Estimation of Dominance Variance in Purebred Yorkshire Swine

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ABSTRACT: We used 179,485 Yorkshire reproductive and 239,354 Yorkshire growth records to estimate additive and dominance variances by Method Fraktur $\mathfrak{R}$. Estimates were obtained for number born alive (NBA), 21-d litter weight (LWT), days to 104.5 kg (DAYS), and backfat at 104.5 kg (BF). The single-trait models for NBA and LWT included the fixed effects of contemporary group and regression on inbreeding percentage and the random effects mate within contemporary group, animal permanent environment, animal additive, and parental dominance. The single-trait models for DAYS and BF included the fixed effects of contemporary group, sex, and regression on inbreeding percentage and the random effects litter of birth, dam permanent environment, animal additive, and parental dominance. Final estimates were obtained from six samples for each trait. Regression coefficients for 10% inbreeding were found to be −.23 for NBA, −.52 kg for LWT, 2.1 d for DAYS, and 0 mm for BF. Estimates of additive and dominance variances expressed as a percentage of phenotypic variances were, respectively, 8.8 ± .5 and 2.2 ± .7 for NBA, 8.1 ± 1.1 and 6.3 ± .9 for LWT, 33.2 ± .4 and 10.3 ± 1.5 for DAYS, and 43.6 ± .9 and 4.8 ± .7 for BF. The ratio of dominance to additive variances ranged from .78 to .11.

Key Words: Pigs, Inbreeding, Dominance, Genetic Parameters

Introduction

Across-herd genetic evaluation in swine currently uses an additive genetic model. However, fitness traits, similar to the litter traits in swine, may have a substantially higher heritability in the broad sense relative to the narrow sense (Hill and Webb, 1982; Bidanel et al., 1989; Falconer, 1989). Under these conditions, selection accuracy is reduced under an additive model (Uimari and Maki-Tanila, 1991).

The prediction of additive and dominance genetic effects concurrently should allow for a more precise prediction of total genetic merit and may prove beneficial in the estimation of dominance effects for a mate selection program (Henderson, 1985, 1989). These conditions are particularly valid in populations with a large number of dominance relationships (i.e., full-sibs) and populations that use specialized sire and dam lines (DeStefano and Hoeschele, 1992). Therefore, because swine are a litter-bearing species with a large percentage of dominance relationships and possible magnitude of dominance effects in reproductive traits, swine genetic evaluation seems well-suited for dominance models. However, before implementation, the relative importance of dominance genetic effects must be characterized. Consequently, the objective of this study was to estimate dominance variance for reproductive and growth traits in swine.

Materials and Methods

Data were obtained from the National Swine Registry and included 179,485 reproductive and 239,354 growth records from purebred Yorkshire swine. The data sets were edited to ensure connectedness and eliminate biological extremes greater than 4 SD from the mean. Growth records were then adjusted to a constant weight (NSIF, 1988). Litter records were adjusted for parity, age of dam, age of litter at weaning, and number after transfer (Culbertson, 1997). Phenotypic means and standard deviations are presented in Table 1. The average full-sib family contained approximately three full-sibs. Contemporary groups were determined by the National Swine Registry. Growth contemporary groups were defined

Table 1. Means and standard deviations for number born alive (NBA), 21-d litter weight (LWT), days to 104.5 kg (DAYS), and backfat at 104.5 kg (BF)

Item	NBA	LWT[a]	DAYS	BF[b]
Mean[c]	10.21	56.0	165.2	17.3
SD	2.8	14.7	16.8	4.8

[a]Expressed in kilograms.
[b]Expressed in millimeters.
[c]Based on adjusted data after editing as described in the text.

as a group of animals farrowed, weaned, and tested together under common management and environmental conditions. Reproductive contemporary groups were defined as a group of sows that were bred, gestated, and farrowed in a group under the same management and environmental conditions.

The dominance relationship matrix was formed using the method of Hoeschele and VanRaden (1991). In this method, dominance effects are defined and predicted as a specific mating pair or parental dominance class.

Number born alive ($\mathbf{NBA}$) and 21-d litter weaning weight ($\mathbf{LWT}$) were analyzed separately using the model

$$\mathbf{y} = \mathbf{X}\beta + \mathbf{Zb}\Delta + \mathbf{Za} + \mathbf{Wf} + \mathbf{Zp} + \mathbf{Ms} + \mathbf{e}$$

where $\mathbf{y}$ is the vector of records, β is the vector of contemporary group effects, Δ is the regression of y on inbreeding coefficient; $\mathbf{b}$ is the vector of inbreeding coefficients, $\mathbf{a}$ is the vector of additive animal effects, $\mathbf{f}$ is the vector of parental dominance effects, $\mathbf{p}$ is the vector of animal permanent environmental effects, $\mathbf{s}$ is the vector of mate within contemporary group effects, $\mathbf{e}$ is the vector of residuals, and $\mathbf{X}$, $\mathbf{Z}$, $\mathbf{W}$, and $\mathbf{M}$ are known matrices that relate records to respective effects. The variances of this model are

$$\text{var}\begin{bmatrix}\mathbf{a}\\\mathbf{d}\\\mathbf{p}\\\mathbf{s}\\\mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{A}\sigma_a^2 & 0 & 0 & 0 & 0\\0 & \mathbf{F}\sigma_f^2 & 0 & 0 & 0\\0 & 0 & \mathbf{I}\sigma_p^2 & 0 & 0\\0 & 0 & 0 & \mathbf{I}\sigma_s^2 & 0\\0 & 0 & 0 & 0 & \mathbf{I}\sigma_e^2\end{bmatrix}$$

where σ_a^2 is the additive variance, σ_f^2 is the parental dominance variance and thus 1/4 of the total dominance variance σ_d^2, σ_p^2 is the animal permanent environmental variance, σ_s^2 is the mate within contemporary group variance, σ_e^2 is the residual variance, $\mathbf{A}$ is the additive relationship matrix, and $\mathbf{F}$ is the parental dominance relationship matrix.

Days to 104.5 kg ($\mathbf{DAYS}$) and backfat at 104.5 kg ($\mathbf{BF}$) were analyzed separately using the model

$$\mathbf{y} = \mathbf{X}\beta + \mathbf{Zb}\Delta + \mathbf{Za} + \mathbf{Wf} + \mathbf{Ml} + \mathbf{Zp} + \mathbf{e}$$

where, $\mathbf{l}$ is the vector of litter of birth effects, $\mathbf{p}$ is the vector of dam permanent environmental effects, and $\mathbf{M}$ is a known matrix that relates records to their respective effects. The corresponding variances are

$$\text{var}\begin{bmatrix}\mathbf{a}\\\mathbf{d}\\\mathbf{l}\\\mathbf{p}\\\mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{A}\sigma_a^2 & 0 & 0 & 0 & 0\\0 & \mathbf{F}\sigma_f^2 & 0 & 0 & 0\\0 & 0 & \mathbf{I}\sigma_l^2 & 0 & 0\\0 & 0 & 0 & \mathbf{I}\sigma_p^2 & 0\\0 & 0 & 0 & 0 & \mathbf{I}\sigma_e^2\end{bmatrix}$$

where σ_l^2 is the litter variance, σ_p^2 is the dam permanent environmental variance, and all other effects are the same as defined with the reproductive model.

Estimates were obtained by Method $\Re$ (Reverter et al., 1994) following the procedures by Misztal (1997). Each trait was analyzed with six samples of the data, containing 50% of the total data, selected by a random number generator. The convergence criterion was $r_i = 1 \pm .0001$, where r_i is the regression from random effect i. Sampling standard deviation was defined as the standard deviation of the six estimates from the subsamples.

Results and Discussion

Estimates of inbreeding depression and variances for NBA and LWT are presented in Table 2. All variances are expressed as a percentage of the phenotypic variance. Estimates of inbreeding depression were considerable for both traits. For example, sows produced by a mating of half-sibs, 12.5% inbred, would have their record adjusted approximately .3 of a pig and .65 kg for NBA and LWT, respectively. These estimates of inbreeding depression are in general agreement with previous work on reproductive traits (Craft, 1958; Bereskin et al., 1968). Estimates of additive, permanent environmental, and mate variances are in general agreement with previous studies for both traits (Mabry et al., 1988; Kaplon et al., 1991; Ferraz and Johnson, 1993). Estimates of dominance variance were 25 and 78% of additive variance for NBA and LWT, respectively.

Estimates of inbreeding depression and variances for DAYS and BF are found in Table 3. Estimates of inbreeding depression were larger in magnitude for DAYS relative to BF. Previous research has also found negligible effects of inbreeding for measures of lean percentage similar to BF (Leymaster et al., 1979) with more substantial effects on measures of growth such as DAYS (Craft, 1958; Bereskin et al., 1968). Permanent environment of the dam, although estimated to be of little importance, was included in the estimation model to further define all sources of variation and allow for more precise estimates of dominance variance.

Table 2. Estimate of regression on inbreeding percentage and means and standard
deviations for estimates of additive, dominance, permanent environment,
and mate within contemporary group variances for number
born alive (NBA) and 21-d litter weight (LWT)

| Trait | Inbreeding depression[a] | Variance (% of phenotypic)[b] | | | |
		Additive	Dominance[c]	PE[d]	Mate[e]
NBA	−.23 ± .001	8.8 ± .5	2.2 ± .7	6.2 ± .4	3.4 ± .2
LWT[f]	−.52 ± .001	8.1 ± 1.1	6.3 ± .9	4.6 ± 1.0	4.0 ± .5

[a]Per 10% inbreeding.
[b]Based on six runs of Method $\Re$.
[c]Calculated as $4 \times \sigma_f^2$.
[d]Animal permanent environment.
[e]Mate within contemporary group.
[f]Expressed in kilograms.

Table 3. Estimates of regression of inbreeding percentage and means
and standard deviations for estimates of additive, dominance, litter,
and maternal permanent environment variances for days to
104.5 kg (DAYS) and backfat at 104.5 kg (BF)

| Traits | Inbreeding depression[a] | Variance (% of phenotypic variation)[b] | | | |
		Additive	Dominance[c]	Litter	PE[d]
DAYS	2.10 ± .001 d	33.2 ± .4	10.3 ± 1.5	12.7 ± .6	1.2 ± .4
BF	.00 ± .001 mm	43.6 ± .9	4.8 ± .7	7.3 ± .3	1.0 ± .2

[a]Per 10% inbreeding.
[b]Based on six runs of Method $\Re$.
[c]Calculated as $4 \times \sigma_f^2$.
[d]Maternal permanent environment.

Additive and litter variances for DAYS and BF were in general agreement with estimates from previous studies (Ferraz and Johnson, 1993; Li and Kennedy, 1994). Dominance variance for DAYS was estimated to be about a third of the additive variance and approximately 10% of the phenotypic variance. Conversely, dominance variance for BF, the trait with the highest heritability in the narrow sense, was found to be only 11% of the additive. Although the dominance variance for DAYS would seem large, similar results were found for growth traits in beef cattle (Gengler et al., 1997).

Implications

The results indicate that dominance effects may be important for reproductive and growth traits in swine. Therefore, specific mating systems may allow for selection of dominance effects for these traits and, subsequently, increased phenotypic performance. Additional studies also need be conducted to analyze the relative improvement in prediction of additive effects by accounting for dominance and inbreeding in the analysis model.

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