# SIRE X HERD INTERACTION EFFECT IN BREEDPLAN

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## SUMMARY

Significant sire x herd interactions have been identified for most BREEDPLAN data. Consequently, sire x herd (sh) effects for each trait has been included into the analytical software for BREEDPLAN. Some results for birth weight in a European breed are presented. These indicate that EBVs for sires with progeny in only one herd will be most affected. Their EBVs will be closer to their midparent value. Sire x herd effects for birth weight in herds of origin tend to be more negative than the average sh effect for the same sire used in an outside herd.

**Keywords**: BREEDPLAN, Sire x herd interaction, EBVs

## INTRODUCTION

Numerous studies on Australian beef cattle data have identified a small but significant sire x herd and even sire x herd-year variance for all performance recorded traits (Notter *et al.* 1992, Meyer and Graser 1999). This variance accounts for between 1 and 10 % of total variation depending on the trait and data set. Furthermore, inclusion of a sire x herd effect into the analytical model resulted in a drastic reduction of the negative covariance between direct and maternal genetic effects for 200-day weight (Bradfield 1999). The source of this variation is not well established but could be due to preferential treatment of sire progeny groups, misrecording of management groups, true sire by environment (herd) effects or genetic interactions between individual sires and the dam lines of their mates (so-called "nicking" effect).

As a consequence of these findings BREEDPLAN analytical software was modified to accommodate sire x herd (sh) interaction effects as part of the mixed model equations. In this paper we discuss how this modification affects estimated breeding values and report some results.

## METHOD OF ESTIMATING SIRE X HERD INTERACTIONS EFFECT

In BREEDPLAN V4.1 a sire x herd effect is estimated for each trait and each sire x herd combination. Sire x herd effects are assumed to be independently distributed with expectation E(sh) = 0 and variance matrix I*SH, where SH has a matrix with dimension of number of traits in the analysis which describes the variance and covariance of one sire's sh effects. The * represents the Kronecker product. These covariances have been estimated for most trait combinations. It has been found that within sires the sh effect for similar traits are highly correlated (Meyer and Graser 1999, Bradfield 1999).

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## RESULTS AND DISCUSSION

As the variance of the sh effect for some traits is nearly as large as the sire variance [Var(s) = $1/4\ \sigma_a^2$] the deviation of progeny performance from their contemporaries will be equally divided between the EBV and sh if a sire has all his progeny in only one herd. Therefore the largest changes in EBVs were observed for sires with large numbers of progeny recorded in only one herd and when the EBV of the sires were well above or below the midparent value. For sires that have few progeny in each of many herds, the strong regression of each sh effect towards zero results in only small changes to their EBVs. Table 1 shows some statistics of the sh effect for birth weight in a European breed. Almost 70 % of all sires in this data set are only used in one herd and only 1 year.

**Table 1. Statistics for birth weight sire x herd effects (kg) in a European breed for differently used sires**

| Sire group | N | Standard Dev. | Minimum | Maximum |
|---|---|---|---|---|
| One herd 5 – 10 progeny | 339 | 0.33 | -1.7 | 1.3 |
| One herd > 10 progeny | 318 | 0.46 | -1.9 | 1.3 |
| ≥ 5 herds with 5 - 10 progeny each | | | | |
| Mean sire x herd | 64 | 0.11 | 0.3 | 0.3 |
| Individual sh | 608 | 0.36 | -1.2 | 1.3 |
| ≥ 5 herds with > 10 progeny each | | | | |
| Mean sire x herd | 26 | 0.19 | -0.4 | 0.4 |
| Individual sh | 190 | 0.49 | -1.4 | 1.5 |

With increasing numbers of progeny in a herd, the random sh effect are regressed less and the standard deviation of the sh effect increases. While this is true for all sh effects for sires that have progeny in many herds the mean sh effect is important, as it is responsible for changes in EBV. As can be seen in Table 1 the mean sh effect varies much less for sires used in five or more herds compared to sires used in only one herd. However, while sires used in many herds are little affected by the change in the model, progeny of sires in herds with large sh effect will still be affected as their performance is adjusted by these larger sh effects. Extreme deviations from midparent values of progeny groups in individual herds are less rewarded and the effect of preferential treatment of progeny groups will be buffered, making the EBVs of young animals more accurate.

Investigating the sh effect for birth weight more closely in this breed found some interesting results. When comparing the sh effect of the small number of sires used in more than one herd, the sh effects in the herd where the sires were bred tended to be smaller (more negative) than in herds where he was introduced. We can speculate about reasons for this effect; is it preferential treatment such as rounding off of birth weights, or does within herd selection against high birth weights create genotype x environmental interactions or genotype by genotype interactions?

## REFERENCES

Bradfield, M. (1999) PhD. Thesis UNE Armidale

Meyer, K. and Graser, H. -U. (1999) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **13**:385

Notter, D. R., Tier, B. and Meyer, K. (1992) *J. Anim. Sci.* **70**:2359