Early genetic evaluation of morphology and some wood properties of *Tectona grandis* L. clones

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Abstract

An early genetic evaluation of morphology and wood properties of *Tectona grandis* L. (teak) used two 4-yr-old trials with 36 clones x 3 blocks x 1 ramet (216 trees). Morphologic traits (breast height (DBH), heartwood (HWP), tree height) and some easily measured wood properties (specify gravity, tangential, radial and volumetric shrinkage; growth strain, and dynamic elastic modulus measured in standing tree, in logs, in green lumber and in dried lumber) were evaluated to establish clonal variations and their heritabilities. The broad-sense heritability ($\hat{H}^2$) is greater than 0.3 for *DBH*, radial and volume shrinkage, growth strain and dynamic elastic modulus of standing trees and logs. *DBH* and tree height were not genetically correlated with any wood properties, although *DBH* was genetically correlated with tree height and the dynamic elastic modulus in dried-lumber. According with above results, the evaluation of heritability and genetic control of wood properties is limited when it is evaluated in the juvenile stage of *T. grandis* clones. However morphology (*DBH* and tree height), and two wood properties (radial and tangential shrinkage) and the dynamic elastic modulus of dried-lumber present opportunities in the heritability or genetic control values in juvenile and they can be introduced in the genetic program.

Key words: early evaluation, correlation genotypic, heritability.

Introduction

Teak is a tropical species that is widely planted in Costa Rica (PÉREZ and KANINNEN, 2005). It is a species with potential to produce high quality wood (BHAT, 2000; BHAT et al., 2001) because of its good physical and mechanical properties (MOYA and PÉREZ, 2008) and color, which set market acceptance (TEWARI, 1999; THULASIDAS et al., 2006; ZOBEL and SPRAGUE, 1998). In clonal plantations wood quality is influenced by intensity of management and correct selection of clone phenotypic characteristics (height, diameter, and morphology) (GALLOWAY et al., 2001; PÉREZ and KANINNEN, 2005).

Traditionally morphological characteristics of trees, such as diameter and height have been used as the main predictors of individual internal characteristics (ZOBEL and VAN BUIJTENEN, 1989; ZOBEL and SPRAGUE, 1998). In recent years, the genetic selection of plus trees have been used for wood properties selection (CALLISTERY and COLLINS, 2008).

General evaluations of wood properties are limited and restricted to trees over 8 years old (BHAT and INDIRA, 2005; INDIRA and BHAT, 1998; RAO and SHASAHIKALA, 2003; NANARAYAN et al., 2009). However, assessments at an early age (PANDE and SINGH, 2005; SOTELO et al., 2007a and 2007b; WEBER and SOTELO, 2008) using non-destructive techniques (GRABIANOWSKI et al., 2006; LINDSTROM et al., 2004; MOYA and MARÍN, 2011; SOTELO et al., 2007a) should permit genetic evaluation without inhibiting tree growth.

Assessment of wood properties, their correlation with morphological characteristics and changes as the tree gets older (GOH and MONTEUUIS, 2005; SOTELO et al., 2007a and 2007b) are needed to determine the best age for genetic selection of individuals. For example, the study 39 month-old *Calycophyllum grandiflorum*, demonstrated that it would be suitable for structural uses (SOTELO et al., 2007a).

Considering the importance of *Tectona grandis*, the present work examined the genetic control of morphological characteristics of the tree and the wood coming from plantations of fast-growing trees. Diameter at breast height (*DBH*), diameter of the second log and total height of tree were the primary morphological traits assessed. Dynamic modulus of elasticity at different stages of processing (standing tree, logs and green and dry lumber), specific gravity, longitudinal growth strains and shrinkages (radial, tangential, and volumetric shrinkage) were the wood quality attributes that were assessed. Gathering such phenotypic and genotypic data will help in future prediction and development of clonal plantations from an early age.

Material and Methods

Trees samples: Trees were taken from two trials located in Costa Rica's northern region. Both sites belong to Grupo Ecodirecta S.A. The first trial is situated in the district of Los Chiles, in the village of Combate (N10° 57' 36" and W84° 35' 30"). There is no well-defined dry season. The soil is an ultisol-type soil, with an umbricepipedon and argillic horizon and a moderate to high acidity with an acid saturation greater than 30% and a slope of less than 3% with regular surface and

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without erosion. The second trial is located in the district of Pocosol, in the village of San Cristobal (N10°49'47" and W84°27'54"). At this site also, there is no well-defined dry season. The soil is an ultisol-type soil, with an argillic horizon and acidity varies slightly between acid and neutral. The topography is irregular with slope variations ranging between 15 and 30%. Both sites have an average annual rainfall of 2592.5 mm and a mean annual temperature of 25.3 °C.

Trial Characteristics: The trees were 4 years old at the time of sampling, which corresponded to a first genetic thinning. Trials used a randomized complete block design with 3 blocks of 684 trees each; each block had all 36 clones. Plus trees were selected from throughout regular plantations (older than 5 years old) in northeastern Costa Rica, based on growth rate and stem quality. Average selection rate was 1 plus tree per 25 individuals. Trees were cloned directly by taking stem sprouts and, in some cases, collecting stump sprouts after felling the selected trees. Propagules (cuttings) were brought to greenhouse facilities and rooted (MURILLO and BADILLA, 2004). Once all plus trees had been vegetatively propagated, small clonal gardens were established and utilized in multiplication of all materials for establishing genetic tests. Each clone was repeated 18 times at 3 x 3 m spacing between trees (36 clones x 18 repetitions x 3 blocks = 2052 trees) in each block.

Sampling: six trees were selected for each clone (1 tree x 3 blocks x 2 sites) for a total of 216 trees. Of the trees marked for thinning, the best ones were selected. The selected trees had straight trunk, normal branching, and no disease or pest symptoms. Prior to tree felling, the diameter a breast height (*DBH*), total height (*h*), and transverse and longitudinal ultrasound velocity were measured (USV_T and USV_L respectively). The trees were then cut to obtain a 230 cm log (from the stump to a height of 230 cm), and immediately above that a second log 180 cm long. End diameter of the second log was measured and it was named as diameter of second log (d_2). A 3 cm thick disc was extracted from the lower end of each log.

Ultrasound velocity (*USV*) under bark was first determined in the standing tree along the longitudinal and radial directions using SYLVATESTDUO ultrasound equipment with 22 kHz transducers. After felling two logs were extracted and *USV* was measured in the first log. The log was sawn and *USV* was measured in the green lumber. Finally the lumber was kiln dried and the *USV* was remeasured. *USV* was calculated by time of ultrasound propagation (Equation 1) and they were measured according to this methodology:

1. Standing trees: Before felling, their north-facing side was marked and times of ultrasound pulse propagation in longitudinal and transversal direction were obtained. The longitudinal ultrasound pulse propagation time was determined on the north- and south-facing sides of the tree and was measured over a 130 cm-long section, from 30 cm above ground level to a height of 160 cm with the probes inclined at 45 degrees. In the transverse direction the ultrasound pulse was measured at the breast height (*DBH*) in north-south and west-east direction.

2. Logs: Ultrasound pulse propagation in the longitudinal direction of the first log was measured at three radial points (10%, 50% and 95% from the pith) on the exposed ends on the north side of the log and values were averaged (*Figure 1a*).

3. Green lumber: the first log was sawn to obtain a 3 cm-wide plank that contained the same points of measurement for time of ultrasound as those in the log (*Figure 1b*). The time of ultrasound pulse propagation was determined immediately after obtaining the lumber and therefore, corresponded to green wood.

4. Kiln-dried lumber: The wood was dried for approximately 10 days to obtain an equilibrium moisture content of 12%. The planks were then taken from the kiln and left to rest for 24 hours so that measurements were obtained at room temperature. The points of measurement were the same as those used in logs and green wood (*Figure 1b*).

Ultrasound velocity and dynamic elastic modulus (*E*): The *USV* was obtained using to Equation 1, while the longitudinal and transversal dynamic elastic modulus in standing trees (E_T and E_L, respectively), dynamic elastic modulus in logs (E_{log}), dynamic elastic modulus in green lumber (ED_{lumber}) and dry lumber (ED_{dried}) were derived from Equation 2. For standing trees and logs green density was used in Equation 2. In the case of green and dry lumber, a 2 cm x 2 cm x 2 cm wood sample was taken from the section where *USV* was measured (*Figure 1b*). Weight and volume were determined for this sample using the water displacement method specified by standard ASTM D-2395-02 (ASTM, 2003a).

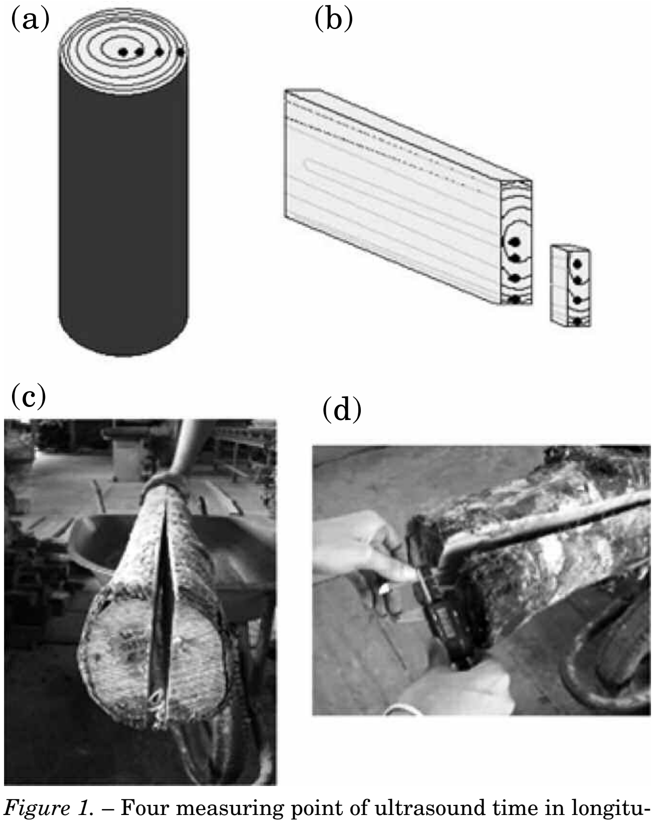

Figure 1. – Four measuring point of ultrasound time in longitudinal direction in log (a), and four measuring point in lumber (b) with SilvaTest Duo and log sawed (c) and opening measurement from young trees of *Tectona grandis*.

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$$V = \frac{L}{T} \quad (1)$$

$$ED = V^2 \times d \times 10^{-6} \quad (2)$$

Where:

V = ultrasound velocity in m s^{-1}

L = sample length in meters

T = time required by ultrasound pulse propagation to travel from one end of board to the other in µs

ED = dynamic elastic modulus in GPa

d = wood density in kg m^{-3}

Longitudinal growth strain was measured on the second log using the procedure described by CHAUHAN and ENTWISTLE (2010). The log was cut longitudinally along the centre-line, from end to end (*Figure 1c*) using a band saw. On being split in two, the relaxation of inherent growth stresses (compressive stresses at the core and tensile stresses at the periphery) results the two half-rounds bending away from each other. The two halves were clamped together at the mid-point and the outward "log-opening" measured using a digital caliper (*Figure 1d*). The log opening data was used to estimate longitudinal surface growth strain according to equation 3, as proposed by CHAUHAN and ENTWISTLE (2010):

$$\varepsilon = \frac{Yu \times Ravg}{0.87\ x\ L^2} \quad (3)$$

Where:

ε = longitudinal growth strain

Yu = free end deflection

$Ravg$ = average diameter between the smallest and largest diameter

L = length log

Heartwood percentage and physical properties of the wood: Heartwood percentage (*HWP*) was determined in the 3 cm disc cut from the base of the tree. Diameter (over bark) was measured as well as heartwood diameter in two directions (north-south and east-west). *HWP* was calculated using total heartwood area in relation to the total disk area expressed as a percentage.

Radial (*RS*), tangential (*TS*), and volumetric shrinkage (*VS*) and specific gravity (*SG*) were determined using the disc cut from the bottom of the second log. A 3 cm-wide block was cut along the center, from north-south (including the pith), of each disc and divided into two subsamples (cut into half). The east and west sides of the disc were used to measure *RS* and *TS*. Refer to *Figure 1* (MOYA and PÉREZ, 2008) for details regarding type of sample cut. The weight and volume of both diametral subsamples were determined when green according to standard ASTM D-2395-02 (ASTM, 2003a) and then the samples were kiln dried at 105 °C for 24 hours to determine the weight and volume of dry wood. The green and kiln-dried weight and volume were used to calculate *SG* and *VS*. Sample dimensions for *RS* and *TS* complied with standard ASTM D-143-94 (ASTM, 2003b).

Statistical Analysis: Average values were obtained for the variables measured and the data was tested for normal distribution using the SAS System PROC UNIVARIATE procedure Version 8.1 for Windows (SAS INSTITUTE, 1997). The normality distribution and homogeneity of variances of data was examined and some transformations were necessary for some variables. Logarithmic transformations were applied to *DBH*, *TS* and ED_L. In the case of *SG* and ED_{log}, an x^2 transformation was required; an inverse transformation (1/x) was used for *RS* and *GS*; *VS* was transformed with $x^{-1.5}$; and ED_{dried} with $x^{1.5}$.

The mixed linear model was used in the analysis of variance of wood properties (Equation 4). The model included the following sources of variation: clone (c), site (s), the interactions between clone and site and block within site (Equation 4).

$$Y_{ijk} = \mu + c_i + s_j + c*s_{ij} + s(b)_{jk} + e_{ijk} \quad (4)$$

where Y_{ijk} is the single observation of each wood property of the ijkth-tree, μ is the overall mean, c is the i^{th}-clone random effect, s is j^{th}-site fixed effect, $c*s_{ij}$ is the random interaction between the i^{th} clone and the j^{th} site and $s(b)_{jk}$ is the fixed effect of k^{th} block within j^{th} site, and e_{ijk} is the residual random effect. The GLM procedure from SAS (SAS INSTITUTE, 1997) was applied to estimate the significance of sources of variation.

Estimates of variance components were obtained using model 23 of SELEGEN software (random block: test of clones with one ramet per trial in two sites) (RESENDE, 2002). Broad-sense heritability was estimated for wood variables based on equation 5:

$$\hat{H}^2 = \frac{\hat{\sigma}^2{}_c}{\hat{\sigma}^2{}_c + \hat{\sigma}^2{}_{c*s} + \hat{\sigma}^2{}_e} \quad (5)$$

where $\hat{\sigma}^2_c$, $\hat{\sigma}^2_{c*s}$ and $\hat{\sigma}^2_e$ are variance components for clonal, GxE interaction (clone by site), and error or residual effects, respectively. The phenotypic Pearson correlation matrix was obtained using PROC CORR of SAS software (SAS INSTITUTE, 1997). The genotypic correlation was calculated with model 103 of SELEGEN software on within clone values. After the removal of environmental effects, genetic correlations among all wood traits were estimated (Equation 6) through SELEGEN software again (RESENDE, 2002). And their significances were tested using t-student test (Equation 7).

$$r_{a(x,y)} = \frac{\mathrm{cov}_{\hat{a}(x,y)}}{\hat{\sigma}_{\hat{a}x}\hat{\sigma}_{\hat{a}y}} \quad (6)$$

$$t = \frac{r_{a(x,y)}}{\sqrt{\frac{1 - r_{a(x,y)}}{N-2}}} \quad (7)$$

where, $\mathrm{cov}_{\hat{a}(x,y)}$ is the genetic covariance between traits "x" and "y", while $\hat{\sigma}_{\hat{a}x}$ and $\hat{\sigma}_{\hat{a}y}$ are the genetic standard deviations (square roots of variances) of trait "x" and trait "y" respectively.

Results and Discussion

Effect of site and clone on wood properties

The effect of the variables site and clone, the block and their interactions on morphological properties of the tree and the wood is shown in *Table 1*. Despite the fact

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that the trials were located in similar geographical areas with similar climatic conditions (temperature and rainfall), soil properties and chemical properties, there were significant differences between sites ($p > 0.01$) in the majority of properties, with the exception of the *RS* and *TS*, where the site was not statistically significant (*Table 1*). Note that *DBH* and *h* separately were affected significantly by the site as were the wood properties *VS*, ED_T, *SG*, ED_{lumber} and ED_{dried}. Nevertheless, the site explained less than 12.75% of the variation of these properties. While in the case of *h*, d_2, heartwood, ED_L and ED_{log}, the site explains the variation of data in the range of 19.57% to 36.54% (*Table 1*).

MOYA and PÉREZ (2008) explored the effect of soil fertility on wood properties of *T. grandis* in mature trees and concluded that the chemical soil composition affects many physical properties of wood which they attributed to variations in soil fertility. There is topographical and soil characteristics differ among the studied tests. The experiment "Combate" presents a regular topography, with a soil type umbricepipedon and argillic horizon with high saturation of acidity, and on the other hand "San Cristobal" presents ultisol-type soil, with an argillic horizon and pH tend to be neutral.

Numerous studies with clones of coniferous species report the effect of site on wood properties in older trees (GAPARE et al., 2010; HANNRUP et al., 2004; ZOBEL and VAN BUIJTENEN, 1989) but there has been less work on tropical hardwood species most notably with *Guazuma crinita* (WEBER and SOTELO, 2008), *Dalbergia sissoo* (PANDE and SINGH, 2005), *Calycophyllum grandiflorum* (SOTELO et al., 2007a), *Bombacopsis quinata* (HODGE et al., 2002) and *Alnus acuminata* (HERNÁNDEZ and RESTREPO, 1995), which are consistent with the effect of sites found in this work. Specifically in *T. grandis* in mature trees (14 years old), INDIRA and BHAT (1998) showed that site has a great influence on wood density.

The *DBH*, *h*, *HWP* and *SG* show statistically significant differences ($\alpha < 0.01$) between sites for 4 yr-old trees of *T. grandis* and the variance of data for these parameters ranged from 12.75% to 36.54%. Several studies in others tropical species in juvenile stage had found similar differences in these properties of clones according to the site, for example, 8 yr-old *Dalbergia sisso* (PANDE and SINGH, 2005) and < 18 month-old clones of *Guazuma crinita* (WEBER and SOTELO, 2008). However with 39 month-old clones of *Calycophyllum grandiflorum*, there were no significant differences in density between sites (SOTELO et al., 2007a).

Other properties such as *RS*, *VS* and several types of *ED* introduced differences between sites with variance between 2 and 12.75%. This variance can be attributed

Table 1. – Estimated variance component a broad sense-heritabilities in 4-year-old *Tectona grandis* clones from two sites northern Costa Rica ($n = 216$).

Wood properties	Site effect (d.f.=1)		Clone effect (d.f.=35)		Clone x Site effect (d.f.=35)		Site(Block) (d.f.=2)		Error (d.f.=142)		Broadsense heritability*	
	F-valor	% Var	F-valor	% Var	F-valor	% Var	F-valor	% Var	MS	% Var	H^2	CV %
DHB (Log10)	72.3**	32.0	2.7**	10.3	1.5^{ns}	7.4	1.7^{ns}	1.0	0.0	49.3	0.36	5.5
HWP	48.3**	28.5	1.5^{ns}	4.7	1.1^{ns}	1.4	0.5^{ns}	0.3	65.5	65.0	0.27	14.5
d_2	37.8**	19.6	2.9**	14.9	1.4^{ns}	6.7	1.3^{ns}	0.4	2.7	58.4	0.53	7.7
h	106**	36.5	2.0**	2.1	1.7*	9.6	10.0**	10.3	2.2	41.4	0.15	2.7
SG (x^2)	22.4**	12.7	1.3^{ns}	4.9	0.8^{ns}	4.4	3.6**	5.3	$7.6x10^8$	72.8	0.18	1.2
RS (1/x)	0.40^{ns}	0.1	1.7**	13.4	0.7^{ns}	7.6	0.8^{ns}	0.4	0.0	78.5	0.47	14.8
TS (Log10)	1.6^{ns}	0.2	1.4^{ns}	2.3	1.3^{ns}	8.3	1.1^{ns}	0.2	0.0	88.9	0.05	2.2
VS ($x^{-1.5}$)	7.2**	4.3	1.6*	9.6	0.9^{ns}	1.9	1.7^{ns}	1.5	$3.8x10^{-5}$	82.6	0.44	4.9
GS (1/x)	0.22^{ns}	0.1	1.4^{ns}	18.5	1.7*	22.3	3.3*	5.0	$2.6x10^3$	54.0	0.02	1.2
ED_T	18.8**	2.3	1.5*	3.4	1.2^{ns}	4.2	14.9**	25.1	$7.8x10^5$	65.0	0.21	7.9
ED_L (Log10)	57.6**	26.7	1.4^{ns}	2.2	1.2^{ns}	4.1	6.9**	9.4	0.2	57.5	0.04	12.7
ED_{log} (x^2)	38.7**	24.8	1.0^{ns}	1.3	0.9^{ns}	2.9	1.0^{ns}	0.1	3.5	70.9	0.02	0.9
ED_{lumber}	11.5**	6.9	2.1**	6.5	1.6*	13.8	0.5^{ns}	1.0	$1.1x10^6$	71.8	0.26	2.0
ED_{dried} ($x^{1,5}$)	16.3**	11.3	1.7*	8.7	1.1^{ns}	1.7	0.4^{ns}	1.3	$1.3x10^{14}$	76.9	0.15	2.1

* statistically significant at 95% confidence level, *NS*: not significantly different, *DBH* = diameter at breast height, *HWP* = heartwood percentage, d_2 = diameter of second log, *h* = Tree height, *SG*: specific gravity, *RS* = Radial shrinkage, *TS* = Tangential shrinkage, *VS* = Volume shrinkage, *GS* = growth strain, ED_T = transversal dynamic elastic modulus in standing tree, ED_L = longitudinal dynamic elastic modulus in standing tree, ED_{log} = dynamic elastic modulus in log, ED_{lumber} = dynamic elastic modulus in green lumber, ED_{dried} = dynamic elastic modulus in dry lumber, Var = variance, CV = coefficient of variation.

** Statistically significant at 99% confidence level.

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to the difference in fertility between sites (MOYA and PÉREZ, 2008). The mechanical resistance (stiffness) of wood is influenced by the composition and distribution of anatomical elements of wood which in turn are determined by the conditions of growth, management and fertility – conditions that also define tree development (ZOBEL and VAN BUIJTENEN, 1989). The variation between sites of different type of *ED* can be attributed to differences in the composition and distribution of the anatomical elements of wood and they are influenced by soil fertility (MOYA and PÉREZ, 2008).

With regard to clones, there was a highly significant genetic effect for *DBH*, *h*, ED_{lumber} and *RS* ($\alpha < 0.01$). In the case of ED_T and *VS*, they have significant differences at *P-value* < 0.05. Similar situation happens with site effect, the variance of data for clone effect is very low for those parameters of wood, which varied between 2.11% and 13.38% (*Table 1*). Studies related to genetic component for wood properties are limited and many of them are focus on morphological characters of the tree in mature stage, such as *DBH* and *h* (SÁNCHEZ et al., 2005; CALLISTER and COLLINS, 2008) or properties of wood like *HWP*, *SG*, *VS* and *ED* (BHAT and INDIRA, 2005; CHERRY et al., 2008; DUNGEY et al., 2006; HANNRUP et al., 2004; KUMAR, 2004; SOTELO et al., 2007a and 2007b, NANARAYAN et al., 2009) for older trees.

However, some recent studies carried out with *C. grandiflorum* (SOTELO et al., 2007a and 2007b) and *D. ssiso* (PANDE and SINGH, 2005) found that the properties of wood changed significantly between clones in the juvenile stage. LINDSTROM et al. (2004) discussing the use of clones of *Pinus radiata* mention that there is a genetic selection potential of juvenile wood using *ED*, which is also consistent with the data obtained for ED_{lumber}, ED_{dried} and ED_T of 4 yr-old *T. grandis* in this study.

The interaction site × clone presented a statistically significant effect for *h*, *GS* and ED_{lumber} ($p < 0.05$), explaining the total data variance between 9.59% and 13.79%, similar to the weak interaction found in 19 yr-old clones of *Picea abies* (HANNRUP et al., 2004). In contrast, SOTELO et al. (2007) did not find any influence of the interaction clone × site for ED in families of 39 month-old *C. grandiflorum*. In summary the interaction clone × site on ED_{lumber} should be taken with great caution, because this interaction was not present in other measurements of *ED*, and in this circumstance could be present on ED_{lumber} due to a random effect of the variables.

On a uniform site the layout of blocks should have no effect on morphological features or wood properties. This is not always the case. The effect of block within sites was also examined (*Table 1*) and it was found that the variables *h*, *SG*, ED_T and ED_L were affected significantly ($p < 0.01$) by the block effect within site. For these properties of wood, the variance accounted for 3.64 to 14.90% (*Table 1*). A less significant relationship ($p < 0.05$) was presented for the *GS*; however this variable only explains 2.70 of the variance of data (*Table 1*). In a genetic study conducted by MOYA and MARÍN (2011) for 10 yr-old *T. grandis*, there were no effects due to block on wood properties. Those findings slightly contradict the results obtained in the present study with young trees as mentioned. Some morphological parameters and mechanical resistance of the tree (ED_T and ED_L) were affected significantly. This may be due to a deficiency of the experimental design of the blocks test, either the blocks were not properly distributed within site or the site was too variable.

Finally it was observed that the variance due to the error varied from 41.41% to 88.95%, where the lowest percentage of variance is for *HWP* and *h*, with 49.33% and 41.41% respectively. The greater dispersion of data is obtained for the shrinkages where the model produces a variance of data between 78.52 and 88.95%. Silvicultural variables such as d_2 and *h* are affected by site and clone; the model can predict more than 50%, while variables such as shrinkages did not predict a significant percentage (*Table 1*). Then, variables such as those can be affected by inherent characteristics of anatomical composition of wood, as opposed to other variables that are susceptible to management and control of both silvicultural and genetic.

According to above analysis, the results indicate that it is possible to establish the differences in all morphological properties and wood, with the exception of the ratio *d/h*, *RS* and *VS*, between sites at an early age teak clones and this results aggress with other tropical species in mature stage. Thus the practical implications of the evaluation in juvenile stage of clones can shorten the time to know the differences of wood properties among sites.

Heritability of wood properties

Heritability ($\hat{H}^2$) in a broad sense is obtained for each of the parameters of the tree and wood properties are detailed in *Table 1*. It is possible to note that only two morphological variables (*DBH* and d_2), and other 2 properties of wood (*RS* and *VS*) have a value of $\hat{H}^2$ greater than 0.3 a similar value of 0.38 reported in "ramets" 3.5 years old of *T. grandis* (CALLISTER and COLLINS, 2008). While, variables such as *h*, *SG, TS, GS*, ED_L and ED_{log} present values of H^2 low, less than 0.3 (*Table 1*). Although these are considered to be low, they are relevant for the manifestation of character for future "ramets" (CALLISTER and COLLINS, 2008). In a study with clones of 3.5 years old *T. grandis*, CALLISTER and COLLINS (2008), SWAIN et al. (1999) and NARAYANAN et al. (2009) have found a value of $\hat{H}^2$ of 0.28, 0.38 and 0.34, respectively for tree height, which authors considered low but relevant. But SWAIN et al. (1999) found too high $\hat{H}^2$ with 12 years old trees. These reported values are greater than the one obtained in this study with trees of 4 years of age. This difference can be attributed to the trial in the study of CALLISTER and COLLINS (2008), because they used more trees (N = 696) in comparison with the sampled in this study (N = 216) and higher number of ramets per clone which improves the level of prediction and also the estimate of heritability in general.

There are genetic studies about *HWP* in *T. grandis* and in hardwood species overall (MURILLO and BADILLA, 2004; MOYA and MARÍN, 2011), in spite of the commercial

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importance of this property, it requires analysis to identify patterns of heritability and consider it as a criterion for selection (MURILLO and BADILLA, 2004). For example KJÆR et al. (1999) and VARGHESE et al. (2000) found that heartwood were significantly different between provenances in mature trees. Heritability of 0.27 is low for *HWP* but similar in families of *T. grandis* of similar age (MURILLO and BADILLA, 2004). But NARAYANAN et al. (2009) found high heritability ($\hat{H}^2 = 0.77$) in the *HWP* for 27 year old trees. Nonetheless, this low heritability found in our study or those obtained by CALLISTER and COLLINS (2008) in 4- year-old *T. grandis* should be taken with great caution. According to FUJIMOTO et al. (2006), genetic control increases with age. Other studies with teak trees more than 10 years of age confirm this statement (HARSHAP and SOERIANEGARA, 1977; MOYA and MARÍN, 2011; RAO and SHASHIKALA, 2003).

There were significant difference in *RS* and *VS* between two sites sampled and the $\hat{H}^2$ was greater than 0.47 (*Table 1*). Differences in shrinkage due to planting sites have been reported in *T. grandis* by MOYA and PÉREZ (2008) and MOYA et al. (2011), however scarce references mentioned $\hat{H}^2$ of these shrinkage, with exception of MOYA and MARÍN (2011). SOTELA et al. (2007b) studied 39 months old *C. grandiflorum* (tropical species) and found heritability over 0.29 in radial, tangential and volume shrinkage, which are similar to that found in the present study (*Table 1*). Considering only the $\hat{H}^2$ of these shrinkages, selection would be most effective in juvenile stage if based on other wood properties, as wood density, because they did not present any important heritability. Shrinkage is one of the most important properties of dimensional stability of wood (SOTELA et al., 2007b), then tree selection with low shrinkage values can contribute to superior dimensional stability lumber, especially if they extracted from plantation in juvenile stage. However, this performance can be changed in mature stage.

With regard to the mechanical resistance (stiffness) of wood in different degrees of processing, it was found that ED_{lumber}, ED_{dried} and ED_T possess low heritability, less than 0.3 (*Table 1*). These results are conflicting with those obtained by MOYA and Marín (2011) for 10 years old trees, which registered a H^2 of 0.34 in dry wood. Inheritance of *ED* have been investigated during the last decade mainly concentrated in temperate species (CHERRY et al., 2008; DUNGEY et al., 2006; HANNRUP et al., 2004; KUMAR, 2004) and only few of them were on tropical hardwood species (CALLISTER and COLLINS, 2008; SOTELO et al., 2007a; WEBER and SOTELO, 2008). In general, these studies reported similar heritability numbers compared to those found in clones of *T. grandis*; for example *ED* values from 0.14 to 0.17 in 19-year-old clones of *Picea abies* (HANNRUP et al., 2004), from 0.22 to 0.31 in 39 months old *C. grandiflorum* (SOTELO et al., 2007b) and 0.30 in mature douglas fir (CHERRY et al., 2008), 0.01 to 0.40 in 21 years old *Pinus radiata* (DUNGEY et al., 2006; GAPARE et al., 2010; KUMAR, 2004).

According to the results obtained here, heritability of wood properties is low when it is evaluated in juvenile stage of *T. grandis* clones. But some important morphologic (*DBH* and d_2), and two wood properties (*RS* and *VS*) present promissory results in the heritability values in juvenile stage.

Genotypic correlation

The characteristic of the tree was not genetically associated to other properties of wood (*Table 2*); but they were genetically correlated between them, with the highest coefficients, from 0.73 to 0.79. These results confirmed the low heritability of wood properties in juvenile

Table 2. – Genotypic correlations among morphological tree parameters, wood properties and dynamic elastic modulus in 4-year-old *Tectona grandis* clones from two sites in Costa Rica ($n = 216$).

	DBH	d_2	*H*	HWP	*SG*	*RS*	*TS*	*VS*	*GS*	ED_T	ED_L	ED_{log}	ED_{lumber}	ED_{dried}
DBH	1													
d_2	0.93**	1												
h	0.79*	0.73*	1											
HWP	-	-	-	1										
SG	-	-	-	-	1									
RS	-	-	-	-	-	1								
TS	-	-	-	-	-	-	1							
VS	-	-	-	-	-	-	-	1						
GS	-	-	-	-	-	-	-	-	1					
ED_T	-	-	-	-	-	-	-	-	-	1				
ED_L	-	-	-	-	-	-	-	-	-	-	1			
ED_{log}	-	-	-	-	-	-	-	-	-	-	-	1		
ED_{lumber}	-	-	-	-	-	-	-	-	-	-	-	-	1	
ED_{dried}	-	-	-	-	-	-	-	-	-	-	-	-	0.76*	1

Numbers in boldface statistically significant (* denotes $p < 0.05$; ** denotes $p < 0.01$) based on Equation 6 for genotypic correlations.

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stage of *T. grandis*, mentioned previously. The absence of any significant genetic correlation between morphological traits and wood properties observed in this study contradicts with other studies carried out at juvenile stage. For example, SOTELO et al. (2007a) reported genetic correlation of *DBH* with the parameters related to color of wood and elastic modulus in 4 years old *C. grandiflorum*. HANNRUP et al. (2004) also found high genetic correlation of *HWP* and *h* with some wood properties, including *SG* and *ED* 19 years old clones of *Picea abies*. The lack of significant genetic correlation between morphology and wood characteristic might be attributed to small number of sampling as only 6 ramets per clone (2 sites, 3 blocks and 1 ramete per block) were used for the study.

KUMAR (2004) and KUMAR et al. (2002) mention that the study of this variable should be continued and it should be very careful because most genetic programs are based on the selection of individuals for fast production and this has a negative impact on the mechanical properties of the tree (FUJIMOTO et al., 2006).

Among wood properties, only ED_{lumber} and ED_{dried} exhibited a significantly positive genetic correlation. This is expected as both represent the same property with only difference is in their moisture content. Shrinkage parameters (*RS*, *TS*, *VS*), specific gravity and stiffness parameters (*ED*) were found to be independent of each other with no genetic correlation.

This study shown that limited wood properties (*RS* and *VS*) and specific morphological characters of the tree such as *DBH* and *h* presented moderate genetic control and that none of the morphology characteristics are genetically correlated with any wood properties early ages for teak. The results suggest that for the selection of superior breeding material for wood quality, all the wood quality parameters needs to be assessed individually as they are not genetically correlated. However, this also implies that genotypes with superior wood quality could be selected at an early age without compromising on growth parameters. For that reason LINDSTROM et al. (2004) indicates that there is a genetic potential in young timber, because at early ages those trees are defining genetic relationships of importance such ED_{lumber} as it is the case in our study.

Heritability, however, increases or changes with age of trees, so it is important to continue the study at older ages and using mature wood to determine the best age to have a genetic selection. While in the present study with teak, comparison of the relationships of young and adult wood have not been done, other studies have made this comparison (FUJIMOTO et al., 2006) and they have concluded that it is possible to make an effective selection of clones at early ages without altering the quality of adult trees.

In general, genetic breeding programs have been assessed by evaluations of properties at ages close to 10 years. Although we have established important relationships between the properties of wood with morphological aspects or parameters of wood which are determined in a non-destructive way, it is also necessary to establish whether all measured variables are inherited from an early age to incorporate them more effectively in programs of reforestation with this species.

Conclusion

It is possible to establish the differences in all morphological properties and wood, with the exception of the ratio *d/h*, *RS* and *VS*, between sites at an early age teak clones. Thus the practical implications of the evaluation in juvenile stage of clones can shorten the time to know the differences of wood properties among sites. On the other hand, heritability of wood properties is limited when it is evaluated in juvenile stage. But *DBH*, d_2, *RS* and *VS* presents promising results in the heritability values at the juvenile stage. Finally, this study has shown that, none of the wood properties was genetically correlated with the morphologic characteristics at the early ages for teak. Thus, these characteristics could be used in breeding program in *T. grandis* to select superior genotypes to produce quality lumber at short rotation without having any significant impact on growth parameters.

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