Wood physical properties, color, decay resistance and stiffness in Tectona grandis clones with evidence of genetic control

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Abstract

Tectona grandis (teak) plantations are being produced with trees from genetic improvement programs, including clonal selection. However, limited information about inheritance of wood properties is available. For studying genetic parameters of T. grandis wood properties and stem diameter two 10-yr-old trials were studied involving nominally 2 sites x 20 clones x 3 replicates x 1 ramet. Clonal variation was observed in: heartwood (HWP), pit (PP) and bark (BP) percentages; green moisture content (IMC) and density (GD); tangential (TS), radial (RS) and volumetric (VS) shrinkage and ratio tangential-radial: shrinkage (ratio T/R); L*a*b* color parameters; and stiffness and specific gravity (SG). Some wood properties evidenced strong across-sites genotypic control. The higher broad-sense heritability estimates (over 0.36) were for PP, IMC, SG, TS, VS and L*a*, and b* color coordinates and stiffness. Low and non-significant values were estimated for HWP, BP, GD, RS, ratio T/R and decay resistance of supwood and heartwood to Trametes versicolor and Pycnoporus sanguineus. However, HWP showed marked clone x site interaction. Phenotypic and tentatively estimated genotypic correlations indicate that selecting faster-growing clones will improve some important wood properties, such as increasing HWP, and decreasing PP and BP, without affecting other wood properties. Selecting clones for denser wood, as expected, improved stiffness, should decrease IMC and affect negatively b* (yellow/blue) color. Clone selection with lower L*a* values could increase redness (a*) of wood.

Key words: teak, genetic parameters, broad-sense heritability, genotypic correlations, wood properties, heartwood color, wood decay.

Introduction

Among tropical forest species, teak (Tectona grandis L.f.) has become one of the most important in the market due to its physical, mechanical and aesthetic timber properties. Its excellent workability properties, strong decay resistance, excellent dimensional stability, and highly desired wood color, have allowed this tree species to become one of the most planted and marketable (Goh and Monteuuis, 2005). Today teak is being planted in Costa Rica as a solid-wood crop, with sitting, site preparation, breeding programs and management all rapidly improved in the last few years (Murillo, 2005). One of the most practical and effective strategies in improving productivity has been developing new plantations through clonal forestry (Xavier and Ottoni, 2009). Clonal deployment from properly developed breeding programs allows more uniform plantations, higher yield and shorter rotations, among other benefits (Monteuuis and Goh, 1999; Monteuuis and Maitre, 2007). More advanced breeding generations may provide better clone-to-site matching and disease resistance (Xavier and Ottoni, 2009).

Most teak breeding efforts have only addressed volume growth, stem quality, branch exertion angle, and buttress reduction, among other external traits (Goh and Monteuuis, 2005; Callister and Collins, 2008). Therefore, there is a major need to incorporate wood traits into breeding and plantation management procedures, in order to improve lumber prices in international markets. Some reports include heritability estimates for traits like wood quality, heartwood diameter, bark thickness, wood calcium and silica contents, and wood density and durability (Kjær et al., 1999 and 1996; Varghese et al., 2000). However, none of all these investigations has involved clonal material, but instead regular provenance and progeny tests.

Today, wood color is being considered as another important attribute in teak lumber coming from plantations, especially at the market (Thulasidas et al., 2006). Even though there are no reports in literature about teak on genetic control for wood color, other investigations report mixed findings for other tree species (Rink, 1987; Sotelo et al., 2008; Hannrup et al., 2004; Mosedale et al., 1996). Other wood properties, like shrinkage, density, durability and mechanical properties, have received great attention in breeding and clonal forestry (Zobel and Jett, 1995), but again, very little in the case of teak. Recent investigations on breeding for stiffness have shown that, using ultrasound techniques, it is possible to get the proper information for selecting trees with sufficient effective heritabilities (Solorzano et al., 2012b).

This research was aimed at generating new information about teak wood properties and their genetic control, especially in the following traits: specific gravity, green density, some tree traits (heartwood percentage
and bark thickness), wood shrinkage (tangential, radial and volume) color parameters (through CIE L*a*b* system), fungal decay, and stiffness.

Material and Methods

**Study site description:** The study involved in two teak clonal trials located in two different sites in northern Costa Rica. Site 1 (Garza) has an average rainfall of 1594 mm, a mean annual temperature of 26°C, and a 4-month dry season without rain. The soil is a loam, is moderately acid to neutral (pH 6-7) and moderately fertile but with low organic matter content, and the slope is less than 3%. Site 2 (Peñas Blancas) has an average rainfall of 1745 mm, a mean temperature of 27°C, and a 5-month dry season without rain. The soil has a loam to clay loam texture, is moderately acid (pH 5-6), and is moderately fertile soil with moderate organic matter content, while the slope is less than 3%.

**Tree selection and stand conditions:** Plus trees were selected as part of a breeding program at Precious Woods company throughout more than 2000 planted ha in northeastern Costa Rica, as well as from provenance trials (mostly asean origin) established in several sites. Therefore, selections comprehend quite a large genetic variation. Selection criteria were based mostly on growth rate and stem quality. Selected trees were cloned directly by taking stem sprouts and, in some cases, collecting stump sprouts after felling them down. Propagules (cuttings) were brought to greenhouse facilities and rooted (VÍQUEZ and PÉREZ, 2005). Once all plus trees were vegetatively propagated, small clonal gardens were established within a greenhouse and utilized in multiplication of all materials for establishing genetic tests. Clonal trial age was 10 years at the time of this investigation, which corresponds to the second commercial thinning. Clonal trial cites were used by cattle in the past. Originally, the experiment included 40 clones planted in five blocks, with two single ramets randomly distributed within each block (Figure 1a). This resulted in a total of 80 trees per block at 3 x 3 m spacing with uniform spacing between road and columns. The trials had a 50% thinning at age 5, but including mortality, only 20 from the original 40 clones remained with most of their trees alive in good conditions at age 10. Therefore, the clones that were included in this investigation were the ones with the largest number of standing trees at all three blocks within each of the two sites, aiming to ensure some statistical balance in data. Thus, clones with the best possible representativeness in both trials was their main selection criteria for this investigation. Some more detailed information about the sampled trees was included in Table 1.

**Sampling procedures:** One tree from each clone in the first three blocks at each site was selected, that is, 1 tree per clone x 2 sites x 3 replicates (a total of 6 trees per clone). Trees felled had straight trunks, low branching thickness and near 90° insertion angle, and non visible disease or pest symptoms. The north-facing side of each tree was marked before being felling down. Then a 100 cm-long log sample was taken from 0.3 m to 1.3 m (Figure 1b). Additionally, two 3 cm-thick discs were obtained at DBH. A full-length 3 cm-thick diametric section was cut from the log from north to south (Figure 1b). These samples were conditioned at 22°C and at a relative humidity of 66%, in order to obtain a 12% equilibrium moisture content. Several wood samples exhibiting knots, evidence of rot, or any other defects, had to be discarded since they could interfere with ultrasonic waves used within the probe.

**Heartwood, pith and bark percentage determination:** These traits were determined on each stem cross-section. Heartwood and pith diameter were obtained from the average of two complete cross-sectional measurements (direction north-south and east-west). The total mean diameter (with and without bark) was calculated following the same procedure. Bark thickness was defined as half the difference between inside and outside-bark diameters. The sectional area of each component was determined as an assumed circle and the

![Figure 1. – Wood probes sampling procedure for testing wood properties in teak clonal investigation.](image-url)
corresponding percentages calculated. Heartwood percentage (HWP) was obtained by the average of two heartwood diameters related to total inside bark-area. Pith percentage (PP) and bark percentage (BP) were then obtained through its proportion with respect to total inside-bark disc area.

**Determining ultrasound velocity and dynamic stiffness:** Longitudinal ultrasound velocity measurements were taken on the diametric boards cut from the logs along a radial transect at four distances from the pith (near to pith, midway between pith and sapwood/heartwood boundary, sapwood/heartwood boundary, and halfway into sapwood thickness). The time required by the wave to travel from one end of the board to the other was measured twice at each distance. Tests were conducted using SYLVATESTDUO ultrasound equipment with two 22 kHz transducers. This device was set to four readings per measurement. Ultrasound velocity was calculated (Equation 1) and dynamic stiffness (Ed) by Equation 2. In order to calculate density, a 2x2x 2 cm sample was extracted from where ultrasound velocity was measured. This sample was used to calculate weight and volume using the water displacement method as specified by D2395 (ASTM, 2003).

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

\[
Ed = V^2 \times d \times 10^{-6} \quad (2)
\]

Where: \(V\) = ultrasound velocity in m s\(^{-1}\), \(L\) = sample length in meters, \(T\) = time required by ultrasound wave to travel from one end of board to the other in µs, \(Ed\) = dynamic stiffness in GPa and \(d\) = wood density in kg m\(^{-3}\).

**Wood color determination:** In order to determine wood color, a cross-section was taken at DBH and a 3 cm-wide diametric section was cut (Figure 1b). Then a 2x2x 2 cm sample was produced at the same four distances (near to pith, midway between pith and sapwood/heartwood boundary, sapwood/heartwood boundary, and halfway into sapwood thickness) from the pith as for ultrasound velocity determination. A nominal total of 960 specimens (8 per cross-section x 3 replicates x 20 clones x 2 sites) were obtained from the sampled clones. Wood color was determined on the block's tangential face in accordance with ASTM D-2244 (ASTM, 2005). A HunterLab Miniscan® XE Plus spectrophotometer was used. Measurements were taken at room temperature and color characteristics were determined using CIELab system (parameters \(L^*\), \(a^*\), and \(b^*\)). Measurement range was from 400 to 700 nm, with a 13 mm aperture at the measurement point. Specular component (SCI mode) was included to observe reflection at a 10° angle, which is normal for this specimen surface (D65/10), as well as a 2° field of vision (standard observer, CIE 1931), and standard D65 illumination (corresponds to daylight at 6500 K). According to HUNTERLAB (1995), CIELab color system estimates wood color in three coordinates: \(L^*\) for lightness represents the position on the black-white axis (\(L^*=0\) for black, \(L^*=100\) for white), \(a^*\) for chroma value and defines the position on the red-green axis (+100 values for red shades, −100 values for green shades), and,
b* for chroma value and defines the position of yellow–blue axis (+100 values for yellow shades, –100 values for blue shades).

**Decay resistance:** Wood specimens measuring 2.5 x 2.5 x 2.5 cm were obtained from each wood probe. White-rot fungi *Trametes versicolor* L. Fr. and *Pycnoporus sanguineus* (L.) Merrill were utilized in testing natural decay resistance following ASTM Standard D-2017-81 (ASTM, 2003). The relative resistance of each test block to decay was measured as a percentage loss in oven-dry weight during 16-week exposure to fungi. Therefore, four wood characteristics were determined: heartwood loss weight under *T. versicolor* (TV-HRW) and under *P. sanguineus* (PS-HRW); and sapwood loss weight under *T. versicolor* and *P. sanguineus*, coded as TV-SAP and PS-SAP respectively.

**Wood physical properties determination:** Another group of wood physical properties were determined for each clone, based on the second cross-section at DBH. These properties were: radial shrinkage (RS), tangential shrinkage (TS) and total volume shrinkage (VS), ratio of tangential shrinkage/radial shrinkage (Ratio T/R), wood density at green condition (GD), initial or green moisture content (IMC) and specific gravity (SG). The rest of wood samples from each clone were obtained as shown in Figure 1b. Green weight and volume from each subsample were determined according to norm D-2395-02 (ASTM, 2003). Wood samples were oven-dried at 105o for 24 hours, and then reweighed. This final oven-dried weight was utilized in order to determine GD, VS, IMC, and SG. Both, TS and RS were determined according to ASTM D-2395-02.

**Statistical analyses:** HWP, PP and BP, RS, TS and VS were assessed based on single-tree values. All other wood properties were estimated based on a mean of two (IMC, GD, SO) or four samples per single tree (color parameters, stiffness and weight loss due to fungi). The individual-tree coefficient of variation (CV) was estimated for each wood property and on each site. It was estimated as the ratio of the standard deviation to the mean. Before analysis of variance was performed, data were checked for normality of distribution and homogeneity of variances of data. PP, RS, GD, SG, ED, TS, VS, ratio T/R, TV-SAP and PS-SAP presented problem with normality and homogeneity of variance. Then logarithmic transformations were applied in PP, RS, TS and VS, ratio T/R, TV-SAP and color coordinate a*. GD was transformed to X²; SG was transformed to its inverse (1/X); stiffness (Ed) was transformed to its square root, and PS-SAP to X₁.⁵.

Joint analysis on both sites was performed using SELEGEN REML/BLUP software (Reesende, 2002). The statistical model is presented in Equation 3, where, “Y” is the data vector. “r” is a repetition effects vector.

### Table 2. – Phenotypic variation in replicated 10-year-old teak clonal test at the two sites (N=110).

<table>
<thead>
<tr>
<th>Wood properties</th>
<th>Both site Mean (CV)</th>
<th>Garza Mean (CV)</th>
<th>Lowest and highest Value</th>
<th>Peñas Blancas Mean (CV)</th>
<th>Lowest and highest Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>DBH (cm)</td>
<td>19.8 (15.2)</td>
<td>19.4 (15.7)</td>
<td>12.9-25.9</td>
<td>20.3 (14.6)</td>
<td>14.0-28.7</td>
</tr>
<tr>
<td>HWP (%)</td>
<td>38.3 (19.5)</td>
<td>37.2 (21.2)</td>
<td>16.5-55.3</td>
<td>39.5 (17.4)</td>
<td>22.9-54.1</td>
</tr>
<tr>
<td>BP (%)</td>
<td>19.2 (25.0)</td>
<td>16.5 (29.5)</td>
<td>9.3-28.3</td>
<td>22.0 (12.1)</td>
<td>15.9-27.3</td>
</tr>
<tr>
<td>PP (%)</td>
<td>0.162 (31.6)</td>
<td>0.17 (55.7)</td>
<td>0.02-0.48</td>
<td>0.15 (70.7)</td>
<td>0.03-0.51</td>
</tr>
<tr>
<td>IMC (%)</td>
<td>10.4 (23.3)</td>
<td>87.9 (23.4)</td>
<td>45.2-128.7</td>
<td>121.4 (11.6)</td>
<td>89.8-138.0</td>
</tr>
<tr>
<td>GD (g/cm³)</td>
<td>1.04 (10.4)</td>
<td>0.91 (10.7)</td>
<td>0.60-1.19</td>
<td>1.18 (4.2)</td>
<td>0.90-1.21</td>
</tr>
<tr>
<td>SG</td>
<td>0.48 (8.0)</td>
<td>0.50 (7.2)</td>
<td>0.43-0.59</td>
<td>0.49 (8.7)</td>
<td>0.41-0.62</td>
</tr>
<tr>
<td>VS (%)</td>
<td>12.8 (18.9)</td>
<td>6.9 (15.1)</td>
<td>4.7-9.8</td>
<td>7.1 (21.0)</td>
<td>4.2-12.2</td>
</tr>
<tr>
<td>TS (%)</td>
<td>4.2 (19.3)</td>
<td>3.6 (18.6)</td>
<td>2.5-5.8</td>
<td>4.7 (10.8)</td>
<td>3.4-6.0</td>
</tr>
<tr>
<td>RS (%)</td>
<td>2.7 (29.8)</td>
<td>2.1 (17.1)</td>
<td>1.3-3.1</td>
<td>3.4 (18.2)</td>
<td>2.1-4.6</td>
</tr>
<tr>
<td>Ratio T/R</td>
<td>1.5 (19.0)</td>
<td>1.7 (14.9)</td>
<td>1.0-2.1</td>
<td>1.4 (19.9)</td>
<td>1.0-2.2</td>
</tr>
<tr>
<td>L*</td>
<td>52.7 (5.7)</td>
<td>63.3 (6.1)</td>
<td>51.5-72.4</td>
<td>62.0 (5.1)</td>
<td>54.8-70.0</td>
</tr>
<tr>
<td>a*</td>
<td>9.5 (10.6)</td>
<td>9.0 (9.2)</td>
<td>7.1-10.5</td>
<td>9.9 (9.8)</td>
<td>7.7-11.7</td>
</tr>
<tr>
<td>b*</td>
<td>28.6 (6.5)</td>
<td>27.8 (5.9)</td>
<td>23.0-31.1</td>
<td>29.5 (5.6)</td>
<td>25.2-33.2</td>
</tr>
<tr>
<td>Ed (GPa)</td>
<td>12.8 (13.7)</td>
<td>13.2 (14.8)</td>
<td>9.3-16.5</td>
<td>12.4 (11.5)</td>
<td>9.2-15.1</td>
</tr>
<tr>
<td>TV-HRW (%)</td>
<td>16.9 (73.4)</td>
<td>27.6 (26.8)</td>
<td>14.5-52.5</td>
<td>5.9 (72.5)</td>
<td>1.3-18.6</td>
</tr>
<tr>
<td>PS-HRW (%)</td>
<td>7.3 (40.7)</td>
<td>5.1 (54.9)</td>
<td>1.2-11.8</td>
<td>9.1 (64.0)</td>
<td>1.4-26.8</td>
</tr>
<tr>
<td>TV-SAP (%)</td>
<td>30.5 (41.1)</td>
<td>39.3 (15.6)</td>
<td>23.3-52.3</td>
<td>21.5 (51.3)</td>
<td>3.5-46.4</td>
</tr>
<tr>
<td>PS-SAP (%)</td>
<td>15.1 (51.3)</td>
<td>10.3 (51.2)</td>
<td>1.2-23.8</td>
<td>20.0 (33.6)</td>
<td>2.8-43.8</td>
</tr>
</tbody>
</table>

CV = coefficient of variation, DBH = diameter at breast height, HWP = heartwood percentage, BP = bark percentage, PP = pith percentage, IMC = initial moisture content, GD = green density, SG = specific gravity, VS = Volume shrinkage, TS = Tangential shrinkage, RS = Radial shrinkage, Ratio T/R = relation tangential and radial shrinkage, “L*”, “a*” and “b*” are color coordinates, Ed = stiffness, TV-HRW = weight loss with *Trametes versicolor* fungi in heartwood, PS-HRW = weight loss with *Pycnoporus sanguineus* fungi in heartwood, TV-SAP = weight loss with *Trametes versicolor* fungi in sapwood, PS-SAP = weight loss with *Pycnoporus sanguineus* fungi in sapwood.
(assumed as random) and added to general mean value, “a” is an individual additive genetic effects vector (assumed as random), “p” is a plot effects vector (assumed as random), “i” is the genotype x environment interaction effects vector (random), and “e” is the residual vector (random). Capital letters denote incidence matrices for mentioned effects. Vector “r” includes all repetitions in both locations (adjusting repetition x location combinations). In this case, site effects and repetitions within locations are considered.

\[ Y = Xr + Za + Wp + Ti + e_i \]  

(3)

Variance component estimates were obtained using model 23 of SELEGEN software (Randomized Block Design with three repetitions and established at two locations, RESENDE, 2002). Clonal heritability was estimated for all individual wood traits based on equation 4:

\[ \hat{H}^2 = \frac{\hat{\sigma}^2_c}{\hat{\sigma}^2_c + \hat{\sigma}^2_e + \hat{\sigma}^2_x + \hat{\sigma}^2_e} \]  

(4)

where \( \hat{\sigma}^2_c \), \( \hat{\sigma}^2_x \), \( \hat{\sigma}^2_e \) and \( \hat{\sigma}^2_e \) are respectively variance components for clonal, GxE interaction (clone by site), and error or residual effects. The Pearson phenotypic (clonal-means) correlation matrix was obtained using PROC CORR of SAS software (SAS INSTITUTE, 1997).

Results

Variation of wood properties: Average wood property values are presented in Table 2. Weight loss of heartwood due to fungi (TV-HRW and PS-HRW) exhibited the highest coefficient of variation (CV) values, both over 70%. Sapwood weight loss exhibited lower CV values, [its significances were tested using t-student test (STEEL and TORRIE, 1980, pp 279) (Equation 6).]

\[ r_{x,y} = \frac{Cov(x,y)}{\hat{\sigma}_x \hat{\sigma}_y} \]

(5)

\[ t = \sqrt{\frac{1 - r_{x,y}^2}{n-2}} \]

(6)

Where, \( Cov(x,y) \) is the genetic covariance between traits “x” and “y”, while \( \hat{\sigma}_x \) and \( \hat{\sigma}_y \) are the genetic standard deviations (square roots of variances) of trait “x” and trait “y” respectively.

Table 3. – Analysis of variance, variance component effects and broad sense heritabilities in 10-year-old Tectona grandis clones from two sites in Costa Rica (n = 110).

<table>
<thead>
<tr>
<th>Wood traits</th>
<th>Site effect</th>
<th>Clonal effect</th>
<th>Clonal x Site effect</th>
<th>Block(Site)</th>
<th>Broad sense heritability</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>(d.f.=1)</td>
<td>(d.f.=19)</td>
<td>(d.f.=18)</td>
<td>(d.f.=18)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>g</td>
<td>% VAR</td>
<td>g</td>
<td>% VAR</td>
<td>g</td>
</tr>
<tr>
<td>DBH</td>
<td>3.68**</td>
<td>1.03</td>
<td>3.90**</td>
<td>30.00</td>
<td>1.13**</td>
</tr>
<tr>
<td>HWP</td>
<td>3.47**</td>
<td>0.00</td>
<td>3.34**</td>
<td>0.00</td>
<td>2.02*</td>
</tr>
<tr>
<td>BP</td>
<td>65.46**</td>
<td>32.51</td>
<td>2.28**</td>
<td>12.85</td>
<td>0.92**</td>
</tr>
<tr>
<td>PP10</td>
<td>4.86**</td>
<td>1.37</td>
<td>3.77**</td>
<td>30.52</td>
<td>1.07*</td>
</tr>
<tr>
<td>PP110</td>
<td>166.2**</td>
<td>48.06</td>
<td>4.90**</td>
<td>20.92</td>
<td>0.97**</td>
</tr>
<tr>
<td>GD(x)</td>
<td>142.3**</td>
<td>43.51</td>
<td>2.92**</td>
<td>13.72</td>
<td>2.60*</td>
</tr>
<tr>
<td>SG(10)</td>
<td>7.53**</td>
<td>1.52</td>
<td>9.46**</td>
<td>45.26</td>
<td>2.27**</td>
</tr>
<tr>
<td>TS10</td>
<td>10.43**</td>
<td>4.61</td>
<td>7.65**</td>
<td>42.72</td>
<td>1.84*</td>
</tr>
<tr>
<td>TS110</td>
<td>216.5**</td>
<td>44.68</td>
<td>7.24**</td>
<td>21.40</td>
<td>2.28**</td>
</tr>
<tr>
<td>RS10</td>
<td>228.2**</td>
<td>62.33</td>
<td>2.45**</td>
<td>6.61</td>
<td>1.24*</td>
</tr>
<tr>
<td>RS110</td>
<td>28.21**</td>
<td>19.76</td>
<td>1.08*</td>
<td>1.59</td>
<td>0.84*</td>
</tr>
<tr>
<td>L</td>
<td>10.53**</td>
<td>3.56</td>
<td>10.54**</td>
<td>53.38</td>
<td>1.53*</td>
</tr>
<tr>
<td>a* (10Log10)</td>
<td>46.75**</td>
<td>19.41</td>
<td>5.43**</td>
<td>31.17</td>
<td>1.33*</td>
</tr>
<tr>
<td>b*</td>
<td>76.33**</td>
<td>24.22</td>
<td>8.66**</td>
<td>13.05</td>
<td>1.04*</td>
</tr>
<tr>
<td>Ed (J/g)</td>
<td>21.25**</td>
<td>2.95</td>
<td>17.08**</td>
<td>16.26</td>
<td>1.4*</td>
</tr>
<tr>
<td>TV-HRW</td>
<td>321.9**</td>
<td>75.87</td>
<td>12.11</td>
<td>1.32</td>
<td>0.56*</td>
</tr>
<tr>
<td>PS-HRW</td>
<td>22.14**</td>
<td>14.69</td>
<td>0.92*</td>
<td>0.00</td>
<td>1.42*</td>
</tr>
<tr>
<td>TV-SAP (Log10)</td>
<td>114.0**</td>
<td>59.05</td>
<td>1.18</td>
<td>2.28</td>
<td>0.98*</td>
</tr>
<tr>
<td>PS-SAP (x105)</td>
<td>73.09**</td>
<td>40.33</td>
<td>0.82*</td>
<td>0.00</td>
<td>1.12*</td>
</tr>
</tbody>
</table>

Legend: ** Statistically significant at p<0.01; * statistically significant at p<0.05, NS: not significantly different.

Abbreviations: DBH = diameter at breast height, HWP = heartwood percentage, BP = bark percentage, PP = pith percentage, IMC = initial moisture content, GD = green density, SG = specific gravity, VS = Volume shrinkage, TS = Tangential shrinkage, RS = Radial shrinkage, Ratio T/R = relation tangential and radial shrinkage, “L”*, “a”* and “b”* are color coordinates, Ed = stiffness, TV-HRW = weight loss with Trametes versicolor fungi in heartwood, PS-HRW = weight loss with Pycnoporus sanguineus fungi in heartwood, TV-SAP = weight loss with Trametes versicolor fungi in sapwood, PS-SAP = weight loss with Pycnoporus sanguineus fungi in sapwood.
from 41 to 51%. *PP* values registered a large CV of 63% as well. Meanwhile, color parameters, and *SG* and *GD* estimates exhibited the lowest CV values, all below 11%.

Some differences were established between Site 1 and Site 2. Analyses of variance and genetic control: Results of the analyses of variance are presented in Table 3 for all the wood traits and *DBH*. Significant differences (*p* < 0.01) between the two sites were observed for all variables, except *HWP*. The estimated variance component due to site (environment) ranged from 1.4 to 75.9% of the total (‘random-effect’) variation (Table 3). The largest site effect (over 50%) was exhibited by *TV-SAP*, *RS* and *TV-HRW*, indicating a strong environmental effect on these traits. In contrast, low site effects (from 14 to 33%) were recorded in *PS-HRW*, ratio *T/R*, *BP*, *color coordinates a* and *b*, while the least site effects were observed for *VS*, *Ed*, *SG*, *PP* and color coordinate *L*, indicating a stronger genetic control for these traits.

The clonal effect was significant (*p* < 0.01) for *BP*, *PP*, *IMC*, *GD*, *SG*, all shrinkage parameters (except in ratio *T/R*), all wood color parameters, and *Ed*. The color coordinate *L* exhibited the highest variance proportion explained by clonal effect, with 53.4% of its total estimated random variation. For the traits *PP*, *SV*, *SG*, *Ed*, and color coordinates *a* and *b*, the estimated clonal variance percentages varied from 20.0 to 46.3%. The results of environmental and clonal effects permit conclude that color in teak could be strongly improved through well sound breeding programs. The lowest across-sites clonal variation was observed in traits *HWP*, ratio *T/R*, *TV-HRW*, *PS-HRW*, *TV-SAP* and *PS-SAP*.

Table 3: Phenotypic and genotypic correlation coefficients were estimated with SELEGEN (RESENDE, 2002).

<table>
<thead>
<tr>
<th>Trait</th>
<th><em>DBH</em></th>
<th><em>HWP</em></th>
<th><em>BP</em></th>
<th><em>PP</em></th>
<th><em>IMC</em></th>
<th><em>GD</em></th>
<th><em>SG</em></th>
<th><em>VS</em></th>
<th><em>TS</em></th>
<th><em>RS</em></th>
<th><em>Ratio T/R</em></th>
<th><em>L</em></th>
<th><em>a</em></th>
<th><em>b</em></th>
<th><em>Ed</em></th>
<th><em>TV-HRW</em></th>
<th><em>PS-HRW</em></th>
<th><em>TV-SAP</em></th>
<th><em>PS-SAP</em></th>
</tr>
</thead>
<tbody>
<tr>
<td><em>DBH</em></td>
<td>1</td>
<td>0.57**</td>
<td>1</td>
<td>-0.44*</td>
<td>-0.46*</td>
<td>0.33</td>
<td>-0.09</td>
<td>-0.63</td>
<td>-0.22</td>
<td>-0.19</td>
<td>-0.87</td>
<td>-0.16</td>
<td>-0.64</td>
<td>-0.04</td>
<td>0.05</td>
<td>-0.32</td>
<td>-0.31</td>
<td>0.24</td>
<td>0.04</td>
</tr>
<tr>
<td><em>HWP</em></td>
<td>0.57**</td>
<td>1</td>
<td>0.26</td>
<td>-0.29</td>
<td>0.20</td>
<td>0.52*</td>
<td>0.19</td>
<td>0.11</td>
<td>0.11</td>
<td>-0.09</td>
<td>0.02</td>
<td>-0.20</td>
<td>0.35</td>
<td>0.11</td>
<td>0.14</td>
<td>0.17</td>
<td>0.03</td>
<td>0.06</td>
<td>-0.22</td>
</tr>
<tr>
<td><em>BP</em></td>
<td>-0.26</td>
<td>-0.29</td>
<td>0.20</td>
<td>0.52*</td>
<td>0.19</td>
<td>0.11</td>
<td>-0.09</td>
<td>0.02</td>
<td>0.20</td>
<td>0.35</td>
<td>-0.09</td>
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<td>0.35</td>
<td>0.11</td>
<td>0.14</td>
<td>0.03</td>
<td>0.06</td>
<td>-0.22</td>
</tr>
<tr>
<td><em>PP</em></td>
<td>0.45</td>
<td>-0.18</td>
<td>-0.05</td>
<td>1</td>
<td>-0.21</td>
<td>-0.61</td>
<td>-0.11</td>
<td>0.29</td>
<td>0.23</td>
<td>0.43</td>
<td>0.45*</td>
<td>-0.21</td>
<td>-0.41</td>
<td>0.21</td>
<td>0.12</td>
<td>0.14</td>
<td>0.16</td>
<td>-0.18</td>
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<tr>
<td><em>IMC</em></td>
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<td>0.17</td>
<td>0.31</td>
<td>-0.14</td>
<td>1</td>
<td>0.32</td>
<td>-0.73**</td>
<td>-0.32</td>
<td>-0.54**</td>
<td>-0.61**</td>
<td>0.17</td>
<td>0.08</td>
<td>0.34</td>
<td>0.45*</td>
<td>-0.44*</td>
<td>0.24</td>
<td>-0.19</td>
<td>0.34</td>
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</tr>
<tr>
<td><em>GD</em></td>
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<td>0.10</td>
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<td>0.33</td>
<td>0.75*</td>
<td>1</td>
<td>0.41</td>
<td>-0.13</td>
<td>-0.17</td>
<td>-0.43</td>
<td>0.04</td>
<td>-0.21</td>
<td>0.40</td>
<td>-0.02</td>
<td>0.14</td>
<td>-0.24</td>
<td>0.04</td>
<td>0.14</td>
<td>0.06</td>
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<tr>
<td><em>SG</em></td>
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<td>0.02</td>
<td>0.20</td>
<td>0.49</td>
<td>0.23</td>
<td>1</td>
<td>0.20</td>
<td>0.41</td>
<td>0.28</td>
<td>-0.04</td>
<td>0.23</td>
<td>0.94</td>
<td>-0.45**</td>
<td>0.53*</td>
<td>-0.40</td>
<td>-0.39</td>
<td>-0.23</td>
<td></td>
</tr>
<tr>
<td><em>VS</em></td>
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<td>-0.18</td>
<td>0.24</td>
<td>0.11</td>
<td>0.10</td>
<td>0.15</td>
<td>-0.68</td>
<td>1</td>
<td>0.82**</td>
<td>0.77**</td>
<td>0.06</td>
<td>0.20</td>
<td>-0.31</td>
<td>-0.22</td>
<td>0.66**</td>
<td>0.18</td>
<td>-0.21</td>
<td>0.27</td>
<td></td>
</tr>
<tr>
<td><em>PS</em></td>
<td>0.04</td>
<td>0.00</td>
<td>0.45*</td>
<td>0.02</td>
<td>0.27*</td>
<td>0.44</td>
<td>-0.65</td>
<td>0.50</td>
<td>1</td>
<td>0.69*</td>
<td>0.11</td>
<td>0.21</td>
<td>-0.19</td>
<td>-0.19</td>
<td>0.67**</td>
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<tr>
<td><em>SS</em></td>
<td>0.64</td>
<td>0.00</td>
<td>0.45*</td>
<td>0.03</td>
<td>0.39</td>
<td>0.46</td>
<td>-0.61</td>
<td>0.43</td>
<td>0.69*</td>
<td>1</td>
<td>-0.33</td>
<td>-0.67</td>
<td>-0.23</td>
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<td>0.52**</td>
<td>0.29</td>
<td>0.06</td>
<td>-0.69</td>
<td>0.19</td>
</tr>
</tbody>
</table>

Table 4. – Phenotypic Pearson (clonal-mean) correlations (below diagonal) and estimated genotypic correlations (above diagonal) in 19 traits (*N* = 100).

Legend: numbers in boldface for statistically significant (* denotes *p* < 0.05, ** denotes *p* < 0.01) based on Equation 6 for genotypic correlations. Abbreviations: see Table 3. Phenotypic and genotypic correlation coefficients were estimated with SELEGEN (RESENDE, 2002).

Note: Selegen Software estimates a Bonferroni correction for type 1 error.

The interactions between site and clone were significant in *HWP*, *GD*, *SG*, *VS*, *TS* and *Ed*, contributing with 10 to 31% to the total estimated variation. Non-significant effects were observed in the remaining wood properties. The block effect was not significant (*p* > 0.05) for all the traits analyzed and contributed 0% or less than 3.5% to the total estimated variation. These results may be explained by very homogenous conditions within both. Finally, the error item contributed over 50% of total variation in traits *BP*, *PS-SAP*, *PP*, *HWP*, ratio *T/R* and *PS-HRW*.

Estimated broad-sense heritabilities (*H*<sup>2</sup>) ranged from 0.00 to 0.57 (Table 3). The highest heritability estimates were recorded for traits *VS*, color parameter *L*, *a* and *b*, *PP*, *IMC* and *SG*. These results indicate that these traits are under an important genetic control, with large variation among clones and good prospects for breeding for these traits. Significant estimates of heritability were found for some wood properties, from 0.38 to 0.57.
Low values were obtained for BP, GD, RS and ratio T/R (H^2 from 0.03 to 0.19), and negligible values for HWP and decay resistance of sapwood and heartwood (Table 3).

Phenotypic and genotypic correlations among wood properties: In Table 4 can be seen both, phenotypic (lower diagonal) and estimated genotypic (above diagonal) correlations among all wood properties investigated. Although we used a small study population of clones, there is a evident positive genetic correlation between DBH and HWP, as well strong but negative relationship between DBH with both, BP and PP. HWP shows a significant negative genetic correlation with Ed. Interestingly to notice is a negative genetic correlation between SG with color factor b* and Ed. Predictably, there are strong genetic correlations between all three shrinkage properties (TS, RS and VS).

On the other hand, there is a lack of significance (p<0.05) in the correlation between SG and DBH, as well as between IMC with GD, TS with RS, RS with TV-HRW, L* with a* and TV-HRW with TV-SAP. Lack of significance in the genetic correlation (p<0.05) between SG with shrinkage properties (VS, TS or RS), are also interesting results to be discussed (Table 4). These results suggest that we could improve SG without materially affecting shrinkage. Another strong but predictable genetic correlations involving SG is its strong negative relationship with IMC (r=-0.73**). Therefore, the highest SG values will result low IMC. Future research must study this issue precisely, based on a larger genetic sample and a better experimental design.

Discussion

Sample size utilized in this investigation was the best possible obtained based on the available remaining trees in these trials. Due to the lack of information, the relevance and the possibility of assessing genetic control on teak wood properties, this investigation was conducted. Clonal trials are usually quite homogeneous, however, 6 ramets per clone are at no doubt quite a small sample size.

Average recorded values for HWP, BP and PP are all below expected and reported for fast-grown teak plantations (Pérez and Kanninen, 2005; Moya and Pérez, 2008, Bhat, 1995, Kocutse et al., 2004). Wood values for GD, SG and shrinkage (VS, TS and RS), fell between reported values from other studies (Moya et al., 2005; Moya and Pérez, 2008). In relation to wood color parameters, Moya and Berrocal (2010) reported similar values in fast-growing teak plantations in Costa Rica. For the case of white-rot fungal attack effect in weight loss, values reported by Moya and Berrocal (2010) and Bhat and Florence (2003), Bhat and Indira (2005), Kocutse et al. (2006) and Lukmandaru and Takahashi (2008) are similar as those reported here with 10-year-old ramets.

While environment affects almost all wood properties, some of them are under strong genetic control as well, as reported frequently (Zobel and Jett, 1995; Zobel and van Bulthuis, 1998). Recently, Moya and Pérez (2008) found that soil characteristics such as calcium content, copper, phosphorus, as well as sandy or salty soil texture, correlated with some physical wood properties in teak. Even though there is still little knowledge of site effects on wood properties in tropical clonal forestry, with the exception of eucalyptus (Miranda et al., 2007; Vancly et al., 2008), there are some reports in minor tree species such as in Dalbergia sissoo (Pande and Singh, 2005) in which site conditions significantly affected wood SG and some other wood anatomy properties. However, other studies reported contradictory results, like in Calycophyllum spruceanum (Soto et al., 2007), where no site effects were found for any wood property, but some genetic control in wood specific gravity.

The significance of clone x site interaction, but lack of either main effect for HWP, is noteworthy and puzzling. According to ours results, environmental factors affect clones differently in different sites; therefore the site was not affecting all clones similarly. However, this result can be considered with care, because 2 sites only and small ramets quantity were studied.

Some wood properties with important effects in processing and utilization, like drying (related to IMC and all shrinkage properties), mechanical properties (related to SG and Ed), and wood color (based on color coordinates L*, a* and b*), exhibited large clonal variation and strong genetic control, for instance, genotypic correlation between L* with a* in this study (Table 4). These results support the possibility of including these traits in future teak breeding programs. However, this does not imply abandonment of good silvicultural practices in order to avoid identifiable effects of growth rate on wood properties (Zobel and Jett, 1995).

There are some previous studies reporting important genetic control in growth traits in teak (Goh and Montefusis, 2005; Callister and Collins, 2008; Solorzano et al., 2012a), but very little on wood properties. Most of the reports are based on SG and HWP (Bhat and Indira, 2005; Indira and Bhat, 1997; Rao and Shashikala, 2003; Solorzano et al., 2012a), reporting similar genetic control values to those found in this study. In contrast, Rao and Shashikala (2003) and Bhat and Indira (2005) reported lower heritabilities in teak SG. Rao and Shashikala (2003) with 16-year-old clonal tests, reported higher heritabilities for HWP than those found in this study.

There is plentiful evidence relating the amount of heartwood in trees to their growing conditions, especially with diameter increments (Perez and Kanninen, 2003 and 2005; Viquez and Perez, 2005). The best explanations are based on the pipe model (Shinozaki et al., 1964, cited by Mortataya et al., 1999), which relates crown growth with diameter increments and the needed sapwood area, and therefore, the resulting heartwood area. In teak, heartwood proportion is a key marketing factor, so it is important to understand its control and possibilities of manipulation. One way of increasing it is through the promotion of higher diameter increments. In this study, we found a clear positive relationship between diameter growth and heartwood proportion (Figure 2a), as reported in similar studies with teak.
largely management (environmental) effects (ZOBEL and
within-clone statistics must be interpreted as reflecting
correlations and non-genetic correlations reflecting
dence of significant genotypic correlations, phenotypic
ever, when for the same two properties there is no evi-
dal estimates, genetic correlations will be involved. How-
strong positive phenotypic correlation ($r = 0.57^{**}$), as
For the clonal teak population ($DBH$ and $HWP$), in this study.
Besides, this relationship was genetically significant
(Table 4). This means that if we increase diameter
growth through good silvicultural practices, we may
increase $HWP$ in teak trees and that if we select trees in
a breeding program for higher $DBH$ (Figure 2a), there
will be more heartwood and less pith and bark content.
Other researchers have established genetic correlations
among wood properties in conifers (HANRUP et al.,
Similar studies with tropical tree species, however, are
limited (SOTELO et al., 2008).

Very promising for breeding are the positive genotypic
and phenotypic correlations between the SG with stiffness ($r = 0.53^{**}$ and 0.36 respectively). Increasing $SG$
improves mechanical properties. This is a very consist-
tent relationship between these two properties, with a
very promising utilization in breeding (ZOBEL and
JETT, 1995). On the other hand, $Ed$ and $DBH$ did not exhibit
significant genetic correlations, but a negative pheno-
typic correlation ($r = −0.36$). However, though the pheno-
typic correlation was significant, it was quite low and
may reflect the low number of clones ($n = 20$) and ramets
per clone in each site ($n = 2$ to 3). Meanwhile, $Ed$
and shrinkage also showed a favorable genotypic correlation
(Table 4). These correlations can be explained by the
shrinkage and $Ed$ being correlated with wood density
(IVKOVIĆ et al., 2009). Another important correlation with $Ed$ is its negative phenotypic correlation with $HWP$
($r = −0.59$), which indicated that increasing $HWP$ (by tree
diameter) would reduce stiffness (lower $Ed$).

Color is a key factor for marketing teak wood. There-
fore, wood color relationships with other wood properties
are amongst the most important in this investigation.
Interesting to note is the strong negative genotypic correlation estimate of $SG$ with $b^*$ ($= −0.45^{*}$) (Figure 2b).
This means that increased $SG$ entails decreased yellow-
ness of wood color so darker colour. The $SG$ may be uti-
lized in future as an indirect indicator for recognizing

(SOLORZANO et al., 2012a). Since $DBH$ showed a strong
clonal variability (Table 3), heartwood proportion could
be indirectly improved in teak through selection and use of
faster-growing genotypes. Other researchers reported in
teak a high to moderate genetic control of $DBH$, with
broad-sense heritabilities varying from 0.22 to over 0.50
in early trials (HARSHAP and SOERIANEGARA, 1977; SHAR-
MA et al., 2000; CALLISTER and COLLINS, 2008). Heart-
wood formation may be genetically influenced not only
by being strongly inherited, but possibly influenced as
well by other tree characteristics not included in this
investigation. For example, it was demonstrated that
heartwood is influenced by site fertility, (MOYA and
PÉREZ, 2008), location (KJÆR et al., 1999; PENG et al.,
2012), and growing conditions (DERKYI et al., 2010;
MOYA and CALVO-ALVARADO, 2012).

Genetic correlations among traits may have biased
effects due to the small sample of trees evaluated. After
thinning, slow-growing trees were eliminated from experi-
ment, as well as those with undesirable phenotypic
stem characteristics. Reduction of these ramets withi-

(diameters) would reduce stiffness ($lower Ed$).

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Genetic correlations among traits may have biased
effects due to the small sample of trees evaluated. After
thinning, slow-growing trees were eliminated from experi-
ment, as well as those with undesirable phenotypic
stem characteristics. Reduction of these ramets within-
clones, tend to produce better vigor estimates for
growing traits, but is not necessarily positive in other
wood traits, which are clearly losing observations. Coef-
ficient of variation estimates will be downward reduced
since they are now based on a smaller number of trees
(MATHESON and RAYMOND, 1984) and therefore, it may
affect not only genetic correlation estimates, but also in
other genetic parameters.

On the other hand, selecting for one of the two wood
properties may induce a correlated effect in other relat-
ed wood properties. Since here we are dealing with clon-
al estimates, genetic correlations will be involved. How-
ever, when for the same two properties there is no evi-
dence of significant genotypic correlations, phenotypic
correlations and non-genetic correlations reflecting
within-clone statistics must be interpreted as reflecting
largely management (environmental) effects (ZOBEL and
JETT, 1995). One good example is the relationship
between the $DBH$ and $HWP$, $BP$ and $PP$, in this study.
For the clonal teak population ($n = 20$) there is a quite
strong positive phenotypic correlation ($r = 0.57^{**}$), as
reported elsewhere (KJÆR et al., 1999; PÉREZ and KANNI-
NEN, 2003, 2005; VIQUEZ and PÉREZ, 2005; SOLORZANO et
al., 2012b). This is a positive result, since a threshold
minimum $HWP$ is required in marketing teak wood.
Besides, this relationship was genetically significant
(Table 4). This means that if we increase diameter
growth through good silvicultural practices, we may
increase $HWP$ in teak trees and that if we select trees in
a breeding program for higher $DBH$ (Figure 2a), there
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ness of wood color so darker colour. The $SG$ may be uti-
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Figure 2. – Phenotypic correlation between heartwood percentage ($HWP$) and diameter at breast height and between $b^*$ color parameter and specify gravity in teak clones tested in northern Pacific from Costa Rica.
wood with better properties. Meanwhile there is a strong genetic correlation between $a^*$ and $L^*$ parameters ($r = -0.64^*$). This is a very promising result for breeding since clones with lower $L^*$ should produce wood with highest $a^*$ values. Moya and Berrocal (2010) established through multiple correlation analysis that $DBH$ is the main characteristic that determines $L^*$ and $a^*$ values in heartwood color in teak trees. Sotelo et al. (2008) established significant genetic correlations between $DBH$ and tree height with $b^*$ color parameter in Calycophyllum spruceanum. Hannrup et al. (2004) reported significant genetic correlations between $a^*$ and $b^*$ color coordinates in Picea abies. However, in this investigation there were no evident association between wood color and DBH.

No genotypic correlation between various wood properties and decay resistance of both sapwood and heartwood was found (Table 4). However, some important properties, such as wood color, can be used as a wood-decay indicator on the basis of phenotype (Table 4). If we look at phenotype correlations for wood-color variables, $b^*$ and $a^*$ coordinates were negatively correlated with sapwood and heartwood decay under Trametes versicolor. But, these color parameters were positively correlated under Pycnoporus sanguineus wood decay. These color correlations are explained by the fungi’s decay effects in the wood, which could be interpreted as an effect from the environmental conditions. Moya and Berrocal (2010) found that wood-color variables were differently correlated with decay in different environmental conditions of Costa Rica. They agree with the contention that decay resistance is an effect of environment. It means also that, when decay resistance is not controlled through breeding programs, it could be controlled by environmental conditions.

Conclusions

These results must be considered as the first ones on teak wood properties genetic control, and therefore treated as non-conclusive. Future investigations are needed in order to validate and contrasts these findings.

This study demonstrates that these teak clones appear to show adequate SG, shrinkage and stiffness. The wood color is similar to that of other fast-grown trees. And it also established that variation in $PP$, $BP$, $IMC$, $GD$, $SG$, different shrinkage- and wood-color variables, and Ed is under important genetic control. Estimated broad-sense heritability was from moderate to high for the color parameter $L^*$ and VS. Low heritabilities were found in $GD$, $RS$ and ratio $T/R$ and negligible values were found for $HWP$ and decay resistance in sapwood and heartwood.

Especially interesting results were obtained for $HWP$, since it is a key factor for marketing teak wood. It was estimated that while variation is present between clones, across-sites heritability is very low. There is plentiful evidence relating the amount of heartwood in trees to their growing conditions. However, $HWP$ can be increased with better silvicultural practices, as well as selecting faster-growing trees. It is important to establish the allometric relationships between heartwood and tree-size variables, to give a better understanding of heartwood formation in clonal forestry.

Phenotypic and estimated genetic correlations indicate that in future breeding programs, selecting trees for faster growth will increase heartwood proportion, while reducing pith and bark content. However, faster-growing trees, through the improvement of $DBH$, should lead to a reduction in wood stiffness and decay resistance. On the other hand, selecting clones with denser wood would improve $Ed$ and would reduce yellowness and probably improve wood color. Finally, clone selection with lower $L^*$ values could be increase redness ($a^*$) of wood. However, decay resistance is not controlled strongly by genotype but more by environment.

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