

Table 2. Cross-validation results for each environment, where V_p (phenotypic variance), h^2 (heritability), and s^2 (sire by site interaction variance ratio) are estimated from a single trait analysis of data for all sites *excluding* the site shown in each row, and b is the regression of offspring performance at the site shown in each row on sire EBVs calculated from all other sites. Standard errors in brackets (s.e.)

Site	Location	V_p (s.e.)	h^2 (s.e.)	s^2 (s.e.)	b (s.e.)
1	Kirby NSW	5.70 (0.12)	0.10 (0.03)	0.07 (0.01)	0.81 (0.19)
2	Trangie NSW	6.56 (0.12)	0.09 (0.02)	0.06 (0.01)	0.33 (0.17)
3	Cowra NSW	6.46 (0.12)	0.09 (0.02)	0.06 (0.01)	0.66 (0.21)
4	Rutherglen VIC	6.76 (0.13)	0.08 (0.02)	0.06 (0.01)	0.39 (0.14)
5	Hamilton VIC	6.55 (0.12)	0.07 (0.02)	0.07 (0.01)	0.63 (0.21)
6	Struan SA	6.30 (0.12)	0.10 (0.02)	0.06 (0.01)	0.33 (0.20)
7	Turretfield SA	6.60 (0.13)	0.09 (0.02)	0.06 (0.01)	0.33 (0.13)
8	Katanning WA	6.54 (0.13)	0.08 (0.02)	0.04 (0.01)	0.53 (0.12)
Mean		6.43	0.09	0.06	0.50

The data used in this study have also been used to develop genomic predictions which are used in the calculation of WEC ASBVs. For Merinos the accuracy of these genomic predictions is estimated to be 0.26 (Swan *et al.*, 2014). The genomic analyses are based on IN data from all sites, and it would be worthwhile to investigate the impact of GxE on these analyses.

CONCLUSIONS

The results presented demonstrate that there are significant GxE for WEC in Merino sheep, but that the analysis method used in industry genetic evaluations can account for these to a degree. Although the accuracy of breeding values is most likely to be lower in an across flock context, ram breeders can have confidence in ASBVs based on performance data collected in their own flocks, and for sires with large numbers of progeny tested across a range of environments.

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