

## Evaluation of white clover breeding lines in the Australasian region

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**Introduction** The accuracy of predicting breeding line performance across target environments is a significant criterion in the development of cultivars with broad or specific adaptation. This paper characterises the type and magnitude of genotype-by-environment (GE) interactions estimated from a multi-site white clover (*Trifolium repens* L.) breeding line evaluation trial conducted across sites in New Zealand and Australia.

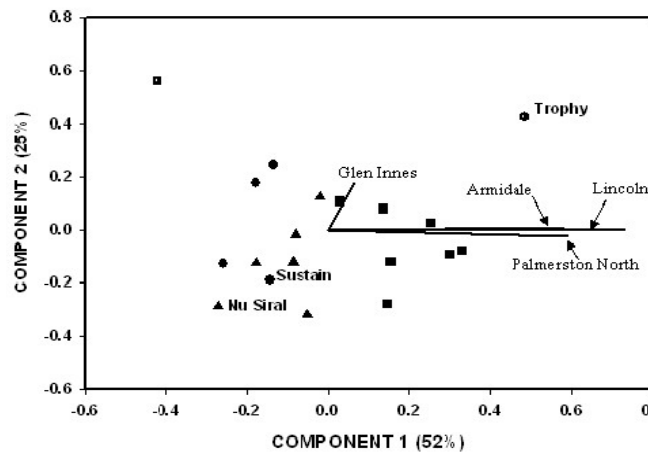
**Materials and methods** A total of 17 experimental breeding lines and 2 control cultivars, Nu Siral and Sustain, were evaluated across 4 sites; Palmerston North and Lincoln in New Zealand, and Armidale and Glen Innes in New South Wales, Australia. Seasonal clover content during years 2 and 3 were expressed as a percentage relative to cultivar Sustain and analysed. Variance component analysis was conducted across years 2 and 3 within sites, and across years and sites, using a random effects linear model. The data were log transformed prior to analysis. The mean values generated from the individual site analysis were used in pattern analyses (Jahufer *et al.*, 2002). Lack of genetic correlation among sites ( $L_c$ ) and heterogeneity of genotypic variance ( $V$ ) were calculated from the line-by-site interaction component (Cooper and DeLacy, 1994).

**Results** There were significant ( $P < 0.05$ ) genotypic differences within lines for mean clover content across years 2 and 3 at all sites. There was a significant ( $P < 0.05$ ) line-by-site interaction. The large  $L_c$  relative to  $V$  indicates changes in relative performance of the lines across the 4 sites (Table 1). The biplot indicates the presence of 3 breeding line groups and two individuals that are distinct from the rest (Figure 1). One of these lines was developed into the new cultivar Grasslands Trophy based on broad adaptation. The directional vectors in figure 1 indicate that Armidale, Lincoln and Palmerston North sites are closely associated in comparison to Glen Innes. Reanalysis of the data without Glen Innes, still indicated significant GE interaction (results not presented).

**Table 1** Genotypic variance components and standard errors from within site analysis of seasonal clover content across years 2 and 3. (P, Palmerston North; L, Lincoln; G, Glen Innes; A, Armidale)

	P	L	G	A	GE
$\sigma^2$	0.055	0.268	0.085	0.017	0.086
$\pm$ SE	0.024	0.094	0.04	0.007	0.019
$L_c$	= 0.079		$V = 0.007$		

GE, genotype by environment interaction variance component from analysis across sites and years,  
 $L_c$ , lack of genetic correlation,  
 $V$ , heterogeneity of genotypic variance



**Figure 1** the vectors in the biplot represent the sites. The symbols represent line groups. Positions of the two controls and the breeding line developed into the new cultivar, Grasslands Trophy, are indicated

**Conclusion** This study indicates the importance of conducting multi-site trials to evaluate breeding lines for selection of superior performers for broad and specific adaptation in the Australasian region.

## References

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