Associations Among Individual Gilt Birth Weight with Subsequent Weights, Selection Rates, and Age to Reach 135 kg. Jefferson Silva¹, Carine M. Vier¹, Amanda P. Siqueira¹, Ray Gonsalves¹, Fernanda Almeida¹, Vanderlei Zappani¹, Evandro Beraldin¹, Geraldo Alberton¹, Diaine Donin¹, Ning Lu¹, Steve dritz², Uislei A. Orlando², ¹Agroceres, ²Genus PIC, ³UMG, ⁴Lar Cooperativa Agroindustrial, ⁵UFPR

Abstract: Our objective was to investigate the associations among individual gilt birth weight (BiWt) of modern genotype gilts with their subsequent weights, age at puberty, and selection rates for the breeding herd. A total of 3,452 PIC gilts (Landrace x Large White) were included in the analysis. Gilts were individually weighed within 12h of birth, and associations with weights at weaning, the end of nursery, and at selection were determined through regression models. Gilts BiWt was also classified into four categories: Below1.04kg, 1.04-1.38kg, 1.38-1.72kg, Above1.72kg. Stimulus for puberty onset started when gilts were 146d old. Gilt age at the first detected heat was recorded. Selection rate was determined as: Selection Rate, % = number of gilts selected at 146d/number of gilts born alive; and Age to 135kg = (135–Selection Weight,kg)/Average Daily Gain from Birth to Selection. Data were analyzed using generalized linear models with the lm and glm functions of R. Results suggested that weaning and end of nursery weights increased (linear, P≤0.05) as the gilt BiWt increased. For each additional 100g in gilt BiWt, weaning and end of nursery weights increased by 131g and 379g, respectively. The weight at selection increased (quadratic, P≤0.05) as gilt BiWt increased. There was no evidence of gilt BiWt impact on age at first detected heat (P>0.10; 170.2, 167.7, 168.2, and 167.4d). Heavier gilts at birth reached 135kg at a reduced age (P≤0.05; 211.8, 201.4, 194.5, and 188.0d) and had greater selection rate (P≤0.05; 44.0, 58.1, 62.2, and 64.9%). In summary, this data indicated that gilts with phenotypically greater birth weight had better chances to be selected for the breeding herd and achieved the minimum weight target (135kg) for the first breeding at a younger age.

Keywords: birth weight, breeding, replacement gilts

Exploring the Statistical Nature of Independent Chromosome Segments. Mary Kate Hollifield¹, Matias Bermann¹, Daniela Lourenco¹, Ignacy Misztal¹, ¹University of Georgia

Abstract: Independent chromosome segments for a population with Nₑ effective population size and L genome length can be approximately defined as 4NₑL non-overlapping haplotypes of L/2 length derived from any Nₑ animals. The number of independent chromosome segments (Mₑ) can be approximated as 4NₑL. The genetic selection with a genomic relationship matrix (GRM) using such haplotypes approaches that with a GRM using the SNP markers. The objective of this study was to investigate the statistical nature of independent chromosome segments. Data were simulated using QMSim and contained a population of ten non-overlapping generations, each including 2,000 animals with Nₑ equal to 20, and a polygenic trait with a heritability of 0.6. The last three generations were genotyped, and each genome contained ten 1 M long chromosomes, for a total genome length of 10 M and 50,000 SNP. Chromosome segments of each animal were organized in non-overlapping haplotypes by the SNP code using in-house software written in Fortran. The effects of the hypothetical independent chromosome segments were estimated using a model that included an overall mean plus the segment effects. To analyze the behavior around Mₑ, the number of segments chosen to estimate segment effects varied around 4NₑL. Accuracies were calculated for animals in the last generation by cor (TBV, Zₐ), where Zₐ is a vector of breeding values based on segments and TBV is a vector of the true breeding values outputted by QMSim. Accuracies of segment effects were compared with the true accuracy, i.e., cor (TBV, GEBV). The maximum accuracy of segment effects was 0.84, and the true accuracy was 0.96. The results suggest that 4NₑL segments contain most of the additive information in the population. However, the accuracy of GBLUP is greater than that of the chromosome segment effects, suggesting that arranging chromosome segments based solely on the statistical nature is not enough to account for all the genetic variation.

Keywords: effective population size, genome length, haplotypes