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Toona ciliata genotype selection with the use of individual BLUP with repeated measures

Rulfe Tavares Ferreira[1], Alexandre Pio Viana[1]*, Déborah Guerra Barroso[2], Marcos Deon Vilela de Resende[3], Antônio Teixeira do Amaral Júnior[1]

[1]UENF/CCTA – Lab. de Melhoramento Genético Vegetal – 28015-610 – Campos dos Goytacazes, RJ – Brasil.
[2]UENF/CCTA – Lab. de Fitotecnia – 28015-610 – Campos dos Goytacazes, RJ – Brasil.
[3]UFV – Depto. de Engenharia Florestal – 36570-000 – Viçosa, MG – Brasil.
*Corresponding author <pirapora@uenf.br>

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ABSTRACT: The increasing demand for raw material for multiple uses of forest products and by-products has attracted the interest for fast growing species, such as the Australian Cedar (*Toona ciliata*), which presents high productive and economic potential. This study aimed at estimating genotypic parameters and values for the species through the use of the BLUP procedure, at individual level, with repeated measures, by means of the conventional evaluation procedures and the introduction of innovative digitalization of the measurements by digital camera with the images provided by the *Imagej* software system. The main objective is to subsidize the beginning of a breeding program for the species. The assays were carried out in private properties, in plantations located in the state of Rio de Janeiro, Brazil. The results generated by three evaluations revealed that the image digital analysis is adequate to quantify characteristics of *Toona ciliata.* It is also an effective and accurate alternative to minimize the costs of data collection in evaluations with the species. There was high accuracy for the characters plant height, diameter at breast height and cylindrical volume. Out of the 90 genotypes evaluated, 38 expressed genotypic values predicted for the diameter at breast height higher than the general average of this character, 33 for the cylindrical volume and 49 for height, allowing gains of up to 24.9 % in average for cylindrical volume. The method of mixed models (REML/BLUP) applied via the SELEGEN software system, using the BLUP procedure at individual level and repeated measures in each individual proved to be adequate to estimate the genetic parameters and predict genotypic values in situations of unbalanced data. Therefore, it is very useful and practical for *Toona ciliata* genetic breeding programs.

Keywords: Australian Cedar, mixed models

Introduction

The increasing demand for raw material for multiple uses of forest products and by-products has attracted the interest in fast growing species with high productive potential and relevant economic return, such as the Australian Cedar (*Toona ciliata*), an exotic species of the family Meliaceae, which, according to Pinheiro et al. (2006), has found absolutely favorable conditions to develop in Brazil.

The adoption of accurate methods in the selection of better individuals in breeding programs with perennial plant species, such as forest species, is directly related to the potential success of the methodology. The success of breeding is related to the unmistakable capacity to select the best individuals that will be the parents of the next generations (Cruz and Carneiro, 2004).

The selection process of perennial plants should be based on the additive genetic values of the individuals that will be used in the recombination and the genotypic values of the individuals to be cloned (Resende, 2002). The individual procedure best linear unbiased prediction (BLUP) has been adequate to predict genetic values in the evaluation of perennial plants, by predicting genetic values of random effects of the statistical model, through observations of the phenotypic characteristics, adjusting the data to the fixed effects and the uneven number of information in the plots, by means of the mixed model methodology (Verardi et al., 2009).

Padilha et al. (2003) and Farias Neto (2002) have emphasized the importance of the repeatability models (parameter associated to the phenotypic correlation among repeated measures in the same individual) for the genetic evaluation of some perennial species, such as erva-mate (*Ilex paraguariensis* St.Hil), and fast growing forest species. The genetic evaluation involving individuals of these species is based on models that consider both the effect of the permanent environment and the mentioned repeatability.

In spite of the potential of the BLUP technique, the quantifications of biometric characteristics in forest species of interest for the market have been currently estimated by conventional procedures, which demand more time and resource. Besides, some characteristics are difficult to be accessed and highly susceptible to errors of inference, such as the canopy diameter. An alternative for this is the use of non-conventional procedures, such as that proposed in this study, which performs the measurement of the desired characteristics in individuals of populations by means of the analysis of images with the use of digital camera with photographical documentation via the *Imagej* software system. Therefore, this study aimed at estimating parameters and genotype values by the BLUP procedure at the individual level, in populations of Australian Cedars, using several individuals and repeated measures, estimated by conventional procedures of measurement and by digitalization of images, aiming at assessing the efficiency of the non-conventional estimates in *Toona ciliata* and subsidize the start of a breeding program with the species.

Materials and Methods

The assays were carried out in commercial plantations of Australian Cedar in three locations: i) Triunfo, located in Santa Maria Madalena-RJ (22°51′ S; 41°09′ W, 118 m a.s.l; ii) Alto Imbé, located in Santa Maria Madalena-RJ (21°59′ S; 41°58′ W; 340 m a.s.l.); and iii) in Trajano de Moraes-RJ (22°07′ S; 42°13′ W; 660 m a.s.l).

The plantations were implanted in the second half of 2005, in the spacing of 3 × 2 m, with seedlings produced by seminal via. The seeds used in Triunfo were from the state of Espírito Santo and those of Alto Imbé and Trajano, from plantations of Viçosa-MG. Thirty individuals were randomly preselected in each plantation, and three measurements were performed, with 6-month intervals between them. After completion, the average was used for all analyses.

Phenotyping via digital and conventional analysis

In this study, in which a new methodology was used for variable measurement by means of a digital camera, the averages of the digitalized images were compared, and then measurements were performed of the diameter at breast height (DBH) and stem diameter (SD) in an image, and height (H) in another image, with the use of the Imagej software system, in comparison to the manual collection using Suta to measure the diameter at breast height (DBH) and stem diameter (SD), and graduated scale to measure height (H), in the same population.

The preselected plants were evaluated as for the following characteristics: plant height (H), diameter at breast height (DBH), cylindrical volume (CV), stem diameter (SD), distance between nodes (Internodes) and canopy diameter (CD). Those were estimated by two procedures: i) measurement using Suta and graduated scale; and the diameter at breast height (DBH) was measured: in centimeters (cm), at 1.3 m of the height of the trunk base. The cylindrical volume (CV): was indirectly estimated, through the use of the equation $(\varpi/4)$ x DBH^2. H, using the measurements of the characteristics mentioned in the equation, which had been previously achieved. The stem diameter (SD): in centimeters (cm), was estimated at the base of the plants. The distance between nodes (Internodes): in centimeters (cm), was achieved through the weighted average of the distances among the nodes immediately superior to 1.30m of height of the base of the trunk. The diameter of the canopy (CD): in centimeters (cm), was quantified at the height of the branches, and the image of the base of the plant was achieved focusing the canopy and ii) measuring the desired characteristics, through the analysis of the images of each individual from two different positions by the *Imagej* software system. The images were achieved with the use of a digital camera, with resolution of 4.1 mega pixels.

The data achieved by the conventional methodology of measurement and by image digital analysis were subjected to the test of homogeneity of variances (F test) and t-test for two independent samples, to assess the validation of the data achieved by means of digitalized image.

In this aspect, the study aimed at investigating if the digital analysis methodology differed from the manual data collection methodology, which is traditionally used. For such, the Student t-test was applied to contrast the differences among population averages, considering the paired data, that is, for the same population, testing the digital analysis of the images and the manual data collection.

Genetic parameter estimates

The genetic values were estimated with the use of the Selegen-REML software system through the individual BLUP procedure with repeated measures for the characteristics plant height (H), diameter at breast height (DBH), cylindrical volume (CV), stem diameter (SD), distance between nodes (Internodes) and canopy diameter (CD).

The prediction of the genetic values followed the statistical model, in the context of the mixed linear models, presented as follows: $y = Xm + Zg + Wi + e$, in which: y is the data vector, m is the vector of the effects of the local combinations and measurements (assumed as fixed) added to the general mean, g is the vector of the genotypic effects added to the vector of the effects of permanent environment (assumed as random), i is the vector of the effects of the genotype × measurement interaction and, e is the vector of errors or residues (random). The capital letters represent the incidence matrices for the mentioned effects. The vector m comprises all the measurements in all the locations and adjusts simultaneously, for the effects of locations, measurement and location × measurement interaction.

The equations of mixed models to estimate the fixed effects and predict the random effects by the BLUP procedure, presented by Resende (2000) are given by:

$$\begin{bmatrix} \hat{m} \\ \hat{g} \\ \hat{i} \end{bmatrix} = \begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + I^{-1}\lambda_1 & Z'W \\ W'X & W'Z & W'W + I\lambda_2 \end{bmatrix}^{-1} \begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix},$$

in which:

$$\lambda_1 = \frac{\sigma_e^2}{\sigma_g^2} = \frac{(1-r)}{r};$$

$$\lambda_2 = \frac{\sigma_e^2}{\sigma_i^2} = \frac{(1-r)}{c^2 gm};$$

To achieve the variance components, the following estimators were used:

Vf: permanent phenotypic variance. $Vfp = \dfrac{m\hat{\rho}}{1+(m-1)\hat{\rho}}$

Vgm: variance of the genotype × measurement interaction. $Vgm = \frac{Vg*}{Vgx \cdot Vgy}$

Ve: temporary residual variance.

Vf: individual phenotypic variance. $Vf = Vg + Vet$

r: repeatability of individual plants. $r = \frac{Vg}{Vf}$

$c_2gm = c_{21}$: coefficient of determination of the effects of the genotype × measurement interaction. $c^2gm = \frac{\sum\left(Y_i^h - \bar{\bar{Y}}_i\right)^2}{\sum\left(Y_i - \bar{\bar{Y}}_i\right)^2}$

rgmed: genotypic correlation through measurements.

rm: repeatability of the average of genotypes (determination). $rm = \frac{m \cdot r}{1 + (m-1)\hat{\rho}}$

Acgen: accuracy in the selection of genotypes. $Acgen = \left[\frac{m \cdot r}{1 + (m-1)\hat{\rho}}\right]^{\frac{1}{2}}$

Results and Discussion

The results achieved for the characteristics diameter at breast height (DBH), stem diameter (SD) and plant height (H) are shown in Table 1. The averages were statistically equal by the t test in the comparison among averages for both methodologies analyzed. This fact guarantees that the results achieved for the variables mentioned by image analysis can be safely used and that it is a viable and effective alternative to measure characteristics for the populations evaluated, facilitating the formation of a "pool" of information, which would be more difficult to be achieved with the use of the conventional procedures.

Table 1 – Averages of the digital and conventional analyses referring to the diameter at breast height (DBH), stem diameter (SD) and plant height (H). The same letters in the column do not differ ("t" test, $p < 0.05$).

	DBH		SD		H	
Method	Average	σ^2	average	σ^2	average	σ^2
Manual	14.02 a	7.44 a	18.12 a	9.72 a	12.00 a	1.16 a
Digital	13.80 a	7.04 a	17.20 a	7.81 a	11.90 a	1.21 a

Estimates of variances, repeatability of the characteristics and accuracy of three evaluations

For the characters growth, diameter at breast height (DBH), plant height (H), cylindrical volume (CV), stem diameter (SD), distance between nodes (internodes) and canopy diameter (CD), the repeatability estimates varied between 0.023876 and 0.269556, as presented in Table 1, and the values for DBH (0.244188), H (0.206068) and CV (0.269556) were consistent with the magnitudes reported by Sampaio et al. (2002), in *Pinus* and by Garcia and Nogueira (2005) in *Eucaliptus*, for the same characteristics evaluated in this study.

The estimates of repeatability for the characteristic CV are located inside the interval of values of heritability estimates achieved by Resende (2002), between 0.14 and 0.62, for timber volume in *Eucalyptus grandis*. The same author, using values found in literature, provides magnitudes of heritability averages for timber volume of 0.2l, based on 528 estimates for many forest species. It is necessary to emphasize that the values of repeatability measured for timber volume in *T. ciliata*, at three years of age, was 0.269556, with value accuracy of 0.855802, according to Table 2, revealing good perspectives of genetic gains in future breeding programs.

The most important function of heritability in genetic studies on the metric character, according to Falconer (1987), is its predictive capacity and the expression of the confidence of the phenotypic value as a guide for the genetic value. Repeatability represents the maximum value that heritability may achieve in the broad sense, because repeatability and heritability are different, since the genotypic variance used to estimate the repeatability is not only of genetic origin, but still masked by the variance components of the permanent environment and among individuals (Cruz et al., 2004). Thus, since the variance caused by the permanent envi-

Table 2 – Estimates of repeatability (r), genotypic variance (Vg), phenotypic variance (Vf), variance of the genotype x measurement interaction (Vgm), temporary residual variance (Ve), coefficient of determination of the effects of the genotype x measurement interaction (c2gm), genotypic correlation through the measurements (rgmed), accuracy in genotype selection (Acgen) for the variables diameter at breast height (DBH), plant height (H), cylindrical volume (CV), stem (SD), distance between nodes (internodes) and canopy diameter (CD).

Estimate	DBH	H	CV	SD	Internodes	CD
Vg	0.4415	0.2312	0.0002	0.5865	1.4927	871.2745
Vgm	0.1465	0.0962	0.0000	0.2608	0.6013	4162.4537
Ve	1.2199	0.7945	0.0006	2.1480	4.9703	31457.6968
Vf	1.8080	1.1220	0.0009	2.9954	7.0644	36491.2512
r	0.2441	0.2060	0.2695	0.1958	0.2113	0.0238
c_2gm	0.0810	0.0857	0.0779	0.0870	0.0851	0.1140
Rgmed	0.7507	0.7060	0.7756	0.6922	0.7128	0.1730
Acgen	0.8398	0.8109	0.8558	0.8019	0.8153	0.3891
General measurement	11.8044	9.7176	0.1120	1.5599	12.1018	245.6525

ronmental effects is minimized, repeatability becomes closer to heritability and they might even be equal, in case the estimate of the genotypic variance is exclusively of genetic nature.

As for the character DBH, works with eucalyptus, such as those developed by Rocha et al. (2007) and Martins et al. (2003), have revealed satisfactory heritability close to 0.3000. Kageyama et al. (1977) evaluated populations of *Pinus patula*, in two locations and achieved estimates of relative heritability for the traits H and DBH, respectively, of 0.2873 and 0.1872 for a location, and 0.1623 and 0.1373 for the second location. The character DBH is considered the most important for the purposes of selection for wood production in *E. urophylla* and *E. grandis* (Rocha et al., 2007). For these species, estimates of heritability of 0.2785 and 0.2247 and accuracies of 0.61 and 0.53, respectively for *E. urophylla* and *E. grandis,* are satisfactory for the genotype selection based on DBH (Rocha et al., 2007). Similarly, repeatability values of 0.2441 and accuracy values of 0.8398 (Table 2) are consistent references for *Toona ciliata*.

Height, with estimated repeatability of 0.206068 and accuracy of 0.81095, is consistent with the interval presented by Garcia and Nogueira (2005) for the selection of clones of eucalyptus and higher than the estimates achieved by Kageyama et al. (1977), for provenances of *Pinus*, indicating that there are real possibilities of genetic gains in the populations of *Toona ciliata* evaluated.

The repeatability estimate achieved for canopy diameter (D.Canopy) of 0.023876 (Table 2) presented the lowest magnitude, indicating the highest irregularity of the superiority of the individuals among the measurements for this character. In this aspect, for ten measurements, it would be possible to achieve accuracy estimate of 0.61. This high irregularity demonstrates that genotype selection based on this trait is not a good strategy. As for the characteristic CV, according to the Table 3, five measurements would be necessary to achieve accuracy slightly higher than 0.90.

The estimates of the parameter accuracy for the variables diameter at breast height (DBH), plant height (H), cylindrical volume (CV), stem diameter (SD) and distance between nodes (Internodes) presented values ranging from 0.801902 to 0.855802. For the canopy diameter (CD), the accuracy estimate was 0.389126. It must be emphasized that Resende and Duarte (2007) proposed the classification of the statistical accuracy as very high (Acgen ≤ 0.90), high (0.70 ≤ Acgen ≤ 0.90), moderate (0.50 ≤ Acgen ≤ 0.70) and low (Acgen ≤ 0.50). Excepting for CD, in this study, the accuracy estimates were high, demonstrating high accuracy in the assessment of the true genetic variation based on the phenotypic variation observed in every trait. For CD, the low accuracy was probably caused by the high environmental influence, which disqualifies this characteristic for selection procedures in *Toona ciliata*.

The low interaction with age, observed by the genotypic correlations during measurements (Rgmed), for the characteristics evaluated, demonstrates that selection can be performed at any of the development stages used for measurements.

The best precision in relation to the uniformity in the repetition of the character CV demonstrates that it is the best characteristic to be used for selection, because it expresses the best genetic control. However, since this variable is more difficult to be quantified, it can be concluded that the best option is the selection by DBH because it expresses high uniformity in the sequential evaluations, it is easy to quantify and presents high correlation with the character CV (Table 4). It corroborates the affirmations of Martins et al. (2003) and Sampaio et

Table 4 – Pearson correlation coefficients among the characteristics diameter at breast height (DBH), stem diameter (SD), distance between nodes (Internodes), canopy diameter (CD), height (H) and cylindrical volume (CV).

Variable	DBH	D.Stem	Internode	CD	H	CV
DBH		0.7353**	0.4073	-0.0094	0.2180	0.9391**
SD	0.7353**		0.3613	-0.1216	0.0098	0.6383*
Internode	0.4073	0.3613		-0.206	0.3547	0.4707
CD	-0.0094	-0.1216	-0.2060		0.3116	0.0896
H	0.2180	0.0098	0.3547	0.3116		0.5149*
CV	0.9391**	0.6383*	0.4707	0.0896	0.5149*	

**,*, significant 1 % and 5 % by the T test.

Table 3 **–** Efficiency of the use of measurements of the same individual over time for the traits diameter at breast height (DBH), height (H), cylindrical volume (CV), stem diameter (SD), distance between nodes (Internodes) and canopy diameter (CD) in *Toona ciliata.*

measurements	Accuracy					
	DBH	H	CV	SD	Internodes	CD
m						
1	0.6662	0.6247	0.6907	0.6125	0.6308	0.2369
2	0.7840	0.7493	0.8037	0.7386	0.7545	0.3260
3	0.8398	0.8109	0.8558	0.8019	0.8153	0.3891
4	0.8726	0.8480	0.8859	0.840	0.8518	0.4383
5	0.8942	0.872	0.9056	0.8661	0.8762	0.4787
6	0.9095	0.8907	0.9195	0.8847	0.8936	0.5128
7	0.9209	0.9042	0.9298	0.8987	0.9068	0.5421
8	0.9298	0.9146	0.9378	0.9097	0.9170	0.5678
9	0.9369	0.9231	0.9441	0.9186	0.9252	0.5904
10	0.9426	0.9300	0.9493	0.9258	0.9319	0.6107

al. (2002), who recommended selection with fulcrum in DBH, also due to easy evaluation and accuracy. However, the most important reason is the high additive genetic correlation with height and volume.

Selection and estimates of gains

Thirty-three genotypes were selected (Table 5), out of the 90, corresponding to 36.6 % of the populations investigated for the characteristic CV. These materials presented averages higher than the general average, achieving relative performance higher than 96 %. The genotype 3, located in Triunfo, occupied the first position in the ranking for CV, with genotypic value equal to 0.0373 and new average of 0.1493 m^3, caused by the increase in 24.9 % in the general average for the character. The genotype presenting the best ranking position for Trajano was that of the order 31, which occupied, for CV, the fourth position in the hierarchy. Its genotypic value was 0.0347 and the new average, 0.1479 m^3, revealing an increase in 24.2 % in the general average. Regarding the location of Imbé, the genotype 61 stood out by achieving the best position in the ranking, occupying the third position for CV, genotypic value of 0.0349 and new average of 0.1483 m^3, characterizing an increase in 24.4 % in the general average for the character. Finally, the genotype of the order 76 was the last to be selected for the characteristic CV, and it was allocated in the 33rd position in the ranking, with genotypic value of 0.0004 and new average of 0.1231 m^3, corresponding to an increase in 9.0 % in the general average for the character.

Table 5 – Genotype ordination for the best genetic value, average and genetic gain, for the trait cylindrical volume (CV).

order	genotype	g	u+g	*Genetic gain*	New average	*u+g+gem*
1	3	0.0373	0.1493	0.0373	0.1493	0.1529
2	9	0.0366	0.1486	0.0369	0.1490	0.1521
3	61	0.0349	0.1470	0.0363	0.1483	0.1503
4	31	0.0347	0.1467	0.0359	0.1479	0.1501
5	36	0.0328	0.1448	0.0353	0.1473	0.1480
6	66	0.0293	0.1413	0.0343	0.1463	0.1441
7	55	0.0150	0.1270	0.0315	0.1435	0.1285
8	85	0.0130	0.1250	0.0292	0.1412	0.1262
9	15	0.0127	0.1247	0.0274	0.1394	0.1260
10	62	0.0102	0.1222	0.0256	0.1377	0.1232
11	32	0.0101	0.1221	0.0242	0.1363	0.1231
12	30	0.0095	0.1215	0.0230	0.1350	0.1224
13	5	0.0089	0.1210	0.0219	0.1339	0.1218
14	48	0.0089	0.1209	0.0210	0.1330	0.1218
15	65	0.0085	0.1205	0.0202	0.1320	0.1214
16	75	0.0074	0.1195	0.0194	0.1314	0.1202
17	64	0.0062	0.1182	0.0186	0.1306	0.1188
18	52	0.0056	0.1176	0.0179	0.1299	0.1181
19	70	0.0051	0.1171	0.0172	0.1292	0.1176
20	68	0.0051	0.1171	0.0166	0.1286	0.1176
21	34	0.0045	0.1165	0.0160	0.1280	0.1170
22	6	0.0037	0.1157	0.0154	0.1275	0.1161
23	60	0.0037	0.1157	0.0149	0.1270	0.1160
24	10	0.0036	0.1157	0.0145	0.1265	0.1160
25	33	0.0032	0.1152	0.0140	0.1260	0.1155
26	18	0.0031	0.1151	0.0136	0.1256	0.1154
27	35	0.0027	0.1147	0.0132	0.1252	0.1150
28	2	0.0025	0.1146	0.0128	0.1248	0.1148
29	11	0.0024	0.1144	0.0124	0.1245	0.1146
30	50	0.0012	0.1133	0.0121	0.1241	0.1134
31	40	0.0007	0.1128	0.0117	0.1237	0.1128
32	78	0.0005	0.1125	0.0114	0.1234	0.1125
33	76	0.0004	0.1124	0.0110	0.1231	0.1125

g= genetic value, u= average, gem=genetic environmental effect.

The progress expected with the selection depends on the heritability of the character, intensity of selection and phenotypic standard deviation of the character (Cruz and Carneiro, 2004). In accordance with that, the values of repeatability achieved in the present research allow the prediction of excellent possibilities of genetic gains, mainly via DBH, by its parametric estimates higher than the height, since it is strongly related to the characteristic CV (Table 4). It allows one to infer that the selection process will also provide satisfactory results for timber volume, which is one of the most economically important characteristics for forest species.

Particularly for the characteristic timber volume, the lower correlation occurred for larger canopy diameter, with diameter at breast height. Through a global analysis, the lower correlation between two characteristics occurred between the canopy diameter and the distance between nodes (Table 4). The characteristics stem diameter (SD) and distance between nodes (Internodes) present values consistent with the values for growth characteristics.

The canopy diameter revealed that, for the genotype 5, it is possible to achieve an increase in 21.13 % in the average, designing a new average of 311.1045 centimeters. However, there must be caution with such inference, since canopy diameter was the characteristic that expressed the lowest correlation with cylindrical volume, according to Table 4.

Stability of genetic values

The results of simultaneous genotype ordering by their genetic values (productivity) and stability, related to the genotypic stability by the harmonic mean method of the genotypic values, according to Resende (2004), found in the Tables 6 and 7, clarify the genotypic behavior through the measurements, since the lower the standard deviation, the higher the harmonic mean of its genotypic values over time.

The prediction based on the harmonic mean allows the selection by productivity and stability, simultaneously, in opposition to the procedure based on arithmetic average, which is suitable for the selection only by productivity. Thus, the selection by the criterion that employs the highest estimates of the harmonic means of the genotypic values (MHVG) is an excellent strategy, allowing safe inferences about the prediction of the genetic values, with the advantage of gathering in a single selection criterion both productivity and stability.

Table 6 – Stability of genetic values (MHVG), for the characteristics diameter at breast height (DBH), height (H) and cylindrical volume (CV).

order	Character					
	genotype	MHVG	genotype	*MHVG*	genotype	*MHVG*
1	9	13.2423	31	10.3120	3	0.1451
2	31	13.1953	3	10.2226	9	0.1448
3	66	13.1358	36	10.1827	31	0.1438
4	36	13.1303	61	10.1059	61	0.1428
5	61	13.0778	63	10.0673	36	0.1408
6	3	12.9111	90	10.0287	66	0.1379
7	85	12.6400	62	9.9829	55	0.1195
8	15	12.6187	33	9.9778	15	0.1189
9	32	12.4201	60	9.9622	85	0.1184
10	55	12.3994	34	9.9161	32	0.1157
11	75	12.2056	48	9.9151	48	0.1141
12	48	12.1274	23	9.8839	62	0.1139
13	18	12.0925	35	9.8548	5	0.1134
14	70	12.0780	89	9.8397	75	0.1128
15	5	12.0409	9	9.8358	30	0.1123
16	52	12.0238	59	9.8315	65	0.1109
17	68	12.0208	17	9.8304	52	0.1108
18	2	12.0058	5	9.8290	70	0.1097
19	10	11.9924	52	9.8230	68	0.1084
20	14	11.9849	88	9.8190	34	0.1084
21	73	11.9828	30	9.8179	64	0.1081
22	11	11.9590	71	9.8167	10	0.1074
23	76	11.9574	25	9.8148	18	0.1072
24	62	11.9383	66	9.8090	60	0.1072
25	6	11..8964	21	9.7827	6	0.1066
26	8	11.8779	29	9.7815	33	0.1063
27	69	11.8577	65	9.7810	2	0.1063
28	50	11.8497	16	9.7743	35	0.1055
29	34	11.8425	80	9.7711	11	0.1053
30	78	11.8360	55	9.7578	50	0.1048
31	64	11.8109	56	9.7517	71	0.1041
32	65	11.8026	54	9.7173	17	0.1036
33	60	11.7525	44	9.7051	76	0.1029

Table 7 – Stability of genetic values (MHVG), for the characteristics stem diameter (SD), distance between nodes (internodes) and canopy diameter (D.Canopy).

order	Character					
	genotype	MHVG	genotype	*MHVG*	genotype	*MHVG*
1	85	16.1023	89	14.3659	5	350.7697
2	66	15.6169	63	14.1522	61	264.1766
3	14	15.6003	74	13.6092	31	257.3581
4	52	15.4751	59	13.6023	35	256.6419
5	68	15.4074	72	13.5812	76	254.2714
6	36	15.3843	19	13.5797	68	253.5553
7	9	15.3782	46	13.5103	74	253.4823
8	70	15.3648	66	13.4577	34	253.0608
9	55	15.3027	33	13.4116	32	252.4194
10	40	15.1854	32	13.3576	18	250.9397
11	32	15.1524	15	13.3495	69	250.0714
12	15	15.0589	80	13.3417	30	249.3698
13	64	15.0552	44	13.2445	46	248.0189
14	67	15.0157	28	13.2241	67	247.9460
15	48	15.0092	42	13.2184	66	247.8256
16	28	14.9853	26	13.1891	37	247.7625
17	26	14.9176	3	12.9538	78	246.9891
18	50	14.8963	62	12.9121	33	246.8231
19	18	14.8861	57	12.9071	50	246.3116
20	27	14.8760	36	12.8112	14	245.9909
21	59	14.8545	5	12.6722	56	245.5374
22	61	14.8064	1	12.6569	53	245.4124
23	75	14.7842	25	12.6357	62	245.0744
24	29	14.7280	50	12.5980	70	244.7079
25	69	14.7091	20	12.5771	64	244.4918
26	83	14.6988	22	12.5609	58	244.2800
27	37	14.6607	61	12.5428	73	244.2194
28	57	14.6501	76	12.5427	86	243.7336
29	8	14.6406	48	12.4796	43	243.5996
30	82	14.6339	2	12.4762	65	243.4292
31	53	14.5971	41	12.4527	40	243.4207
32	31	14.5517	51	12.4078	60	243.1728
33	3	14.5298	87	12.3995	85	242.7503

The selection of the 45 individuals ranked according to the highest genetic values is concordant in 92.10 % for DBH, in 91.11 % for height and in 96.96 % for cylindrical volume, with the ranking according the average components. Genotype 9 stood out for DBH, while for H, the 31 was the first and for CV, the genotype 3 was the best.

The identification of genotypes with high yield and yield stability and wide adaptability to various environments is one of the main goals of forest species breeding programs; in this case the method MHVG is a breakthrough because it is based on an analysis of predicted genotypic values via a mixed model methodology (Verardi et al., 2009).

The method of mixed models (REML/BLUP) applied via the SELEGEN software system, using the BLUP procedure at individual level and repeated measures in each individual proved to be adequate to estimate the genetic parameters and predict genotypic values in situations of unbalanced data. Therefore, it is very useful and practical for *Toona ciliata* genetic breeding programs.

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