ESTIMATION AND UTILIZATION OF INBREEDING AND DOMINANCE GENETIC EFFECTS IN GENETIC EVALUATION OF PUREBRED AMERICAN SWINE

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SUMMARY
Genetic evaluation in swine is currently conducted utilizing additive genetic models. Historical studies have examined the relative influence of inbreeding on phenotypic performance; however, until recently estimation of dominance genetic effects from large populations have proven prohibitive. Utilizing Method R, single-trait estimation of inbreeding and dominance genetic effects were conducted for a population of purebred American Yorkshire swine. The traits analyzed included number born alive (NBA), 21-day litter weight (LWT), days to 104.5 kg (DAYS), and backfat at 104.5 kg (BF). Dominance and inbreeding were found to have sizeable influence for the reproductive and growth traits analyzed. Subsequent analysis analyzed the changes in prediction of additive breeding values when including inbreeding or dominance and inbreeding effects in the genetic prediction model. Inbreeding had greatest influence on prediction of additive breeding value for inbred individuals or families. On average, inclusion of dominance genetic effects seemed to influence smaller changes.
Keywords: dominance, inbreeding, genetic prediction, pigs

INTRODUCTION
The goal of genetic improvement programs have long been the improvement of phenotypic performance by enhancing genetic merit through selection programs and mating systems. Although the increased use of Best Linear Unbiased Prediction (BLUP) has dramatically increased the rate of genetic improvement in recent years, avenues of genetic improvement may be further improved through use of dominance genetic models (Henderson, 1985; Henderson, 1989). Misztal (1995) discussed the historical problems associated with inclusion of dominance genetic effects; however, recent computing and methodology advancements have greatly reduced many of these concerns (Misztal, 1997). The structure of swine populations, with a large number of dominance relationships and selection on fitness-type traits like number born alive, may provide a species where dominance models show added value for genetic prediction and mating pair allocation. Therefore, the objectives of this work were to 1) estimate dominance variance for traits of importance of swine and 2) to evaluate changes in prediction of additive merit due to inclusion of inbreeding and dominance.

MATERIALS AND METHODS
179,485 reproductive records and 239,354 growth records from purebred American Yorkshire swine were obtained from the National Swine Registry. Data sets were initially edited to insure

connectedness and eliminate biological extremes and were adjusted to a constant basis (NSIF, 1987; Culbertson, 1997). NBA and LWT were analyzed univariately with a model which included the fixed effects of contemporary group and regression on inbreeding percentage and the random effects of additive genetic, parental dominance, animal permanent environment, and mate within contemporary group. DAYS and BF were analyzed univariately with a model which included the fixed effects of contemporary group, sex, and regression on inbreeding and the random effects of additive genetic, dominance genetic, litter of birth, and maternal permanent environment. Estimates were obtained by Method R (Reverter et al., 1994) following the procedures of Misztal (1997). Dominance variance was estimated as four times the parental dominance estimate. Each trait was analyzed with 6 samples of the data selected by a random number generator. The convergence criterion was $r_i = 1 \pm .0001$, where r_i is the regression from the random effect i. Sampling standard deviation was defmed as the standard deviation of the 6 estimates from the subsamples.

After estimating the relative variances, additive breeding values were predicted for all animals using univariate procedures and three separate prediction models differing in the inclusion of inbreeding and dominance genetic effects. The first model contained only additive genetic effects, the second model contained additive genetic and regression on inbreeding, and the third model contained additive genetic, regression on inbreeding, and dominance genetic. Additive breeding values were compared between alternative models and trends and differences in specific groups of animals were analyzed.

RESULTS AND DISCUSSIONS
Estimates of inbreeding depression and variances for NBA and LWT are presented in Table 1. All variances are expressed as a percentage of phenotypic variation. Estimates of inbreeding depression were found to be sizeable for both traits and similar to those found by Bereskin et al. (1968). For example, a sow with an own inbreeding level of F=.125 would have her record adjusted by approximately .3 of a pig for NBA. Dominance variance was found to be larger for LWT, 78% of additive variance, relative to NBA, 25% of additive variance.

Table I. Means (standard deviations) of estimates of inbreeding depression and additive, dominance, permanent environment (PE), and mate within contemporary group (mate) variances for NBA and LWT

Trait	Inbreeding Depression	Variance [% of phenotypic]			
		Additive	Dominance	PE	Mate
NBA	-.23	8.8 (.5)	2.2 (.7)	6.2 (.4)	3.4 (.2)
LWT	-.52	8.1 (1.1)	6.3 (.9)	4.6 (1 .0)	4.0 (.5)

[1]Per 10% of inbreeding

Estimates of inbreeding depression and variances for DAYS and BF are presented in Table 2. Inbreeding effects were found to be significant for DAYS and negligible for BF. Dominance variance for DAYS was found to be approximately 10% of phenotypic variation and a third of additive genetic variance.

Table 2. Means (standard deviations) of estimates of inbreeding depression and additive, dominance, litter, and maternal permanent environmental variances (PE) for days to 104.5 kg (DAYS) and backfat at 104.5 kg (BF)

Trait	Inbreeding Depression'	Variance [% of phenotypic variation]			
		Additive	Dominance	Litter	PE
DAYS	2.10	33.2 (.4)	10.3 (1.5)	12.7 (.6)	1.2 (.4)
BF	.00	43.6 (.9)	4.8 (.7)	7.3 (.3)	1.0 (.2)

'Per 10% of inbreeding

Additive breeding values were obtained after fitting of the three alternative prediction models. For all 4 traits, the correlation between additive breeding values after fitting of the three models were > .99. This would suggest, on average, that accounting for inbreeding and dominance effects has little effect on prediction of additive genetic merit. However, by identifying groups of animals which are the most affected it may be possible to determine types of populations where dominance models are most beneficial. Table 3 presents changes in sires' additive breeding for LWT due to inclusion of regression of inbreeding with classes based upon number and average inbreeding of daughters. Table 5 shows changes in additive breeding value for inclusion of dominance genetic effecs with classes based upon the number of full-sibs, i.e. the amount of available dominance information. Changes for individual animals were noticeable for all traits except BF. Inbreeding caused greatest change in prediction of additive merit for inbred animals and those with inbred progeny. Changes in prediction due to dominance genetic effects were generally smaller than those due to inbreeding effects and were found to increase as the amount of dominance information available for a given family increases.

In addition to improving prediction of additive genetic merit, utilization of a more complete prediction model with inbreeding and dominance genetic effects may allow for increased phenotypic performance through a mate allocation program. A small simulation study determined that utilizing conservative assumptions of 1 sire to 15 dams, no parental combinations previously tested, and an average off-diagonal of the parental dominance relationship matrix of .05, the expectation for increase would be approximately 5% of the parental dominance standard deviation. However, if 20% of the parental combinations are previously tested the increase then becomes approximately 35% of the parental dominance standard deviation. Utilizing these results and economic values of $17 per additional pig, $1.10 per kilogram of litter weight., $. 17 per day to 104.5 kg and $.60 per millimeter of BF, increased revenue may be up to $1.24 per litter for NBA,

$0.69 per litter LWT, $0.11 per pig for DAYS, and $0.09 per pig for BF.

Table 3. Change in sire additive breeding value for LWT due to inclusion of inbreeding in the genetic prediction model with classes based on average inbreeding of daughters (Number of sires in paranthesis)

Number of daughters	Average inbreeding of daughters			
	0. 000- 0. 049	0.05-0.099	0.100-0.199	≥ 0. 200
1-5	0.05 (4, 191)	0. 06 (564)	0.09 (378)	0. 20 (56)
6- 10	0.05 (1, 349)	0.10 (199)	0.19 (64)	0. 29 (7)
>10	0. 06 (1, 703)	0. 14 (245)	0. 30 (51)	0. 59 (5)

Table 4. Change in additive breeding value for LWT due to inclusion of dominance genetic effects in the genetic prediction model (number of animals in parenthesis)

Animal	Number of full-sibs			
	o-1	2- 5	6- 10	> 10
Sire	0. 06 (3, 519)	0. 06 (4, 529)	0.07 (695)	0.11 (69)
Dam	0. 05 (25, 009)	0. 05 (42, 203)	0. 05 (4, 550)	0. 07 (344)

The inclusion of dominance genetic and inbreeding effects in a genetic prediction model may prove more beneficial for smaller, closed populations of swine similar to those maintained by most commercial breeding organizations. In addition, future research should be conducted to look at mating programs and genetic system designs which may be able to maximize the potential return of a mating scheme which incorporates these effects.

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