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**Phenotypic examination of variation occurring  
both among families and among genotypes within  
a *T. repens* x (*T. ambiguum* x *T. occidentale*) BC<sub>1</sub>F<sub>2</sub>  
hybrid population.**

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## Abstract

Development of white clover cultivars with increased vegetative persistence, particularly in dryland farming systems has been a major goal within breeding programmes, however little useful genetic variation for survival and growth in these environments has been found. Consequently, it has become necessary to look towards white clovers wild relatives as sources of genetic variation. *T. repens* x (*T. ambiguum* x *T. occidentale*) tri-species hybrids have been developed, however, their morphologies have not been evaluated, and little is known about optimal breeding strategies in these populations.

An experiment was designed to characterise the magnitude of phenotypic variation for a range of root, shoot, and floral traits, and to ascertain optimal breeding strategies within a *T. repens* x (*T. ambiguum* x *T. occidentale*) BC<sub>1</sub>F<sub>2</sub> hybrid plant population. The experiment was designed such that it could be analysed in two ways;

- a) Investigated levels of phenotypic variation occurring among hybrid families, compared to representatives of their F<sub>1</sub> parents
- b) Investigated levels of phenotypic variation among individual hybrid genotypes, again compared to representatives of their F<sub>1</sub> parents.

Analysis (a) found a relative lack of among hybrid family variation. With significant ( $P < 0.05$ ) family variance components for 11 of the 18 traits measured, and generally only occurring between the upper and lower extremes. Repeatability estimates on a family mean basis were low (less than 0.51 for all traits).

Analysis (b) found significant ( $P < 0.05$ ) genotypic variance components for all of the traits measured. Repeatability estimates ranged from 0.47-0.88, indicating a relatively high level of genetic determination for the majority of traits.

Pattern analysis allowed the identification of hybrid genotypes showing the combined expression of key shoot, and root traits. These genotypes may provide a route to hybrid clover cultivars showing increased vegetative persistence via increased nodal and tap-root size, combined with good dry matter production.

The wide range of phenotypic variation and high repeatability estimates among hybrid genotypes, combined with the relative lack of variation and low repeatability estimates among hybrid families allowed us to conclude that phenotypic recurrent selection based on individual genotypes should be practised in these early generation hybrids populations.

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## List of abbreviations

<b>Abbreviation</b>	<b>Parameter</b>	<b>Units</b>
F <sub>1</sub>	First filial generation	
BC <sub>1</sub> F <sub>1</sub>	First generation backcross one hybrid	
BC <sub>1</sub> F <sub>2</sub>	Second generation backcross one hybrid	
AAOO	( <i>T. ambiguum</i> x <i>T. occidentale</i> ) hybrid	
cv.	Cultivar	
OP	Open pollinated	
PS	Pollen stainability	%
PDL	Peduncle length	mm
FPI	Florets per inflorescence	
LL	Leaflet length	mm
LW	Leaflet width	mm
LL:LW	Leaflet length to leaflet width ratio	
PTL	Petiole length	mm
SD	Stolon diameter	mm
IL	Internode length	mm
SL	Stolon length	mm
SA	Stolon anchoring	mm
NRD	Nodal root diameter	mm
NRL	Nodal root length	mm
TRL	Tap root length	mm
TRD	Tap root diameter	mm
LDW	Leaf dry weight	g
SDW	Stolon dry weight	g
RDW	Root dry weight	g