Breeding and Genetics:
Applications and Methods in Animal Breeding—Pigs

180 Survival analysis of mice divergently selected for heat loss. A. S. Bhatnagar* and M. K. Nielsen, *University of Nebraska-Lincoln, Lincoln.*

Improvement in feed efficiency was achieved by reducing maintenance energy requirement without changing output in mice divergently selected for heat loss (MH = high, ML = low, MC = control). In 3 replicates of selection, feed intake at the same mature weight differs greatly (MH/ML~1.38). However, correlated decline in reproductive stayability may negate the benefit in reduced feed intake. For each line by replicate combination, 21 mating pairs were sampled at 7 wk of age (189 pairs). Pairs were culled due to death or illness of either member, no first parity by 42 d cohabitation, 2 consecutive litters with none born alive, 3 consecutive litters with none weaned, 42 d between parities, or average size of most recent 2 litters less than half the average of first 3 litters. All pairs were culled by 1 yr cohabitation. Survival curves were produced from Kaplan-Meier estimates and hazard ratios were produced using Cox proportional hazard model. Data were analyzed over the entire study and in 2 periods (P1: ≤ 5 parities, P2: > 5 parities). A competitive risk analysis was performed to explore risk of culling for each criterion. Log-rank tests of survival curves and hazard ratios showed similar trends. Overall, there was no difference in hazard rates between MH and ML mice. However, MH mice were 2.57 more likely to be culled than ML mice in P1 ($P < 0.04$) but 0.55 times less likely in P2 ($P < 0.04$). MH and ML mice had an increased hazard over MC mice ($P < 0.03$ and $P < 0.01$, respectively). MH mice carried an increased risk of 3.49 ($P < 0.02$) in P1, while ML mice carried an increased risk of 2.58 ($P < 0.01$) in P2 compared with MC mice. There were no differences found in the competitive risk analysis between MH and ML mice for any culling criteria. Results indicate that MH mice are more likely to be culled early and ML mice later, but MC mice have greater survival rates. For systems where smaller maximum parities are desirable, ML mice have less involuntary losses and thus enhanced efficiency in addition to their lower maintenance. But this advantage erodes in systems allowing larger numbers of parities.

Key Words: survival, feed efficiency, mice

181 Genome-wide association mapping including phenotypes from relatives without genotypes for three traits in broiler chickens. H. Wang*[1], I. Misztal[1], I. Aguilar[2], A. Legarra[3], W. Muir[4], R. Fernando[5], and R. Hawken[6], *[1]University of Georgia, Athens, [2]INIA, Las Brujas, Uruguay, [3]INRA, Toulouse, France, [4]Purdue University, West Lafayette, IN, [5]Iowa State University, Ames, [6]Cobb-Vantress Inc., Siloam Springs, AR.*

The purpose of this study is to extend genome-wide association studies using a single-step method (ssGBLUP) for a multi-trait model in broiler chickens. Data set consisted of 2 pure lines (L1 and L2) across 5 generations for 3 traits: body weight at 6 wk (BW6), ultrasound measurement of breast meat (BM), and leg score (LS) coded 1 = no and 2 = yes for leg defect. In total, there were 294,632 and 274,776 individuals in pedigree for L1 and L2, of which 4667 and 4553 were genotyped using a SNP 60k panel. After standard quality control, 40,615 SNP markers remained for analyses. For BM, there were ~74% missing phenotypes in both lines. Pedigree, phenotypic and genomic information were combined, and a multi-trait linear model was used through ssGBLUP. Genomic breeding values were calculated for all individuals in pedigree and converted to SNP effects. Variances of markers were calculated from SNP solutions and included as weights in a new genomic relationship matrix. The last step was repeated 5 times. Manhattan plots were constructed as proportion of genetic variance explained by each region consisting of 20 consecutive SNP markers. Several peaks explaining >1% of the genetic variation were found for BW6; however, peaks for L1 and L2 are on different chromosomes. No strong peaks have been observed for BM and LS, and each region for these traits explained <1% of total genetic variance. BM and LS seem to follow the infinitesimal model. Different peaks for the 2 lines for BW6 suggest different selection goals. The ssGBLUP approach allows for simple GWAS with complex models and easy accommodation of information from genotyped animals.

Key Words: chicken, genome-wide association, multi-trait model

182 Accuracy of estimation of genomic breeding values in pigs using low density genotypes and imputation. Y. M. Badke*[1], R. O. Bates[1], C. W. Ernst[1], J. Fix[3], and J. P. Steibel[1,2], *[1]Department of Animal Science, Michigan State University, East Lansing [2]Department of Fisheries & Wildlife, Michigan State University, East Lansing, [3]National Swine Registry, West Lafayette, IN.*

Genomic selection has the potential to increase genetic progress. Genotype imputation of high density SNP genotypes can improve cost efficiency of genomic breeding value (GEBV) prediction for pig breeding. Consequently, the objectives of this work were to (1) estimate accuracy of GEBV in a Yorkshire population and (2) quantify the loss in accuracy of GEBV prediction when genotypes were imputed (accuracy = 0.95) in selection candidates. Phenotypes (Table) and genotypes obtained with the PorcineSNP60 BeadChip were available for 965 Yorkshire boars. Genotypes of selection candidates were masked and imputed using tagSNP in the GeneSeek Genomic Profiler (10K). Imputation was performed with BEAGLE using 128 haplotypes as reference panel. SNP effects were estimated with ridge regression using de-regressed breeding values as response variables. Accuracy of GEBV was estimated as the squared correlation between estimated breeding values (EBV) and GEBV in a 10-fold cross validation design. Accuracy of GEBV prediction from observed genotypes (r^2_{obs}) ranged from 0.03 for LBW to 0.47 for BF (Table). Variation in accuracy between traits largely depended on the number of boars (N) with usable EBV. Using imputed genotypes for GEBV estimation caused a slight decrease in the accuracy of GEBV (r^2_{imp}) with the proportion of r^2_{imp} to r^2_{obs} ranging from 0.87 to 0.99. GEBV prediction from imputed genotypes is a cost efficient alternative for implementation of genomic selection in pigs. Furthermore, genotyping animals at lower cost and low density, followed by imputation, can result in increased accuracy by allowing more animals into the training panel.

Table 1. Accuracy of genomic prediction

	Backfat thickness	Days to 250 lb	Litter birth weight	Loin muscle area	Litter weaning weight	No. born alive	No. weaned	Wean to estrus
Boars with usable EBV (no.)	965	936	302	938	612	532	482	332
h^2	0.45	0.26	0.19	0.47	0.065	0.08	0.02	0.33
r^2obs	0.47	0.45	0.03	0.45	0.25	0.18	0.21	0.14
r^2imp	0.45	0.44	0.06	0.40	0.23	0.16	0.18	0.13
r^2imp/r^2obs	0.95	0.99	NA	0.89	0.91	0.93	0.87	0.90

Key Words: genomic prediction, pig, imputation

183 Estimation of US Yorkshire breed composition using genomic data. Y. Huang*[1], R. O. Bates[1], C. W. Ernst[1], J. S. Fix[2], and J. P. Steibel[1,3], *[1]Department of Animal Science, Michigan State University, East Lansing, [2]National Swine Registry, West Lafayette, IN, [3]Department of Fisheries and Wildlife, Michigan State University, East Lansing.*

White coat color, as an indication of breed purity has been a long-time selection requirement for the Yorkshire breed. Currently, color verification is completed using a test mating program, which creates an inefficient use of time and resources. In this study, genomic information from local chromosomal regions surrounding the positions where coat color genes are physically mapped, as well as the whole genome were applied to estimate breed composition of purebred Yorkshire animals. Genotypes for ~60,000 SNP from the Illumina PorcineSNP60 Beadchip (60K), including ~8,500 SNP from the GeneSeek Genomic Profiler for PorcineLD (GGP) (GeneSeek, Lincoln, NE) were available for reference animals, in which the genetic background was known, and study animals, that included Yorkshire sires (Tes_York, n = 889), and known crossbred animals that had Yorkshire heritage (Tes_U, n = 12). Haplotypes of 9 SNPs flanking the KIT gene (Dominant white) were developed for reference animals for the Duroc (n = 60), Hampshire (n = 52), Landrace (n = 56), Yorkshire (n = 64) and Pietrain (n = 15) breeds. Haplotypes observed in white reference breeds (Yorkshire and Landrace) were detected in 97% and 62% of haplotypes from Tes_York and Tes_U, respectively. Therefore, multi-SNP haplotypes flanking KIT can be used to classify animals that are not of Yorkshire or Landrace breed origin. In addition, whole genome SNP information was used in regression analyses to further differentiate breed composition. Using 60K SNP, regression coefficients for Yorkshire, indicating relative Yorkshire composition, ranged from 0.79 to 1.07 and 0.52 to 1.06 in Tes_York and Tes_U, respectively. Regression coefficients for Hampshire ranged from −0.029 to 0.052 and −0.005 to 0.38 in Tes_York and Tes_U, respectively. Animals in Tes_U were likely of Yorkshire and Hampshire breed origin. Correlation of regression coefficients for breed composition obtained by using the 60K and GGP SNP panel was 0.99. Genomic information can be used as a tool to describe an animal's breed composition and reduce the need for progeny testing for white coat color verification.

Key Words: haplotype, regression, SNP

184 Genome-wide association for human nose score of boar taint using single-SNP analysis. Y. G. Tesfayonas*[1,2], *[1]Wageningen University, Wageningen, the Netherlands, [2]Swedish University of Agriculture Sciences, Uppsala, Sweden.*

Human nose score (HNS) is one method used to reduce boar taint without castration. It involves the scoring of the level of boar taint in boars by sensory panel. The objective of this study was to identify SNPs that are associated with HNS and to determine the phenotype variation explained by the SNPs. Boar taint is the unpleasant odor released when cooking meat from entire male pigs. It is mainly caused by increased accumulation of androstenone and skatole in adipose tissue. Producers castrate male pigs to remove boar taint; however, this practice has raised animal welfare concerns from consumers. HNS of 1835 intact boars from 5 purebred (1,438) and 3 crossbred (397) lines genotyped with Porcine 60K SNP Bead chip, and 46,751 SNPs were used for the genome wide association study; boars that were part of the purebred and crossbred both contained sire and sow lines. The design of the study was population based. GRAMMAR approach in R package-GenABEL was employed for the genome wide association analysis. This study revealed genome wide SNP (FDR ≤0.05) on SSC5. The SNP had minor allele frequency of 0.04% and it explained 19% of the phenotype variation. In addition, Boars heterozygous for the SNP had a mean score (0.72) higher than the 2 homozygous genotypes (0.56 and 0.63) which suggests over dominance. Moreover, chromosome wide significant SNPs (FDR ≤0.05) were found on SSC2, SSC7 and SSC17. Some of the SNPs correspond to QTLs of androstenone and skatole. Therefore, HNS can be used to alleviate boar taint through breeding.

Key Words: human nose score, boar taint, SNP

185 Identification of a major QTL associated with N-specific IgG response in piglets experimentally infected with porcine reproductive and respiratory syndrome virus. A. S. Hess*[1], B. R. Trible[2], Y. Wang[2], N. J. Boddicker[1], R. R. R. Rowland[2], J. K. Lunney[3], and J. C. M. Dekkers[1], *[1]Iowa State University, Ames, [2]Kansas State University, Manhattan, [3]USDA, ARS, BARC, APDL, Beltsville, MD.*

Porcine reproductive and respiratory syndrome virus (PRRSv) costs the US pork industry $664 million annually; therefore, much emphasis has been placed on identification of genomic markers and pathways associated with host response. Serum level of immunoglobulin G (IgG) likely contributes to observed variability in health when infected with PRRSv. This study examined serum virus N protein-specific IgG levels, measured by fluorescent microsphere immunoassay. Serum and other data were collected on 462 Large White × Landrace piglets infected with PRRSv isolate NVSL 97-7895. 1:400 dilutions of sera, collected 42 post-infection, were added to virus N protein coupled beads. Antibody was detected by addition of biotin-conjugated goat anti-swine IgG, followed by addition of streptavidin-conjugated phycoerythrin. MAGPIX was used to obtain mean fluorescence intensity (MFI). Three standards were run on each plate: a negative control (no pig serum), a medium positive (serum with a median MFI), and a high positive (serum with a high MFI). Subtraction of the background and standardization using high positive resulted in a sample:positive ratio with the least between plate variation (4.6 ± 4.2% of total variance) and was used for analysis. Pedigree-based heritability was 13.5 ± 13.2%. In a genome-wide association study using 60k SNP data, the proportion of markers with no effect (π) was estimated to be 0.9999 using BayesCPi in GenSel. The 1-Mb region that explained the most genetic variation was on chromosome 7 in a region harboring the major histocompatibility (MHC) class I antigen genes, and was estimated to explain 54.2% of genetic variation. Analysis with Bayes B supported these results, indicating the presence of a major QTL associated with IgG levels. This is indicative of response to the N protein of PRRSv and is consistent with the presence of the MHC class I genes in the region, which play a direct role in immune response to viruses. Supported by NPB grant #12–120, Genome Canada, the National Pork Board and breeding companies of the PRRS Host Genetics Consortium.

Key Words: PRRSv, pig, antibody

186 eQTL analysis of blood RNA from pigs challenged with PRRSV reveal numerous differentially expressed transcripts associated with viral load QTL region. J. P. Steibel*[1], I. Choi[4], M. Arceo[1,3], C. W. Ernst[1], N. Raney[1], Z. Hu[2], C. K. Tuggle[2], N. Boddicker[2], J. Dekkers[2], R. R. R. Rowland[5], and J. K. Lunney[4], *[1]Michigan State University, East Lansing [2]Iowa State University, Ames, [3]North Carolina State University, Raleigh, [4]BARC-USDA, Belltsville, MD, [5]Kansas State University, Manhattan.*

This study's aim was to assess differentially expressed (DE) genes in pigs segregating for SNP WUR10000125 on SSC4, which has been reported as associated with porcine reproductive and respiratory syndrome virus (PRRSV) load post infection. Healthy pigs (n = 39) from a PRRS Host

Genetics Consortium (PHGC) trial were inoculated with PRRSV isolate NVSL 97–7985. RNA was prepared from blood Tempus tube samples collected at 0, 4, and 7 d post-infection. Pigs were assigned into 4 phenotypic groups according to the pigs' serum viral level and weight gain: (1) high viral level (Hv)-high growth (Hg), (2) Hv-low growth (Lg), (3) low viral level (Lv)-Hg and (4) LvLg. RNA was hybridized to the 20K 70-mer oligonucleotide Pigoligoarray in a blocked reference design with time 0 of each individual animal as the reference sample. Microarray data was analyzed using a linear mixed model with fixed effects of dye, time, phenotypic group (viral load × weight gain), WUR10000125 SNP genotype, interactions of SNP genotype × time and time × group, and random effects of array and pig. Nine oligonucleotides representing genes close to the WUR10000125 SNP were tested separately to assess cis-effects; a suggestive cis-acting association was detected for GBP4 ($P = 0.007$). A total of 107 oligonucleotides spanning 99 known genes across the genome were DE with respect to genotype within time effects (FDR <10%). Enrichment analyses for these 99 genes were performed with Ingenuity Pathways Analysis software. Top biological functions were Inflammatory Response, Cell-mediated Immune Response, and Lymphoid Tissue Structure And Development. Top canonical pathways included CCR5 Signaling in Macrophages, Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells, Calcium-induced T Lymphocyte Apoptosis and T Cell Receptor Signaling. Finally, TRAT1 and IL15 were identified as the top upstream regulators. These results provide insight into potential eQTL and mechanisms involved in the genetic control of gene expression in relation to PRRSV infection. A larger sample size is being processed to confirm these results in a broader eQTL scan.

Key Words: porcine reproductive and respiratory syndrome (PRRSV), eQTL, PRRS Host Genetics Consortium (PHGC)

187 Include birth weight in your breeding goal in the right way.

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The objective of our study was to examine optimal use individual birth weight (IBWT) observations to improve the genetic model for average daily gain (ADG). Data on ± 25,000 crossbred finishers were collected at TOPIGS Research farm in Beilen (NL). Pigs weighing 0.9 kg at birth had a grow-finish ADG of 828 g/d, while their 1.8-kg littermates gained 885 g/d, resulting in a reduction of 7 d to market. Pig breeding companies have been successful in selecting for increased litter size. As litter size increased, average birth weights tended to decline (b = −37 g/pig). When pig birth weight drops, the probability of preweaning death increases. Increasing birth weight by genetic selection seems, therefore, to be an attractive alternative. Several studies show that the heritability of IBWT is 0.30 or higher. A similar estimate was found in this data set. Birth weight, however, is not a characteristic of the piglet, but a characteristic of the sow. Analyzing IBWT with a direct–maternal genetic model reduced the heritability for the direct effect to 0.02 while the heritability for the maternal component was 0.15. The statistical properties of the latter model showed that this model is, by far, preferable to a direct genetic model. A bivariate model for IBWT and ADG showed that ADG and the direct effect of IBWT were uncorrelated and that ADG and the maternal component of IBWT had a moderate genetic correlation ($r_g = 0.34$). Since sows with a high genetic merit for ADG are heavier when giving birth (Bergsma et al., 2008), this genetic correlation showed that these sows give birth to heavier piglets because they are heavier themselves. As a bonus the genetic variance for ADG increased by 9%. The low heritability for the direct effect for IBWT also means that the sire of the litter hardly affects IBWT. This, together with the observation that IBWT and ADG are genetically uncorrelated, justifies the conclusion that selection for IBWT in sire lines is not relevant. Add IBWT as a direct–maternal effect to your genetic evaluation of ADG. This improves the perspective for selection for ADG and allows you to select for increased average birth weight (in dam lines) via increased litter weight.

Key Words: pig breeding, birth weight, daily gain

188 Genetic analysis of pig survival in a crossbred population.

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The aim of this study was to estimate genetic parameters for survival traits at different steps of the fattening period and their relationships with final weight in a commercial crossbred population of pigs. The edited data set consisted of 24,376 crossbred pigs from 197 purebred Duroc sires and 1,671 non-pedigreed Large White x Landrace dams. Traits analyzed were preweaning mortality (PWM); farrow dock (FAD) defined as culling between farrowing and nursery site; nursery dock (NUD) defined as culling between nursery and finisher site; finisher dock (FID) defined as culling before packing plant; hot carcass weight (HCW). Genetic parameters were estimated with a threshold-linear sire model because of the combination of categorical (PWM, FAD, NUD, and FID) and continuous (HCW) traits. Fixed effects were sex and dam parity. Random effects were year × month of birth, sire, litter and residual. The PWM was 16.99%, FAD was 0.71%, NUD was 0.90%, and FID was 1.02%. The mean HCW was 93.4 kg. Estimates of heritability were low to moderate (0.04 for PWM, 0.02 for FAD, 0.14 for NUD, 0.07 for FID, 0.12 for HCW). The sire genetic effects, defined as the ratio between the estimated sire variance and the total variance, were even lower and followed the same pattern than heritability. Estimates of common litter effect were higher and decreased with time for survival traits (0.11 for PWM, 0.19 for FAD, 0.10 for NUD, 0.04 for FID). Estimate of genetic correlation was 0.10 between PWM and FAD. Estimates of genetic correlations were negatives between PWM and NUD (−0.51), between PWM and FID (−0.10), between FAD and NUD (−0.50), and between FAD and FID (−0.21); NUD was positively correlated with FID (0.41). Estimates of genetic correlation between survival traits and HCW were 0.08 for PWM, −0.11 for FAD, 0.03 for NUD, and −0.27 for FID. Survival at the beginning of the fattening period (PWM and FAD) is not a good predictor for survival until harvesting and high market weight. Docking at nursery and finisher stages are more similar traits than docking at farrowing stage. The influence of the sire line on the survival of crossbred pigs is small.

Key Words: genetic parameter, pig, survival

189 Survival from birth to weaning in gilts.

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The aim of this study was to evaluate the influence of birth weight on gilt survival. For the US pig industry to remain globally competitive production efficiencies must continue to be improved. Improved methods for producing pork that reduce inputs, minimize environmental impact, maximize pig well-being, and ensure a safe, nutritious pork supply are needed. To improve reproductive efficiency, pigs have been genetically selected for increased litter size at birth. However as number born alive increases, individual piglet birth weight decreases. Low piglet birth weights can result in increased pre-weaning mortality and reduced wean-to-finish growth performance. Information on 12,968 gilts from 2 genetic multiplier farms in eastern North Carolina was recorded. Gilts were individually tagged and birth weights were recorded within 24 h of birth. Mortality was recorded based on date of death and reason. Average birth weight was 1250 g (±320). From the 12,968 gilts that were born, 10,742 (82.8%) survived to weaning. The average wean age of the gilts is 22.06 d (±2.74). Glimmix procedure was used to examine the effect of birth weight on survivability in gilts. A binomial distribution was used for death (1 = alive, 0 = dead). Birth week, parity, cross-foster, and farm were fixed effects. Number born, birth weight, and number nursed were covariates. All effects in the model were significant ($P < 0.05$). Piglets with a 100g increase in birth weight are 1.16 times more likely to survive. When increasing number born and number nursed by one piglet, the odds of survival are 0.84 and a 0.95, respectively. Survival decreased 9.5% when piglets were cross-fostered. Producers should develop genetic and management strategies to select on birth weight and survivability. It was concluded that cross-fostering piglets decreased survivability.

Key Words: pig, survival, cross-fostering

190 Genetic parameters of maternal traits related to sow feed efficiency during lactation.

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Over the past few decades, the productivity of commercial sows has increased and this has resulted in higher energy requirements and greater mobilization of body reserves, which can negatively affect the longevity and later production performance of sows. One way to overcome this is to increase feed efficiency during lactation. The objective of this study was to estimate genetic parameters for traits related to feed intake and efficiency of sows during lactation. The data were provided by Genesus Inc. and included data on 1239 farrowings from 478 Yorkshires and 457 Landrace sows recorded between July 2011 and December 2012. Sow body weight and back fat were measured ~5 d before farrowing, and at weaning. Daily feed intake was recorded using the Gestal feed recording system. Heritabilities were estimated separately for each breed using a single trait linear mixed model analysis using ASReml. All models included fixed effects of parity (5 levels), contemporary group (farrowing year and season–7 levels), random animal and permanent environmental effects. Sow residual feed intake (RFI) and lactation energy balance (EB) were used to evaluate the overall efficiency of sows during lactation. Heritability estimates for RFI and EB were 0.21 and 0.12 for Landrace and 0.25 and 0.06 for Yorkshire sows. The major traits that contribute to the calculation of RFI and EB are total feed intake of sow (FI), Protein loss (PL), fat mass loss (FML), sow body weight loss (WL), litter birth weight (LBW) and litter weaning weight (LWW) and these traits exhibited moderate heritabilities (0.18, 0.36, 0.20, 0.32, 0.41 and 0.11 for Landrace and 0.33, 0.24, 0.12, 0.24, 0.32 and 0.10 for Yorkshire). Proportions of variance due to permanent environmental effects ranged from 0 to 0.10 for all traits except LWW, for which it was 0.24 and 0.18 for Landrace and Yorkshire sows respectively. These results suggest that for the population studied, selection based on these traits can result in reasonable genetic improvement for feed efficiency during lactation.

Key Words: sow lactation, feed efficiency, genetic parameter

191 Random regression models for daily feed intake in Danish Duroc pigs.

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The objective of this study was to develop random regression models and estimate covariance functions for daily feed intake (DFI) in Danish Duroc pigs. A total of 476201 DFI records were available on 6542 Duroc boars between 70 to 160 d of age. The data originated from the National test station and were recorded using ACEMO electronic feeders in the period of 2008 to 2011. The pedigree was traced back to 1995 and included 17222 animals. The phenotypic feed intake curve was decomposed into a fixed curve, being specific to the barn-year-season effect and curves associated with the random pen-year-season, permanent, and animal genetic effects. The functional form was based on Legendre polynomials (LP). A total of 64 models for random regressions were initially ranked by BIC to identify the approximate order for the LP using AI-REML. The parsimonious model included Legendre polynomials of 2nd order for genetic and permanent environmental curves and a heterogeneous residual variance, allowing the daily residual variance to change along the age trajectory due to scale effects. The parameters of the model were estimated in a Bayesian framework, using the RJMC module of the DMU package, where weakly informative priors were derived from preliminary AI-REML analysis. We used a burn-in of 10k followed by 90k rounds, interleaving every 10th sample. Posterior mean heritabilities were low for DFI, but increased from 0.07 to 0.12 at 100 d of age and then decreased fluctuating to around 0.08. The low heritabilities were due to a higher residual variance when using individual DFI records compared with average DFI records over the entire test period. The heritability of DFI for the entire test period was 0.28, corresponding closely to the estimate derived from analysis of average DFI records. Eigenvalues of the genetic covariance function showed that 33% of genetic variability was explained by the individual genetic curve of the pigs. This proportion was covered by linear (27%) and quadratic (6%) coefficients. Genetic eigenfunctions revealed that altering the shape of the feed intake curve by selection may be an option in Danish Duroc pigs.

Key Words: random regression model, Gibbs sampling, genetic parameter