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ARTICLE

Classifying coefficients of genetic variation and heritability for *Eucalyptus* spp.

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Abstract: *The objective of this study was to establish classification ranges for genetic and additive genetic coefficients of variation, as well as for broad and narrow sense heritability, as a function of growth and wood quality traits for Eucalyptus* spp. *We conducted statistical analyses to determine differences in this classification the types of coefficients used. The selected studies that met the inclusion criteria, 58 presented genetic variation coefficients (448 data points) and 53 presented heritability coefficients (423 data points). To descriptive statistics and the Shapiro-Wilk test, we confirmed that it was necessary to separate coefficients and traits into groups. Inconsistencies for growth traits were observed, confirming the influence of experimental error, indirect estimation methods, and environmental effects on coefficient estimates. We recommend the use of the classification tables included in this literature review to interpret results in studies so as to standardize the classification of coefficients of genetic variation and heritability.*

Keywords: *Eucalyptus, genetic parameters, coefficient of genetic variation, coefficient of heritability*

INTRODUCTION

According to a report published by the Brazilian Tree Industry (IBÁ 2021) in 2020, *Eucalyptus* is the most commonly planted genus and crop in commercial forestry in Brazil, occurring on 77% of the total area of planted forests, for a total of 6.97 million hectares. Brazil is a prominent player worldwide in terms of genetic improvement programs. Therefore, potential studies related to the genetic improvement of Eucalypt species are important in the global context.

Currently, research on *Eucalyptus* spp. is aimed at the selection of individuals based on both quantitative genetic parameters and the combination of quantitative and molecular genetics. Therefore, well-conducted experiments are extremely important. In agricultural and forestry studies, experimental coefficients of variation (CV_e) are frequently estimated to obtain the degree of precision and infer errors in data analysis. Pimentel-Gomes (1985) established classification ranges for the experimental coefficient of variation for agricultural species, and four years later, Garcia (1989) proposed a methodology to classify these coefficients with data from *Eucalyptus* spp. Later, Mora and Arriagada (2016) further complemented these studies with the classification of wood quality and growth variables, also based on the experimental coefficient of variation for *Eucalyptus* spp.

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Another frequently estimated parameter is the coefficient of heritability that indicate the success of breeding with selection. Resende (2002) established a general classification range for this parameter, categorizing genetic heritability within the range of 0.1 to 15% as low, 15 to 50% as moderate, and greater than 50% as high.

However, to understand the genetic variation existing in experiments using progenies or clones, two coefficients are generally used: coefficients of genetic variation (CV_g , CV_{gi}), based on the method described by Burton (1952); and coefficients of heritability (h^2_g , h^2_a) defined between 1918 and 1940 by Fisher, Wright, and Lush (Visscher et al. 2008).

To ensure success in the selection of genetic materials with desirable traits, coefficients of genetic variation help to identify, quantify, and compare the genetic variability of traits that can be maintained, thus making inferences about the possible outcomes of selection (Resende 1991, Houle 1992, Santos et al. 2018). Along with heritability coefficients, which offer estimates of the genetic contribution for each trait or quantify the genetic origins of phenotypic variation, it is possible to infer and analyze the proportion of traits that are inherited, the genetic control over traits, and the impact of non-heritable factors, such as environmental effects.

These parameters have been used in several studies and applied to several species. However, more specific classification ranges are needed for *Eucalyptus*. In particular, statistical analyses are required to determine whether there are differences in classification between the coefficients of genetic variation and additive genetic variation, and between broad and narrow sense genetic heritability, as a function of *Eucalyptus* spp. growth and wood quality traits. Both of these issues are objectives of the present study.

MATERIAL AND METHODS

The values of the coefficients of genetic variation (CV_g and CV_{gi}) and genetic heritability (h^2_g and h^2_a) were obtained from selected studies through a systematic review of Brazilian and international research on species of the genus *Eucalyptus* published between 1990 and 2021. The inclusion criteria included only scientific articles that present one or both coefficients of genetic variation (CV_g , CV_{gi}) or coefficients of genetic heritability (h^2_g , h^2_a) in the field of genetics and forest improvement. Coefficients are calculated based on genetic variance, whether additive or non-additive, and obtained through estimation for each trait. As for nomenclature, the genetic parameters differ depending on the analyzed genetic material: a) CV_g and h^2_g are used for data obtained from clonal tests; b) CV_{gi} and h^2_a for data obtained from progenies.

From a total of 64 identified studies, 58 on *Eucalyptus* spp. met the inclusion criteria for coefficients of genetic variation, while 53 presented heritability coefficients for the most common traits of interest for wood quality and growth. Data presented for coefficients of genetic variation and heritability were collected for the following traits: tree height (*H*, *m*), diameter at breast height (*DBH*, *cm*), volume (*VOL*, m^3), mean annual increment (*MAI*, m^3), basic wood density (*BWD*, $kg\ m^{-3}$), stem straightness (*STR*) and survival (*SURV*., %). The coefficients of genetic variation and heritability of all traits were expressed as a percentage (%).

We used the Shapiro-Wilk test to assess normality in three scenarios: a) normality test for all traits without separating the two coefficients of variation (*CV*) or the two heritability estimates (h^2); b) normality test for each trait independent of the coefficients of genetic variation or heritability; c) normality test for each trait for each group (coefficient of genetic variation or heritability considered separately or together) established in the previous steps. These analyses were performed to filter the data and identify common and divergent groups between the traits and the two coefficients of variation. According to the second scenario (b), *CV* and *CVs* and h^2 are defined as common groups, that is, the traits that follow the normality of the data do not require the separation of the coefficients according to the type of genetic material.

After this separation, we estimated the number of observations for each situation and trait (*n*), the minimum value (*min*), the maximum value (*max*), the average ($\overline{x}$) and the standard deviation (*SD*), to describe the shape of distribution. Statistical analyses were performed in the R statistical environment (R Core Team 2017), using the “fBasics” package through the “basicStats” function.

The classification of coefficients of variation and heritability were established according to the methodology proposed by Costa et al. (2002), in which an independent interpretation of the normality of the data is proposed. Intervals of coefficients of variation were developed as a function of the median (*MD*) and pseudo-sigma (*PS*). According to the methodology presented by Costa et al. (2002), the pseudo-sigma is a standard deviation based on the interquartile range that can be used independently of a normal distribution (W) hen there is no normal data distribution, the use of pseudo-sigma is more robust than the standard deviation.

The median (MD) was estimated using the formula: $MD = \frac{(Q_1 + Q_3)}{2}$, where $Q1$ is the first quartile and $Q3$ is the third quartile. The pseudo-sigma (PS) was calculated with the formula: $PS = \frac{(Q_3 - Q_1)}{1.35}$. The classification ranges of the coefficients of variation were determined as follows:

a) low (CV_g, CV_{gi} or $CV_S \leq MD - PS$);

b) moderate ($MD - PS < CV_g$, CV_{gi} or $CV_S \leq MD + PS$);

c) high ($MD + PS < CV_g$, CV_{gi} or $CV_S \leq MD + 2PS$)

d) very high (CV_g, CV_{gi} or $CV_S > MD + 2PS$).

The classification ranges for coefficients of heritability:

a) low (h^2_g, h^2_a or $h^2 \leq MD - PS$)

b) moderate ($MD - PS < h^2_g$, h^2_a or $h^2 \leq MD + PS$);

c) high ($MD + PS < h^2_g$, h^2_a or $h^2 \leq MD + PS$);

d) very high (h^2_g, h^2_a or $h^2 > MD + 2PS$).

In this classification, negative values and values above 100% were not considered, as heritability coefficients do not fall below zero or above 100%.

RESULTS AND DISCUSSION

Genetic coefficients of variation

Of the 58 identified studies on different *Eucalyptus* species, 448 data points for coefficients of genetic variation were obtained. From 53 studies we found 423 data points for heritability. For both parameters, data for the traits diameter (*DBH*) and height (*H*) were the most frequent.

According to the Shapiro-Wilk test, the normality of the data without separating the coefficients of variation (CV_g and CV_{gi}) and regardless of the traits, provided a *p value* $< 2.2 \times 10^{-16}$, indicating that there is no normal distribution of data between the two coefficients of variation. Thus, it is possible to treat them separately.

The results obtained for the normality of the data without separating either the coefficients of genetic variation or the coefficients of heritability, we identified a significant difference between the data due to variations found in the published research, such as the types of genetic materials used (seminal or clonal), small sample sizes used in studies on clones, and environmental effects. Pimentel-Gomes (1985) suggests that the data should be stratified when it does not follow a normal distribution, enabling separation into variables and covariates according to the normality of the data. As such, herein we used the median and pseudo-sigma proposed by Costa et al. (2002).

Regarding the differences between the minimum and maximum values of the coefficients, for wood quality (*BWD*) low values were obtained (*min* = 2.75%; *max* = 7.32%). For traits related to growth, volume (*VOL*) showed a wider range of variability between the minimum and maximum values (CV_{gi} *min* = 6.0%; *max* = 40.38%). For (*VOL*) when considering the coefficient of genetic variation (CV_g) *min* = 7.60%; *max* = 87.10%).

When we separated the traits as independent of the type of coefficient of genetic variation (CV_g and CV_{gi}), we observed a normal distribution of data for the following traits: a) mean annual increment (*MAI – p value* = 0.2246); b) survival (*SURV – p value* = 0.05211) and c) stem straightness (*STR – p value* = 0.5266), suggest that these traits do not depend on the coefficients of genetic variation (CV_g or CV_{gi}),being treated separately, thus it is possible to establish a common range for the interpretation and classification of these traits. For height (*H – p value* = 1.696×10^{-05}); diameter (*DBH – p value* = 9.231×10^{-09}); volume (*VOL – p value* = 2.068×10^{-06}) and basic wood density it was (*BWD – p value* = 1.703×10^{-07}) we observed that the data do not follow a normal distribution at a significance level of 5%, suggesting the need to separate traits as a function of each coefficient of genetic variation (CV_g or CV_{gi}) (Table 1). Based on the analysis of normality, we tabulated the results for the traits separating the two coefficients of genetic variation (CV_g) (Table 1A); CV_{gi} (Table 1B) and created a common group ($CV_S = CV_g$ and CV_{gi}, Table 1C) for traits that can be interpreted independently of the differentiation of these two coefficients.

Although the coefficients and traits were stratified, we did detect a normal distribution in the data for the coefficient of additive genetic variation (CV_{gi}) with the traits volume (*VOL*) and basic wood density (*BWD*). In these cases, there were no significant differences between their means or as a function of sample size, i.e., with small sample sizes there is insufficient data to detect the effects.

For height, diameter, volume, and *BWD*, the classification ranges for the coefficients of genetic variation (CV_g) and additive genetic variation (CV_{gi}) must be unique and interpreted individually. For *MAI*, survival, and stem straightness, they can be classified with a common range, regardless of the nomenclature used for the coefficients of genetic variation.

As for the interval ranges for the coefficients of genetic variation (CV_g), we found an overall average classification of values below 5.66% as low, from 5.66 to 18.34% as moderate, 18.34 to 24.68% high, and above 28.68% very high. The traits height, diameter, and *BWD* presented classifications similar to the overall average, while volume showed a classification of values below 12.31% as low, from 12.31 to 35.44% as moderate, from 35.44 to 47% as high, and above 47% as very high.

The results presented indicate high levels of significance between the data for the coefficients of genetic variation (CV_g) even after stratification. This is likely due to the differentiation found in the data from studies with clones of *Eucalyptus* spp., which can be attributed to the sample size of the tested genetic material. According to Gonçalves et al. (2001) a large number of clones should be tested to increase the chance of selecting individuals and obtaining better clones than the existing ones. Thus, we suggest that for these studies a greater number of clonal materials should be included so that they are representative and effective for future selection.

Table 1. Shapiro-Wilk test, descriptive statistics, and classification range for coefficients of variation: A - genetic (CV_g), B - additive genetic (CV_{gi}) and C - common range group ($CV = CV_g$ and CV_{gi}) for *Eucalyptus* spp

Trait	***n***	***P(W)***	***min***	***máx***	$\bar{X}$	***SD***	***MD***	***PS***	**Interval** (%)			
									Low	**Moderate**	**High**	**Very high**
A - CV_g (%)												
H	77	0.001	1.8	20.0	8.1	3.9	7.9	3.1	$CV_g \leq 4.80$	$4.80 < CV_g \leq 10.97$	$10.97 < CV_g \leq 14.06$	$CV_g > 14.06$
DBH	76	0.0004	2.3	23.7	10.0	4.9	9.3	4.6	$CV_g \leq 4.69$	$4.69 < CV_g \leq 13.93$	$13.93 < CV_g \leq 18.54$	$CV_g > 18.54$
VOL	33	0.0001	7.6	87.1	25.7	16.7	23.9	11.6	$CV_g \leq 12.31$	$12.31 < CV_g \leq 35.44$	$35.44 < CV_g \leq 47.00$	$CV_g > 47.00$
BWD	8	0.0064	2.4	27.9	8.4	8.7	6.9	6.1	$CV_g \leq 0.85$	$0.85 < CV_g \leq 13.03$	$13.03 < CV_g \leq 19.12$	$CV_g > 19.12$
Mean	49	0.0019	3.5	39.7	13.1	8.6	12.0	6.4	$CV_g \leq 5.66$	$5.66 < CV_g \leq 18.34$	$18.34 < CV_g \leq 24.68$	$CV_g > 24.68$
B - CV_{gi} (%)												
H	62	0.0101	1.7	23.3	9.0	4.8	8.1	4.5	$CV_{gi} \leq 3.57$	$3.57 < CV_{gi} \leq 12.63$	$12.63 < CV_{gi} \leq 17.17$	$CV_{gi} > 17.17$
DBH	84	0.0121	3.0	32.4	12.4	6.9	11.2	6.0	$CV_{gi} \leq 5.16$	$5.16 < CV_{gi} \leq 17.21$	$17.21 < CV_{gi} \leq 23.23$	$CV_{gi} > 23.23$
VOL	28	0.050*	6.0	40.4	20.9	10.0	21.8	13.3	$CV_{gi} \leq 8.52$	$8.52 < CV_{gi} \leq 35.12$	$35.12 < CV_{gi} \leq 48.43$	$CV_{gi} > 48.43$
BWD	19	0.388*	2.8	7.3	5.6	1.2	5.8	1.1	$CV_{gi} \leq 4.75$	$4.75 < CV_{gi} \leq 6.89$	$6.89 < CV_{gi} \leq 7.95$	$CV_{gi} > 7.95$
Mean	48	0.1150*	3.4	25.9	12.0	5.7	11.7	6.2	$CV_{gi} \leq 5.50$	$5.50 < CV_{gi} \leq 17.96$	$17.96 < CV_{gi} \leq 24.19$	$CV_{gi} > 24.19$
C - $CV = CV_g$ (%) and CV_{gi} (%)												
MAI	24	0.225*	6.6	52.1	28.2	12.5	27.7	11.0	$CV_S \leq 16.73$	$16.73 < CV_S \leq 38.64$	$38.64 < CV_S \leq 49.59$	$CV_S > 49.59$
SURV.	12	0.050*	1.0	39.6	14.2	11.5	12.3	7.7	$CV_S \leq 4.61$	$4.61 < CV_S \leq 19.97$	$19.97 < CV_S \leq 27.64$	$CV_S > 27.64$
STR	25	0.527*	0.6	20.0	11.0	5.5	11.5	5.2	$CV_S \leq 6.31$	$6.31 < CV_S \leq 16.69$	$16.69 < CV_S \leq 21.87$	$CV_S > 21.87$
Mean	20	0.2673*	2.7	37.2	17.8	9.8	17.2	8.0	$CV_S \leq 9.22$	$9.22 < CV_S \leq 25.10$	$25.10 < CV_S \leq 33.04$	$CV_S > 19.12$
Overall	448											

CV_g (%) – Coefficient of genetic variation; CV_{gi} (%) – Coefficient of additive genetic variation; *CV* – Common range group for coefficient of genetic and additive genetic variation; *H* (*m*) - height; *DBH* (*cm*) – diameter; *VOL* (m^3) — wood volume; *BWD* ($kg\ m^{-3}$) – basic wood density; *MAI* (*m*3) – mean annual increase; *SURV*.(%) – survival; *STR* - stem straightness; *n* – number of observations; *P*(*W*) = ($p > 0.05$) (*)indicates that data are distributed normally according to the Shapiro-Wilk test; *min* - minimum value; *máx* - maximum value; $\bar{X}$ - average; *SD* - standard deviation; *MD*– median; *PS* – pseudo-sigma.

For coefficients of additive genetic variation (CV_{gi}), the general classification showed values below 5.50% as low, from 5.50 to 17.96% moderate, from 17.96 to 24.19% high, and greater than 24.19% very high. The traits height and diameter were similar to the average classification intervals, while volume and BWD presented different ranges. For volume, we established values below 8.52% as low, from 8.52 to 35.12% as moderate, from 35.12 to 48.43% high, and above 48.43% very high. For *BWD*, values below 4.75% were interpreted as low, from 4.75 to 6.89% as moderate, from 6.89 to 7.95% as high, and above 7.95 % rated very high.

The additive genetic variation coefficient (CV_{gi}) the basic wood density (BWD) is noteworthy due to the limited variation between minimum and maximum values, suggesting that this wood quality trait tends to be more stable or may be less severely affected by environmental factors (O'Brien et al. 2007, Fritsche Neto et al. 2012). The same was not observed for volume (*VOL*), considering either the coefficient of genetic variation (CV_g) or the additive genetic variation (CV_{gi}). This result indicates that this growth trait is unstable and influenced by experimental errors, indirect estimates, as well as environmental factors.

For the common range group (CV_S), there was an overall average classification of values below 9.22% as low, from 9.22 to 25.10% as moderate, from 25.10 to 33.04% as high, and greater than 33.04% very high. The traits survival and stem straightness showed intervals similar to the observed overall average. *MAI* presented intervals that differed from the average, with values below 16.73% classified as low, from 16.73 to 38.64% as moderate, from 38.64 to 49.59% as high, and above 49.59% as very high.

Heritability coefficients

According to the Shapiro-Wilk test, when checking the normality of the data without separating the heritability coefficients (h^2_g and h^2_a) regardless of the traits, we found a p-value of $< 2.2 \times 10^{-16}$, indicating no normal distribution of the data.

When we consider traits independent of the type of heritability coefficient (h^2_g and h^2_a), we observed a normal distribution of data for the following traits: a) *BWD* (*p value* = 0.365) and b) stem straightness (*STR – p value* = 0.1273). This suggests that these traits do not depend on the separation of the heritability coefficients (h^2_g and h^2_a) and it is therefore possible to establish a common range of coefficients for the interpretation and classification of these traits. For height (*H – p value* = 3.842×10^{-05}); diameter (*BWD – p value* = 1.175×10^{-10}); volume (*VOL – p value* = 1.675×10^{-05}); mean annual increment (*MAI – p value* = 0.01055) and survival (*SURV – p value* = 0.008447) the data does not follow a normal distribution at a significance level of 5%, suggesting the need to separate traits according to each heritability coefficient (h^2_gor h^2_a) (Table 2).

Based on the analysis of normality, the separation of traits for the heritability coefficients was performed (h^2_g) (Table 2A) or h^2_a h^2_g (Table 2B). The common range group ($h^2 = h^2_g$ and h^2_a, Table 2C) included the traits that can be interpreted independently of the nomenclature used or whether these coefficients are treated separately.

According to the descriptive statistics of broad sense heritability, we observed relatively high and similar median and pseudo-sigma values for diameter (*DBH*), height (*H*) and volume (*VOL*). Similar results were found for mean annual increment (*MAI*) with narrow sense heritability. Meanwhile, basic wood density *BWD* for the common heritability group had high median values and moderate pseudo-sigma.

The classification range of heritability coefficients (h^2_g or h^2_a) for height, diameter, volume, mean annual increment, and survival must be treated separately and interpreted individually. Basic wood density and stem straightness were classified according to a common range, regardless of the difference in nomenclature used for the coefficients.

For broad sense heritability (h^2_g) a mean average classification range was established in which values below 4.5% were classified as low, from 4.5 to 63.5% as moderate, from 63.5 to 80.6% as high, and above 80.6% very high. All traits showed wide variation, with survival presenting the smallest variation with the most similar values to the mean classification interval in relation to the others. Thus, for survival, values below 1.23% were classified as low, from 1.23 to 10.60% as moderate, from 10.60 to 15.28% as high, and greater than 15.28% very high.

According to the results obtained for broad sense heritability, the median and pseudo-sigma values related to the

Table 2. Shapiro-Wilk test, descriptive statistics, and range for genetic heritability: A - in the broad sense (h_g^2), B - in the narrow sense (h_a^2) and C - both combined for *Eucalyptus* spp

Trait	***n***	***P*(*W*)**	***mín***	***máx***	$\bar{X}$	***SD***	***MD***	***PS***	**Interval** (%)			
									Low	**Moderate**	**High**	**Very High**
A - h_g^2 (%)												
H	48	0.0010	1.0	95.0	38.7	30.4	38.0	39.6	$h_g^2 = 0$	$0 < h_g^2 \leq 77.63$	$77.63 < h_g^2 \leq 100$	$h_g^2 = 100$
DBH	47	0.0011	1.0	93.0	40.1	30.3	39.3	33.7	$h_g^2 \leq 5.53$	$5.53 < h_g^2 \leq 72.95$	$72.95 < h_g^2 \leq 100$	$h_g^2 = 100$
VOL	33	0.0061	4.0	93.0	50.8	29.3	53.0	43.0	$h_g^2 \leq 10.04$	$10.04 < h_g^2 \leq 95.96$	$95.96 < h_g^2 \leq 100$	$h_g^2 = 100$
MAI	11	0.0166	6.0	92.2	36.3	31.2	33.0	27.5	$h_g^2 \leq 5.47$	$5.47 < h_g^2 \leq 60.43$	$60.43 < h_g^2 \leq 87.91$	$h_g^2 > 87.91$
SURV.	8	0.3479*	1.0	11.2	6.3	4.0	5.9	4.7	$h_g^2 \leq 1.23$	$1.23 < h_g^2 \leq 10.60$	$10.60 < h_g^2 \leq 15.28$	$h_g^2 > 15.28$
Mean	29	0.0062	2.6	76.9	34.4	25.0	33.8	29.7	$h_g^2 \leq 4.5$	$4.5 < h_g^2 \leq 63.5$	$63.5 < h_g^2 \leq 80.6$	$h_g^2 > 80.6$
B - h_a^2 (%)												
H	75	0.0000	3.0	92.0	21.9	17.3	18.8	15.5	$h_a^2 \leq 3.29$	$3.29 < h_a^2 \leq 34.25$	$34.25 < h_a^2 \leq 49.73$	$h_a^2 > 49.73$
DBH	97	0.0000	2.0	99.8	23.3	18.4	21.5	15.6	$h_a^2 \leq 5.94$	$5.94 < h_a^2 \leq 37.06$	$37.06 < h_a^2 \leq 52.61$	$h_a^2 > 52.61$
VOL	33	0.0017	3.0	60.0	20.0	15.8	19.6	16.8	$h_a^2 \leq 2.79$	$2.79 < h_a^2 \leq 36.47$	$36.47 < h_a^2 \leq 53.32$	$h_a^2 > 53.32$
MAI	9	0.6149*	14.0	64.4	33.6	16.7	34.5	17.0	$h_a^2 \leq 17.46$	$17.46 < h_a^2 \leq 51.54$	$51.54 < h_a^2 \leq 68.57$	$h_a^2 > 68.57$
SURV.	5	0.3351*	0.5	35.0	21.8	15.1	23.7	16.8	$h_a^2 \leq 6.88$	$6.88 < h_a^2 \leq 40.46$	$40.46 < h_a^2 \leq 57.24$	$h_a^2 > 57.24$
Mean	44	0.1903*	4.5	70.2	24.1	16.7	23.6	16.3	$h_a^2 \leq 7.3$	$7.3 < h_a^2 \leq 40.0$	$40.0 < h_a^2 \leq 56.3$	$h_a^2 > 56.3$
C - $h^2 = h_g^2$ (%) and h_a^2 (%)												
BWD	27	0.3950*	11.0	96.0	51.1	21.4	49.6	15.0	$h^2 \leq 34.63$	$34.63 < h^2 \leq 64.58$	$64.58 < h^2 \leq 79.55$	$h^2 > 79.55$
STR	30	0.1273*	2.0	47.0	20.5	12.6	19.8	12.2	$h^2 \leq 7.57$	$7.57 < h^2 \leq 32.01$	$32.01 < h^2 \leq 44.23$	$h^2 > 44.23$
Mean	29	0.2611*	6.5	71.5	35.8	17.0	34.7	13.6	$h^2 \leq 21.1$	$21.1 < h^2 \leq 48.3$	$48.3 < h^2 \leq 61.9$	$h^2 > 61.9$
Overall	423											

h_g^2 – broad sense heritability; h_a^2 – narrow sense heritability; h^2– Common range group for broad and narrow sense heritability; *H* (*m*) - height; *DBH* (*cm*) – diameter; *VOL* (m^3) – wood volume; *BWD* (kg/m^3) – basic wood density; *MAI* (m^3) – average annual increase; *SURV*. (%) – survival; *STR* - stem straightness; *n* – number of observations; *P*(*W*) = ($p > 0.05$)(*) indicates that data are distributed normally according to the Shapiro-Wilk test; *min* - minimum value; *máx* - maximum value; $\bar{X}$ - average; *SD* - standard deviation; *MD* – median; *PS* – pseudo-sigma.

growth traits were high and relatively similar, showing a wide variation in the data. Estimates of genetic parameters obtained in clonal tests of *Eucalyptus* spp. showed that variations in broad sense genetic heritability depend on growth traits, which is consistent to what was observed in this article; however, the general averages of these values were similar among them and close to 0.5 for diameter, height and volume (Furlan et al. 2020).

In relation to the coefficient of narrow sense heritability (h_a^2), the average overall classification considers values below 7.3% as low, from 7.3 to 40.0% as moderate, 40.0 to 56.3% high, and above 56.3% as very high. The traits height, diameter, volume, and survival presented classifications similar to the general average, while *MAI* was classified with values below 17.46% as low, from 17.46 to 51.54% as moderate, from 51.54 to 68.57% high, and greater than 68.57% as very high.

Again, this indicates that growth traits are unstable, with diameter and height measurement errors associated with the use of equations that directly influence the accuracy of the estimate, i.e., volume. Furthermore, these results can be influenced by environmental effects, making genetic control difficult, an issue that is not observed for narrow sense heritability. According to Vencovsky (1987) the lower the genetic control over the traits the greater the influence of environmental factors and vice versa. Another possibility is that there is a reduction in preexisting genetic variability due to the number of clonal materials tested in the studies (similar to what occurs for coefficients of genetic variation) and the fact that clonal materials have a non-additive genetic variance and are not used of crosses to obtain selected clones. Again, the greater the number of clones tested, the greater the genetic variability and, consequently, the greater the potential to select superior clones (Gonçalves et al. 2001).

In terms of the common range for heritability coefficients (h^2), the average classification showed values below 21.1% as low, from 21.1 to 48.3% as moderate, from 48.3 to 61.9% as high, and above 61.9% as very high. The two traits included in this group presented classifications similar to the general average, but with variation. For example, *BWD* values below 34.63% were interpreted as low, from 34.63 to 64.58% as moderate, from 64.58 to 79.55% as high, and above 79.55% as very high, while stem straightness (*STR*) showed less variation, with values below 7.57% classified as low, from 7.57

to 32.01% as moderate, from 32.01 to 44.23% as high, and above 44.23% as very high.

The *MAI* for the narrow sense heritability and *BWD* for the common heritability group showed similar median values (*MD*) but differed due to high and moderate pseudo-sigma, respectively. This suggests that there is better data distribution than that obtained for the broad sense heritability data. Materials obtained from progenies ($CV_{gi}$and h^2_a, which have a high magnitude of genetic control (Resende et al. 1995) due to a lower degree of relatedness and selection, will consequently have greater genetic variability and greater additive genetic variance (Tambarussi et al. 2018).

When analyzing the estimated average for the traits, we found that the average values fall within the moderate classification range, regardless of the separation of the coefficients of genetic variation or heritability. This supports the work of Burdon (2008) who states that the mean must be close to the moderate range so that the correction and interpretation of the scales of variation of the traits are effective. In general, the average heritability of *BWD* was greater than the other traits; however, *BWD* has a low average coefficient of genetic variation, which is a limiting factor for the selection of potential genetic materials (Houle 1992), as was observed by Hamilton and Potts (2008).

In conservation, forest improvement programs and genetics studies, many authors have considered values of coefficients of genetic variation above 7% as high, referring to a study carried out by Sebbenn et al. (1998) with the forest species Cabreúva (*Myroxylon peruiferum* LF Allemão), or have compared their work to this previous study to interpret the results. Through statistical analyses, the present study provides a basis to specifically interpret each parameter and trait.

As observed herein, there is distinct nomenclature for the coefficients of genetic variation and heritability, which is due to the type of genetic variance used to calculate these parameters and is a function of the genetic material in question. For progenies, the coefficient of additive genetic variation (CV_{gi}) is calculated, from which narrow sense heritability (h^2_a) is estimated. Similarly, for clones, the coefficient of genetic variation (CV_g) is calculated and broad sense heritability (h^2_g) is based on the total genetic variance (additive, dominance, and epistatic).

When analyzing data from previous research, it is possible that different types of progenies were used in each study, and the lack of information about the type of progenies, whether half- or full-sibs, can directly influence the estimates of coefficients of heritability and genetic variation. However, the more pronounced influence on the classification ranges for heritability is attributed to their estimation and uncertainty around inbreeding coefficients in open pollinated progeny tests in the forest and not the classification proposed in this article.

Generally, in breeding programs, a selection intensity of 10% is established in the short term and 50% in the long term; thus, the higher the coefficient of genetic variation, the greater the possibility of genetic gains. Cornelius (1994) states that genetic selection must be based mainly on the coefficient of genetic variation in addition to heritability and from that the selection intensity can be defined. When selection intensity is defined solely based on heritability, we may wrongly assume the level of genetic variation, thus creating problems in the future. When estimating a parameter considering inappropriate genetic variances for that genetic material or stating that the coefficient of genetic variation is high or low without proper classification, that mistakes can be made in the selection of individuals which in turn will affect the desired outcome for genetic variability. According to a study of genetic variability in *Eucalyptus* progenies, estimates of the genetic variation coefficients can characterize the existence of genetic variability among progenies and indicate the genetic nature of the material; therefore, the classification proposed in this article may inform the genetic variability through the classification intervals for each trait, complementing and explaining the information obtained in the estimates (Moraes et al. 2015).

CONCLUSIONS

Through the present literature review, we obtained data from studies published in journals on species of the genus *Eucalyptus* and found the need for a universal classification for coefficients of genetic variation and heritability for studies on forest improvement and genetics. The present study provides a basis for classifying and interpreting genetic variation and heritability coefficients for diameter, height, volume, *BWD*, *MAI*, survival, and stem straightness in analyses on the *Eucalyptus* genus. The use of the classification interval tables (Tables 1 and 2) presented herein is recommended for the interpretation of results in future studies, which can help to standardize and simplify the classification of coefficients of genetic variation and heritability.

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