

SIRE BY FLOCK-YEAR INTERACTIONS FOR BODY WEIGHT IN POLL DORSET SHEEP

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SUMMARY

The performance of sires across flocks and years are likely to vary due to factors such as interactions with the environment, differences in ewe genotypes, errors in recording, non-random mating, and preferential treatment of progeny. Research in other breeds and species has shown that these sire by flock-year interactions typically account for less than 5% of the phenotypic variance. This paper examines the significance of sire by flock-year effects for weight traits in Poll Dorset sheep. The results demonstrate that while the sire by flock-year effects explained between 2 and 4% of the phenotypic variance, they significantly improved the fit of the model and resulted in a direct-maternal genetic correlation closer to zero. However, heritabilities were reduced significantly by up to 50%, indicating that sire by flock-year effects may be removing too much genetic variation for traits with maternal effects. On balance however, it seems advisable to include sire by flock-year interaction effects in the across flock evaluation.

INTRODUCTION

The sheep genetic evaluation system in Australia (Brown *et al.* 2007) contains performance data from flocks located across Australia. As the use of performance recording and Estimated Breeding Values (EBVs) increases, many sires are being used across many different environments and possibly very different ewe genotypes. It is possible that sires may perform differently across these flocks and years, requiring inclusion of sire by flock-year effects in evaluation models. Significant heterosis between Merino bloodlines has also been observed (Mortimer and Atkins 1987). It is possible that including sire by flock-year effects will remove some of the non-additive variance associated with heterosis or genotype by genotype interactions, to improve the reliability of EBVs.

Including a term for sire by herd interaction has been shown to significantly improve genetic analysis models for many traits in beef cattle (Robinson 1996; Lee and Pollak 1997; Meyer 1997; Meyer 2003; Dodenhoff *et al.* 1999) and to reduce the bias caused by unrecorded or inadequately recorded management and mating groups (Meyer 2003). Inclusion of sire by herd effects also resulted in reductions in the correlation between direct and maternal genetic effects (Meyer 1997; Berweger Baschnagel *et al.* 1999; Dodenhoff *et al.* 1999; Maniatis and Pollott 2002).

Accurate estimation of sire by flock variance requires sires, or related sires, to be used in multiple flocks. Confounding of sires or groups of sires within flocks (typically through using home-bred sires) makes it difficult to partition sire variance between the sires' main effects and interaction effects (Meyer 2003). However, in the terminal sire genetic evaluation program (LAMBPLAN) there is increasing information from sires used across flocks, allowing the effect to be investigated. Therefore the aim of this study was to examine the significance of sire by flock-year interactions on the body weight traits in industry recorded Poll Dorset sheep data.

MATERIALS AND METHODS

Data. Pedigree and performance data were extracted from the Sheep Genetics LAMBPLAN

* AGBU is a joint venture of NSW Department of Primary Industries and University of New England

database (Brown *et al.* 2007). This database consists of pedigree and performance records submitted by Australian ram breeders which are used for genetic evaluation purposes.

As the complete Poll Dorset database was too large for parameter estimation analyses, a subset of 39 of the best linked flocks was selected. Within these flocks, all straightbred Poll Dorset animals with full pedigree and born since 1995 were included. Data were extracted for weaning (Wwt), post weaning (Pwt) and yearling body weight (Ywt). All contemporary groups were transformed to a common mean of 35, 50 and 60kg for weaning, post weaning and yearling weight respectively, as is done routinely for Sheep Genetic analyses (Brown *et al.* 2007). A summary of the data used for each trait is shown in Table 1. The pedigree was built using 1 generation of ancestral information. Depending on the trait, this resulted in pedigree files comprising between 52,065 and 166,582 animals and data files comprising between 35,858 and 146,547 animals. The data originated from 39 flocks across 14 years. Only 7% of the animals studied had records on all three traits however 65% on the animals had weights record at 2 different ages.

Table 1. Summary of the data used in this study

Trait	Number of animals	Number of records	Number of sires	Number of dams	Sire Flock Yrs	Number of CGs	Mean	SD	Min	Max
Wwt	166,582	146,547	2,406	49,069	5,610	6,039	35.0	6.1	10.4	72.6
Pwt	159,083	138,514	2,463	49,226	5,726	4,320	50.0	6.6	14.9	89.1
Ywt	52,065	35,858	1,269	20,133	2,372	1,275	60.0	6.5	27.7	103.4

Models of analysis. Parameters were estimated in univariate analyses for each trait, fitting an animal model in ASReml (Gilmour *et al.* 2006). The base model (model 1) fitted the fixed effects of contemporary group, birth type, rearing type, age of dam, and animal's age at measurement. Contemporary group was defined as flock, year of birth, sex, date of measurement, management group subclass. Random effects fitted included correlated direct and maternal genetic effects and a maternal permanent environment effect. This is the model currently used in LAMBPLAN routine genetic evaluations for these traits. Model 2 included the additional random environmental effect of sire by flock-year (no relationships), with the two models compared using likelihood ratio tests.

To examine the impact of data structure, additional analyses were conducted using the same data sets with restrictions on which records were fitted with a sire by flock-year effect. To avoid the confounding caused by sires used within single flock-years, the additional analyses were conducted using the same data set and fixed effect models however the sire by flock-year effects were only fitted for records from progeny of sires used across multiple flock-years. Heterogeneous residuals were also fitted so that records without sire by flock-year fitted had a different residual variance to those with sire by flock-year effects fitted. The genetic parameters are presented for both records with and without the sire by flock-year fitted.

RESULTS AND DISCUSSION

Genetic parameters. The genetic parameters estimated for each model are summarised in Table 2. For all three traits there is a significant improvement in the log likelihood with the inclusion of sire by flock-year, although the effect only explained 2 to 4% of the phenotypic variance. The inclusion of the sire by flock-year effect also resulted in a significant reduction in the direct heritability and magnitude of the direct-maternal genetic correlation. For post weaning weight and yearling weight the direct-maternal correlation was not significantly different to zero. These observations agree with the studies of Meyer (1997), Berweger Baschnagel *et al.* (1997),

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Dodenhoff *et al.* (1999) and Maniatis and Pollott (2002).

The reduction in the direct heritability is quite extreme for these traits, and appears to be related to the difficulty in partitioning variances in the presence of correlated maternal genetic effects. Results not presented for the same early weight traits in other LAMBPLAN breeds show very similar trends. By contrast, analyses for traits unaffected by maternal effects and measured on the Poll Dorset animals used in this paper (fat depth and eye muscle depth) show significant sire by flock-year interactions, but only marginal reduction in heritability. Anecdotally, it seems unlikely that the heritabilities for early weight traits are as low as shown in Table 2 given the improvement made in growth in this breed since the early 1990's. Meyer (2003) presented an alternative partitioning of variance for this problem which may give better results, but we are yet to implement the method in these data.

Table 2. Phenotypic variance (σ_p^2), direct (h_d^2) and maternal (h_m^2) heritabilities, direct-maternal genetic correlation (r_{am}), maternal permanent environmental (c^2) and sire by flock-year (s^2) effects as a proportion of phenotypic variance with and without sire by flock-year interactions included in the model (se in parentheses). LLR = difference in log likelihood relative to model 1.

Trait	Model	σ_p^2	h_d^2	h_m^2	c^2	r_{am}	s^2	LLR
Wwt	1	25.80 (0.11)	0.10 (0.01)	0.08 (0.01)	0.11 (0.00)	-0.36 (0.04)		0
Wwt	2	25.80 (0.11)	0.05 (0.01)	0.07 (0.01)	0.11 (0.00)	-0.18 (0.07)	0.02 (0.00)	163
Pwt	1	35.26 (0.16)	0.15 (0.01)	0.06 (0.01)	0.07 (0.00)	-0.27 (0.04)		0
Pwt	2	35.17 (0.16)	0.08 (0.01)	0.05 (0.01)	0.07 (0.00)	0.10 (0.08)	0.03 (0.00)	273
Ywt	1	37.86 (0.34)	0.23 (0.02)	0.08 (0.01)	0.06 (0.01)	-0.44 (0.06)		0
Ywt	2	37.69 (0.33)	0.12 (0.02)	0.05 (0.01)	0.06 (0.01)	-0.07 (0.14)	0.04 (0.00)	53

Data structure. In the data used for this study, 65 to 79% of the progeny with records are from sires used in more than one flock and year. On average sires have progeny in 2.3 flock years and 20% of progeny come from sires used across 10 or more flock years. The progeny that come from sires used only in 1 flock and year provide no information to estimate their sire by flock-year effects.

Table 3. Phenotypic variance (σ_p^2), direct (h_d^2) and maternal (h_m^2) heritabilities, direct-maternal genetic correlation (r_{am}), and sire by flock-year (s^2) effects with sire by flock-year effects only fitted for progeny of sires used across at least 2, 5 or 10 flock-years (FYs). Parameters reported for both records with and without sire by flock-year effects.

Trait FYs	No sire by flock-year			With sire by flock-year					FYs [#] %
	σ_p^2	h_d^2	h_m^2	σ_p^2	h_d^2	h_m^2	r_{am}	s^2	
Wwt 2	25.20 (0.20)	0.07 (0.01)	0.08 (0.01)	26.08 (0.13)	0.07 (0.01)	0.07 (0.01)	-0.30 (0.06)	0.02 (0.00)	79%
Wwt 5	25.18 (0.13)	0.09 (0.01)	0.08 (0.01)	27.07 (0.17)	0.08 (0.01)	0.07 (0.01)	-0.36 (0.05)	0.03 (0.00)	39%
Wwt 10	25.34 (0.12)	0.10 (0.01)	0.08 (0.01)	28.59 (0.26)	0.09 (0.01)	0.07 (0.01)	-0.36 (0.05)	0.03 (0.00)	16%
Pwt 2	35.27 (0.29)	0.11 (0.01)	0.05 (0.01)	35.53 (0.18)	0.11 (0.01)	0.05 (0.01)	-0.09 (0.06)	0.03 (0.00)	79%
Pwt 5	34.36 (0.18)	0.14 (0.01)	0.06 (0.01)	37.37 (0.25)	0.13 (0.01)	0.06 (0.01)	-0.22 (0.05)	0.04 (0.00)	39%
Pwt 10	34.84 (0.17)	0.15 (0.01)	0.06 (0.01)	38.53 (0.36)	0.13 (0.01)	0.06 (0.01)	-0.26 (0.04)	0.03 (0.00)	18%
Ywt 2	37.61 (0.49)	0.21 (0.02)	0.07 (0.01)	38.11 (0.41)	0.20 (0.02)	0.07 (0.01)	-0.37 (0.08)	0.03 (0.00)	65%
Ywt 5	37.08 (0.35)	0.24 (0.02)	0.08 (0.01)	41.99 (0.78)	0.21 (0.02)	0.07 (0.01)	-0.43 (0.07)	0.02 (0.01)	17%
Ywt 10	37.61 (0.34)	0.24 (0.02)	0.08 (0.01)	41.54 (1.15)	0.21 (0.02)	0.07 (0.01)	-0.44 (0.06)	0.01 (0.01)	7%

[#]Proportion of records with the sire by flock-year effects fitted

To separate the influences of these within-flock-year sires additional analyses of the same data were conducted in which sire by flock-year effects were only fitted for animals from sires used across multiple flock-years. The genetic parameters from these analyses are show in Table 3. Fitting effects only for progeny of sires used across flock-years resulted in less reduction in the heritability and direct-maternal genetic correlation. The remaining genetic parameters remained relatively constant between analyses.

With the exception of the phenotypic variance the genetic parameters from the models with sire by flock-year effects only fitted to progeny from sires used across 10 or more flock-years are the same as the model with no sire by flock-year effects included (Model 1 in Table 2). The phenotypic variance for animals with sire by flock-year effects in Table 3 increases as the number of flock-years increases from 2 to 10. As fewer animals receive the sire by flock-year effect the direct-maternal correlation becomes more negative in Table 3, approaching the estimate for Model 1 in Table 2.

In fitting sire by flock-year interaction effects we are implicitly estimating an average breeding value across flocks, with deviations from this average within individual flock-years removed by the interaction term. This is desirable when the deviations are caused by factors such as recording errors, non-random mating, or preferential treatment of progeny, but it may not be desirable in other situations in which useful genetic variation is removed by fitting the interaction term. The difficulty is that it is not possible to separate these two cases. On balance however, given that the goal of LAMBPLAN is to evaluate the across flock merit of animals, it seems appropriate to include sire by flock-year effects in the evaluation model.

CONCLUSIONS

Sire by flock-year effects are in a sense a “necessary evil” in LAMBPLAN genetic evaluations. On the one hand they are useful in dealing with data quality problems across flocks and years, but on the other, they may be removing too much genetic variation. This seems to be particularly the case for traits which are modelled with correlated direct and maternal genetic effects. More research is needed in this area, possibly using estimation models which partition the variation differently, but ideally using better structured data. One possibility will be to base studies on the Sheep CRC Information Nucleus flock, where all sires involved are being used at all sites.

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