ON THE VALUE OF INCORPORATING DOMINANCE EFFECTS IN GENETIC EVALUATION OF DAIRY CATTLE

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INTRODUCTION

Current genetic evaluations ignore dominance effects. However, their incorporation might result in gain of accuracy of breeding values depending on dominance variance and on the number of animals with dominance relationships (Misztal *et al.*, 1995). Furthermore, dominance effets can be used to implement mating systems (DeStefano and Hoeschele, 1992; Varona and Misztal, 1999). With the development of algorithms for large datasets using models with nonadditive genetic components, rapid inversion of dominance relationship matrices, and Method $\Re$ for computation of variance components with large data sets, there has been an interest in dominance effects over the last years. This interest is also due to datasets that include more relationships (e.g. fullsibs) necessary for estimating nonadditive genetic effects.

The objectives of this papers were to 1) discuss previously estimated variance components for dominance effects in dairy cattle and to 2) use these components to draw conclusions on the value of incorporating dominance effects in genetic evaluation of dairy cattle.

MATERIAL AND METHODS

Dominance variance estimation. Most of the studies reviewed in Table 1 estimated dominance variance through the estimation of the parental dominance variance which is one quarter of the dominance variance (Hoeschele and Van Raden, 1991). Lately, parental dominance variance was estimated with Method $\Re$ (Misztal, 1997) which can handle large data sets as those required with dominance models.

Changes in breeding values. The changes consecutive to the incorporation of dominance effects were studied in Varona et al. (1998), Druet *et al.* (2001) and Druet (2002). In each case, the changes were analyzed separately for different categories of animals : young bulls, proven bulls, dams, and cows with records. Differences between breeding values (with and without incorporation of dominance effects in the model) or rank correlations among these breeding values were analyzed.

Prediction of specific combining abilities. Varona and Misztal (1999) proposed to predict parental dominance effects from existing parental dominance combinations. $f_{S,D}$ is the average dominance effect of many hypothetical fullsibs produced by sire (S) and dam (D) or it reflects the average dominance effects of the daughters resulting from the mating of the sire S with the cow D. These dominance effects could for instance influence the milk production of these

daughters, some 3 to 4 years after the insemination. $f_{S,D}$, the parental dominance effect, would be predicted through parental dominance combinations among parents (S and D) and grandparents and the variances and covariances among these parental dominance effects (Varona and Misztal, 1999).

However, it is extremely important to mention that the method should be able to predict the value of a parental dominance class for animals whose parents were never actually mated. The information comes then only from parental dominance effects of some of their parents and grandparents that were already mated: class between the sire of sire or the dam of sire and the dam, between the sire of dam or the dam of dam and the sire. Classes containing the dam would use information from previous matings of this dam with half-sibs of the sire or with the sire of the sire, this information would be very limited and restrictive since this cow can only have been mated a limited number of times before and because performances of daughters resulting from these matings are known only some years later. Only the information from matings between half-sibs of the dam with the sire can be important. The number of half-sibs coming from the dam of dam would be limited while the number of half-sibs coming from sire of dam could be more important. Only a small fraction of these half-sibs would already have been mated with the concerned sire.

In conclusion, only matings between some of the daughters of the sire of the dam and the sire are likely to have already been realized : most information for prediction of parental dominance subclass effects comes from the sire of dam by sire parental dominance class. Sire by maternal grandsire dam classes were already used by Allaire and Henderson (1965) and Toro (1998) for the development of mating plans.

The estimation of the sire by maternal grandsire parental dominance class effect can be compared to the prediction of the breeding value of a sire through performances of his daughters:

- the sire contributes half of the genes of his daughters and the sire by maternal grandsire parental class contributes half of the interactions between genes in the cows,
- in consequence, genes of the sires contribute one quarter of the additive genetic variation of the records of their daughters and interactions between genes of the sire and the maternal gransire contribute one quarter of the parental genetic variance of the records of animals within this class.

Therefore :

$$\sigma^2_{\mathbf{s-mgs}} = 0.25\sigma^2_{\mathbf{f}} = 0.0625\sigma^2_{\mathbf{d}} \ (1)$$

where **s-mgs** denotes sire-maternal gransire parental subclass dominance genetic variance, **f** represents parental subclass dominance genetic variance and **d** indicates dominance genetic variance. Equation 1 was in agreement with Allaire and Henderson (1965) or DeStefano and Hoeschele (1992).

The reliability of the estimation can be approximated as :

$$\frac{n}{n + \dfrac{\sigma_e^2}{\sigma_{s-mgs}^2}} \quad (2)$$

where n is the number of daughter equivalents within the class and σ_e^2 is computed as total variance minus sire-maternal grandsire parental subclass dominance variance. For dominance variance of 8 %, 800 daughters with same sire and maternal grandsire would be needed for a reliability of 0.8.

RESULTS AND DISCUSSION

Dominance variance estimation. In comparison with additive effects, dominance effects seem limited in production traits, low to moderate in conformation traits (conformation traits with the largest relative dominance variance were presented) and high in fitness traits like fertility, stillbirth or length of productive life. For somatic cell score, results were especially low despite the fact that health traits are considered as fitness traits.

Table 1. Estimates of additive genetic variance (h²) and dominance genetic variance (d²) expressed in % of total phenotypic variance in previous studies

Authors	Trait	h²	d²
Druet *et al.* (2001)	Non-return rate (female)	0.9	1.4
Druet (2002)	Calving ease (direct)	8.7	0.7
	Calving ease (maternal)	4.4	0.7
	Stillbirth (direct)	1.4	2.4
	Stillbirth (maternal)	1.6	0.1
Fürst and Sölkner (1994)	Calving interval	2	4
	Length of productive life	13	21
Hoeschele (1991)	Days open	2.0	2.3
	Service period	0.8	2.8
Miglior *et al.* (1995)	Somatic cell counts	16.5	1.3
Misztal *et al.* (1997)	Stature	45.3	6.9
	Strength	27.8	8.0
	Body depth	34.5	9.8
	Dairy form	23.4	5.3
	Fore udder attachment	24.3	4.7
Tempelman and Burnside (1990)	Milk yield	40	6
Van Tassell *et al.* (2000)	Milk yield	34.2	5.3
	Fat yield	33.8	5.0
	Protein yield	31.2	5.2
	Somatic cell score	16.6	1.0
	Productive life	11.8	5.7

Changes in breeding values. In studies of Varona et al. (1998), Druet et al. (2001) and Druet (2002), changes due to incorporation of dominance effects were very limited, for most

categories of animals and especially for proven sires. One category of animals where changes could be substantial was ET donors with a single mate. Another category to a smaller extent was ET fullsibs without own information. All authors concluded that the main benefit of inclusion of dominance effects into the models would result from using specific combining abilities in mating programs.

Prediction of specific combining abilities. It seems that some classes of interactions between a sire by maternal grandsire contain thousands of records. However, the number of records is important at a time when a sire is used. When a sire has generally only information from first crop daughters, it has 50 to 200 records approximately for maternal effects. If these records are equally distributed over more than 20 maternal grandsires, then there are less than 10 records per class. Considering that only one quarter of the dominance variance can be exploited, the reliability of the prediction of a parental subclass effect computed with equation 2 is low, in the order of 0-10 %. Only when 2nd crop daughters of a bull arrive can this reliability be better because some sire by maternal grandsire classes are large. If we consider traits like growth or direct calving ease, records are available earlier and in larger quantities. In addition, genetic gain through dominance effects is lost at every generation and in such mating program there is little re-ranking of the bulls in comparison with selection based only on additive effects. In conclusion, in purebred dairy cattle, use of dominance effects does not seem to yield in important improvement of breeding schemes.

REFERENCES
Allaire, F.R. and Henderson, R. (1965) *J. Dairy Sci*. **48** : 1096-1100.
DeStefano, A.L. and Hoeschele, I. (1992) *J. Dairy Sci*. **75** : 1680-1690.
Druet, T., Sölkner, J., Groen, A.F. and Gengler, N. (2001) *J. Dairy Sci*. **84** : 987.
Druet, T. (2002) PhD Thesis, Gembloux Agricultural University, Gembloux, Belgium.
Fürst, C. and Sölkner, J. (1994) *J. Dairy Sci*. **77** : 1114-1125.
Hoeschele, I. (1991) *J. Dairy Sci*. **74** : 1743-1752.
Hoeschele, I. and VanRaden, P.M. (1991) *J. Dairy Sci*. **74** : 557-569.
Miglior, F., Burnside, E.B. and Dekkers, J.C. (1995) *J. Dairy. Sci*. **78** : 1168-1173.
Misztal, I. (1997) *J. Dairy Sci*. **80** : 965-974.
Misztal, I., Varona, L., Culberston, M., Gengler, N., Bertrand, J.K., Mabry, J., Lawlor, T.J. and
        Van Tassell, C.P. (1998) *Proc 6th WCGALP* **25** : 513-516.
Misztal, I., Lawlor, T.J. and Gengler, N. (1997) *Genet. Sel. Evol*. **29** : 319-326.
Tempelman, R.J. and Burnside, E.B. (1990) *J. Dairy Sci*. **73** : 2206-2213.
Toro, M.A. (1998) *Genet. Sel. Evol*. **30** : 339-349.
Van Tassell, C.P., Misztal, I. and Varona, L. (2000) *J. Dairy Sci*. **83** : 1873-1877.
Varona, L., Misztal, I., Bertrand, J.K. and Lawlor, T.J. (1998) *J. Dairy Sci*. **81** : 1126-1135.
Varona, L. and Misztal, I. (1999) *J. Dairy Sci*. **82** : 2186-2191.