

Breeding and Genetics: Current Issues in Swine Breeding

529 Genetics of piglet survival: Additive, maternal and foster contributions. E. F. Knol*, M. J. M. Rutten, D. Roelofs-Prins, and J. W. M. Merks, *IPG, Institute for Pig Genetics B.V., Beuningen, The Netherlands.*

Phenotypic and genetic trends for litter size are clearly positive in most parts of the world, similar trends for number weaned are lower. As a consequence phenotypic trends in stillborn and pre-weaning mortality are positive. This is partly the result of reduced input of labor, and partly because of negative correlated genetic trends of litter size. To optimize selection for current markets, we re-addressed the two traditional survival traits: farrowing survival (FS: complement of stillborn) and pre-weaning survival (PWS).

FS was modeled by both additive-genetic and maternal-genetic effects; PWS was modeled including an extra genetic effect for foster-dam. The models log-likelihoods justified inclusion of the direct additive genetic effect. When the majority of the piglets are raised by their own dam, the genetic foster dam effects and genetic maternal effects are confounded. Therefore, sufficient cross-fostering of piglets in the data is required to be able to disentangle these effects.

The dataset consisted of 75,765 records of individually recorded piglets with known cross-fostering status on a closed TOPIGS multiplication farm with a pedigree of 78,572 animals. Variance estimates for FS: error 623.5, additive genetic 3.79, and maternal genetic 15.50; for PWS: error 819.8, additive genetic 7.29, maternal genetic 7.87 and foster dam genetic 30.09. Absolute genetic correlations were lower than 0.1 within traits and lower than 0.4 among traits. Heritabilities were low, but the sum of the genetic variance components of 19.3 for FS and 45.3 for PWS are very promising for selection.

Interpretation: 'maternal' is the influence of the uterine environment and partly of the first colostrum; 'foster' represents the mothering ability of the sow, behavior and quality of the udder, and 'additive' includes contribution of the sire, which is especially relevant in crossbred data. Large scale recording of birth weight, cross-fostering and survival data is necessary for a successful selection program against mortality.

Key Words: Pig, Survival, Mothering-Ability

530 Genetic parameters of farrowing survival in purebred and crossbred pigs. A. Cecchinato*¹, G. de los Campos², D. Gianola², L. Gallo¹, and P. Carnier¹, ¹*University of Padova, Legnaro, Padova, Italy,* ²*University of Wisconsin, Madison.*

In commercial swine production, an important breeding objective is to improve performance of crossbred animals. However, selection is largely carried out in nuclei of purebreds. A question is whether purebred performance (in the nucleus) predicts accurately outcomes in crossbreds (commercial tier). This can be investigated by considering the two performances as different traits in a model and by estimating the genetic correlation. The objective of this study was to infer (co)variance components for farrowing survival in purebred (P) and crossbred (C) pigs; the latter were from crosses between P boars and Large White-derived crossbred sows. If the genetic correlation between C and P traits is large enough, selection in P would produce a correlated response in

C. Data were from 13,643 (1,213 litters) C and 30,919 (3,162 litters) P pigs, produced by mating the same 168 P boars to 319 Large White derived crossbred females and 1,413 P sows, respectively. The outcome variable was pig survival at birth as a binary trait. A Bayesian bivariate threshold model was implemented via Gibbs sampling. Effects of sex, parity of the dam, litter size and year-month of birth were assigned flat priors; those of litters, dams and sires were given Gaussian prior distributions. Marginal posterior means (SD) of the sire, dam and litter variances in P were 0.018 (0.008), 0.077 (0.020), 0.347 (0.025), respectively in the liability scale. For C, corresponding estimates were 0.030 (0.018), 0.120 (0.034), and 0.189 (0.032), respectively. The posterior means (SD) of heritability of survival in P and C, and of the genetic correlation between these traits were 0.049 (0.023), 0.091 (0.054) and 0.248 (0.336), respectively. Heritability estimates were low and in agreement with previous reports. The genetic correlation was also low, and a 95% Bayesian confidence region (-0.406, 0.821) included zero. Even though variation of estimates is large, results suggest that genetic progress expected in C when selection is based on P may be nil.

Key Words: Threshold Models, Pigs, Heritability

531 Heritability of longevity in Yorkshire females. M. D. Hoge*¹ and R. O. Bates², ¹*Western Illinois University, Macomb,* ²*Michigan State University, East Lansing.*

The length of adult sow life is recognized as both an economical and welfare concern. However there are not consistent definitions to measure sow longevity. This study assessed the genetic variation described by six different descriptions of longevity. Heritability was estimated for four different descriptions of longevity using a proportional hazards model with an underlying Weibull distribution. The definitions included herd life (time from first farrowing to culling), lifespan (number of parities a female has accumulated before culling), lifetime prolificacy (the number of piglets born alive during the lifetime of the sow), and a combination of prolificacy and length of productive life (the number of pigs produced per day of life). Data consisted of 7,632 records of Yorkshire females with at least one farrowing record, from both nucleus and multiplication herds across 21 farms from four seedstock systems. A threshold model was used to estimate heritability for two descriptions of stayability (probability of producing 40 pigs or probability of reaching 4 parities) on a subset of the original data (n=5803) that did not include censored observations. Terms for both models included, first litter performance effects of; age at first farrowing, number born alive, number of stillborns, adjusted 21 day weaning weight, and length of lactation along with the number born alive at last recorded farrowing. Additionally, the number born alive, litter birth weight and percentage of gilts born in a female's birth litter and her growth and backfat records were included. These variables were treated as fixed and time-independent. A random effect of sire was included in all models. Heritability estimates ranged from 0.16 to 0.21 for the Weibull analyses and 0.52 for the threshold analyses. Sufficient genetic variation exists, regardless of definition, to improve sow longevity.

Key Words: Sow Longevity, Genetics, Heritability

532 Use of serial pig body weights for genetic improvement. B. Zumbach^{1,3}, I. Misztal^{*1}, C. Y. Chen¹, S. Tsuruta¹, W. O. Herring², T. Long², and M. Culbertson², ¹University of Georgia, Athens, ²Smithfield Premium Genetics Group, Rose Hill, NC, ³Norsvin, Hamar, Norway.

This study examined the utility of serial weights from FIRE (Feed Intake Recording Equipment, Osborne Industries, Inc., Osborne, KS) stations for a longitudinal analysis of body gain. Data included 884,132 body weight records from 3,888 purebred Duroc pigs. Pigs entered the feeder station at age 77-149 d and left at age 95-184 d. A substantial number of records were abnormal, showing weight close to 0 or up to twice the average weight. Plots of weights for some animals indicated two parallel growth curves. Data were cleaned using robust regression based on M-estimation (weight function: bisquare, $c=2$; scale parameter: median), with age used as both a linear and a quadratic covariable. In order to maintain variability in the data and discard outliers at the same time, a cutoff value of $k=1.5$ was chosen. After discarding the outliers detected by the M-estimation, 607,597 body weight records remained. Daily weight (170,443 records) was calculated as an average of cleaned body weight records for each animal in one day. Daily gain was calculated as the difference in body weight between consecutive days. The number of records for daily gain was 152,636, and the average daily gain was 0.85 kg (SD = 1.16 kg). As a second step of cleaning, only animals with ≥ 50 body weight records and a standard error of the residual ≤ 2 kg were included, reducing the data to 89,257 records. After removing records outside of 3 SD from the mean, the final data set included 69,068 records of daily gain from 1,921 animals. Daily gain based on daily, weekly and monthly records was analyzed using repeatability models. Heritability estimates were 0.02%, 3.3% and 13%, respectively. SE of the estimate on daily records was larger than the estimate. After extensive editing, weight records from automatic feeding stations are useful for genetic analyses of daily gain from weekly or monthly but not daily data.

Key Words: Body Weight, FIRE Feeder Station, Robust Regression

533 Estimates of genetic correlations among growth traits including competition effects. C. Y. Chen^{*1}, R. K. Johnson¹, S. D. Kachman¹, and L. D. Van Vleck^{1,2}, ¹University of Nebraska, Lincoln, ²ARS, USDA, U.S. Meat Animal Research Center, Clay Center, NE.

The objective was to estimate genetic parameters of direct and competition effects for traits measured at the end of a growth test utilizing multi-trait analyses. A total of 9,720 boars were tested with 15 boars per pen from about 71 to 161 d of age and weight from 31 to 120 kg. Traits analyzed with initial age on test as a covariate were average daily gain during test (ADG), days to 110 kg (D110), and daily feed intake (DFI). Backfat measured at the p2 point (BF) and muscle depth (MD) were analyzed with age off test as a covariate. Fixed effects of line and contemporary group, with random direct genetic, competition genetic, and competition environmental effects were also in the statistical model. For single-trait analyses, estimates of direct heritability were 0.30, 0.26, 0.20, 0.46, and 0.33 for ADG, D110, DFI, BF, and MD, respectively. Estimates of heritability for competition effects were near to zero for all traits. Estimates of genetic correlation between direct and competition effects were 0.06, -0.13, -0.32, 0.22, and 0.36 for ADG, D110, DFI, BF, and MD, respectively but these are based on very small estimates of variance of competition effects. For two-trait analyses, estimates of direct genetic correlations were -0.96, 0.15, 0.44, -0.14, -0.42, 0.38, 0.16, and 0.04 for ADG-D110, ADG-BF, ADG-MD, D110-BF, D110-MD, DFI-BF, DFI-MD, and BF-MD, respectively.

Estimates of direct genetic correlations for ADG-DFI and D110-DFI, however, could not be obtained because global convergence failed to be met. Estimates of competition genetic correlations among the five traits might have little meaning because estimates of variances of competition effects were close to zero for all five traits. Difficulty of analyses including competition effects with two-trait models was apparent when the average information matrix failed to provide reasonable information. Interpretation of antagonisms among traits associated with competition effects was limited in this study.

Key Words: Competition, Genetic Parameters, Swine

534 Associations between body structure and overall leg action in crossbred gilts. M. Nikkilä^{*1}, K. Stalder¹, B. Mote¹, J. Lampe², B. Thorn³, M. Rothschild¹, A. Johnson¹, L. Karriker¹, and T. Serenius⁴, ¹Iowa State University, Ames, ²Swine Graphics Enterprises, Webster City, IA, ³Newsham Genetics, West Des Moines, IA, ⁴FABA Breeding, Vantaa, Finland.

The goal of this study was to investigate genetic parameters of body structure traits and overall leg action. The study was conducted at a commercial farm and involved 1449 females. The gilts were from two genetic lines and were progeny of 58 known sires and 836 dams. Sire information from 52 animals was unavailable. Gilts averaged 190 ± 7 days of age and 124 ± 11 kg body weight at the time of evaluation. Body structure evaluation included both body size (length, depth, width) and body shape traits (top line, hip structure, rib shape). Structure traits and overall leg action were independently evaluated by two experienced scorers using a 9 point scale. Top line was divided into two traits (weak/high top line) prior to analyses. AI-REML and the DMU-package were used to estimate variance components using a multivariate animal model. The statistical model included gilt line, evaluation day and scorer as fixed effects, animal as a random effect and weight at evaluation as a linear covariate. Heritability estimates were moderate for body size traits ($h^2=0.25-0.34$), low to moderate for body shape traits ($h^2=0.11-0.26$), and relatively low for leg action ($h^2=0.12$). Body size traits were genetically highly correlated with each other ($r_g=-0.80-0.92$) and with top line and rib shape ($r_g=-0.93-0.88$). Among body shape traits, high top line was genetically correlated with hip structure and rib shape ($r_g=0.63-0.92$). Long and shallow body, high top line and steep hip structure were associated with inferior leg action ($r_g=0.56-0.75$). Since body structure has high favorable genetic correlations with overall leg action, genetic progress in leg action can be enhanced not only by selecting animals with superior feet and leg soundness, but also by utilizing information about body structure. Satisfactory leg action is crucial for increasing sow productive lifetime, since lameness is one of the primary causes of early culling.

Key Words: Gilts, Body Structure, Leg Action

535 Genetic parameters for longitudinal feed intake and weight gain in Durocs. C. Y. Chen^{*1}, I. Misztal¹, S. Tsuruta¹, W. O. Herring², T. Long², and M. Culbertson², ¹University of Georgia, Athens, ²Smithfield Premium Genetics Group, Rose Hill, NC.

The objective was to investigate the genetic parameters for daily feed intake (DFI, g) and daily gain (DG, g) with records obtained from elec-

tronic feeder stations. After editing, data included DFI and DG from 81 to 167 d of age of 1,921 Duroc boars. The boars were housed in 112 pens, each equipped with one feeder, and allowed ad libitum feeding; most animals were tested only for 7-8 weeks. Because of large variation in daily records, weekly averages were used. Six traits were defined as DG and DFI during 81-109 (period 1), 110-138 (period 2), and 139-160 d of age (period 3). A six-trait model included age as a covariate with fixed effect of year-week and random effects of pen-year-week, litter, animal, and permanent environment. Variance components were estimated by a Bayesian approach using Gibbs sampling algorithm. Estimates of heritability for respective periods were 10.3, 10.7, and 11.6% for DFI and 7.0, 5.0, and 7.2% for DG. For DFI, genetic correlations between periods 1-2 were 0.76, periods 2-3 were 0.61, and periods 1-3 were 0.08. For DG, the same correlations were 0.68, 0.72, and 0.33. The correlations between DFI in period 1 and DG in periods 1-3 were 0.80, 0.61, and 0.49. The correlations between DFI in period 2 and DG in periods 1-3 were 0.38, 0.52, and 0.33. The correlations between DFI in period 3 and DG in periods 1-3 were -0.24, -0.09, and -0.27. Standard errors of correlations varied from 0.14 to 0.23. Low correlations for DG and DFI between extreme periods suggests that DG and DFI in these periods are different traits. Negative correlations between DFI and DG may indicate compensatory growth, competition for feeders, or the data structure of few animals with records in periods 1 and 3.

Key Words: Daily Gain, Genetic Parameters, Swine

536 Relationship between feed intake during growth and lactation in a mouse model. W. M. Rauw^{*1}, S. Hermes², K. Bunter², and L. Gomez Raya¹, ¹*University of Nevada, Reno*, ²*University of New England, Armidale, Australia*.

The major part of selection pressure in pig breeding programs has been directed toward improvement of lean growth efficiency by selecting for

increased growth rate, reduced body fatness, and improved feed efficiency. However, because leanness and feed efficiency are negatively correlated with feed intake, selection for improvement in these traits has led to a decrease in voluntary feed intake. It has been argued that voluntary feed intake should be considered in breeding programs. This study investigated the phenotypic correlation between feed intake during growth, at maturity, and during lactation in a mouse model in a selection experiment for litter size at birth. Data were available on 42 control and 48 selection line dams and litters. Feed intake was recorded every 3 d between 21 and 69 d of age, and daily between littering and weaning. A linear function was fitted to relate individual data on cumulative feed intake to age in virgin females and to days in lactation in lactating females. Selection line females, but not those of the control line, with higher intake during growth and at maturity had higher lactation intakes ($r = 0.37$, $P < 0.05$, and $r = 0.46$, $P < 0.001$, respectively). As this relationship will be positive only when animals eat to their potential, the results suggest that selection line females have been genetically "programmed" to eat to their potential intake capacity as a correlated effect, allowing for maximum litter sizes. Commercial lean types of pigs can be expected to produce to their maximum potential as well. However, when food intake is insufficient to meet the energy requirements during lactation, sows mobilize body reserves. When food intake capacity is limited and increased milk production in lactating sows is accounted for by a considerable mobilization of body reserves, the relationship between feed intake during growth and during lactation may be reflected in the relationship between growth intake and body condition instead.

Key Words: Selection, Feed Intake, Lactation