Breeding and Genetics: Swine Breeding

815   Estimation of genetic parameters for birth weight, pre-weaning mortality and hot carcass weight in a crossbred population of pigs. M. Dufrasne*[1,2], I. Misztal[3], S. Tsuruta[3], J. Holl[4], K. A. Gray[4], and N. Gengler[1], [1]*Animal Science Unit, Gembloux Agro-Bio Tech, University of Liege, Gembloux, Belgium,* [2]*FRIA, Brussels, Belgium,* [3]*Department of Animal and Dairy Science, University of Georgia, Athens,* [4]*Smithfield Premium Genetics Group, Rose Hill, NC.*

Economically important traits, such as piglet mortality and growth potential, are both associated with birth weight (BRW) and therefore it is possible that BRW could be used as an early indicator for indirect selection for piglet survival and final weight. The aim of this study was to estimate genetic parameters for BRW, weaning mortality and growth traits in a commercial crossbred population of pigs to improve selection in a purebred terminal sire line. The edited data set consisted of 21,618 crossbred pigs from 262 purebred Duroc sires and 1,987 crossbred non-pedigreed Large White x Landrace dams. Traits analyzed were BRW, pre-weaning mortality (PWM) and hot carcass weight (HCW). All pigs had BRW and PWM records and 15,946 of these pigs had records for HCW. A multiple trait model with fixed effects of sex, dam parity and contemporary group, defined as month by year of birth, and random effects of sire, dam, litter and residual was utilized in the analysis. The mean BRW was 1.41 kg, the mean HCW was 93.4 kg and the percentage of PWM was 19.7%. PWM and HCW were nonlinear functions of BRW. PWM (HCW) were 75.51% (88.24 kg) for BW < 0.7 kg, 38.76% (91.71 kg) for BW <1.2 kg and 11.75% (94.03 kg) for BW >1.4 kg. The phenotypic correlations between BRW and HCW and between BRW and PWM were 0.11 and −0.28, respectively. Estimates of heritability and common litter effect were 0.19 and 0.11 for BRW, 0.04 and 0.06 for PWM, and 0.05 and 0.09 for HCW, respectively. Estimated genetic correlations were −0.75 between BRW and PWM, 0.49 between BRW and HCW, and −0.33 between PWM and HCW. Selection for increased birth weight in purebred terminal sire line may improve pre-weaning survival and final weight in the crossbred population.

Key Words: birth weight, genetic correlation, growth traits

816   Effect of within-year variation on growth performance and subsequent reproductive performance in gilts. C. R. G. Lewis*[1,2], K. L. Bunter[1], and S. Hermesch[1], [1]*Animal Genetics and Breeding Unit (AGBU), University of New England (UNE), Armidale, NSW, Australia,* [2]*PIC North America, Hendersonville, TN.*

Uniform performance is required for optimal production. This study aimed to examine within-year variation observed on gilts for production traits and their subsequent breeding performance. Data consisted of 5060 gilts from 3 breeds (Large White, Landrace and Duroc) and 3 herds in Australia over 15 years. Production traits were average daily again (ADG μ = 662g/d) and backfat (BF μ = 10.9mm) recorded at a live weight (WT) of 100kg. Reproduction traits were total born (TB μ = 10.6), the number born alive (NBA μ = 9.76), the number of stillbirths (SB μ = 0.83) and farrowing age (FA μ = 384) recorded in the first parity. General linear models were utilized to examine variation associated with month (12 levels, calendar month) at recording. Significant effects for all traits were herd, year, month, breed and the interaction between month and breed, which were fully cross-classified in these data. Farrowing age was fitted as a linear covariate for TB, NBA and SB, and TB was a linear covariate for SB. The production traits were also corrected for dam parity and birth litter size. Models for reproduction traits also included the animal's performance traits fitted within month. Least squares means (LSM) and associated P-values by breed, month and the month*breed interaction were assessed to examine differences in the within-year variation for traits and any possible breed (genetic) differences. The ranges in LSM for the effects of month were ADG = 50g/d, BF = 1.1mm, TB = 0.67, NBA = 0.72, SB = 0.23 and FA = 15.7d (min and max for all traits $P < 0.05$ difference). Growth rate was higher and BF was lower in cooler months. The differences between winter and summer were larger in magnitude for Duroc in comparison to the other 2 breeds. For reproduction traits, less TB were produced in cooler months (mated during the summer) and SB was higher for summer farrowings. Further analyses showed that if variation is generated in growth performance before breeding, then there is a differential effect on variation in the reproductive traits. Linear regressions of FA on ADG nested within month of farrowing resulted in ADG solutions of −0.35d/g in winter and −0.12d/g in summer. Quantifying the different sources of within-year variation and their interactions is of economic importance and could suggest paths for intervention strategies to increase uniformity in performance.

Key Words: gilts, variation, growth

817   Towards robust sows: Heat tolerance expressed in fecundity traits. S. Bloemhof*[1,2], E. Knol[1], E. van der Waaij[2], and I. Misztal[3], [1]*TOPIGS Research, Beuningen, the Netherlands,* [2]*Animal Breeding and Genomics Centre, Wageningen, the Netherlands,* [3]*Department of Animal and Dairy Science, University of Georgia, Athens, Georgia, United States of America.*

Globalization results in increased pork production, especially in warm climates such as Latin America and Asia. This requires a robust sow that is tolerant to environmental perturbations such as disease and heat tolerance, without compromising production. Objective of this study is to evaluate the effect of heat stress during the reproduction cycle of the sow on farrowing rate (FR) and litter size (LS). This as a start for genetic improvement of heat tolerance in sows and genetic selection for robust sows. Data included 22,750 observations on FR (0 or 1) and LS (1–25), on 5,024 sows. Sows of a purebred Yorkshire dam line were located on 16 farms in Spain and Portugal. Outside temperature data were available. Sows are exposed to heat stress when temperature exceeds the upper critical temperature (UCT). In a previous study the UCT for FR was estimated to be 19.2°C and for LS to be 21.7°C. Heat load can be calculated as temperature-UCT. To simplify the analysis, the effect of heat stress was studied as the effect of temperature or heat load per day on FR or LS; analyses included temperatures/heat loads from 28 d before until 75 d after insemination. Correlations were estimated between temperature/heat load and LS and FR for each day. Strongest correlation between temperature and FR was −0.09 on d 22 before insemination; −0.13 on d 16 before insemination in gilts, and −0.09 on d 18 before insemination in sows (parity > 1). Correlations increased marginally when estimated between FR and heat load instead of temperature. Heat load had the largest effect on FR on d 21 before insemination. Strongest correlation between temperature and LS was −0.04 on d 10 after insemination; −0.08 on d 10 after insemination in gilts. Correlations increased when estimated between LS and heat load instead of temperature. Heat load had the largest effect on LS on d 10 after insemination, intriguingly this is 2 d before implantation. In conclusion, gilts are more susceptible for heat stress than older sows. A genetic model for genetic improvement of heat tolerance in sows for LS

and FR should include heat load instead of temperature as correlations between LS/FR were strongest with heat load.

Key Words: sows, fecundity, heat stress

818   A comparison of methods for predicting litter size in commercial pig lines. L. Tusell*[1], P. Perez[1], S. Forni[2], X. L. Wu[1], and D. Gianola[1], *[1]Department of Animal Sciences, University of Wisconsin, Madison, [2]Genus Plc, Hendersonville, TN.*

Genome-assisted evaluation requires statistical models capable of dealing with high-dimensional genotype data while yielding accurate predictions of merit of selection candidates. Various methods have been proposed for genome-enabled selection. Here, several procedures were compared with regard to their ability to predict phenotypes in 2 purebred pig lines and their cross. Data represented 2,598, 1,604 and 1,879 sows from 2 purebred and one crossbred line, respectively. Phenotype was the average number of piglets born, pre-corrected for systematic environmental effects. Genotypes were obtained using the Illumina PorcineSNP60 BeadChip. SNPs with minor allele frequency <0.05 and call rate >0.95 were excluded, yielding 46,855, 45,597 and 50,151 SNPs for the 2 purebred and crossbred lines, respectively. Missing genotypes were imputed from average allele frequencies at each locus. A 10-fold cross-validation assessed predictive ability of Bayesian Lasso, Bayesian Ridge Regression, Genomic BLUP, Reproducing Kernel Hilbert Spaces with kernel averaging, and a Radial Basis Function Neural Network using either the additive genomic relationship matrix (RBF-G) or principal component scores of the SNP matrix (RBF-UD) as inputs. Within line, methods yielded similar predictive ability, except for RBF models. The average correlation between observed and predicted phenotypes in testing sets (r) was higher in the crossbred line (0.27) than in purebred lines (0.19–0.23). RBF-G had the worst predictive ability in all lines: r = 0.10 and 0.17 in purebreds, and 0.21 in crossbreds. On the other hand, RBF-UD yielded the best predictive ability (r = 0.30) in crossbreds. This suggests that population structure affects predictive ability. When prediction was assessed in a large data set, principal component scores of the SNP matrix led to better predictive results, possibly because these scores are more informative than genomic relationships.

Key Words: genomic selection, neural networks, pigs

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