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Heritabilities of pre-weaning traits in a multibreed beef cattle herd fitting models with or without a sire genotype x dam genotype interaction

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Introduction

Animal breeders are concerned with unbiased estimation of genetic parameters, since it also has an influence on the accuracy of predicted breeding values. In many studies, additive genetic variances are often either over- or under-estimated. In multibreed (crossbred or composite breeds) evaluations these parameters are sometimes overestimated when it is assumed that non-additive differences are absent. Estimates will especially be biased if the correct covariance structure is not employed (Komender & Hoeschele, 1989), such as where there is a non-random distribution of sires across genotypes, i.e. if certain sires are more frequently used within certain groups than in others. Animal (or sire) effects are then confounded with group effects, thus resulting in the biased estimates. The objective of this investigation was to compare heritabilities where the sire genotype x dam genotype interaction was fitted into the model to account for non-additive variances and the non-random distribution of sire genotypes compared to where it was not fitted.

Material and Methods

Data were obtained from the multibreed beef cattle herd of the Johannesburg Metropolitan Council. Management practices were reported previously (Patterson *et al*, 1980; Schoeman & Jordaan, 1999). The original data set, after editing, consisted of 40522 birth weight (BW) and weaning weight (WW) records of 636 different genotypes with varying levels of the 10 foundation breeds. Owing to a large number of genotypes with small numbers of observations (in many cases only one observation per genotype), the dataset was reduced to 24492 observations of 315 different genotypes with varying composition involving only Afrikaner, Hereford, Simmentaler, Charolais and Bonsmara, since these breeds made the biggest contribution to the herd (Schoeman *et al*, submitted). The VCE (version 4.2.5) package of Groeneveld (1997) was used in the analysis of the data. The model included the following effects: year (26 levels), farm (2 levels), sex (2 levels) month of birth (11 levels), dam age (9 levels), genotype (315 levels) and for WW, weaning age was used as a covariate. The sire genotype x dam genotype interaction was either included or excluded. Both unitrait (with or without the maternal effect) and two-trait (without the maternal effect) models were fitted.

Results and Discussion

In both the unitrait and two-trait models h^2 estimates for both BW and WW were considerably lower where the sire genotype x dam genotype interaction (**I**) was fitted, compared to where it was not fitted. In those models where **I** was fitted, the obtained h^2 estimates were in closer agreement with the mean estimates reported by Mohiuddin (1993) and Koots *et al*. (1994a) in their respective reviews, probably indicating less biased estimates. Similarly, corresponding higher h^2 estimates were also reported by Tawah *et al*. (1993) in a synthetic herd in Cameroon, while higher h^2_a estimates were also obtained by Meyer (1992) in a Zebu crossbred population than in purebreds in the more comprehensive and best fitting models. When fitting models which accounted for the maternal effect (Table 2), estimates of h^2_a were generally lower for both BW and WW than where it were not fitted (Table 1).

In models where **I** was included, h^2_a estimates were slightly higher and h^2_m slightly lower than where it was not included. It therefore seems that in models where the maternal effect is included, genotypic differences amongst dams were accounted for, making the inclusion of **I** unnecessary. The correlation between direct and maternal effects (r_{am}) were in all cases close to zero, which differs from the negative estimates for WW mostly reported in the literature (Meyer, 1992; Koots *et al.*, 1994b).

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Table 1 Direct heritability estimates (±SE) for BW and WW from unitrait and two-trait analyses fitting models without or with a sire genotype x dam genotype interaction (**I**)

Traits	Without **I**	With **I**
Unitrait		
BW	0.58 ± 0.011	0.29 ± 0.008
WW	0.40 ± 0.012	0.24 ± 0.007
Two-trait		
BW	0.57 ± 0.010	0.27 ± 0.007
WW	0.39 ± 0.012	0.23 ± 0.007
r_g	0.55 ± 0.016	0.55 ± 0.018

Table 2 Direct (h^2_a) and maternal (h^2_m) heritabilities for BW and WW from unitrait analyses fitting models with or without a sire genotype x dam genotype interaction (**I**).

Traits	Without **I**	With **I**
BW		
h^2_a	0.47	0.51
h^2_m	0.09	0.08
r_{am}	0.06	0.05
Log **L**	48716.4	49008.4
WW		
h^2_a	0.25	0.33
h^2_m	0.14	0.11
r_{am}	0.09	0.05
Log **L**	43287.8	43471.5

Conclusions

Over-estimation of additive genetic values is likely when it is assumed that non-additive differences are absent or of minor importance. Additive values predicted from multibreed evaluations do not predict progeny differences between prospective parents of different breed composition (Pollak & Quaas, 1998). The inclusion of a sire genotype x dam genotype interaction in models where the maternal effect is not accounted for seems to be a way of handling this problem. Modelling has indeed become a very complex but extremely important exercise.

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