

Identification of superior hybrid clones for fibre biometry in *Eucalyptus camaldulensis* × *E. tereticornis* using multi trait stability index

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Abstract

Genotype × environment (G×E) interaction is a major challenge in selecting superior genotypes based on growth traits in *Eucalyptus* since phenotypic variability is significantly affected by environmental heterogeneity. The aim of the present investigation was to understand the relationship between wood property traits and fibre biometry in the bi-parental mapping population of *E. camaldulensis* × *E. tereticornis* across three locations and identify stable genotypes based on multiple traits to improve prediction accuracy in breeding programs. High broad-sense heritability was documented for fibre parameters indicating a good prospect of these traits for genotype selection in hybrid breeding programmes in *Eucalyptus*. Significant positive correlation of fibre parameters with cellulose, acoustic velocity, DMOE and negative correlation with lignin reiterate that the fibre traits can be improved by the selection of genotype for improved wood property traits. Multi-Trait Stability Index (MTSI) and weighted average of absolute scores of the genotype index (WAASB) short-listed four genotypes (C343, C327, C246 and C161) with improved wood property traits and the mean of selected genotypes for all traits was significantly higher than the grand mean of the overall genotypes. The identified superior and stable genotypes with improved wood properties and fibre biometry can be used in plantation programs or as genitors in breeding programs.

Keywords: *Genotype-by-environment interaction, Eucalyptus, Multi-environment trials (METs), Multi-Trait Stability Index (MTSI), wood properties, fibre biometry.*

Introduction

Eucalyptus is a fast-growing and high-yielding species predominantly used as raw material for the pulp and paper industry. *Eucalyptus* plantation occupies more than 22.57 million hectares worldwide (Zhang et al. 2021) and India is one of the major *Eucalyptus* growing country with planted area of around 2.5 million hectares (Kaur et al. 2021). The wider adaptability to various edaphic and climatic conditions makes *Eucalyptus camaldulensis* and *E. tereticornis* the major tropical species for establishing plantations in India (Rajasugunasekar et al. 2015). In low annual rainfall and long hot dry season prevailing regions of southern India, interspecific hybrids of *E. camaldulensis* and *E. tereticornis* would be highly suitable compared to the other species (Varghese et al. 2008).

The important wood quality traits to consider in a *Eucalyptus* breeding program focusing on paper and pulp production includes growth, basic wood density, and pulp yield (Silva et al. 2009; Hamilton et al. 2017), lignin and extractive contents (Gomide et al. 2010) and wood structure and anatomy including fibre biometry (Ohshima et al. 2005). At ICFRE-Institute of Forest Genetics and Tree Breeding, Coimbatore, India the genetic improvement programme for *E. camaldulensis* and *E. tereticornis* was initiated in 1995 and superior performing clones were released (Varghese et al. 2008). Subsequently, interspecific hybrids were developed with superior wood property traits (Rajasugunasekar et al. 2015; Muneera Parveen et al. 2021).

Success of genetic improvement program relies on the selection of superior and stable genotypes (Silva et al. 2019) which requires an understanding of genotype × environment (G×E) interactions. It affects the stability and adaptability of the genotypes and causes reduction in genetic gain owing to

simultaneous selections in different environments (de Araujo et al. 2019; Oliveira et al. 2018) leading to reduced prediction accuracy and trait selection bias (Pollak et al. 1984). Superior genotype selection based on the growth traits alone emphasizes local selection to attain maximum gain (Gallo et al. 2018; Silva et al. 2019). Significant effect of genotype $\times$ environment (G $\times$ E) interaction were reported for growth traits in *Eucalyptus globulus* (Costa e Silva et al. 2006), *E. camaldulensis* (Kien et al. 2010), *E. dunnii* (Gallo et al. 2018), *E. urophylla* $\times$ *E. tereticornis* (Weng et al. 2014; Chen et al. 2018; Yang et al. 2018), *E. grandis* (Osorio et al. 2001; Silva et al. 2019) and in the hybrids of *Eucalyptus* (Hardner et al. 2010). Hence, selection based on multiple traits from multi-environment trials (METs) improves the prediction accuracy for low-heritability traits that are genetically correlated with a high-heritability trait (Hung et al. 2015; Jiang et al. 2015; Montesinos-López et al. 2016).

Further, multiple environment trials (METs) allow identification of genotypes with adaptability to several environments (Yan and Kang, 2003). Commonly used statistical techniques to estimate the G $\times$ E interactions in multi-environment trials include additive main effect and multiplicative interaction (AMMI) analysis (Gauch, 2013) and genotype plus genotype-versus-environment (GGE) interaction (Yan and Kang, 2003). AMMI analysis has been extensively used to assess the stability of single growth traits mainly tree volume (Nair et al. 2021a), Stem form Quotient (Nair et al. 2021b) and yield (Chandrasekar et al. 2017) in *E. camaldulensis*, diameter at breast height (DBH) in *E. urophylla* (Pupin et al. 2018), tree height and DBH in *Eucalyptus* hybrids (Karuntimi, 2012) and tree height in *E. grandis* (Lavoranti et al. 2007). However, MET analysis based on multi-trait is considered highly reliable compared to the recommendation of genotypes based on a single trait (Zuffo et al. 2020; Hussain et al. 2021).

The metan (multi-environment trial analysis) allows simultaneous selection for mean performance and stability considering several traits and the Multi-Trait Stability Index (MTSI) enables an easy to interpret selection process considering the correlation among traits (Olivoto et al. 2019a, b). This technique has been successfully used to select stable genotypes in *Fragaria* $\times$ *ananassa* (Olivoto et al. 2021), *Cicer arietinum* L. (Hussain et al. 2021), *Zea mays* L. (Singamsetti et al. 2021), *Cymopsis tetragonoloba* L. (Benakanahalli et al. 2021), *Hordeum vulgare* L. (Pour-Aboughadareh et al. 2021), *Lens culinaris* Medik. (Sellami et al. 2021), *Glycine max* (L.) Merr. (Zuffo et al. 2020; Abdelghany et al. 2021) and in wild genotypes of *Aegilops* and *Triticum*, (Pour-Aboughadareh and Poczaí, 2021).

Our team has earlier reported the quantitative genetic analysis of wood property traits including diameter, density, ultrasonic velocity, modulus of elasticity, total lignin and cellulose content in the interspecific cross of *E. camaldulensis* (Ec111) $\times$ *E. tereticornis* (Et86) for two locations (Muneera Parveen et al. 2021). However, superior genotypes with adaptability to multiple environments were not evaluated. Hence, the present study was taken up to catalogue stable superior performing hybrid clones based on Multi-Trait Stability Index.

Materials and methods

Eucalyptus pedigree details and multi-environment experimental trials

Inter-specific controlled cross between *E. camaldulensis* (Ec111) $\times$ *E. tereticornis* (Et86) was conducted to develop the bi-parental mapping population (Rajasugunasekar et al. 2015). Et86 is a selection from Seed Production Area established by the Institute at Pudukottai, Tamil Nadu, India while Ec111 belongs to the Kennedy River provenance from Queensland, Australia (CSIRO seed lot No. 17864) selected from Provenance Resource Stand at Pudukottai, Tamil Nadu, India.

A total of 160 progenies were planted in three locations at Karur, Muthupettai and Pudukottai Tamil Nadu in 2011 in an area of 1 hectare. Two tree plot with spacing of 3 $\times$ 1.5 m in four replications was established in completely randomized block design (Table 1). However, due to severe drought conditions, the survivability of the hybrid clones was significantly affected in Karur. Hence, the study was restricted to 23 hybrid clones common across all three locations and three replications per clone were harvested at an approximate age of 2 years and six months. The wood logs were air dried for six months and wood discs were processed for proximate analysis and acoustic studies.

Phenotyping of wood property traits

In the present study, 14 (10 measured and 4 derived) wood related traits were estimated in two parents and 23 hybrid clones with 2-3 ramets per clone across all three locations. Total lignin (TL) and total cellulose (TC) were estimated using acetyl bromide and anthrone method. Air dry acoustic velocity (AV) and Air dry Dynamic Modulus of elasticity (DMOE) were determined using UltraSonic timer at 90 KHz frequency (Fakopp, Enterprise BT, Agfalva, Hungary) with spiked probe. Fibre traits including fibre area (FA), fibre perimeter (FP), fibre length (FL), fibre diameter (FD), lumen diameter (LD) and double wall thickness (DWT) were measured in 10 fibres per replicate and the derived wood properties including Runkel ratio (RR), flexibility coefficient (FC), slenderness ratio (SR) and rigidity coefficient (RC) were calculated from the measured fibre dimensions in 25 individuals including parents and hybrids. The details of the phenotyped traits and the protocol used are presented in table 2.

Statistics and quantitative genetic analysis of wood property traits

All wood property traits were analyzed individually using analysis of variance (ANOVA) and Tukey's honest significant difference (Tukey HSD) tests. Multivariate ANOVA (MANOVA) was performed to infer differences due to genotype, environment and their interaction using SPSS v. 19.0 (SPSS Inc., Chicago, IL, USA). Broad sense heritability (H^2), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and expected genetic advance (GA) for all three locations combined were estimated as described by Muneera Parveen et al. (2021). Further, to determine inter-trait correlation between total cellulose (TC), total lignin (TL) contents, Acoustic velocity

Table 1
Location and description of study sites

	Karur, Tamil Nadu	Muthupettai, Tamil Nadu	Pudhukottai, Tamil Nadu
Latitude	10° 57'27.41" N	10° 23'44.52" N	10° 23'44.52" N
Longitude	78° 04' 38.75" E	79° 29' 41.96" E	79° 29' 41.96" E
Altitude (m)	137	9	88
Annual rainfall (mm)	595	1196	921
Soil	Sandy loam	Coastal Alluvial soil	Red sandy loam
Mean annual temperature (°C)	28.7	30.8	28.8
Absolute minimum temperature (°C)	17	26.39	17.8
Absolute maximum temperature (°C)	39	35.19	39.7
Spacing (m)	3 x 1.5	3 x 1.5	3 x 1.5
Trees/Plot	2	2	2
Replications	4	4	4

Table 2
Method used for estimation of wood property traits in the present study

S.No.	Trait	Abbreviation	Unit	Method of analysis
Measured wood property traits				
1	Cellulose	TC	%	A micro protocol of Updegraff (1969) optimized according to Kumar and Turner (2015) with few modifications
2	Total Lignin	TL	%	Acetyl bromide method with minor modification (Rodrigues et.al., 1999; Moreira-Vilar et al., 2014)
3	Air dry acoustic velocity	AV	Km/s	V = Sample length / (Pulse transit time -15)
4	Air dry Dynamic Modulus of elasticity	DMOE	GPa	
5	Fibre Area	FA	µm2	Schultz's method (Jane, 1956)
6	Fibre Perimeter	FP	µm	
7	Fibre Length	FL	µm	
8	Fibre Diameter	FD	µm	
9	Lumen Diameter	LD	µm	
10	Double Wall Thickness	DWT	µm	
Derived wood property traits				
11	Runkel Ratio	RR	-	Runkel ratio = 2 × Fibre cell wall thickness / Lumen diameter
12	Flexibility Coefficient	FC	-	Flexibility coefficient = Lumen diameter / Fibre diameter
13	Slenderness Ratio	SR	-	Slenderness ratio = Fibre length / Fibre diameter
14	Rigidity Coefficient	RC	-	Rigidity coefficient = 2 x Cell wall thickness / Fibre diameter

(AV) and Dynamic Modulus of elasticity (DMOE) and fibre parameters, phenotypic and genotypic correlations and path coefficient analysis were conducted using GENRES Version 7.01.

Combined Stability Analysis of wood property traits

The combined Additive main effect and multiplicative interaction (AMMI) analysis was performed across environments to determine the stability of the genotypes using CROP STAT 7.2. AMMI stability value (ASV) was calculated as described in Nduwumuremyi et al. (2017) for each genotype to measure and rank them based on their stability. The lower the ASV, the more stable the genotype. The ranking based on genotype performance, ASV, and genotype stability index (GSI) was used to determine the best-performing stable genotypes across all three environments. GSI was also calculated as described in Nduwumuremyi et al. (2017).

WAASBY index, which allows weighting between mean performance and stability across multi-environment trials (METs) and multi trait stability index (MTSI) was calculated using software package metan-MET analysis (Olivoto et al. 2019) in the RStudio software (R Core Team, 2020).

Results

Mean performance for wood property traits across three environments

A total of 14 wood property traits were recorded in the parents (*E. camaldulensis* and *E. tereticornis*) and 23 hybrids across three locations (Table S1). The phenotypic variation for all traits in three locations is presented in Table S2, while the combined location result is presented in Table 3. The mean of all traits evaluated in three locations showed that they were consistently higher in Karur, except for FC, RC and TC which was marginally high in Muthupettai and AV, DMOE were high in Pudhukottai (Table S2). In combined location analysis, the parents were significantly different for the fibre area (FA) and the derived parameters including RR, FC and RC was higher in *E. camaldulensis* (Ec111) when compared to *E. tereticornis* (Et86). In hybrids, wide phenotypic variation was recorded and the mean of all recorded traits was intermediate between the parents, indicating additive genetic control. FA, FP, FL, SR, TC and TL showed significant differences among the hybrids. All traits except LD, RR, FC and SR followed normal distribution based on skewness and kurtosis values (Table 3).

The results of MANOVA for genotypes showed significant variations for most of the documented traits except FD and LD. The effect of environment was not significant for LD, RR, RC and DMOE indicating that they were not influenced by locations. Genotype $\times$ environment interaction also indicated significant variations for FA, FP, FL, SR, FC, TC and TL (Table 4) demonstrating the combined effects of G $\times$ E on the expression of these traits.

Broad sense heritability (H^2) based on all locations combined data ranged from 0.10–0.60 with maximum H^2 for fibre

parameters including RR (0.60), RC (0.59), DWT (0.53) and FA (0.45), indicating good prospects of selection gains for these traits. The lowest H^2 was registered for FC (0.10) and FD (0.18) (Table 4). The highest predicted genetic advance as a percentage of mean (GAM) was for RR (30.4 %) followed by FA (21.8 %) and DWT (20.3 %) (Table 4).

Phenotypic and genotypic correlations between wood quality traits and fibre parameters

Phenotypic and genotypic correlations among the traits considered in the study showed that the genotypic correlation was higher than the corresponding phenotypic correlation for most of the studied traits (Table 5). The genotypic correlation coefficient among the wood property traits revealed highly positive significant correlation of TC with all the fibre parameters except DWT, whereas highly negative significant genotypic correlation was recorded for TL with FD ($rg = -0.974$, $p \leq 0.01$) (Table 5). Similarly, AV and DMOE showed a highly significant positive correlation with all the fibre parameters except LD, which recorded a significant negative correlation with AV ($rg = -0.411$, $p \leq 0.05$) and DMOE ($rg = -0.589$, $p \leq 0.01$). A highly significant negative genotypic correlation was documented between TC and TL ($rg = -0.695$, $p \leq 0.01$) (Table 5). FA had the highest statistically significant correlations with all fibre parameters including FL ($rp = 0.851$; $p \leq 0.01$), followed by FP ($rp = 0.850$; $p \leq 0.01$) and DWT ($rp = 0.335$; $p \leq 0.01$). AV and DMOE showed positive phenotypic correlation with DWT.

Path analysis for fibre parameters with TC, TL, AV and DMOE

To understand the genotypic association of different fibre parameters with wood property traits, path coefficient analysis was conducted to partition their direct and indirect effects. FA had a maximum positive direct effect on TC (1.919) followed by LD (0.613), while FP documented maximum direct negative effect (-1.142) followed by FD (-1.131), FL (-0.234), and DWT (-0.105) on cellulose content in the wood. The highest positive effect of TL was exhibited on FP (1.238), followed by FA (0.584) and FD (0.562), whereas DWT (-1.387), FL (0.519) and LD (-0.263) showed direct negative effects. FL had the maximum positive direct effect on AV (2.892) and DMOE (2.567) followed by DWT, whereas all the other fibre parameters exhibited direct negative effects on the acoustic traits (Table 6).

AMMI analysis of variance for wood property traits

The Additive Main Effects and Multiplicative Interaction (AMMI) results revealed that the interaction principal component analysis (IPCA1) was significant for FA, FP, FL, TL ($p \leq 0.001$), TC ($p \leq 0.01$), FD and DWT ($p \leq 0.05$). IPCA2 showed significant variation for FA and TL ($p \leq 0.05$) (Table 7). The percent variation due to environment was higher than the percent variation due to genotype for all traits except LD, TC, AV and DMOE indicating the effect of environment on FA, FP, FL, FD, DWT and TL. The percent variation in LD, TC, TL, AV and DMOE revealed that G $\times$ E interaction accounted for higher percent variation than that for genotype and environment individually,

Table 3

Phenotypic analysis for wood property traits in parents and hybrids of *E. camaldulensis* (Ec111) x *E. tereticornis* (Et86)

Trait	Parents		p value	Hybrids			p value	Kurtosis	Skewness
	<i>E. camaldulensis</i> (Ec111)	<i>E. tereticornis</i> (Et86)		Min	Max	Mean $\pm$ SD			
FA	7764.28 $\pm$ 1622.99	7289.48 $\pm$ 1502.22	<0.05	4824.24	11236.40	7186.34 $\pm$ 1685.15	<0.001	-1.11	0.48
FP	1432.1 $\pm$ 188.17	1400.43 $\pm$ 175.95	ns	1124.45	1691.71	1388.75 $\pm$ 163.79	<0.001	-1.36	0.31
FL	713.94 $\pm$ 84.06	699.38 $\pm$ 81.99	ns	562.47	834.98	687.81 $\pm$ 79.32	<0.001	-1.33	0.30
FD	12.2 $\pm$ 2.11	13.36 $\pm$ 2.43	ns	10.17	19.10	13.54 $\pm$ 2.05	ns	-0.30	0.81
LD	4.97 $\pm$ 0.17	6.12 $\pm$ 1.49	ns	4.67	12.29	6.9 $\pm$ 1.37	ns	3.29	1.42
DWT	7.23 $\pm$ 2.28	7.25 $\pm$ 0.94	ns	4.68	9.35	6.8 $\pm$ 1.10	ns	-0.46	0.57
RR	1.48 $\pm$ 0.53	1.21 $\pm$ 0.11	<0.05	0.66	1.48	1.02 $\pm$ 0.17	ns	7.86	1.76
FC	0.42 $\pm$ 0.08	0.45 $\pm$ 0.02	<0.05	0.40	1.09	0.51 $\pm$ 0.09	ns	26.44	4.25
SR	59.51 $\pm$ 8.53	52.83 $\pm$ 4.1	ns	38.50	71.00	51.63 $\pm$ 5.95	<0.01	2.61	1.10
RC	0.58 $\pm$ 0.08	0.55 $\pm$ 0.02	<0.05	0.40	0.65	0.5 $\pm$ 0.05	ns	1.57	0.47
TC	42.33 $\pm$ 0.68	37.78 $\pm$ 2.64	ns	30.02	45.04	37.45 $\pm$ 3.89	<0.05	-0.92	0.02
TL	15.27 $\pm$ 2.19	16.31 $\pm$ 1.68	ns	12.03	19.86	15.58 $\pm$ 1.77	<0.001	-0.27	0.41
AV	3.58 $\pm$ 0.03	3.9 $\pm$ 0.1	ns	2.94	4.30	3.64 $\pm$ 0.30	ns	-0.22	0.01
DMOE	8.45 $\pm$ 0.49	9.79 $\pm$ 0.69	ns	5.38	11.53	8.63 $\pm$ 1.39	ns	-0.43	0.16

P value shows the significant differences for the clones across locations.

Table 4

Estimates of variances at genotypic, phenotypic and residual level, broad sense heritability coefficient (H²) and genetic advance in percentage of mean for the wood property and fibre traits in bi-parental population of *E. camaldulensis* (Ec111) x *E. tereticornis* (Et86) based on combined location analysis

Trait	Significance			GCV (%)	PCV (%)	ECV (%)	H ²	GAM (%)
	Genotype	Environment	Genotype X Environment					
FA	***	***	***	14.0	20.8	8.3	0.5	21.8
FP	**	***	***	5.0	9.0	5.8	0.3	8.0
FL	***	***	***	5.6	9.4	5.8	0.4	9.0
FD	ns	***	ns	5.2	12.2	11.6	0.2	6.4
LD	ns	ns	ns	10.8	22.5	25.1	0.2	12.9
DWT	***	***	ns	11.3	15.6	11.8	0.5	20.3
RR	***	ns	ns	21.5	27.7	21.0	0.6	30.4
SR	*	***	*	9.0	15.2	11.5	0.4	10.2
FC	***	***	***	6.2	19.9	25.5	0.1	4.9
RC	***	ns	ns	10.7	14.0	10.0	0.6	14.6
TC	**	*	**	8.7	13.6	9.8	0.4	10.4
TL	***	***	***	8.2	12.4	7.8	0.4	11.1
AV	**	**	ns	6.6	10.2	9.1	0.4	8.9
DMOE	*	ns	ns	13.1	20.4	19.4	0.4	17.6

Two-way ANOVA was performed for linear model, on raw data. Significance: *p $\leq$ 0.05, **p $\leq$ 0.01, ***p $\leq$ 0.001 and ns indicates not significant.GCV %, genotypic coefficient of variation; PCV %, phenotypic coefficient of variation; ECV %, environmental coefficient of variation; H², Broad sense heritability coefficient; GAM (%), genetic advance as a percentage of mean

Table 5

Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among the wood property traits in bi-parental population of *E. camaldulensis* (Ec111) x *E. tereticornis* (Et86)

	FA	FP	FL	FD	LD	DWT	TC	TL	AV	DMOE
FA	1	0.866 **	0.851 **	-0.147 ns	-0.260 ns	0.942 **	0.639 **	-0.106 ns	0.550 **	0.540 **
FP	0.850 **	1	0.976 **	-1.114 **	-0.941 **	0.698 **	0.903 **	-0.111 ns	0.624 **	0.658 **
FL	0.851 **	0.988 **	1	-0.835 **	-0.819 **	0.684 **	0.656 **	-0.018 ns	0.676 **	0.685 **
FD	0.260 **	0.141 ns	0.142 ns	1	0.732 **	0.224 ns	0.481 *	-0.974 **	1.407 **	1.269 **
LD	0.190 *	0.075 ns	0.060 ns	0.562 **	1	-0.585 **	0.612 **	0.068 ns	-0.411 *	-0.589 **
DWT	0.335 **	0.184 *	0.199 *	0.579 **	0.134 ns	1	0.131 ns	-0.048 ns	0.978 **	0.983 **
TC	0.012 ns	0.026 ns	-0.002 ns	0.037 ns	-0.103 ns	0.141 ns	1	-0.695 **	0.023 ns	-0.064 ns
TL	0.040 ns	0.032 ns	0.034 ns	0.043 ns	0.103 ns	-0.012 ns	-0.076 ns	1	-0.459 *	-0.501 *
AV	0.073 ns	0.105 ns	0.115 ns	0.064 ns	-0.053 ns	0.179 *	0.086 ns	0.056 ns	1	0.999 **
DMOE	0.087 ns	0.103 ns	0.114 ns	0.060 ns	-0.050 ns	0.179 *	0.084 ns	0.044 ns	0.963 **	1

Statistically significant correlation: * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$ and ns indicates not significant.

Table 6

Direct (bold diagonal and underlined) and indirect effects of different fibre parameters on Cellulose (TC), Total lignin (TL), Acoustic velocity (AV) and Dynamic Modulus of elasticity (DMOE) in bi-parental population of *E. camaldulensis* (Ec111) x *E. tereticornis* (Et86)

Cellulose (TC)							
	FA	FP	FL	FD	LD	DWT	rg
FA	<u>1.919</u>	-0.99	-0.199	0.166	-0.159	-0.099	0.6385 **
FP	1.662	<u>-1.142</u>	-0.228	1.261	-0.577	-0.073	0.9032 **
FL	1.633	-1.115	<u>-0.234</u>	0.945	-0.502	-0.072	0.656 **
FD	-0.282	1.274	0.195	<u>-1.131</u>	0.449	-0.024	0.4812 *
LD	-0.499	1.075	0.191	-0.829	<u>0.613</u>	0.061	0.612 **
DWT	1.807	-0.798	-0.16	-0.254	-0.358	<u>-0.105</u>	0.1316 ns
Total lignin (TL)							
FA	<u>0.58356</u>	1.07248	-0.44196	-0.08262	0.0683	-1.30554	-0.1058 ns
FP	0.50557	<u>1.23793</u>	-0.50678	-0.62634	0.24707	-0.96853	-0.1112 ns
FL	0.49659	1.20795	<u>-0.51936</u>	-0.46932	0.21494	-0.94902	-0.0183 ns
FD	-0.08583	-1.38022	0.43389	<u>0.56177</u>	-0.19252	-0.3112	-0.9742 **
LD	-0.15173	-1.16441	0.42498	0.41173	<u>-0.26267</u>	0.81064	0.0683 ns
DWT	0.54944	0.86469	-0.35546	0.12608	0.15356	<u>-1.3866</u>	-0.0484 ns
Acoustic velocity (AV)							
FA	<u>-0.24935</u>	-3.11512	2.46108	0.00378	0.17733	1.27249	0.5503 **
FP	-0.21602	<u>-3.59568</u>	2.82204	0.02863	0.64151	0.94401	0.6244 **
FL	-0.21219	-3.50861	<u>2.89207</u>	0.02145	0.55807	0.92499	0.6758 **
FD	0.03667	4.009	-2.41615	<u>-0.02568</u>	-0.49987	0.30332	1.4072 **
LD	0.06483	3.38214	-2.3665	-0.01882	<u>-0.68201</u>	-0.79012	-0.4109 *
DWT	-0.23477	-2.51156	1.9794	-0.00576	0.39872	<u>1.3515</u>	0.9776 **
Dynamic Modulus of elasticity (DMOE)							
FA	<u>-0.47843</u>	-2.77549	2.18413	0.00621	0.18604	1.4174	0.5398 **
FP	-0.41449	<u>-3.20366</u>	2.50446	0.0471	0.67304	1.05151	0.6579 **
FL	-0.40713	-3.12608	<u>2.56662</u>	0.03529	0.5855	1.03033	0.6846 **
FD	0.07036	3.57191	-2.14425	<u>-0.04224</u>	-0.52444	0.33786	1.2692 **
LD	0.12439	3.0134	-2.10019	-0.03096	<u>-0.71554</u>	-0.88009	-0.5891 **
DWT	-0.45046	-2.23774	1.75665	-0.00948	0.41832	<u>1.5054</u>	0.9827 **

Residual Effect=1.07 (TC), 1.29 (TL), 0.37 (AV), 0.49 (DMOE).

rg – Genotypic correlation coefficient.

Statistically significant correlation: * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$ and ns indicates not significant.

Table 7

Combined AMMI analysis for wood property and fibre traits in parents and hybrids of *E. camaldulensis* (Ec111) x *E. tereticornis* (Et86)

Source of Variation	df	Mean squares									
		FA	FP	FL	FD	LD	DWT	TC	TL	AV	DMOE
Genotype (G)	24	2380000***	16157**	4597***	3.40 ^{ns}	3.99 ^{ns}	1.84***	36.63***	4.79***	0.22*	5.40*
Environment (E)	2	118000000***	1306134***	286465***	184.61**	33.74 ^{ns}	53.63***	61.54**	82.27**	0.78*	6.26 ^{ns}
Interaction (GXE)	48	2380000***	19274***	4837***	3.59 ^{ns}	2.64 ^{ns}	0.85 ^{ns}	25.55**	3.75***	0.12 ^{ns}	2.73 ^{ns}
IPCA1	25	4010000***	29313***	7344***	4.90*	3.23 ^{ns}	1.13*	35.34**	4.58***	0.13 ^{ns}	3.48 ^{ns}
IPCA2	23	604000*	8361 ^{ns}	2112 ^{ns}	2.16 ^{ns}	2.00 ^{ns}	0.54 ^{ns}	14.91 ^{ns}	2.86*	0.11 ^{ns}	1.90 ^{ns}
Residual	72	369000	6592	1625	2.47	2.65	0.67	13.96	1.46	0.11	2.91
Total	197	2780000	27066	6427	4.96	3.22	1.43	22.67	3.81	0.14	3.13
Sum of squares											
Genotype (G)	24	57100000	387777	110333	81.52	95.80	44.16	879.23	115.08	5.38	129.58
Environment (E)	2	237000000	2612269	572931	369.23	67.50	107.25	123.08	164.54	1.56	12.51
Interaction (GXE)	48	114000000	925134	232177	172.26	126.70	40.79	1226.47	180.18	5.96	130.80
IPCA1	25	100000000	732821	183607	122.60	80.70	28.32	883.62	114.50	3.35	87.08
IPCA2	23	13900000	192313	48570	49.66	46.00	12.47	342.85	65.69	2.61	43.73
Residual	72	26500000	474654	117017	177.94	191.10	48.28	1005.11	105.23	7.98	209.73
Total	197	548000000	5331922	1266102	977.38	634.90	281.46	4466.04	751.44	27.03	616.29
% Variation due to G		13.99	9.88	12.05	13.08	33.03	22.98	39.45	25.03	41.69	47.48
% Variation due to E		58.07	66.55	62.59	59.27	23.28	55.80	5.52	35.79	12.09	4.58
% Variation due to GXE		27.93	23.57	25.36	27.65	43.69	21.22	55.03	39.19	46.22	47.93
% GXE due to IPCA1		71.23	52.35	52.58	35.01	25.39	31.80	39.60	40.12	24.02	25.57
% GXE due to IPCA2		9.90	13.74	13.91	14.18	14.47	14.00	15.36	23.02	18.74	12.84
% residual		18.87	33.91	33.51	50.81	60.13	54.21	45.04	36.87	57.24	61.59

Statistically significant correlation: *p ≤ 0.05, **p ≤ 0.01, ***p ≤ 0.001 and ns indicates not significant.

IPCA1 - interaction principal component axis 1; IPCA2 - interaction principal component axis 2.

Table 8

Eigenvalues, explained variance, factorial loadings after varimax rotation, and communalities obtained in the factor analysis for wood property and fibre traits in parents and hybrids of *E. camaldulensis* (Ec111) x *E. tereticornis* (Et86)

Trait	FA1§	FA2	FA3	FA4	Communality
FA	-0.910	0.152	0.228	0.028	0.903
FP	-0.963	0.082	0.011	-0.093	0.943
FL	-0.966	0.113	0.052	-0.058	0.952
FD	-0.099	0.132	0.950	-0.049	0.932
LD	-0.007	-0.316	0.727	-0.081	0.635
DWT	-0.273	0.417	0.638	0.251	0.719
TC	-0.225	-0.228	-0.044	-0.784	0.719
TL	0.092	0.157	0.062	-0.915	0.875
AV	-0.194	0.945	0.005	0.061	0.934
DMOE	-0.084	0.963	0.000	-0.029	0.936
Eigenvalues #	3.48	1.96	1.71	1.40	
Variance (%) #	34.82	19.62	17.05	13.99	
Accumulated (%) #	34.82	54.44	71.49	85.49	

§ FA, Factor retained

The values for all factors are provided in Table S4.

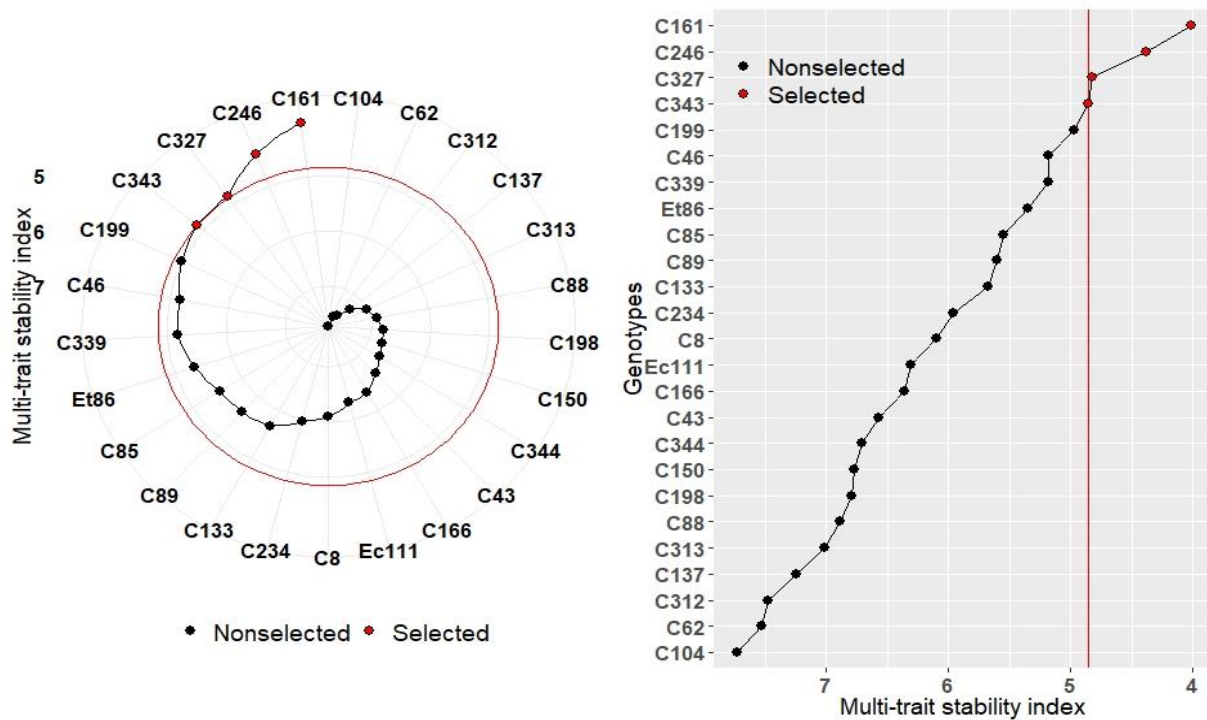


Fig. 1
Genotype ranking and selected genotypes for the multitrait stability index considering a selection intensity of 15 % from bi-parental population of *E. camaldulensis* (Ec111) x *E. tereticornis* (Et86)

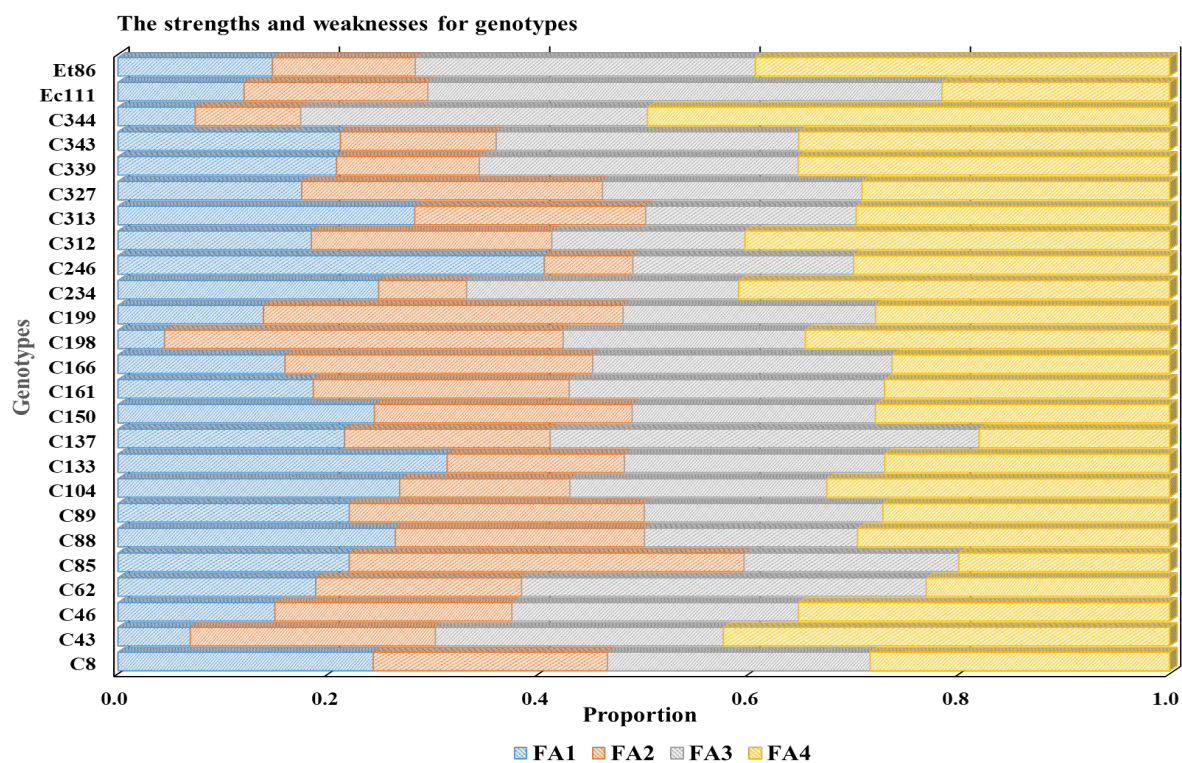


Fig. 2
Strengths and weaknesses view of genotypes assessed from bi-parental population of *E. camaldulensis* (Ec111) x *E. tereticornis* (Et86). The y-axis presents the ratio of each factor on the calculated MTSI of the selected genotypes. The minimum the proportions explicated by a factor, the nearer the traits within that factor are to the ideotype. FA stands for factor

Table 9

Selection differential of the WAASBY index for wood property and fibre traits in parents and hybrids of *E. camaldulensis* (Ec111) x *E. tereticornis* (Et86)

Factor	Trait	Xo	Xs	Selection Differential	Selection Differential (%)
FA 1	FA	49.85	56.69	6.85	13.74
	FP	53.28	60.98	7.70	14.45
	FL	49.45	56.36	6.91	13.98
FA 2	AV	48.84	58.02	9.18	18.80
	DMOE	46.93	63.09	16.15	34.42
FA 3	FD	48.89	65.94	17.05	34.88
	LD	57.78	63.51	5.73	9.91
	DWT	62.68	78.48	15.80	25.21
FA 4	TC	49.29	57.50	8.21	16.65
	TL	47.96	64.56	16.60	34.62
Mean		51.49	62.51	11.02	21.66

Xo, WAASBY index of the original population

Xs, WAASBY index of the selected genotypes (C161, C246, C327, C343)

indicating the influence of G×E interaction on the expression of these traits (Table 7).

The G×E interaction variation assigned to IPCA1 and IPCA2 showed that IPCA1 contributed to a significantly higher percentage of variation compared to IPCA2. The IPCA1 accounted for almost twice as much variation as IPCA2 all traits except FA, where it explained 71.2 %, while IPCA2 explained 9.9 % (Table 7). IPCA1 accounted for 24.0 (AV) to 71.2 % (FA) variation and the variation of IPCA2 ranged from 9.9 % (FA) to 23.0 % (TL). The residual percent variation was notably higher for FD, LD, DWT, TC, AV and DMOE, indicating that these traits could be influenced by unknown factors in G×E interactions (Table 7).

Mean genotype performance, AMMI stability analysis and genotype selection index were calculated for each genotype (Table S3). The genotypes with the least ASV represent high stability of genotypes with low G×E interaction and the genotype with the lowest rank sum for GSI was considered the best clone across traits.

Genotype selection based on MTSI and contribution of factors to the MTSI

In the factor analysis performed with the WAASBY index, four principal factors were maintained, and the accumulated variance in these factors was 85.5 % (Table 8). After varimax rotation, mean communality (h) was 0.86 ($LD\ 0.64 \leq h \leq 0.95\ FL$) signifying that the higher ratio of each trait variance was influenced by the factors. Ten wood property traits clustered into four different factors. FA1 (FA, FP and FL) included traits with fibre biometry that are critical determinants of paper quality; FA2 (AV and DMOE) included traits used to assess intrinsic wood properties and mechanical strength; FA3 (FD and LD) also had traits related to fibre biometry and FA4 (TC and TL) included traits related to kraft pulp yield from wood (Table 8).

Figure 1 shows the genotype ranking for the MTSI, assuming 15 % selection intensity. Four hybrid clones which were short-listed based on the analysis were C343, C327, C246 and C161.

The contribution of each factor in the MTSI indicates the strengths and weakness of genotypes (Fig. 2). The less involvement of a FA (factor), the nearer the characters within that factor are to the ideotype. FA1 (FA, FP and FL) was the factor with the least contribution to MTSI of C161 and C327 indicating the higher WAASBY values for these traits (Fig. 2). This implies that positive gains are desired for FA, FP and FL and indicates that these two genotypes have high values in fibre parameters out of the selected hybrid clones. Further, FA1 was the main causative factor for the MTSI of C246 (41 %), signifying that this genotype had low values for FA, FP and FL. The smallest contribution of FA2 (AV and DMOE) was observed for C246 (8 %) and C343 (15 %) (Fig. 2; Table S4 and Table S5). This implies that these two genotypes are close to the ideotype for the traits (AV and DMOE) which are significant for intrinsic wood properties and mechanical strength when compared to C161 and C327. In C343 (35 %) and C327 (29 %) most of the MTSI was due to FA4 (TC and TL) (Fig. 2; Table S4 and Table S5). The studied traits in FA4 imply that higher magnitudes of TC and lower magnitudes of TL are most desired to determine the kraft pulp yield from wood.

The selection differential (SD) for the WAASBY index was positive for all the selected traits, suggesting that the technique was effective in selecting the best performing and stable genotypes across the studied environments. The mean WAASBY index of the selected genotypes was higher than the mean WAASBY index of the overall population. The mean selection differential for the WAASBY index was 21.7 %, the lowest was for LD (9.9 %) and the highest of 34.9 % was observed for FD (Table 9).

Weighted average of the absolute scores

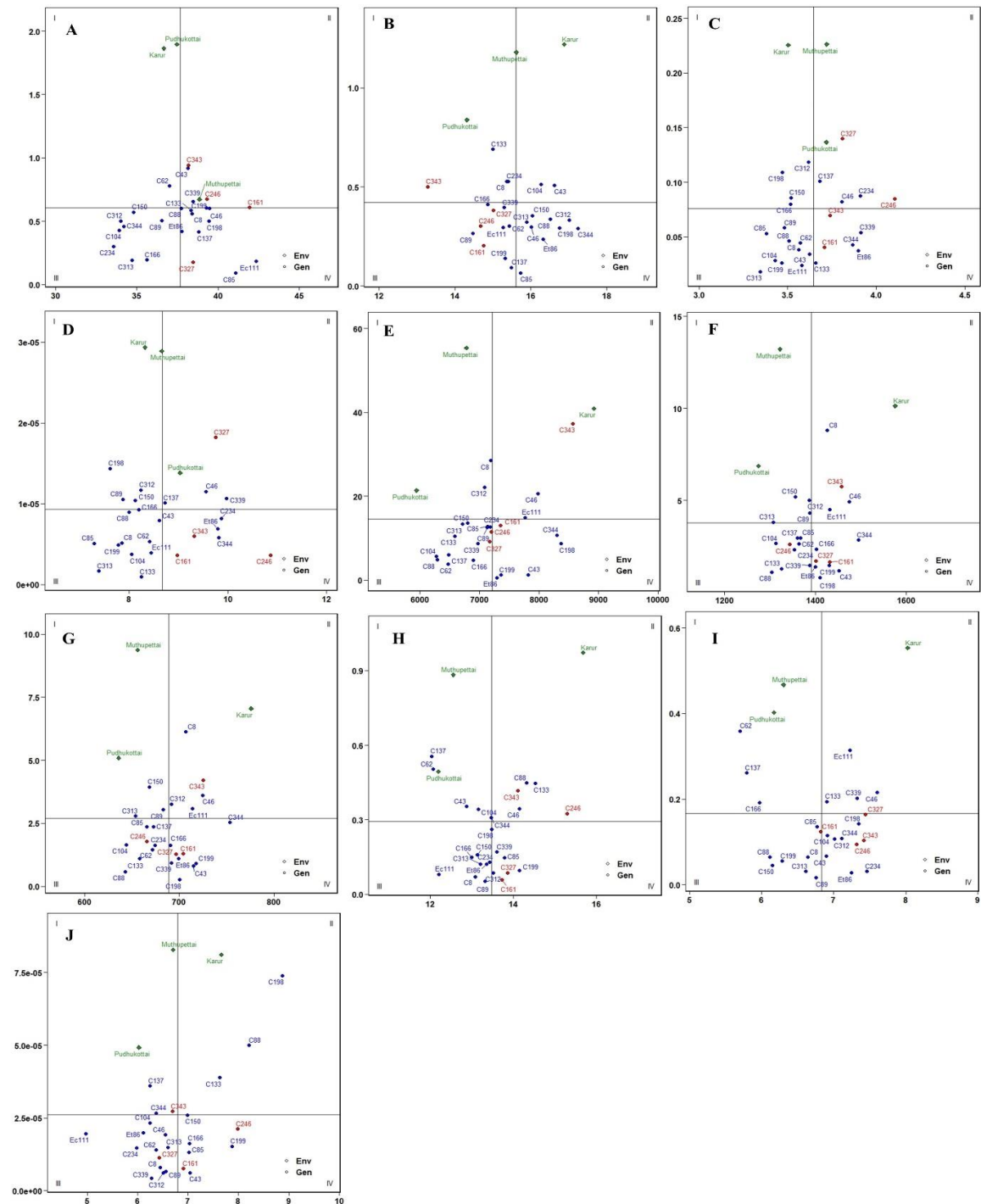


Fig. 3

Joint interpretation for mean performance and stability for wood property traits in parents and hybrids of *E. camaldulensis* (Ec111) x *E. tereticornis* (Et86). (A) TC, (B) TL, (C) AV, (D) DMOE, (E) FA, (F) FP, (G) FL, (H) FD, (I) DWT, (J) LD. The x axis shows the mean for each genotype x environment interaction and the y axis the WAASB index

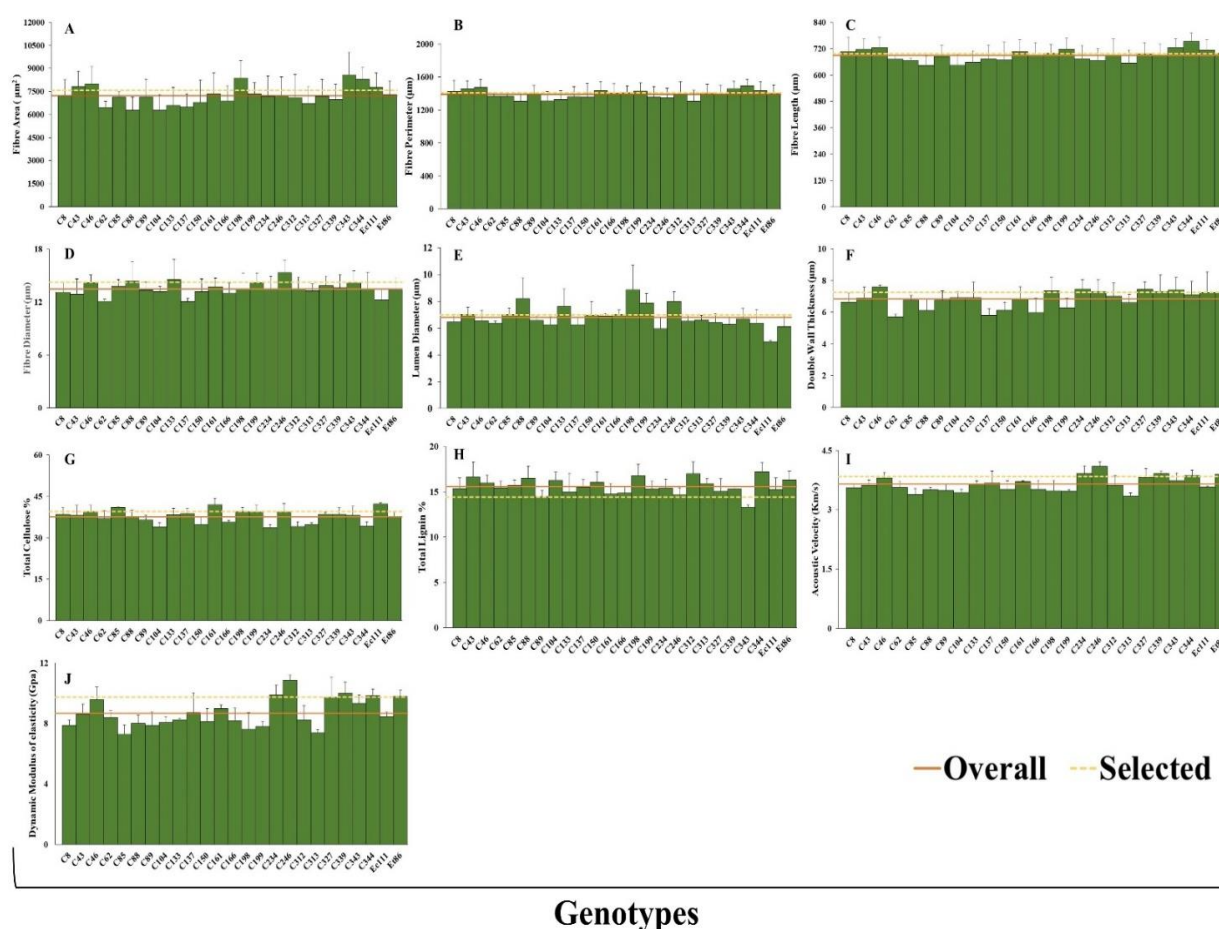


Fig. 4

Observed values for (A) FA, (B) FP, (C) FL, (D) FD, (E) LD, (F) DWT, (G) TC, (H) TL, (I) AV, (J) DMOE in parents and hybrids of *E. camaldulensis* (Ec111) x *E. tereticornis* (Et86) evaluated in three environments. Horizontal solid lines represent the grand mean; dashed lines represent the mean of the selected genotypes. Bars represent means $\pm$ SE ($n = 9$)

Mean performance and stability of selected genotypes

The joint interpretation of mean performance for all the fibre parameters and TC, TL, AV, DMOE is presented in figure 3. The ordinates of WAASBY quantify the stability of the genotypes considering all possible IPCA values whereas the AMMI biplot considers IPCA1 and IPCA2. Genotypes within quadrants I and II are assumed to be unstable. Genotypes within quadrant IV for all fibre parameters, TC, AV, DMOE and within quadrant III for TL are considered to be desirable because they represent a desirable mean and minor variation across environments, which is explained by the WAASB values (Fig. 3). The mean of selected genotypes for all traits is considerably higher than the grand mean of the overall genotypes ranging from 1.3 % (FP) to 12.2 % (DMOE). In case of lignin where the genotypes with lesser mean are considered preferable since it affects the pulping process, a selection differential of -7.5 % was observed (Fig. 4, Table S6). The selected genotypes including C161, C246, C327 and C343 represent the desirable means for kraft pulp

yield, intrinsic wood properties and mechanical strength. The selection differentials of the WAASBY stability index were negative for fibre parameters (-21.4 % (LD) $\leq$ selection differential ≤ -10.6 % (FP and FL) indicating that the selected genotypes were considerably more stable for the documented traits (Table S6). The ranking of genotype for wood property traits based on ASV, GSI and WAASB index is represented in Table S7. ASV and WAASB were highly and positively correlated for most of the studied traits, whereas minor deviations are observed between GSI and WAASB (Table S6).

Discussion

Wood is an abundant biological resource and important raw material for lumber and paper industry. The main objective to meet the rapidly increasing demand for wood without destructing the natural forest is to improve wood quality and

productivity through the use of genetically superior planting stock (Paux et al. 2004; Pillai et al. 2013). The determinant wood quality traits for pulpwood production include growth, physical attributes of fibres including fibre length, diameter and wall thickness, chemical properties including cellulose, lignin and extractive contents that affect the pulping process (Goncalves et al. 2004; Rencoret et al. 2007; Stackpole et al. 2011; Gallo et al. 2018). However, these traits are largely affected by silvicultural interventions, genotype and environmental factors (Macdonald and Hubert 2002; Goncalves et al. 2004). Hence multi-trait selection of genotypes based on multi-location trials would give a better understanding for prudent deployment of stable clones across environments. In the present study, the response of parents (*E. tereticornis* and *E. camaldulensis*) and 23 hybrids to three different environmental conditions was investigated by the AMMI and multi trait stability index (MTSI) on the basis of variations in several wood property traits and fibre parameters.

Phenotypic variation and inter-specific F1 hybrid performance

In this study, a wide range of phenotypic variation was observed between the hybrids for all the wood property traits studied. However, the mean performance of the inter-specific F1 hybrids was intermediate between the parental performances, indicating additive genetic control of the traits. This response does not exclude the fact that certain hybrid clones exhibit outstanding performance in the cross studied. Similar intermediate mean performances of the inter-specific F1 hybrid were reported in *E. nitens* × *E. globulus* (Volker et al. 2008), *E. grandis* and *E. urophylla* with clones of *E. globulus* (Bison et al. 2007), *E. nitens* × *E. globulus* and *E. gunnii* × *E. globulus* (Potts et al. 2000) and *E. ovata* × *E. globulus* (Lopez et al. 2000). Site effects reflect the expression of hybrid superiority, combining ability of the desired wood property traits and the response of the genotypes to edaphic as well as native and regional climatic conditions (Potts and Dungey 2004; Pliura et al. 2006). This explains the significant effect of environment on all traits except LD, RR, RC and DMOE in the combined analysis of all three locations and the variation in the mean performances of the hybrids across locations. The magnitude of available variation across genotype, environment and G×E indicates the possibilities of exploiting these wood property traits for further genetic improvement programmes to enhance wood productivity.

Heritability and genetic advancement of wood property traits

Heritability is an important genetic parameter which quantifies the inheritable fraction of the phenotypic variation that can aid in selection. Comprehensive knowledge of heritability, genetic correlation, additive and non-additive variance of different wood properties is essential for effective tree breeding and to maximize genetic gain (Lima et al. 2019). The phenotypic coefficients of variations were consistently higher than the genotypic coefficient of variations for all the studied wood property traits indicating the influence of environment. All location combined heritability estimates showed moderate

heritability for wood property traits including TC, TL, AV and DMOE. Similar results of heritability were reported in *E. tereticornis* × *E. grandis* (Dasgupta et al. 2021) and *E. grandis* × *E. urophylla* (Tan et al. 2017; Resende et al. 2017; Lima et al. 2019). The maximum broad sense heritability was documented for fibre parameters including RR (0.60), RC (0.59), DWT (0.53) and FA (0.45) and the lowest H^2 for FC (0.10) and FD (0.18). Lima et al. (2019) documented similar results with high broad sense heritability for fibre length (0.52–0.68) and low H^2 for fibre width (0.08–0.33). Kube et al. (2001) also reported moderate to very high site heritability for fibre length (0.25–0.80). However, results obtained in this mapping population were contrasting to the fibre traits reported in *E. tereticornis* × *E. grandis* by Dasgupta et al. (2021) and *E. globulus* (Apiolaza et al. 2005) where low heritability was predicted for fibre length (0.14), which could be attributed to the hybrid genotype and density of the plantation (Chaix et al. 2011), environmental factors, size of the evaluated population and the narrow genetic base (Gion et al. 2011; Hein et al. 2012). High heritability for the fibre parameters accounts for the highest genetic gain for these traits when compared to the other wood property traits. In general, a breeding program should focus on improving the fibre biometry related traits which are a critical determinant of paper quality including strength, opacity, porosity, smoothness and bulk.

Inter-trait genetic correlation between fibre and wood property traits

Genetic correlations between the wood property traits could explain their impact on pulp productivity and provide an indirect response to the selection of one trait over others. High genetic correlations between the traits indicate the pleiotropic relationships between the genes controlling them which could aid in multi-trait genetic selection (Gion et al. 2011; Hung et al. 2015; Chen et al. 2018). A strong additive genetic correlation was observed among TC, AV and DMOE with fibre biometrics. Similarly, in earlier studies, a strong positive correlation was reported between acoustic velocity and cellulose with pulp yield (Apiolaza et al. 2005; Stackpole et al. 2010; Stackpole et al. 2011; Hamilton et al. 2017). Raymond et al. (2010) reported that the significant and positive correlation of velocity and cellulose with pulp yield could be attributed to a positive correlation between AV and fibre length which is possibly due to increased cellulose and decreased lignin content with a corresponding increase in fibre length. The strongly positive genetic correlation between AV with FL observed in the present study concurs with earlier studies on *Pinus radiata* (Albert et al. 2002; Raymond 2008) and *Melia azedarach* (Hasegawa et al. 2015; Duong et al. 2018). Similarly, a significant positive correlation of TC with FL was also reported in *Melia dubia* (Dhaka et al. 2020) and several species of eucalyptus including *E. urograndis* hybrid population (Lima et al. 2019), *E. pellita* (Lukmandaru et al. 2016), *E. globulus* (Apiolaza et al. 2005) and *E. nitens* (Kube et al. 2001).

Lignin content and its composition is one of the key traits that affect the pulping process. High lignin content hinders the pulping process because the delignification process of wood involves separating the extractives including phenols, tannins,

fatty acids, and esters by chemical polymerization which involves high energy and reagents consumption. High cellulose and low extractives and lignin are desirable for high quality pulp production (Hein et al. 2012; Thumma et al. 2016; Carrillo et al. 2017). In this study, TL showed a significant negative genetic correlation with TC, AV, DMOE and FD. Similar results of low to negative genetic correlation of lignin with cellulose were reported in *E. urograndis* hybrid population (Lima et al. 2019), *E. urophylla* × *E. tereticornis* (Yang et al. 2018; Chen et al. 2018), *E. pellita* (Lukmandaru et al. 2016) and *E. globulus* (Stackpole et al. 2011) and with pulp yield in *E. dunnii* (Gallo et al. 2018) and *E. globulus* (Poke et al. 2006; Stackpole et al. 2011). Such negative relationship between cellulose and lignin is predictable due to their physical complementarity in wood structure (Plomion et al. 2001). A significant negative correlation between fibre length and lignin content was also reported by Poke et al. (2006); Lima et al. (2019); and Dhaka et al. (2020).

Thus, the genetic correlation reported here would provide a new perspective to the broad understanding of the relationship between fibre traits with other wood properties. Fibre traits generally showed significant, positive genetic correlation with TC, AV and DMOE but non-significant and negatively significant correlation with TL. This indicates that the average fibre traits can be improved by selecting for improved TC, AV and DMOE and low TL content.

AMMI analysis – Presence and extent of G×E interactions

Genotype-by-environment interaction (G×E) in forest tree species across multi-environments limits the efficiency to select the stable and superior genotypes for adaptation, because of their differential responses to different environments (Li et al. 2017; Nduwumuremyi et al. 2017; Adjebeng-Danquah et al. 2017). Several statistical methods are available to estimate the magnitude of G×E interactions that aid in understanding and evaluating complex data from multi-environment trials. Multivariate statistical methods widely used to assess G×E interactions in forest tree breeding programs include cluster analysis, principal component analysis, linear discriminant analysis, additive main effects and multiplicative interaction (AMMI) and genotype main effects and G×E effects (GGE) (Li et al. 2017).

The AMMI analysis indicated that the environmental variation outweighed the genetic variation, emphasizing the need for multi-location trials to identify stable genotypes adapted to the environments. G×E interaction significantly affected FA, FP, FL, SR, FC, TC and TL demonstrating the combined effects of environment and genotype on the expression of these traits. The findings on G×E interaction agreed with earlier studies (Kube et al. 2001; Yang et al. 2018; Gallo et al. 2018; Muneera Parveen et al. 2021; Dasgupta et al. 2021) indicating that G×E interaction analysis is important for identifying genotypes with adequate adaptation to target environments. The insignificant G×E interaction for FD, LD, DWT, AV and DMOE indicated the possibility of evaluating the trait in any environment and explained the stable performance of genotypes across various locations. However, genotype selection based on ASV and GSI

would lead to selection bias, since the traits were analysed individually and some of the evaluated wood property traits were negatively correlated.

Selection of stable genotypes across environments based on MTSI

The selection of high-performance and stable genotypes for the desirable traits is the ultimate goal of breeding programs. However, the AMMI and GGE biplots explain the stability and performance of the genotypes considering a single trait alone. Multi Trait Stability Index is a useful technique to identify stable genotypes in multi-environment trials where numerous traits are targeted for improvement and the WAASB (Weighted Average of Absolute Scores) index could be an indicator for the selection of superior genotypes (Olivoto et al. 2019a, b). In this study, four stable genotypes (C343, C327, C246 and C161) were identified out of 25 genotypes based on 15 wood property traits across three environments. The mean of selected genotypes for all the documented traits was higher than the overall mean of the 25 genotypes. Further, the genotypes C199 and C46 were closer to the red circle and it would be interesting to investigate the performance of these genotypes that are nearer or closer to the cutpoint (Olivoto et al. 2019a, b; Olivoto and Nardino 2020). In *Eucalyptus*, Multiple-trait BLUP has proven efficient in genetic selection compared to single trait selection (Alves et al. 2018). However, the use of MTSI has been limited to *Fragaria* × *ananassa* (Olivoto et al. 2021), *Cicer arietinum* L. (Hussain et al. 2021), *Zea mays* L. (Singamsetti et al. 2021), *Cymopsis tetragonoloba* L. (Benakanahalli et al. 2021), *Hordeum vulgare* L. (Pour-Aboughadareh et al. 2021), *Lens culinaris* Medik. (Sellami et al. 2021), *Glycine max* (L.) Merr. (Zuffo et al. 2020; Abdelghany et al. 2021) and in wild genotypes of *Aegilops* and *Triticum* (Pour-Aboughadareh and Pocza, 2021). Hence, MTSI and WAASBY index would be highly useful for the selection of stable and superior genotypes across multiple environments in tree species.

Conclusion

In the present investigation, a total of 14 wood property traits in *E. camaldulensis* × *E. tereticornis* and their hybrids across three locations documented significant G×E interactions for FA, FP, FL, SR, FC, TC and TL. The fibre parameters including RR, RC, DWT and FA documented high broad-sense heritability, indicating the good prospects of these traits for genotype selection in *Eucalyptus* hybrid breeding programmes. Similarly, the significant positive correlation of fibre parameters with TC, AV, DMOE and negative correlation with lignin indicate that the fibre traits can be improved by the selection of genotype for improved TC, AV and DMOE and low TL content. AMMI documented insignificant G×E interaction for FD, LD, DWT, AV and DMOE traits suggesting the possibility of selecting these traits for the selection of stable genotypes across locations. However, if the traits are analysed individually it could result in

selection bias, since few of the traits could be negatively correlated. Hence, selection of stable and superior genotypes across multiple environments using the MTSI and WAASBY index can be a viable strategy in tree breeding programs. In the present study, four hybrid clones including C343, C327, C246 and C161 were selected based on 14 wood property traits. The identified superior and stable hybrid genotypes can be used as genitors in the *Eucalyptus* breeding programs.

Statements and Declarations

Conflict of interest: The authors declare that no conflict of interest could have appeared to influence the work reported in this paper.

Author Contributions: ABMP, MM, NK, SSC performed the phenotyping for wood property traits, JK, MM, performed the phenotyping for fibre biometry, BN, AM conducted the controlled hybridization, DR, VP, SS, VKWB conducted the field trials, VS identified the parents, ABMP performed the statistical analysis and prepared the manuscript and MGD designed and planned the experiment and finalized the manuscript. All authors have approved the manuscript.

Data Archiving Statement: This manuscript has no associated data.

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