The University Of Queensland AUSTRALIA | QAAFI Queensland Alliance for Agriculture and Food Innovation
School of Agr. & Food Science

Multi-trait, multi-environment models in forestry

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Motivating study

- Prediction of genetic values for clonally replicated eucalypt hybrids for selection for reafforestation of saline affected lands
- Hybrids of *E. camaldulensis*, *E. globulus* and *E. grandis*
- In total, 841 genotypes tested over 21 sites
- Previous analysis of tree diameter at 3 years
- Other traits of interest

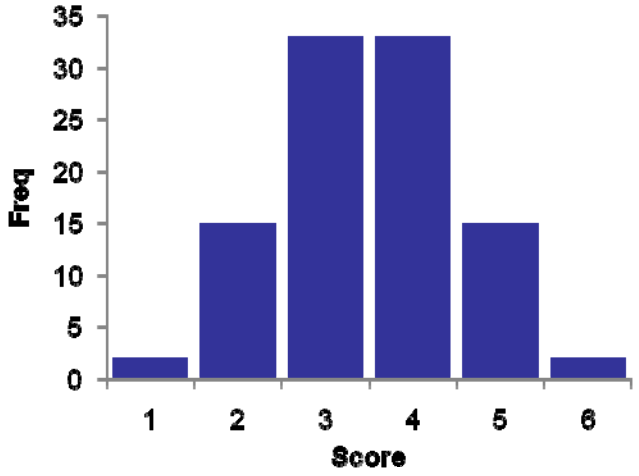
Assessment of traits

Stem height (HT) – wood volume

Branch angle (BA) & size (BS) – knots affect wood strength and appearance

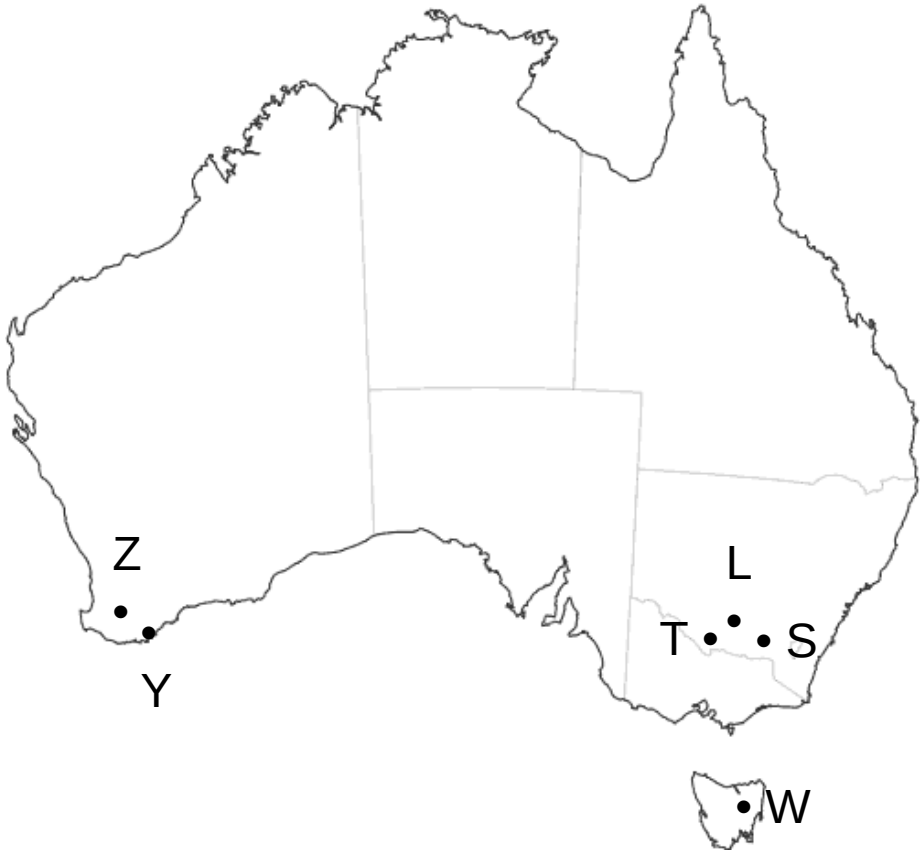
Stem straightness (SS) – can affect recovery and strength

6-point scale used for BA, BS and SS



Experimental structure

Location of trials



Congruence of genotypes

	L	S	T	W	Y	Z
L	50	5	24	6	4	4
S		79	50	12	5	5
T			601	48	38	38
W				105	7	7
Y					49	49
Z						49

General model - overview

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_u\mathbf{u} + \mathbf{Z}_g\mathbf{g} + \boldsymbol{\varepsilon}$$

mu + E + lin(Row) + lin(Col)

Block + Row + Col + spl(Row) + spl(Col)

$$\text{var}(\mathbf{y}) = \mathbf{V} = \mathbf{Z}_u\mathbf{G}_u\mathbf{Z}_u' + \mathbf{Z}_g\mathbf{G}_g\mathbf{Z}_g' + \mathbf{R}$$

$$\mathbf{G}_g = \mathbf{G}_{TE} \otimes \mathbf{I}_m$$

For E=*j*

$$\mathbf{R}_j = \mathbf{R}_{T_j} \otimes \mathbf{C}_{j(Row)}(\rho_{j(Row)}) \otimes \mathbf{C}_{j(Colum)}(\rho_{j(Column)})$$

Prediction of clonal effects

$$\begin{bmatrix} \hat{\mathbf{b}} \\ \hat{\mathbf{u}} \\ \hat{\mathbf{g}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}^{\mathrm{T}}\mathbf{R}^{-1}y \\ \mathbf{Z}_u^{\mathrm{T}}\mathbf{R}^{-1}y \\ \mathbf{Z}_g^{\mathrm{T}}\mathbf{R}^{-1}y \end{bmatrix} \begin{bmatrix} \mathbf{X}^{\mathrm{T}}\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}^{\mathrm{T}}\mathbf{R}^{-1}\mathbf{Z}_u & \mathbf{X}^{\mathrm{T}}\mathbf{R}^{-1}\mathbf{Z}_g \\ \mathbf{Z}_u^{\mathrm{T}}\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}_u^{\mathrm{T}}\mathbf{R}^{-1}\mathbf{Z}_u + \mathbf{G}_u^{-1} & \mathbf{Z}_u^{\mathrm{T}}\mathbf{R}^{-1}\mathbf{Z}_g \\ \mathbf{Z}_g^{\mathrm{T}}\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}_g^{\mathrm{T}}\mathbf{R}^{-1}\mathbf{Z}_u & \mathbf{Z}_g^{\mathrm{T}}\mathbf{R}^{-1}\mathbf{Z}_g + \mathbf{G}_g^{-1} \end{bmatrix}^{-1}$$

Estimation of model parameters

1. Single-trait, single-environment analyses
2. Single-trait, multi-environment analyses
3. Multi-trait, multi-environment single-stage analysis

Used ASReml 3-R

LRT to test significant difference of nested models

AIC to compare non-nested models

Large unstructured matrix not feasible

Simplifications to reduce number of parameters

DIAG – heterogeneous variances, no correlation

CORUH – heterogeneous variances, homogeneous correlation

FA – factor analytic (Smith et al 2001)

Single-Trait multi-Env results

Trait	G_E	r_E	H^2
HT	CORUH	0.85	0.43 – 0.81
BA	CORUH	0.54	0.06 – 0.50
BS	CORUH	0.61	0.13 – 0.54
SS	FA1	0.20 – 1.00	0.17 – 0.32

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Two way

$$\mathbf{G}_g = \mathbf{G}_{TE} \otimes \mathbf{I}_{\mathrm{m}}$$

Three way

$$\mathbf{G}_g = \mathbf{G}_T \otimes \mathbf{G}_E \otimes \mathbf{I}_{\mathrm{m}}$$

Results

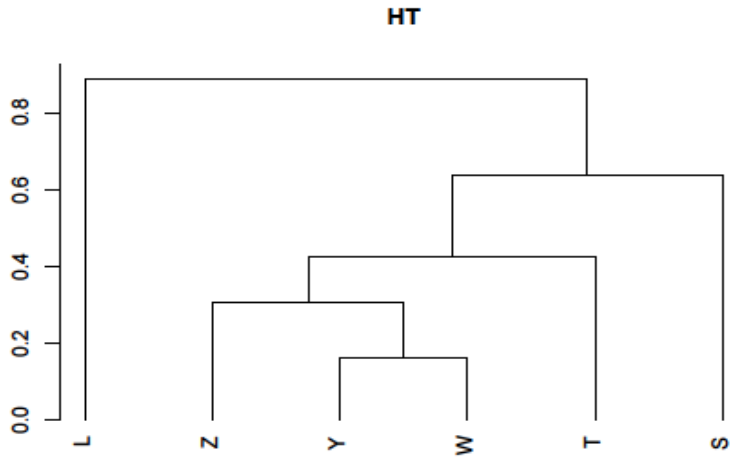
2-way	3-way				
G_{TE}	G_T	G_E	nparam	LogL	AIC
FA3			93	-8434.9	17208
FA4			114	-8406.7	17193
FA5			134	-8395.1	17210
	US	CORUH	17	-8621.9	17430
	US	FA1	22	-8612.4	17421

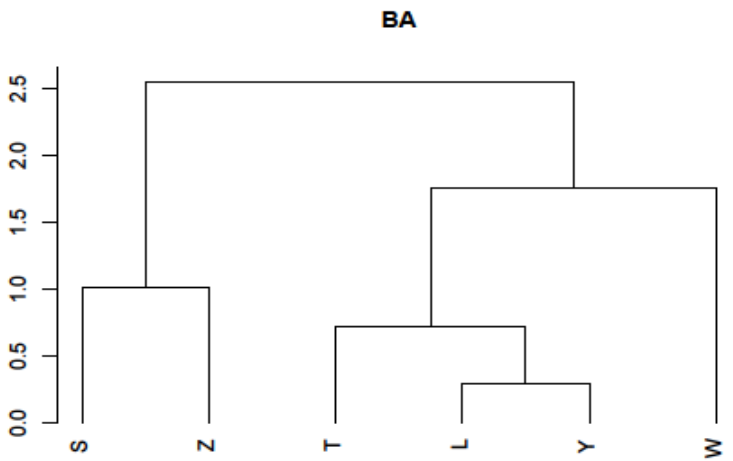
cf. Smith et al 2007 Euphytica 175:253-266.

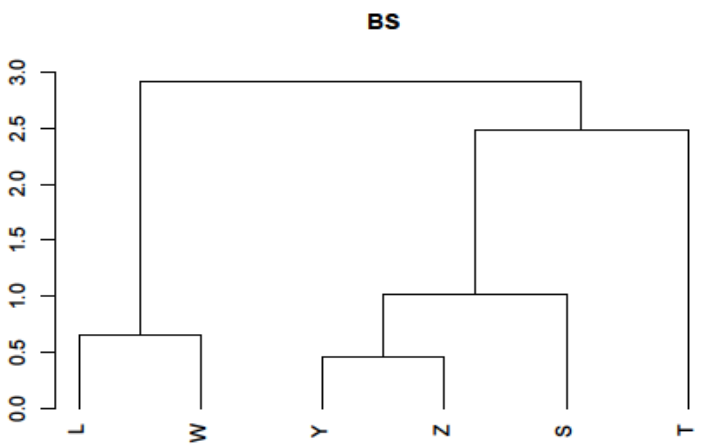
Within trait correlations

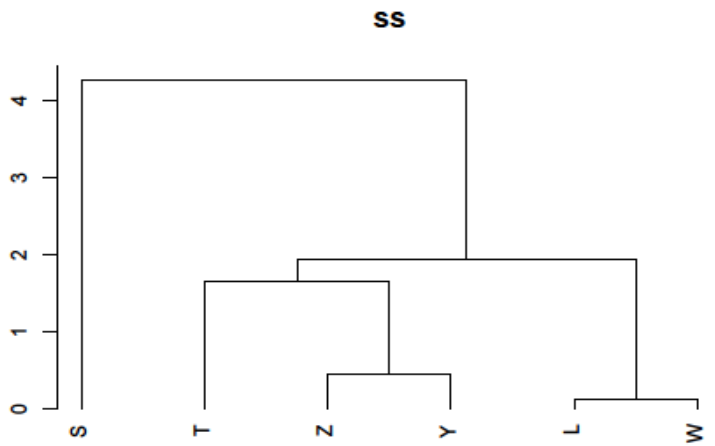
Trait	r_E		H^2	
	Single-trait	Multi-trait	Single-trait	Multi-trait
HT	0.85	0.53 – 0.90	0.43 – 0.81	0.36 – 0.79
BA	0.54	-0.05 – 0.71	0.06 – 0.50	0.05 – 0.51
BS	0.61	-0.23 – 0.77	0.13 – 0.54	0.12 – 0.49
SS	0.20 – 1.00	-0.72 – 0.94	0.17 – 0.32	0.18 – 0.32

Clustering of trials









Among trait correlations

	BA	BS	SS
HT	0.33	-0.34	0.28
BA		-0.33	0.10
BS			-0.32

Summary for this study

1. Solutions possible with FA approaches
2. Multi-trait better than single-trait analysis
3. 2-way parameterisation of G better than 3-way