

## STUDIES ON THE VALUE OF INCORPORATING EFFECT OF DOMINANCE IN GENETIC EVALUATIONS OF DAIRY CATTLE, BEEF CATTLE, AND SWINE

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### SUMMARY

Potential gains from including the dominance effect in genetic evaluations include “purification” of additive values and availability of specific combining abilities for each pair of prospective parents. The magnitude of such gains was tested for dairy and beef cattle and for swine by estimating variance components for several traits and by analyzing changes in additive evaluations when the parental dominance effect was added to the model. Estimates of dominance variance for dairy and beef cattle and for swine were up to 10% of phenotypic variance; estimates were larger for growth traits. As a percentage of additive variance, the estimate of dominance variance reached 78% for 21-day litter weight of swine and 47% for postweaning weight of beef cattle. Changes in additive evaluations after considering dominance are largest for dams of a single large family. These changes were found to be important for dairy cattle especially for dams of full-sibs, but less important for swine.

**Keywords:** Dominance, Evaluation, Variance Components, Method R

### INTRODUCTION

The genotypic model of inheritance includes additive, dominance and epistatic effects (Cockerham, 1954). Genetic evaluations currently ignore effects other than additive. Subsequently, evaluations are less accurate than they could be, and the loss of accuracy is a function of the variance of nonadditive effects and the number of animals with dominance relationships. Issues in nonadditive evaluation were reviewed by Misztal *et al.* (1995).

In the past, computations with dominance were restricted to a few thousand animals (Henderson, 1985). Accurate estimates of dominance variances with the animal model require them to be derived from data sets with at least 30,000 to 100,000 animals for populations with many full-sibs, and even larger data sets for cattle populations. Hoeschele and VanRaden (1991) discovered rules to create the inverse of the dominance relationship matrix at a much lower cost. Their procedures allowed evaluations with the animal model for a data set containing over 400,000 animals; however, processing cost was approximately 40 times higher than for the additive only procedure.

All variance component estimation with larger data sets using the rules of Hoeschele and VanRaden (1991) (e.g., VanRaden *et al.*, 1992) was by a sire model, which considers only about ¼ of the dominance information because full-sibs are treated as ¾ sibs, and 3 of the 4 types of ¾ sibs are ignored. Therefore, estimates of dominance variance with the sire model have inflated standard deviations and are potentially biased.

Misztal (1997) streamlined the computations with dominance by using iteration on data and by estimating variance components by Method R (Reverter *et al.*, 1994). Consequently, an evaluation would be only twice as expensive as with the additive model, and estimation of dominance variance by the animal model could be applied to complete national data sets.

Gains from evaluation with dominance are twofold. First, dominance evaluations can be used for mate selection (DeStefano and Hoeschele, 1992), and the first objective was to estimate the magnitude of dominance variance for various traits of dairy cattle, beef cattle and swine. Second, the additive evaluations can be “purified,” and the second objective was to quantify the contamination of additive evaluations by dominance for various groups of animals when dominance was ignored.

## MATERIALS AND METHODS

Data used in this study included first-lactation production and conformation records on Holsteins (dairy cattle), postweaning gain in Limousin (beef cattle), and reproduction and growth traits in Yorkshire (swine). All computations used the following type of model

$$\mathbf{y} = \mathbf{X}\hat{\mathbf{a}} + \mathbf{ZB}\ddot{\mathbf{A}} + \mathbf{Za} + \mathbf{ZWf} + \dots + \mathbf{e} \quad [1]$$

where  $\mathbf{y}$  is a vector of records,  $\hat{\mathbf{a}}$  is a vector of management and possibly other fixed effects,  $\mathbf{B}$  is a vector of inbreeding coefficients,  $\ddot{\mathbf{A}}$  is a coefficient of inbreeding depression,  $\mathbf{a}$  is a vector of additive animal effects,  $\mathbf{f}$  is a vector of parental dominance effects, and  $\mathbf{e}$  is a vector of residual effects. Models for specific traits/species additionally included effects of permanent environment, mate and/or litter.

Estimation of variance components was done with the JAADOM program, which uses a single level of recursion to build the inverse of the parental dominance matrix, iteration on data with second-order Jacobi for obtaining solutions and Method R for estimation of variance components. Method R has many desirable properties although its estimates can be strongly biased if the model does not include important fixed effects (Misztal *et al.*, 1997b). Estimates with Method R used 50% subsets of the data selected randomly. Each analysis involved six subsets (three for yield traits of Holsteins). Sampling variance of the estimates was approximated as the variance of estimates obtained from different subsets.

To determine the influence of dominance on additive evaluations, differences were examined between additive breeding values (ABV) from the dominance model above and an additive

model (the dominance model without  $f$ ). Expected changes between the models the models were analyzed theoretically for 4 groups of animals: 1) full-sibs with one record each, 2) parents of one full-sib family, 3) parents of half-sibs with one record each, and 4) animal without records and with dam known and a sire with an evaluation with high reliability. Parents had neither records nor parental information, and changes were analyzed as functions of size of full-sib groups.

## RESULTS AND DISCUSSIONS

Estimates of additive and dominance effects as a percentage of phenotypic variance for several traits are in Table 1. Conformation traits with an estimated dominance variance of <4% were omitted.

**Table 1. Estimates of variance components and size of data sets for several traits and species**

Species (breed)	Trait	Percentage of phenotypic variance		Number (1000s)	
		Additive	Dominance	Animals	Records
Dairy cattle (Holstein)	Milk yield	43.5 ± .7	5.7 ± .4	1378	764
	Fat yield	42.6 ± .7	7.0 ± 1.2	1378	764
	Protein yield	40.6 ± .2	4.9 ± .8	1150	371
	Stature	45.3 ± .3	6.9 ± 1.2	732	600
	Strength	27.8 ± .5	8.0 ± .7	732	600
	Body depth	34.5 ± .3	9.8 ± .7	732	600
	Dairy form	23.4 ± .4	5.3 ± 1.0	732	600
	Fore udder attachment	24.3 ± .5	4.7 ± .7	732	600
Swine (Yorkshire)	Number born alive	8.8 ± .5	2.2 ± .7	98	179
	21-day litter weight	8.1 ± 1.1	6.3 ± .9	98	179
	Days to 104.5 kg	33.1 ± .4	10.3 ± 1.5	261	239
	Backfat at 104.5 kg	43.6 ± .9	4.8 ± .7	261	239
Beef cattle (Limousin)	Postweaning gain	21.0 ± 1.1	9.9 ± 1.6	476	215

Theoretical changes in ABV for selected animal groups are in Table 2.

**Table 2. Expected changes in additive evaluations for different animal groups**

Animal group	Size of full-sib family	
	1	$\infty$
Full sibs	$\approx 0$	$0.3 - 0.5 \sigma_d$
Parents of full-sibs	Up to twice the change in progeny	
Parents of half-sibs	$\approx 0$	0
Progeny	Up to half the change in parents	

Changes for stature of Holsteins were calculated using all known records and pedigrees (approximately 3 million animals with 5 million records) and for all traits of Yorkshire were calculated using the same data files as for variance component estimation. Changes for Holstein bulls were small, whereas changes for dams were larger. The largest change was for a dam with 21 fullsib progeny, no individual performance record and with uninformative parents. Her additive breeding value changed by 10 parental dominance standard deviations, and this change was approximately twice the change of her progeny, who changed by approximately 5 parental dominance standard deviations. Changes for Yorkshires were smaller for both dams and sires. Although most Holstein dams had only a single full-sib family, Yorkshire dams averaged 3 such families. Consequently, changes due to dominance were averaged out.

In summary, dominance variation has been found to be moderately important for selected traits of dairy and beef cattle and of swine. The absence of dominance in the evaluation procedures leads to biases of ABV for full-sib families, and particularly dams of embryo-transfer animals for cattle. Changes in ABV of proven sires are small. The dominance information would be utilized best in a mating system (DeStefano and Hoeschele, 1992), which can also utilize the inbreeding information (Boswerger *et al.*, 1994). Based on these results, genetic gains from using dominance information will not be large, but they will outweigh expenditures to derive the information.

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