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ARTICLE

Evaluation of different selection indices combining Pilodyn penetration and growth performance in *Eucalyptus* clones

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Abstract: *The present study aimed to evaluate the selection indices efficiency for Pilodyn penetration combined with growth traits in Eucalyptus clones. It was carried out experiments in a randomized block design, with single tree plots and 30 replications. Diameter at breast height (DBH), total height (TH), and Pilodyn penetration as an indicator of basic density (BD) were measured. The volume was estimated. Based on predicted genotypic values, three indices presented the highest accuracies: I_8 (based on partial correlation), I_7 (based on the concept of multivariate BLUP) and I_3 (based on two variables as ratio, which uses a third heritability estimate associated to the ratio DBH/BD, besides the two heritabilities of DBH and BD). Thus, it is possible to optimize the selection by combining properly the variables using their genetic control, precision and the relationships between them. The best options came from using only two no redundant traits DBH and BD.*

Key words*: Selection criteria, accuracy, wood quality, partial correlation, path analysis.*

INTRODUCTION

Part of the increase in forest production is attributed to breeding programs (Costa et al. 2015). In this scenario, evaluation, characterization and selection of superior genotypes are critical steps in a forest breeding program that aims at maximizing genetic gain (Resende 2002, Bhering et al. 2015). Therefore, it is essential that the breeder carefully sets the goal of the selection, as well as the criteria that will be used to properly manage the breeding population and to generate significant gains in relation to the final commercial product.

Wood quality and volumetric analyses are essential in *Eucalyptus* improvement directed for pulp production (Gomide et al. 2010, Protásio et al. 2014). Although tree volume measurement is commonplace, wood quality studies are costly and time-consuming (Raymond and Apiolaza 2004). Basic density has been considered to be a universal index for assessing the quality of the wood, providing indirect information about other technological traits (Gomide et al. 2010). In spite of basic density importance, its determination is difficult due to high cost and need for tree felling.

Considering these fact, the Pilodyn method has been successfully applied for indirect estimation of wood basic density without to fall the tree (Gouvêa et

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al. 2011, Couto et al. 2013, Neves et al. 2013). With indirect estimation of basic density and information of tree growth (volume), the genetic selection of superior materials is technically correct.

Thus, in order to adopt more complex criteria to select superior genotypes considering several traits simultaneously, selection index theory can be employed. This theory was first described by Smith (1936), and later by Hazel (1943). According to Freitas et al. (2012), indices allow using a single value to select genotypes, since analysis is carried out by linear combinations of phenotypic data of many characters in study, whose weighting coefficients are estimated in order to maximize the correlation between the index and the true breeding values.

In addition, selection index is more efficient than direct selection, since it enables the distribution of gains between the several traits, in a more homogeneous way and in accordance with the purposes of the breeding program, generating higher total gain (Reis et al. 2011, Freitas et al. 2012, Cruz et al. 2014). Thus, these actions may greatly contribute to maximize the cost/benefit of the breeding program.

Several selection indices have been used for multivariate evaluation of characters of interest in different cultures, particularly *Eucalyptus* (Martins et al. 2006, Reis et al. 2011, 2015). Despite their importance, these indices are based on phenotypic values and do not consider the genotypic correlation and the cause and effect relationships between variables. According to Resende et al. (2014), the use of multivariate mixed models with multiple traits and unstructured covariance matrix is theoretically the most efficient method, and allows considering heterogeneity of variances and covariances. However, in practice, this approach is not used, due to the difficulty in convergence of the iterative analysis and the super parameterization (Resende et al. 2014).

Thus, structural equation modeling is an alternative that allows efficiently representing the standard multi-trait model (Resende et al. 2014). With a functional network of studied traits, it is possible to establish cause and effect relationships between the variables of interest and to compose optimum selection indices using the genotypic values predicted by univariate analysis by the REML/BLUP procedure (Maximum Restricted Likelihood/Best Linear Unbiased Prediction) (Resende et al. 2014, Viana and Resende 2014).

Therefore, the present study investigated the effectiveness of new classes of selection criteria based on partial correlations, direct effect of path analysis, ordinary correlations and heritability for *Eucalyptus*, using genotypic values predicted through the mixed models methodology.

MATERIAL AND METHODS

Experimental network

Experiments were carried out in the areas of CMPC Celulose Riograndense Company, in the municipalities of Minas do Leão (lat 30° 11' S, long 52° 00' W, alt 141 m asl, average temperature 17.5 ºC and annual precipitation 1,422 mm), Encruzilhadas do Sul (lat 30° 27' S, long 52° 39' W, alt 250 m asl, average temperature 17 ºC and annual precipitation 1,368 mm), Dom Feliciano (lat 30° 29' S, long 52° 19' W, alt 378 m asl, average temperature 16 ºC and annual precipitation 1,564 mm) and Vila Nova do Sul (lat 30° 14' S, long 53° 49' W, alt 301 m asl, average temperature 16.8 ºC and annual precipitation 1,133 mm), which are located in the state of Rio Grande do Sul (climate Cfa, according to the climatic classification of Koppen) Brazil. A network of clonal trials with 864 *Eucalyptus* clones was set in 2007. Trees were planted at a spacing of 3.5 x 2.6 m. At each site, it was established an experiment in a randomized block design, with single tree plots and 30 replications.

Data collection

For the indirect estimate of basic density, Pilodyn's method (Greaves et al. 1996) was used when trees were three years old. The measurement with Pilodyn was carried out twice, on each north and south cardinal aspects of the tree. For analysis, the considered number was the mean of the two measurements. It was considered the inverse of Pilodyn penetration depth (mm) as the estimated basic density (BD).

Growth data of the trees were collected at three years of age, as well as the estimated basic density. It was measured the diameter at breast height (DBH), in centimeters (cm), and the total height (TH) of trees, in meters (m). DBH was

measured with the aid of a diameter tape, and TH was obtained using a relascope.

To calculate the volume (m^3) without bark (Vol), the model of Leite et al. (1995) was used, as shown below:

$$Vol = 0.000048 \times DBH^{1.720493} \times TH^{1.180736} \times e^{(-3.00555)\times(tx/dbh)x[1-(d/dbh)^{1+0.228531\times d}]} + E$$

In which *DBH*: diameter at 1.3 meters height; *TH*: total height; tx = 0, for the volume with bark and 1 for volume without bark; d: superior commercial diameter; *E* = experimental error.

Statistical analysis

The statistical model for analysis of this experimental network in several environments (Resende 2002), with single tree plots is given by $y = Xr + Zg + Hb + Wge + e$, where: *y*, *r*, *g*, *h*, *ge* and *e* are vectors of data, replication effects (fixed), genotypic effects (random), block effects (random), effects of genotype x environment interaction (G x E) (random), and random errors, respectively. In addition, *X*, *Z*, *H* and *W* are the incidence matrices for *r*, *g*, *h* and *ge*, respectively. Predicted genotypic values free of interaction, considering all the environments were given by $u + g$, in which *u* is the mean of all sites. These values predicted for each variable, using univariate analysis, will be used in the selection indices. In addition, it was also obtained the genetic correlations between the analyzed variables. All analyses were carried out using the Selegen-REML/BLUP software (Resende 2016).

Selection Indices

It follows a description of the index used in this paper (Table 1). Details of them and their accuracies are presented by Viana and Resende (2014) and Resende et al. (2014).

Table 1. Description of the indexes and their accuracies used

Concept	Index[1]	Description	Accuracy[1]
Phenotypic index	I_1	$I_1 = \left(\frac{DBH}{S_{DBH}}\right)\left(\frac{DB}{S_{DB}}\right)$	$r_{g\hat{g}} = \sqrt{\frac{n \times h^2}{1 + (n-1) \times h^2}}$
	I_2	$I_2 = \left(\frac{Vol}{S_{Vol}}\right)\left(\frac{DB}{S_{DB}}\right)$	
Optimum index using a ratio between two variables	I_3	$I_3 = LogDBH - Log(1/BD)$	$r_{g\hat{g}} = \sqrt{\frac{n \times h^2_{y*}}{1 + (n-1) \times h^2_{y*}}}$
	I_4	$I_4 = LogVol - Log(1/BD)$	
Genotypic index	I_5	$I_5 = \left(\frac{VG_{DBH}}{S_{VG_{DBH}}}\right)\left(\frac{VG_{BD}}{S_{VG_{BD}}}\right)$	$Ac_{I5} = \frac{sd(I5) \times Ac(I3)}{sd(I3)}$
	I_6	$I_6 = \left(\frac{VG_{Vol}}{S_{VG_{Vol}}}\right)\left(\frac{VG_{BD}}{S_{VG_{BD}}}\right)$	$Ac_{I6} = \frac{sd(I6) \times Ac(I4)}{sd(I4)}$
Multivariate BLUP index	I_7	$I_7 = b_1 g_0 + b_2 g_{a1} + b_3 g_{a2}$	$r_{g\hat{g}} = \sqrt{Var(Index)/\sigma^2_g}$
Partial correlation index	I_8	$I_8 = b_1 g_0 + b_2 g_{a1} + b_3 g_{a2}$	$r_{g\hat{g}} = \frac{sd(score\ I_x)}{sd(score\ I_{greater})}$
Ordinary correlation index	I_9	$I_9 = b_1 g_0 + b_2 g_{a1} + b_3 g_{a2}$	
Path analysis index	I_{10}	$I_{10} = b_1 g_0 + b_2 g_{a1} + b_3 g_{a2}$	

[1] Description of the indexes components and accuracies: *BD*: basic density indirectly estimated by the Pilodyn's method; *DBH*: diameter at breast height; S_{DBH}: standard deviation of diameter at breast height; S_{Bd}: standard deviation of basic density; *Vol*: volume of wood without bark; S_{Vol}: standard deviation of the volume without bark; *Log*(1/*BD*): inverse of the basic density indirectly estimated by the Pilodyn's method on the logarithmic scale; *LogDBH*: diameter at breast height on the logarithmic scale; *LogVol*: volume of wood without bark on the logarithmic scale; VG_{BD}: genotypic value of the indirectly estimated basic density; VG_{DBH}: genotypic value of the diameter at breast height; $S_{VG_{DBH}}$: standard deviation of the genotypic value of the diameter at breast height; $S_{VG_{BD}}$: standard deviation of the genotypic value of the basic density; VG_{Vol}: genotypic value of volume without bark; $S_{VG_{Vol}}$: standard deviation of the genotypic value of Vol; g_o: standard genotypic value of the objective character (DBHxBD); g_{ai}: is the standard genotypic value of the auxiliary characters (DBH and BD). The weighting coefficients (b_i) of the index are given by (Viana and Resende 2014); r_{gg}: accuracy of the index; *n*: number of individuals per clone; h^2_{y*}: heritability of the ratio between two variables given by Resende et al. (2014); h^2: heritability of the phenotypic index; Ac_{I5}: accuracy of the I_5 genotypic index; *sd*(*I*5): standard deviation of the I_5 genotypic index score; *Ac*(*I*3): accuracy of the I_3 optimum index; *sd*(*I*3): standard deviation of the I_3 optimum index score; Ac_{I6}: accuracy of the I_6 genotypic index; *sd*(*I*6): standard deviation of the I_6 genotypic index score; *Ac*(*I*4): accuracy of the I_4 optimum index; *sd*(*I*4): standard deviation of the I_4 optimum index score; $Var(Index)/\sigma^2_g$: ratio between the index and additive variances of the objective trait; *sd*(*score* I_x): standard deviation of the I_8, I_9 or I_{10} indexes score;*sd*(*score* $I_{greater}$): standard deviation of the score of the index with greater variance among I_7 and I_{10}.

Internal consistency of the indices

As mentioned by Resende et al. (2014), a comparison between alternative selection indices may be carried out by varying the degree of covariance of the variables between each other. Thus, the Cronbach's alpha coefficient (1951) (modified by Resende et al. (2014)) works as an indicator of internal consistency of an index involving n variables. Its formula is given by:

$$\alpha = \frac{n-1}{n}\left(1 - \frac{\Sigma \upsilon_i^2}{\upsilon_t^2}\right)$$

In which $\Sigma \upsilon_i^2$ = sum of the variances of the n variables; υ_t^2 = total variance of the scores of the selection index; n = number of variables.

RESULTS AND DISCUSSION

Genetic parameters and genetic correlations

Genetic parameters of the analyzed traits were estimated (Table 2). Since the present study only aims to evaluate the different selection criteria, genetic parameters related to G × E interactions are not reported here, but the full publication on that can be found in Nunes et al. (2016).

Estimates of individual heritability of the studied characters may be considered low (h_g^2 = 0.07 for TH), moderate (from 0.15 for Vol, to 0.23 for I_1), and high (0.59 for BD), Table 2, according to the classification reported by Resende (2002). Elevated heritability value for basic density (0.64) was found by Wei and Borralho (1997) in *Eucalyptus urophylla* S.T. Blake. Muneri and Raymond (2000) and Kube et al. (2001) also reported high values of heritability for Pilodyn penetration and basic density, ranging from 0.60 to 0.70. In spite of high genetic control of basic density, the heritability for growth traits have been reported in literature ranging from 0.10 to 0.22 (Kube et al. 2001), which corroborates with the present work.

Notwithstanding the estimate of broad sense individual heritability, it is observed that the value of this parameter for I_2 (0.16) was similar to the heritability of Vol (0.15), Table 2. Thus, there is the need to develop an index which enables the estimate of a balanced heritability, i.e., that not only resembles to only one of the traits of the index. The same reasoning can be applied to I_1.

Table 2. Estimates of genetic parameters (individual REML) and genotypic correlations (below the genetic parameters) for basic density (BD in kg m^{-3}), diameter at breast height (DBH in cm), total height (Th in m), volume (Vol in m^3 ha^{-1} year), phenotypic index DBH×BD (I_1), and phenotypic index Vol×BD (I_2) for *Eucalyptus* clones evaluated in the joint analysis between environments, at three years of age

Parameters[1]	BD	DBH	Th	Vol	I_1	I_2
h_g^2	0.59	0.18	0.07	0.15	0.23	0.16
h_{mg}^2	0.95	0.70	0.54	0.65	0.78	0.67
Acgen	0.97	0.84	0.73	0.80	0.88	0.82
c_{bloc}^2	0.24	0.03	0.08	0.05	0.15	0.07
Overall mean	382.64	13.26	14.72	0.08	6.03	44.92
CVgi (%)	12.39	8.16	5.09	17.89	12.04	19.20
CVe (%)	9.70	15.71	16.50	37.80	20.20	40.08
CVr	1.27	0.51	0.30	0.47	0.59	0.47
	BD	DBH	Th	Vol	I_1	I_2
BD	-	-0.27	-0.01	-0.22	0.67	0.26
DBH		-	0.66	0.97	0.49	0.81
Th			-	0.77	0.48	0.71
Vol				-	0.52	0.86
I_1					-	0.86
I_2						-

[1] Description of genetic parameters: h_g^2 : coefficient of individual heritability in the broad-sense (corrected to variance of block), free from interaction; h_{mg}^2 : heritability of clone mean; *Acgen*: genetic accuracy in clone selection; c_{bloc}^2 : coefficient of determination of block; Overall mean: overall mean of characters between different environments; *CVgi* (%): coefficient of genotypic variation; *CVe* (%): coefficient of experimental variation; *CVr* coefficient of relative variation.

Prediction accuracy of genetic values of the clones was high (Table 2). According to Resende and Duarte (2007), accuracies above 0.70 are sufficient for evaluations in a breeding population, and when the goal is the evaluation of the Value of Cultivation and Use, accuracies must be greater than 0.90. These high accuracy levels justify the great experimental quality, the caution and the technical precision in the establishment and evaluation of experiments. Moreover, the high number of replications (30) enabled obtaining reliable results of clones ranking by their predicted genetic values.

The value of coefficient of environmental variation (*CVe*) for I_2 (40.08) was twice as higher as the *CVe* of I_1 (20.20) (Table 2). The prediction accuracy of the breeding values of I_2 (0.82) was relatively lower than the prediction accuracy of I_1 (0.88). These results show that I_1 is more accurate than I_2. This fact corroborates with the highest value of *CVe* of Vol in relation to the *CVe* of DBH (Table 2). Considering that the growth traits Vol and DBH make up the indices I_2 and I_1, respectively, by multiplying by BD, the difference in accuracy and in *CVe* between these two indices is related to greater uncertainty in the estimate of Vol. Thus, since the estimate equation of Vol is composed of DBH and TH, the inclusion of the latter in the estimate of Vol led to higher value of *CVe* and lower accuracy of I_2, in relation to I_1.

Genotypic correlations between characters was estimated (Table 2) and it was found high correlation value between DBH and Vol (0.97). Nunes et al (2016) reported that is advantageous to perform the indirect selection of *Eucalyptus* clones aiming at gains in Vol through DBH. Negative values of genetic correlation between BD and DBH, and BD and Vol evidence the need for the study of selection indices involving wood quality and growth characters, simultaneously. Negative values (Kube et al. 2001, Bison et al. 2006) and positive values (Paula et al. 2002, Reis et al. 2011) of genetic correlation between basic density in *Eucalyptus* and growth characters were reported by different authors. Thus, discrepancies in genetic correlations in each cited work are caused by the genetic variation that exists in the evaluated population and by the different genes that are segregating in relation to the control of growth and wood quality characters (Reis et al. 2011).

Heritability and correlations of optimal indices based on a ratio between two variables

The genetic analyses of a trait using variables as a ratio seems to be unused in forest tree breeding so far. This paper is the first one to evaluate its effectiveness. The results have shown that it is a very promising technique. It was ranked among the three best out of the ten selection indices evaluated.

When comparing the heritability of the phenotypic indices (Table 2), I_1 (0.23) and I_2 (0.16), with the heritability of I_3 and I_4 (Table 3), an increase is observed in the genetic control, and therefore, greater efficiency of these last indices is also observed. For I_3, there was a 37% increase in relation to the phenotypic heritability index, while for I_4, this increase was 18%. These results show that I_3 and I_4 were more efficient than the phenotypic indices in weighing the genotypic values for each variable under study, and thus they were more efficient in weighting the effects of each variable on the index as a whole.

It is observed that the calculated heritability (optimum) of I_4 was lower than the heritability of I_3 (Table 3). This fact can be explained since the elasticity coefficient (K^2) of I_4 (0.53) was lower than the K^2 of I_3 (1.05) (Table 3). Thus, the I_4 had its calculated heritability penalized by the higher variance of volume (Vol), when compared with the variance of the diameter at breast height (DBH). Therefore, I_3 index is more accurate and ideal for selection of superior genotypes in relation to I_4, due to greater accuracy in the measurement of DBH, when compared with the estimate of Vol.

Correlations between indices based on a ratio between two traits and their constituent variables were calculated (Table 3). Genotype correlations of the constituent variables

Table 3. Heritabilities and correlations of a ratio between two variables

Coefficients[1]	I_3	I_4
h^2_{y*}	0.60	0.34
r^g_{y*W*}	0.58	0.65
r^g_{y*x*}	-0.63	-0.61
r^p_{y*W*}	0.30	0.70
r^p_{y*x*}	-0.37	-0.18
k^2	1.05	0.53
k^2_h	1.02	1.77
k	1.03	0.72
k_h	1.01	1.33

[1] Description of the coefficients: h^2_{y*} : heritability of the ratio between two variables (optimum index); r^g_{y*W*}: genotypic correlation of the index with the variable W*, which for I_3 is DBH, and for I_4 is Vol; r^g_{y*x*}: genotypic correlation of the index with variable X*, which for both indices is 1/BD; r^p_{y*W*}: phenotypic correlation of the index with variable W*, which for I_3 is DBH, and for I_4 is Vol; r^p_{y*x*}: phenotypic correlation of the index with the variable X*, which for both indices is 1/BD; k^2: elasticity or relationship between variances, being the phenotypic variance of X (always BD) in the numerator, and the phenotypic variance of W (DBH or Vol) in the denominator; k^2_h: ratio between heritability of variable X (BD) estimated in the original scale and the calculated heritability of the ratio between two variables; k: square root of k^2; k_h: square root of k^2_h. As mentioned in the material and methods, coefficient details can be found in Resende et al. (2014).

of each phenotypic index with these same indices (Table 2) were different from these obtained for I_3 and I_4. The negative correlation between BD and I_3/I_4 is justified, since for calculating the ratio between two variables, it was necessary to carry out analyses considering 1/BD. Therefore, for comparison, it should be noted the magnitude of the correlation, not the negative signal. Thus, it is evident that indices based on the ratio between two variables do not present high correlation with only one of the component character of this index, as found for I_1 and I_2. I_3 and I_4 indices provide a better balance between the two variables that compose it. I_3 presented genotypic correlation with DBH in the order of 0.58 and with 1/BD of -0.63 (Table 3), while I_1 genetic correlation with DBH and BD is 0.49 and 0.67, respectively (Table 2).

Efficiency of selection indices

According to the accuracy values, it can be concluded that the most effective indices are I_8, I_7, I_3, I_5 and I_{10}, while I_6 presents the lowest accuracy value, along with I_9 (Table 4). In general, prediction accuracies were high. This result was obtained due to the high number of replications and consistency in setting up and running the experiment. According to Resende and Duarte (2007), accuracies above 0.90 are considered too high and ensure reliable selection of superior genetic materials, as obtained for I_8, I_7, I_3, I_5, I_{10} and I_4.

This result corroborates the fact that partial correlations and path analyses (I_8 and I_{10}) are more efficient procedures than the ordinary correlations of Pearson (I_9), since they are conditional correlations, unlike the latter (Cruz et al. 2014, Resende et al. 2014). Thus, in the composition of I_8 and I_{10} indices, genotypic values are optimally weighted, and the considered correlations are odd (Resende et al. 2014), and there is no overestimation or underestimation of the index score.

As a report by Resende et al. (2014), for the analysis of a multivariate vector of observations of several traits, the multivariate mixed model is theoretically the most efficient, since it allows considering the complete heterogeneity of variance and covariance. Also, according to these authors, in practice, the use of the multivariate mixed model does not apply, due to the problematic convergence of the iterative analysis and super parametrization. Thus, it is important to use optimum selection indices that incorporate the concept of multivariate BLUP, by global maximization; the use of genotypic correlations and heritabilities; as well as the indices based on the concept of structural equation (Resende et al. 2014). This new approach becomes crucial for the optimization of the selection process, since it generates the same results of the multivariate mixed model, with less effort and high accuracy. In this context, the indices developed in this work can be used for any species and in any situation, in order to optimize the process of selection of superior genetic materials.

According to Resende et al. (2014), the use of structural equations (path analysis) is similar to the use of partial correlation matrices, instead of total correlations. This reduces the complexity of the multivariate mixed model, since it works with clean correlations between each pair of variables, making full rank the covariance matrices (Resende et al. 2014). In the present study, the index of greater efficiency was I_8, which is based on partial correlations between DBH × BD with DBH and BD. However, I_{10}, based on the direct effect of path analysis also showed high accuracy. Thus, it is verified the equivalence of the use of structural equation models and partial correlations, since the path analysis depends on the partial correlations, as reported by Resende et al. (2014).

Among the three best indices, I_3 was slightly higher, since it has greater internal consistency measured by the alpha coefficient. Internal consistency of an index may be studied by the degree of covariance of the variables between each other. Cronbach's alpha coefficient (1951) can be used as an indication of consistency of an index involving these variables (Resende et al. 2014). Thus, the higher the value of the coefficient, the more reliable is the index. I_3, I_5 and I_1 presented the highest internal consistencies (0.50). According to Resende et al. (2014), the lower the specific variance of each variable and the higher the total variance that they produce together, the higher is the alpha coefficient. Thus, when the sum of the variances of the individual variables is reduced, it increases the variance they have in common, that is, the one that ensures the coherence or internal consistency of the index (Resende et al. 2014). Therefore, it is verified that the constituent variables of these indices combine well, i.e., they covary in the index to which they belong (Resende et al. 2014).

The I_5 index presented high accuracy, and was higher than I_1 (Table 4). The index with the use of genotypic values proves to be more efficient, when compared to the phenotypic index. Resende (2002) reports that the use of genotypic

values will be advantageous when genetic correlations of the variables are close to zero, and when prediction accuracies of genetic values for each character, individually, are high. Such conditions for success in the use of genotypic index are found in the present study, in which the genetic correlation between DBH and BD is null (-0.27) (Table 2), and the prediction accuracies for these two characters are high (0.97 for BD, and 0.84 for DBH) (Table 2). If these conditions are not met, I_8, I_7 or indices based on a ratio between two variables should be used, since they take into account the accuracy of each trait, their correlation and the relationship between variances of the constituent variables of the index.

Genotypic index in function of DBH×BD (I_5), which considers only the heritability of the characters, was as efficient as I_3, which optimally weighs the genotypic values by heritability and correlations between variables. However, since I_3 is optimum by the above mentioned reasons, it was more efficient (Table 4), and should be used especially in experiments in which the constituent variables of the index have non-null genotype correlations. Contrary to what happened to I_5 (0.95 accuracy), I_6 (0.78 accuracy) is the least efficient index. This result can be explained given that the conditions for use of the genotypic indices cited by Resende et al. (2002) are not met in the case of I_6, due to the inherent imprecision of Vol.

Table 4. Accuracies and Cronbach's alpha coefficients (1951) for I_1, I_2, I_3, I_4, I_5, I_6, I_7, I_8, I_9, I_{10} indices, which are based on the concepts of phenotypic index, ratio between two variables (Resende et al. 2014), genotypic index, multivariate blup (Viana and Resende 2014), partial correlation (Viana and Resende 2014), ordinary correlation and direct effects of path analysis (Resende et al. 2014), respectively

Concept	Index	Acurracy	Alfa[4]
Partial Correlelation	I_8	1.00	0.18
Mult Blup[2]	I_7	0.97	0.20
RBTV[1]	I_3	0.96	0.50
Genotypic	I_5	0.95	0.50
Path[3]	I_{10}	0.92	0.20
RBTV[1]	I_4	0.91	-[5]
Phenotypic	I_1	0.88	0.50
Phenotypic	I_2	0.82	-[5]
Ordinary correlation	I_9	0.79	0.21
Genotypic	I_6	0.78	0.49

[1] RBTV: Ratio between two variables; [2] Multi Blup: multivariate Blup; [3] Path: direct effect of path analysis; [4] Cronbach's alpha coefficient (1951) modified by Resende et al. (2014); [5] Negative value.

For the first time in the literature, it was compared so many selection indices, using somehow different concepts such as ratio between two variables, multivariate BLUP, partial correlations and direct effects of path analysis as part of the calculation of the weights. Path analysis is of great importance for the identification of direct and indirect effects of given characters in an objective variable (Cruz et al. 2014). Coefficients of path analysis were estimated based on ordinary genetic correlations of the characters, based on predicted genotypic values calculated by the REML/BLUP approach. Silva et al. (2009) report that path analysis becomes more effective when it is based on predicted genotypic values than when it is applied on phenotypic values. Thus, efficiency of the breeding program increases. Brasileiro et al. (2013), studied the consistency of path analyses using phenotypic and genotypic correlation, and concluded that in unbalanced cases, the use of genetic correlation produces more consistent results. Thus, it is noteworthy the precision of the analysis carried out in this study by the use of genotypic correlations obtained via REML/BLUP.

The five most efficient indices were those based on partial correlation, on the concept of multivariate BLUP, on two variables as a ratio and direct effects from path analysis. Basically, this can be attributed to the use of the following basic quantities: the genetic control of the trait, reliability and precision of the predicted genotypic values, and partial correlations between traits and the breeding objective. For the two variable as a ratio an additional feature is taken into account, the heritability of a third variable which is the own ratio. Thus, the use of indices based on these cited concepts are efficient and effective alternatives in selecting superior *Eucalyptus* genotypes based on several characters, without the complex procedures of multivariate mixed models.

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