

## GENOTYPE BY ENVIRONMENT INTERACTION IN AUSTRALIAN MATERNAL AND TERMINAL SHEEP

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### SUMMARY

Genotype by environment interactions (GxE) for economically important traits in Australian maternal and terminal sheep were investigated by both sire by flock interactions and multi-trait methods for performance data observed in eight flocks (sites) across Australia. The traits included growth traits: birth weight (bwt), weaning weight (wwt), post-weaning weight (pwt); carcass composition traits: carcass eye muscle depth (cemd), carcass fat (ccfat), lean meat yield (lmy) and dressing percentage (dressperc), and meat quality traits: intra-muscular fat (imf) and shear force (sf5). Univariate analyses showed that variation between genetic groups was relatively large compared to direct genetic variance and that maternal effects were significant for growth traits. The estimates of heritability were low for growth traits (from 0.08 to 0.11), moderate for most carcass composition traits (except for lmy) and sf5 (from 0.24 to 0.26), and high for lmy (0.44) and imf (0.50). Significant sire by flock interactions were found for growth traits and sf5. The average genetic correlations over pairs of flocks for each trait were 0.35 (bwt), 0.44 (wwt), 0.43 (pwt), 0.78 (cemd), 0.70 (ccfat), 0.77 (dressperc), 0.83 (lmy), 0.91 (imf) and 0.72 (sf5), respectively. Both the interaction term and multi-trait methods demonstrate that significant GxE existed for growth traits. The industry genetic evaluation should account for GxE for these traits.

### INTRODUCTION

The Australian sheep industry has generated substantial gains through use of Australian Sheep Breeding Values and Indexes generated by Sheep Genetics (Swan, 2017). Where they are significant, genotype by environment interactions (GxE) result in changes in ranking across environments, with potential effects on selection response. Therefore, it is important to understand the magnitude of GxE for traits included in Australian sheep breeding programs. To date there have been no studies reporting GxE in meat quality and carcass traits in the terminal and maternal sheep breeds in Australia.

A well-structured distribution of genotypes across environments is crucial to detect GxE effects. The Sheep CRC Information Nucleus (INF, van der Werf *et al.* 2010) is an ideal resource to study GxE because a large number of sires were progeny tested at eight research flocks that represent the diversity of Australian sheep production environments. An extensive measurement program of meat quality traits was undertaken on individual animals at these eight flocks over a five-year period. In this study, these data were used to investigate the magnitude of GxE quantified by fitting a sire by flock interaction term and multi-trait methods for some economically important traits in terminal and maternal sheep breeds.

### MATERIALS AND METHODS

**Animals and data.** The Sheep CRC IN flocks represented three sire breed types, Merino, Maternal and Terminal in the initial experimental design at eight research flocks. In this study performance data from progeny of Maternal and Terminal sire breed types mated to Merino or Border Leicester

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x Merino dams were combined to conduct genetic analyses. The research flocks included Armidale, NSW (IN01); Trangie, NSW (IN02); Cowra, NSW (IN03); Rutherglen, Vic. (IN04); Hamilton, Vic. (IN05); Struan, SA (IN06); Turretfield, SA (IN07); and Katanning, WA (IN08). The measurement program was run for five years with animals born between 2007 and 2011. Pedigree and performance data of nine traits were extracted from the IN database. The traits analysed included three growth traits: birthweight (bwt, kg), weaning weight (wwt, kg) and post-weaning weight (pwt, kg); four carcass composition traits: carcass eye muscle depth at C site (cemd, mm), carcass fat at C site (ccfat, mm), dressing percentage (dressperc, %) and lean meat yield (lmy, %); two meat quality traits: intramuscular fat (imf, %) and shear force at five days aging at 3–4 °C (sf5, Newtons). All carcass composition and meat quality traits were measured on meat samples post-slaughter. A summary of the numbers of records and sires represented at each flock for each trait is shown in Table 1. The growth traits had the most records, followed by carcass composition traits and meat quality traits. Correspondingly, the total number of sires used differed across traits, varying from 263 for imf to 510 for bwt. However, the average number of sires used across pairs of flocks was not substantially different across traits, ranging from 67 to 82.

**Statistical analyses.** Univariate analyses were used to estimate variance components and heritabilities for each trait. Fixed effects included contemporary group (cg), birth type, rearing type, age of measurement (in days) fitted as a covariate and dam age fitted as linear and quadratic covariates for all traits with the exception that rearing type and age of measurement were not fitted for bwt. Hot carcass weight was included as a linear covariate for meat quality and carcass composition traits except dressperc and lmy. Contemporary group definitions were based on management group, flock, year, sex, breed type and date of measurement, with numbers of cg ranging from 369 (wwt) to 994 (sf5) across traits. Random effects included a genetic group effect (ranging from 124 to 159 genetic groups across traits, representing the original breeds and strains within breeds of the base animals), a direct genetic effect of animal, and sire x flock-year interaction (SF) for each trait. Random maternal effects (representing both maternal genetic and maternal permanent environmental effects) were fitted to growth traits only.

The genetic correlations of animal genetic effects between flocks which modelled each trait in the different flocks as different traits were estimated by two alternative models. The first model used pairwise bivariate analyses, with 28 analyses of all combinations of the eight flocks. The second model was the factor analytic model in which all data was used simultaneously to estimate all genetic correlations in a single analysis with heterogeneous residual variance fitted at the flock level. Both bivariate and factor analytic models used the same fixed and random effects as those used in the univariate analyses for each trait, but excluding the random SF effect. The random sire × flock, rather than a direct genetic of animal effect, was modelled with a factor analytic covariance structure (FA) in the factor analytic model. All analyses were conducted using software ASReml (Gilmour *et al.* 2009) with REML procedures.

## RESULTS AND DISCUSSION

The summary statistics, phenotypic variance and ratios of variances are shown in Table 1. Significant values for the ratio of genetic group variances to direct genetic variances were found for all growth traits, decreasing from 4.73 (bwt) to 2.32 (pwt), showing that genetic groups account for a large proportion of the genetic variation for growth traits. The estimates of heritability were low for growth traits (from 0.08 for bwt to 0.11 for pwt), moderate for most carcass composition traits (except for lmy) and sf5 (from 0.24 to 0.26), and high for lmy (0.44) and imf (0.50). The heritability estimates for growth traits were lower than the weighted means of 0.15 (bwt), 0.18 (wwt) and 0.21 (pwt) reviewed by Safari *et al.* (2005) for meat breeds. Brown *et al.* (2016) also reported slightly higher heritability estimates for

*Breeding Program Design*

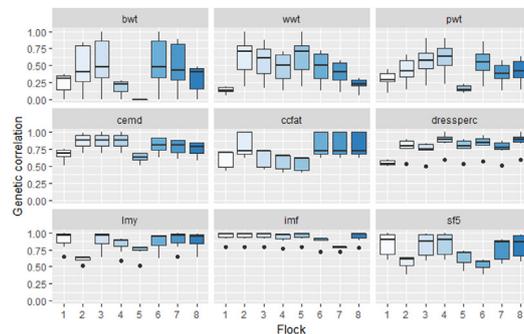
bwt (0.15) and pwt (0.15-0.16) for both maternal and terminal breeds, but with a similar estimate for wwt. This could be due to SF effects which were significant for these traits (variance ratio estimates ranging from 0.02 to 0.03) fitted in the models to account for the GxE across flocks. Negligible SF effects were observed for all carcass composition traits and imf. The heritability estimates for carcass composition traits were similar to those reported in the previous preliminary study by Mortimer et al. (2010) based on 2007-2008 INF data, except for the slightly higher estimate for lmy in this study (0.44 vs 0.34). For meat quality traits, Mortimer et al. (2014) reported similar estimates of heritabilities for imf (0.48) and sf5 (0.27) from INF data, along with a similar magnitude estimate of the SF effect for sf5 (variance ratio of 0.03). Maternal permanent environment effects were significant for all growth traits and decreased as age increased, from 0.34 for bwt to 0.21 for pwt. This trend was consistent with previous findings (sum of maternal genetic and permanent environment effects) but with slightly lower estimates for growth traits by Brown *et al.* (2016).

**Table 1. Number of records (N), total number of sires with progeny data (tot\_sire) across all flocks, average number of sires with progeny data across pairs of flock combinations (ave\_sire), number of genetic groups (N\_gg), number of contempory groups (N\_cg), mean trait value (mean), estimates of phenotypic variance ( $\sigma_p^2$ ), ratio of genetic group to additive genetic variance ( $b^2$ ), direct heritability ( $h^2$ ), sire by flock effect ( $s^2$ ), maternal environmental effect ( $c^2$ ) as a proportion of phenotypic variance, average genetic correlations of across pairs of flock combinations by factor analytic model (rg\_fa) and by bivariate analyses (rg\_bi) with standard errors in subscript for each trait**

	bwt	wwt	pwt	cemd	ccfat	dressperc	lmy	imf	sf5
Unit	kg	kg	kg	mm	mm	kg	%	%	Newtons
N	16190	13144	12373	8996	8793	9483	7272	7016	7174
tot_sire	510	439	426	425	424	425	278	263	278
ave_sire	82	80	82	79	79	79	74	67	74
N_gg	159	159	139	137	138	138	124	125	125
N_cg	742	369	419	633	628	608	568	545	994
mean	4.9	29.4	32.9	31.3	4.6	46.1	58.1	4.2	26.9
$\sigma_p^2$	0.71 <sub>0.01</sub>	17.08 <sub>0.23</sub>	19.88 <sub>0.28</sub>	10.76 <sub>0.18</sub>	3.81 <sub>0.07</sub>	5.15 <sub>0.08</sub>	5.61 <sub>0.12</sub>	0.61 <sub>0.01</sub>	48.41 <sub>0.95</sub>
$b^2$	4.73 <sub>1.85</sub>	3.96 <sub>1.65</sub>	2.32 <sub>1.03</sub>	0.15 <sub>0.11</sub>	0.20 <sub>0.12</sub>	0.06 <sub>0.07</sub>	0.49 <sub>0.20</sub>	0.15 <sub>0.10</sub>	0.12 <sub>0.09</sub>
$h^2$	0.08 <sub>0.02</sub>	0.09 <sub>0.02</sub>	0.11 <sub>0.02</sub>	0.25 <sub>0.03</sub>	0.27 <sub>0.03</sub>	0.24 <sub>0.03</sub>	0.44 <sub>0.04</sub>	0.50 <sub>0.04</sub>	0.26 <sub>0.03</sub>
$s^2$	0.03 <sub>0.01</sub>	0.02 <sub>0.01</sub>	0.03 <sub>0.01</sub>	0.01 <sub>0.01</sub>	0.01 <sub>0.01</sub>	0.01 <sub>0.01</sub>	0.01 <sub>0.01</sub>	0	0.03 <sub>0.01</sub>
$c^2$	0.34 <sub>0.01</sub>	0.24 <sub>0.01</sub>	0.21 <sub>0.01</sub>	-	-	-	-	-	-
rg_fa	0.35 <sub>0.26</sub>	0.44 <sub>0.34</sub>	0.43 <sub>0.26</sub>	0.78 <sub>0.18</sub>	0.70 <sub>0.14</sub>	0.77 <sub>0.20</sub>	0.83 <sub>0.14</sub>	0.91 <sub>0.10</sub>	0.72 <sub>0.18</sub>
rg_bi	0.41 <sub>0.45</sub>	0.41 <sub>0.59</sub>	0.41 <sub>0.46</sub>	0.82 <sub>0.39</sub>	0.61 <sub>0.34</sub>	0.75 <sub>0.34</sub>	0.77 <sub>0.26</sub>	0.82 <sub>0.25</sub>	0.74 <sub>0.35</sub>

The average genetic correlations over all pairs of flocks from both the factor analytic model (rg\_fa) and a series of bivariate analyses (rg\_bi) are shown in Table 1. Similar magnitudes of genetic correlations were found from both approaches for all traits. However, the standard errors of genetic correlations from the factor analytic model were much smaller (from 0.10 to 0.34) than those from the bivariate analyses (from 0.25 to 0.59) across all traits, demonstrating that the factor analytic model is a more reliable and parsimonious approach to analyse eight flocks data simultaneously in this study. The results from the factor analytic model indicated low to moderate genetic correlations (between 0.35 and 0.44) for growth traits, and moderate to high genetic correlations (between 0.70 and 0.91) for both

carcass composition and meat quality traits. These results are consistent with the significant level for sire by flock interaction term in the univariate analyses for most of the traits except for sf5. Although a significant SF effect was detected for sf5, a much higher average genetic correlation across flocks was found for sf5 than for the growth traits. The distributions of genetic correlations between each flock and other flocks for each trait is shown in Figure 1. What can be clearly seen in this figure is that low genetic correlations were generally found for each flock with other flocks for growth traits; imf had consistently high genetic correlations for each flock with other flocks; and for the carcass composition traits and sf5, most of the flocks had high genetic correlations with other flocks, but there was at least one flock that had only moderate genetic correlations with other flocks (e.g. dressperc and lmy for one and sf5 for three flocks).



**Figure 1. Genetic correlations of each flock with other flocks by using Factor analytic models**

## CONCLUSIONS

The results from both SF interaction and multi-trait models demonstrated that there were significant GxE for all growth traits (bwt, wwt and pwt) and negligible GxE were found in all flocks for imf and in most of the flocks for the carcass composition traits in maternal and terminal sheep. Our industry genetic evaluations should be able to account for these GxE effects by fitting a sire by environment interaction term in the models for these traits with significant GxE.

## ACKNOWLEDGEMENTS

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