ALTERNATE METHODS FOR ESTIMATING BREEDING VALUES FOR FAECAL EGG COUNT DATA FROM MERINO STUDS ACROSS AUSTRALIA

D. J. Brown and B. Tier
Animal Genetics and Breeding Unit*, University of New England, Armidale, NSW 2351

SUMMARY
Selection for resistance to internal parasites is of interest to many sheep breeders. However, the genetic evaluation of faecal egg count is problematic due to the variable levels of expression, as a result of interactions with the environment, the species of parasite, and its skewed distribution. Transformation, variance standardisation and adjustment for heterogeneous variances are used to overcome these problems. This study aims to identify which combination of techniques produces the most accurate estimated breeding values (EBVs).

The EBVs from analysis of cube root transformed faecal egg count with (EBV_S) and without (EBV_3) variance standardisation are highly correlated (0.96). Furthermore the genetic correlation between these traits was also very high (0.95) indicating that genetically these traits are the same. EBVs estimated after homogenising the residual variances across groups produced EBVs less influenced by the level of variance in the raw data. Analysing faecal egg counts without variance standardisation did not significantly reduce the accuracy of the genetic evaluation. However, the EBVs need to be expressed on a scale that breeders can interpret.
Keywords: EBVs, Faecal Egg Count, FEC, genetic evaluation

INTRODUCTION
Internal parasites cost Australian sheep producers hundreds of millions of dollars each year in treatment and lost production. Genetic variation in resistance to internal parasites exists and genetic progress is achievable through selection. An increasing number of faecal egg count (FEC) observations are entering the genetic evaluation systems across Australia as sheep breeders adopt selection for resistance to internal parasites. However, the genetic evaluation of faecal egg count is problematic due to the variable levels of expression across different environments and years, type and representation of various species of internal parasite and the skewed distribution of the data. The skewed distribution of raw FEC observations is a result of the majority of animals having low faecal egg counts and a small number having very high counts. These data are commonly transformed with a cube root to normalise the data prior to genetic evaluation.

In addition, variance of observed FEC is correlated with its mean. Different levels of variance across groups can bias EBVs for animals in groups where variance is larger or smaller than expected. Variance standardisation is used by most genetic service providers to overcome different levels of variance across groups of sheep. This technique was reviewed by Eady (1995) who found that variance standardisation was required as a disproportionate amount of animals would be selected from groups with higher mean and variance in faecal egg counts. OVIS (Brown *et al.* 2000) does not

* AGBU is a joint institute of NSW Agriculture and The University of New England

perform variance standardisation but adjusts residuals to accommodate heterogeneous variances (Reverter *et al.* 1997). This study compares the qualities of the different techniques.

MATERIALS AND METHODS

Pedigree and yearling faecal egg count (FEC) records were obtained from the Merino Genetic Services database. This database consists of pedigree and performance records from Australian and New Zealand Merino studs and is used for genetic evaluation purposes.

Only data that met the following criteria were used: 1) date of measurement and current owner recorded, 2) at least sire or dam known, 3) date of birth known, 4) sex identified as male or female, 5) pure-bred Horn or Poll Merino, and 6) age of dam less than 12 years. To remove possible outliers observations more than 3 standard deviations outside the mean of their contemporaries were deleted. Also contemporary groups (CGs) with fewer than 10 animals were deleted. The pedigree was built using all available ancestors. This resulted in a pedigree of 24,636 animals and records on 16,495 animals. There were 595 sire and 6337 dams from 29 flocks across 12 years and 86 CGs.

Using the observed FEC data two traits for analysis were created; FEC_3 and FEC_S. FEC_3 was the cube root transformed data. FEC_S was the FEC_3 data with a standardised variance within CGs. Groups were defined by breed, flock, sex, year and management group. Standardisation was achieved using the following formula; FEC_S = (FEC_3 – Mean) / SD, where Mean and SD were the mean and standard deviation respectively of FEC_3 for the animals in each CG.

The data for each of these traits are summarised in Table 1. The means of FEC_3 ranged between 2.7 and 21.9 with an overall mean of 9.1. The standard deviations averaged 2.6, ranged between 1.3 and 6.0.

Univariate breeding values were then estimated for each trait using OVIS (Brown *et al.* 2000). Four analyses were performed to estimate breeding values; 1) FEC_S (EBV_S), 2) FEC_3 without heterogeneous variance adjustment (EBV_N), 3) FEC_3 with normal OVIS heterogeneous variance adjustment (Reverter *et al.* 1997) (EBV_3) and 4) FEC_H with residual variance homogenisation achieved using a modified version of the Reverter *et al.* (1997) technique which resulted in all groups having the same residual variance (that defined in the OVIS genetic parameters) (EBV_H). The correlation between EBVs from each analysis were compared.

Table 1. Mean, standard deviation (SD), minimum and maximum for each trait (n=16,495)

Trait[A]	Mean	SD	Minimum	Maximum
FEC	1,368	2,418	0	35,937
FEC_3	9.07	4.54	0.00	33.00
FEC_S	-0.04	0.95	-5.09	4.74

[A] FEC= raw faecal egg counts, FEC_3= cube root FEC, FEC_S= Standardised FEC

Genetic parameters and correlations were estimated for FEC_3 and FEC_S using bivariate analyses in ASREML (Gilmour *et al.* 1999) and the model; $\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{a} + \mathbf{e}$, where $\mathbf{y}$ is a vector of

observations, b a vector of fixed effects (mean and CG), **a** vector of direct breeding values, **X** and **Z** are incidence matrices relating observations and effects, and **e** is the vector of random residuals, also with Var(**a**) = **G**, **G** = **A*****G**$_0$, Var(**e**) = **R** and **R**= **I*** **R**$_0$. **G**$_0$ and **R**$_0$ are the genetic and residual covariance matrices among traits, respectively.

RESULTS AND DISCUSSION

The correlation between OVIS EBVs for each trait across all animals were all very high (Table 2). Adjustment for heterogeneous variance slightly increased the correlation between EBV_3 and EBV_S while homogenising the residual variance resulted in EBVs that were perfectly correlated with EBV_S.

Table 2. Correlation between EBVs for FEC_3, EBV_3, EBV_S, EBV_N and EBV_H(n=86)

	EBV_S	**EBV_N**	**EBV_3**	**EBV_H**
EBV_S	1.00			
EBV_N	0.95	1.00		
EBV_3	0.96	1.00	1.00	
EBV_H	1.00	0.95	0.96	1.00

Groups with higher mean FEC_3 had greater variation in FEC_3 (r=0.42). While the variances of EBV_S and EBV_H were not correlated with variances in FEC_3 (r=0.08 and 0.17 respectively) the variation in EBV_N and EBV_3 was highly correlated with the variance in the raw data (r=0.84 and 0.82 respectively). Therefore OVIS's adjustment for heterogeneous variance only slightly reduced the correlation between group variance in the data and group variance of the EBVs.

Homogenising the residual variances removed the relationship between the variance in the data and the variance in the EBVs and may be a more appropriate method than the current adjustment for heterogeneous residual variance for these traits. Homogenised residual variance achieves the same result as standardising without removing genetic variance. However standardised or homogenised residual variances may not be ideal as groups may have different levels of genetic and residual variation.

Table 3. The genetic parameters for the bivariate analysis of FEC_3 and FEC_S(n=16,495)

	FEC_3	**FEC_S**
Phenotypic Variance	8.04 (0.09)	0.91 (0.01)
h2[#]	0.25 (0.03)	0.21 (0.02)
rg	0.95 (0.01)	
rp	0.95 (0.00)	

h2= direct heritability, rg= genetic correlation, rp= phenotypic correlation

The genetic parameters for the bivariate analysis of FEC_3 and FEC_S are illustrated in Table 3. The heritability estimate for FEC_3 was slightly higher (+0.04) than that for FEC_S. Both estimates agree with published estimates from sheep of similar ages, which range between 0.00 and 0.55 but average

approximately 0.25 across a range of sheep types and environmental conditions (Ponzoni and Fenton 2000; Raadsma *et al.* 1997). The genetic and phenotypic correlations between FEC_3 and FEC_S were both 0.95 indicating that they are essentially the same trait.

In these data it seems as though there is no significant difference between these traits however the question is whether this is generally the case and if data standardisation results in loss of genetic variation as is suggested by the estimates of heritability. If there is not heterogeneous genetic variation across groups the homogenised residual variance should result in similar EBVs to the standardised data. However, the variation in EBV_S was slightly less related to the variation in FEC_3 than EBV_H suggesting that there may be some difference in the genetic variation across these groups. It is still not clear whether the residual variances should in fact be standardised or homogenised.

Regardless of which method for analysis is best, the EBVs need to be readily understood by breeders and have real meaning such that they can be combined into multiple trait indexes based on their relative economic values.

CONCLUSIONS

The EBVs from analysis of FEC_3 with and without variance standardisation are highly correlated. The results indicate that selection on either trait is selection for both traits. EBV_3 were under adjusted for within group variance of the raw data. OVIS's adjustment for heterogeneous variances changed the EBVs for faecal egg count very little. Homogenisation of residual variance may offer an alternative approach to account for differing levels of variance across groups. To improve the accuracy of the estimated breeding values for FEC more research is required to develop appropriate methods to accommodate different levels of genetic and residual variance between groups.

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