

PARTITIONING GENETIC VARIANCE IN COMPOSITE SHEEP

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SUMMARY

Australian sheep producers have been moving towards an increased use of composite crossbred ewes to achieve higher performance and greater genetic gain, taking advantage of the high value lamb market. Sheep research has traditionally been carried out on purebred flocks or their first and second crosses with replication and uniformity of breed types within the data. Within composite lines, the breed combinations are often complex, with multiple breeds in variable proportions with few sheep per breed combination. To enable estimation of between and within breed genetic effects, the analysis performed in our study included both additive and dominance genetic effects at the breed level. Breed additive effects contributed to 1.3% of the variation in weight. The variance associated with breed dominance effects were significant for both weight and height (10 and 5%). Results from this analysis on the small sub set are promising, and suggest the model will account for breed effects when a larger composite sheep data set is analysed.

INTRODUCTION

Traditionally the Australian sheep industry has been based on the Merino and crossbreeding from a Merino dam base. However, composite flocks are becoming more common, taking advantage of retained heterosis, as producers improve the output of the breeding flock in response to a growing lamb market. Composite flocks involve crossing multiple breeds to take advantage of 'hybrid vigour' and to incorporate specific characteristics of certain breed types. Traditionally this technique has been used to incorporate characteristics such as the double muscling in the Texel breed and the high fertility of the Finn breed.

In flocks containing purebred or simplistic crosses, fitting breed type as a fixed effect allows the estimation of breed effects. This technique is viable when the number of breed types is low, the frequency of each breed type is high and the relationship between breeds is irrelevant. However, fitting breed as a fixed effect will not work for composite flocks due to the large number of breed combinations developed from multiple breeds with low replication of crossbred types

Traditionally composite flocks within research are designed around diallel crosses, with the analysis techniques refined to account for maternal effects and epistasis to successfully analyse composite populations (Gardner and Eberhart 1966, Eisen *et al.* 1983). Recently genetic grouping has been used to account for animals of genetically similar makeup, in most cases breed or strains (Gilmour *et al.* 2006). However, the strength and viability of both these models was dependent on availability of information for all the developed crosses and founding purebreds. The unstructured nature and large number of crosses in the composite flock lead to the use of simulation techniques (Ovaskainen *et al.* 2008) to capture the breed effects within the composite population.

The analysis reported in this paper looks at the separation of phenotypic variance, taking into account the breed additive and dominance variation for a composite flock, along with additive genetic variation (animal model) within and repeatability between individuals.

MATERIAL & METHODS

The data source comprised of 614 ewes (repeat records on 212 ewes so 826 total records) from a maternal composite flock run in Holbrook, New South Wales. The ewes varied from 2 to 5 years

of age, from 26 sires and 429 dams. A complete back pedigree (10753 individuals) was available for the composite flock from which the 614 ewes are a subset. Measurements were taken on the adult ewes in the autumn of 2010 and the following spring at weaning. Weight, fat score and hip height were recorded with descriptive stats presented (Table 1).

Table 1. Description of trait measurements from composite adult ewe flock, Holbrook, NSW

Trait	Records	Minimum	Mean	Maximum	C.V.
Hip height (mm)	826	480	625.7	730	0.08
Weight (kg)	823	50.0	77.0	110.0	0.13
Fat score	825	1	3.4	5	0.24

The composite flock was developed from seven purebred lines (Border Leicester, Coopworth, East Friesian, Finnish Landrace, Poll Dorset, Texel and White Suffolk). From a White Suffolk base the breeds were unevenly incorporated across generations via both the sire and dam lines. Composite rams were used as sires resulting in the inclusion of multiple breeds via the same sire line. Thirteen generations of crossing has allowed the formation of an unstructured composite flock ‘type’ which is phenotypically similar, yet at the breed level is highly varied. The variation at the breed level is highlighted by only 6% of ewes having a single breed contribute greater than 44% of their genotype (Figure 1). With no information available on the purebred individuals and very little on foundation crosses, the model developed from Gardner and Eberhart (1966) for diallel crosses is not suitable. The data is limited as a proportion of the flock pedigree lacks information on breed contributions.

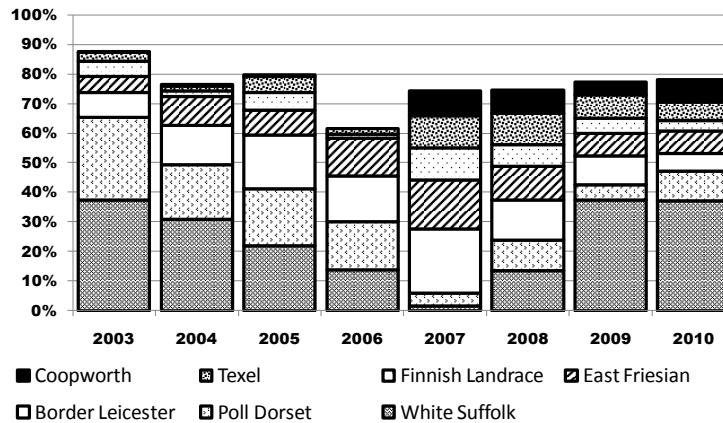


Figure 1. Variation in breed contributions to the flock’s progeny from 2003 to 2010

Each animal was assigned a breed identification developed from the contributions of the seven founder breeds and the parent lines from which the breed was incorporated. The code provides information on the integration of breeds via the maternal and paternal lines for five generations (five generations of back crossing = purebred). A pedigree at the breed level could then be formed (Figure 2). The breed pedigree was based on the seven founder breeds and included the developmental crosses required to reach the composite breed types present within the flock. An eighth breed type (unknown) was included to group breeds with small contributions and to assign a code to individuals missing pedigree information.

The breed level pedigree is like the animal pedigree used regularly within genetic analysis and allows for the formation of a relationship matrix. At the breed level it must be assumed that there

is a level of inbreeding experienced within pure breeds. Breeds breed ‘true’ in that a Texel mated with a Texel will always produce a Texel. Each breed was assigned an inbreeding coefficient depending on the classification guidelines of the breed’s Australian flock book. If a breed required greater than four generations of back crossing it was given an inbreeding coefficient of 0.96875 (East Friesian, Finn, Poll Dorset and Texel). For three generations the value was 0.9375 (Border Leicester) compared to the more open flock books of the Coopworth and White Suffolk which require only two generations and were given a value of 0.875.

The relationship matrices for the flock pedigree were calculated using simulation techniques (Ovaskainen *et al.* 2008) implemented using the ‘asreml.monte’ function in ASReML-R (Butler *et al.* 2009). This produced the additive and dominance matrices encapsulating the 1646 breed combinations within the breed pedigree and providing the additive and dominance genetic effects between these combinations (eg. Additive and Dominance matrices for a simplified breed pedigree, Figure 2).

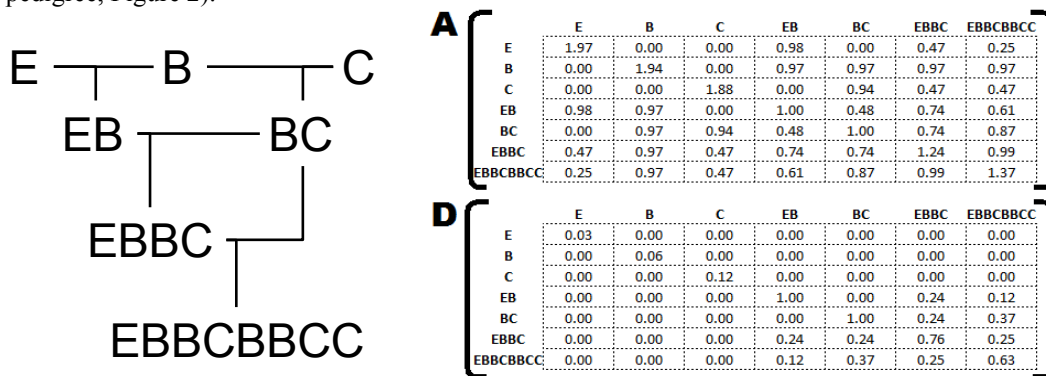


Figure 2. Demonstration of breed pedigree from crossing East Friesian (E), Border Leicester (B) and Coopworth breeds (C) with corresponding additive (A) and dominance (D) matrices.

The data were analysed using ASREML (Gilmour *et al.* 2006) with the importation of the breed additive and dominance matrices formed in ASREML-R (Butler *et al.* 2008). The age of the ewe time of measurement (autumn or spring), number of lambs weaned in 2010 (current year) the length of lactation in 2010 number of lambs weaned in 2009 (previous year) and the length of lactation in 2009 were fitted as fixed effects within the model,

$$\mathbf{y} = \mathbf{x}\bar{\mathbf{t}} + \mathbf{Z}_a\mathbf{a} + \mathbf{Z}_i\mathbf{u} + \mathbf{Z}_{ab}\mathbf{a}_b + \mathbf{Z}_{db}\mathbf{d}_b + \mathbf{e}$$

Where,

\mathbf{y} ; observed value

$\mathbf{x}\bar{\mathbf{t}}$; vectors of fixed effects, as described above

$\mathbf{Z}_a\mathbf{a}$; animal additive effect (\mathbf{a} = additive matrix), assuming, $\mathbf{a} \sim N(\mathbf{0}, \sigma_a^2 \mathbf{A})$

$\mathbf{Z}_i\mathbf{u}$; permanent environment effect, assuming, $\mathbf{u} \sim N(\mathbf{0}, \sigma_i^2 \mathbf{I}_{614})$

$\mathbf{Z}_{ab}\mathbf{a}_b$; breed additive effect (\mathbf{a}_b = breed additive matrix), assuming, $\mathbf{a}_b \sim N(\mathbf{0}, \sigma_{ab}^2 \mathbf{A}_b)$

$\mathbf{Z}_{db}\mathbf{d}_b$; breed dominance effect (\mathbf{d}_b = breed dominance matrix), assuming, $\mathbf{d}_b \sim N(\mathbf{0}, \sigma_{db}^2 \mathbf{D}_b)$

\mathbf{e} ; is the temporary environment effect (residual), assuming, $\mathbf{e} \sim N(\mathbf{0}, \sigma_e^2 \mathbf{I}_{826})$.

RESULTS AND DISCUSSION

The analysis predicted that 1.3% of the variation in weight could be accounted for by the breed additive effect with the estimates of breed additive effects hitting the zero boundary for height and

fat score. It was possible to estimate residual, identity animal, animal and breed dominance variance components for height and weight (Table 2). Ten percent of the variation in height of the ewes could be attributed to the breed dominance effect whilst only accounting for 5% of the variation in weight. Hip height and weight produced heritability estimates of 0.41 and 0.10 respectively, compared to when the breed matrices were not fitted of 0.52 and 0.19. The analysis of fat score did not partition out any breed additive or dominance effects, with fat score having a repeatability of 0.40.

Table 2. Proportion of variance within body measurement traits accounted for by the inclusion of breed additive and dominance effects and phenotypic variance.

Variance	Hip height	Weight	Fat score
Additive	0.41	0.10	0.06
Breed additive	0.00 ^B	0.01	0.00 ^B
Breed dominance	0.10	0.05	0.00 ^B
Between animal residual	0.09	0.49	0.33
Within animal residual	0.39	0.35	0.60
Phenotypic variance	1361	89.18	0.613

^BComponent hit boundary

The correlation between the EBVs of the breed adjusted model and the unadjusted model was 0.56 for weight and 0.72 for height. Incorporating the breed component tightened the variation in EBVs (lowered the additive genetic variance). Not accounting for breed effects resulted in overestimation of EBV magnitude in the unadjusted model.

This technique has shown to be successful at fitting the breed additive and breed dominance effects within the model. Breed dominance effects could be successfully segregated from the genetic variation within the trait. From a biological point of view this variation relates to the effect of heterosis on the measured trait or for producers the combinability of breeds. The ability to separate variation into a dominance component within unstructured composite populations is relatively new and of value to the livestock sector. This will provide producers with the ability to predict the general and specific combining ability of breeds. This technique could also hold value for tree breeding and other species where crosses can be produced cheaply or genotypes can be cloned.

The model was able to segregate the breed additive variance for weight within this small data set. Within composite sheep flocks this should provide producers with a greater understanding of the influence breed combinations are having on production traits. This analysis and model will progress further as more data on the complete composite flock becomes available.

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