailable and therefore these dams were assumed unrelated. In the ST model, direct heritability estimates for purebred animals were 0.38, 0.22 and 0.31 for BW, WW and PG, respectively. For F1, the same estimates were 0.21, 0.34 and 0.34. Genetic correlations estimates between purebreds and crossbreds were 0.4, 0.6 and 0.3 for BW, WW and PG, respectively. The purebred selection is only partially effective on crossbreds, especially for BW and PG. The selection is effective for WW where the lower genetic correlation is compensated by higher heritability. Estimates in this study may be biased by the ignoring of maternal pedigrees in F1.

Key words: crossbreeding, F1, correlation

481 The heritability of lean color and its influence on beef tenderness. P. Johnson^{*1}, D. Moser², and M. Miller¹, ¹Texas Tech University, Lubbock, ²Kansas State University, Manhattan.

The objective of this study was to determine heritability estimates of lean color, as measured by subjective scoring and Hunter Colorimeter readings, and its phenotypic and genetic correlation with tenderness in beef. Data were collected over 5 years on the longissimus dorsi muscle of 1,277 head; 12 different breeds were represented. Tenderness was measured by Warner-Bratzler shear force (WBSF) and quantitative ratings were given for initial tenderness and sustained tenderness by trained sensory panelists. Phenotypic correlations were found using the GLM procedure of SAS and variance and covariance components were obtained using MTDFREML. Lean color was found to be moderately heritable (0.34 ± 0.122) while the heritability estimates of Hunter colorimeter readings varied; 2 were moderately heritable: a* (0.29 ± 0.115) and b* (0.28 ± 0.120), while the third was lowly heritable, L* (0.09 ± 0.087). Phenotypic correlations found to be significant ($P < 0.01$) were: lean color and WBSF, a* value and WBSF, L* value and WBSF, lean color and initial tenderness, L* value and initial tenderness, lean color and sustained tenderness, L* value and a* value, L* value and b* value and a* value and b* value. Both a* and b* values were found to be highly and negatively correlated genetically with WBSF (-0.71 and -0.72 , respectively). The genetic correlation between lean color and WBSF was -0.46 . The genetic correlations of a* value and b* value with WBSF were both high, -0.71 and -0.72 , respectively. The genetic correlation between lean color and initial tenderness was also high, 0.56, while that between a* value and initial tenderness was 0.43; similar to that found between b* value and initial tenderness, 0.44. The genetic correlations between lean color and sustained tenderness, a* value and sustained tenderness and b* value and sustained tenderness were all found to be high at 0.58, 0.70 and 0.58, respectively. The genetic correlation between a* value and b* value was also found to be high, 0.63. In conclusion, regardless of how lean color is measured, it is not only heritable, but has also been shown to be moderately and highly correlated with measurements of tenderness in beef.

Key words: beef, tenderness, color

482 Multivariate characterization of morphological traits in Nigerian sheep. A. Yakubu¹, M. Okpeku², M. Wheto³, S. Amusan³, B. O. Agaviezor⁴, M. A. Adefenwa⁵, B. M. Ilori³, O. Ajayi³, G. O. Onasanya³, J. Ekundayo³, T. Sanni³, C. O. N. Ikeobi³, M. I. Takeet⁶, and I. G. Imumorin^{*7}, ¹Dept of Animal Science, Nasarawa State University, Lafia, Nigeria, ²Department of Livestock Production, Niger Delta University, Amassoma, Nigeria, ³Department of Animal Breeding and Genetics, University of Agriculture, Abeokuta, Nigeria, ⁴Dept of Animal Science and Fisheries, University of Port-Harcourt, Port-Harcourt, Nigeria, ⁵Dept of Cell Biology and Genetics, University of Lagos, Lagos, Nigeria, ⁶Dept of Veterinary Microbiology and Parasitology, University of Agriculture, Abeokuta, Nigeria, ⁷Dept of Animal Science, Cornell University, Ithaca, NY.

Principal component and discriminant analyses were performed to investigate distinction and patterns of morphological variation among 4 indigenous sheep breeds sampled from all over Nigeria. Body weight and 9 linear type traits (withers height, rump height, body length, ear length, fore cannon bone length, tail length, chest girth, chest depth and rump width) were measured in 402 randomly selected West African Dwarf (WAD), Yankasa, Uda and Balami sheep, respectively. The morphometric traits of Uda and Balami sheep were significantly ($P <$

0.05) higher than those of Yankasa sheep, which in turn had a comparative advantage over their WAD counterparts. There was variation in the pattern of the loading traits of the principal components (PCs) of each sheep breed. This was further revealed by the differences in the degree of accuracy when body weight was predicted from the scores derived from the PCs of each genetic group. Based on Mahalanobis distances, the least differentiation was observed between Uda and Balami sheep (0.298) while that between WAD and Balami sheep was longest (18.004). While 93.33% of WAD sheep were correctly assigned into their source genetic group, 63.93% of Yankasa, 45.16% of Uda and 61.15% of Balami sheep were classified into their source population in the nearest neighbor discriminant analysis. The present phenotypic information could be exploited in designing appropriate management, conservation and breeding programs for Nigerian indigenous sheep.

Key words: multivariate analysis, sheep, Nigeria

483 Multivariate analysis of morphological differentiation in Nigerian goats. A. Yakubu*¹, M. Okpeku², M. Wheto³, S. Amusan³, B. O. Agaviezor⁴, M. A. Adefenwa⁵, B. M. Ilori³, O. Ajayi³, G. O. Onasanya³, J. Ekundayo³, T. Sanni³, C. O. N. Ikeobi³, M. I. Takeet⁶, and I. G. Imumorin⁷. ¹Dept of Animal Science, Nasarawa State University, Lafia, Nigeria, ²Department of Livestock Production, Niger Delta University, Amassoma, Nigeria, ³Department of Animal Breeding and Genetics, University of Agriculture, Abeokuta, Nigeria, ⁴Department of Animal Science and Fisheries, University of Port-Harcourt, Port-Harcourt, Nigeria, ⁵Dept of Cell Biology and Genetics, University of Lagos, Lagos, Nigeria, ⁶Dept of Veterinary Microbiology and Parasitology, Abeokuta, Nigeria, ⁷Dept of Animal Science, Cornell University, Ithaca, NY.

The objective of the study was to morphologically characterize Nigerian indigenous goats using multivariate statistical analyses. Body weight and 9 biometric traits were measured in 352 randomly selected West African Dwarf (WAD), Red Sokoto (RS) and Sahel (SH) goats of both sexes categorized into 3 age groups from across Nigeria. The univariate analysis showed that breed, sex and age of the animals significantly ($P < 0.05$) affected the body parameters. The principal component analysis revealed variation in the morphometric characters of the goats. Stepwise discriminant analysis showed chronologically that tail length, rump width, rump height, ear length and body length were the most discriminating variables among different pair-wise breeds' comparisons. In the canonical discriminant analysis, the first canonical variate was significant and accounted for 95.5% of the variability among the goat breeds. The longest Mahalanobis distance was that between WAD and SH goats (11.44; $P < 0.001$) while the shortest was recorded for RS and SH goats (1.50; $P < 0.01$), respectively. The dendrogram showed 2 large clusters indicating that WAD and the 2 other goat breeds are separate genetic entities. Discriminant functions cor-

rectly allocated 65.79% of individual goats to their a priori breeds, although a sort of genetic introgression was observed between RS and SH goats. The present findings combined with molecular characterization could aid the formulation of management, breeding and conservation strategies for Nigerian indigenous goat resources.

Key words: multivariate analysis, goats, Nigeria

484 Searching for causal relationships among five traits of European quails. B. D. Valente*^{1,2}, G. J. M. Rosa^{1,3}, M. A. Silva², R. B. Teixeira⁴, and R. A. Torres⁴. ¹Department of Animal Sciences, University of Wisconsin, Madison, ²Departamento de Zootecnia, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil, ³Department of Biostatistics and Medical Informatics, University of Wisconsin, Madison, ⁴Departamento de Zootecnia, Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.

Structural equation models (SEM) allow modeling multiple traits expressing causal links among them. The number of different causal structures that can be used for fitting a SEM is typically huge, even when only a few traits are studied. In recent applications of SEM in mixed model settings, causal structures were pre-selected based on prior beliefs alone. Alternatively, causal structure spaces can be explored using algorithms that search for structures that are compatible with the joint distribution of the traits. However, in mixed models settings, the search cannot be performed directly on the joint distribution of the phenotypes as causal relationships are possibly masked by genetic covariances. In this context, it has been proposed that such search could be performed by applying the Inductive Causation (IC) algorithm to the joint distribution of phenotypes conditionally to unobservable genetic effects. Here, we applied this approach to a data set of 5 traits of European quails: birth weight (BW), weight at 35 d of age (W35), age at first egg (AFE), average egg weight from 77 to 110 d of age (AEW), and number of eggs laid in the same period (NE). We focus the discussion on the challenges and difficulties resulting from applying this method to field data. Statistical decisions were based on different Highest Posterior Density (HPD) interval contents (70, 75, 80, 85, 90, and 95%). Resulting causal structures were fitted and models were compared using the Deviance Information Criterion (DIC). In addition, we used temporal information to perform additional edge orienting, overriding the algorithm output when necessary. As a result, the final causal structure consisted of 2 separated substructures: $BW \rightarrow AEW$ and $W35 \rightarrow AFE \rightarrow NE$.

Key words: causal relationships, European quails, structural equation models

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