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Plant stand failures effect in genetic parameters estimation procedure in *Eucalyptus* sp.

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Abstract

The objective of this work was to verify the influence of the percentage of failures in a forest genetics experiment in the estimation of genetic parameters. The study consisted in the evaluation of two

experiments of full-sib families under randomized complete block design with three replicates conducted in the state of Minas Gerais, Brazil. The experiment I was evaluated in January 2002, with approximately 60 months of age. The experiment II was evaluated in January 2003, with 45 months of age. In both experiments, the evaluations consisted of the measurement of the diameter at breast height and plant height. For all the investigated genetic parameters, an increase in the amplitude of the estimates was verified due to the increase in the number of experimental failures. Variances and negative heritabilities were detected, from 35% of failure, indicating that in such cases, this proportion of failure may be problematic to estimate genetic values, to estimate the gain with the selective process and for make decision.

Keywords: Eucalypt, biometric statistics, plant genetics, genetic statistics, genetic parameters.

1. Introduction

The economic importance of eucalypt culture in Brazil and worldwide is due to its rapid growth, wood productivity, and the multiplicity of uses of its different species. According to [12], the area covered by planted forests in Brazil corresponds to approximately 7.84 million hectares, of which 5.7 million hectares of eucalypt, 1.6 million hectares of pine trees and 590 thousand hectares with other species, *Acacia* sp., *Hevea brasiliensis*, *Schizolobium amazonicum*, *Tectona grandis*, *Araucaria angustifolia*, among others. Most of these areas are in the states of Minas Gerais (24%), São Paulo (17%) and Mato Grosso do Sul (15%).

Eucalyptus is currently the most widely exotic planted species in Brazil due to its adaptation to climatic and edaphic conditions and to its high productivity and short production cycles compared to native species. With the establishment of the plantations, various research and breeding programs were initiated in order to provide superior individuals. In this sense, obtaining genetic parameters is of great importance, since it allows the estimation of genetic gains with the selection process, as well as the identification of individuals or families more adapted to different environments.

Genetic gain is defined by [9] as the improvement of the average genetic value in a population. Among the main procedures for its estimation, we highlight the analysis of variance (ANOVA) and the REML/BLUP (Restricted Maximum Likelihood Estimation / Best Linear Unbiased Prediction) procedure. In ANOVA, the variance components are obtained from mean square expected values [3], considering the experimental and genetic design. Heritability and other genetic parameters are estimated from the genetic variance components. REML/BLUP, widely used in forest genetics, allows dealing with unbalanced data and treatments with any kinship, being considered a generalization of ANOVA for more complex situations. However, for simple situations, both procedures are equivalent [30].

Although the experiments are conducted in as judicious as possible way, in *eucalyptus* trials, the existence of failures in the parcel is due to various effects (pests, management etc.) that are accentuated due to their period of evaluation in the field. Experiments with failures, or unbalanced, are worrying in the genetic context, because it means that the plants are under different competition conditions, which in the analytical context require appropriate methods to obtain reliable estimates. If they are not considered, the existence of failures in the experiment is able to provide mean estimates and variances unbiased, which may lead to

incorrect decision-making by plant breeders. In this sense, the objective of this work was to verify the influence of the percentage of failures in a forest genetics experiments on the estimation of genetic parameters, that will allow to accurately estimate the gain with the selection process.

2. Material and Methods

The study consisted in the evaluation of two experiments of full-sib families. The experiment I was installed in the municipality of Belo Oriente, MG, Brazil, in December 1996 and evaluated in January 2002, with approximately 60 months of age. It was used a randomized complete block design with three replicates and linear parcel of 10 plants. The treatments consisted of 32 full-sib families whose parents were elite genetic material previously selected for trait of wood yield. In both experiments, the evaluations consisted of the measurement of the diameter at breast height (DBH) and plant height (PH). The two experiments were taken because they presented low percentage of failures (<3.80, 2%) in the plant stand. Prior to the statistical analysis, the plant stand correction method was applied according to [1].

The variables were analyzed using the statistical model [6]:

$$Y_{ijk} = \mu + G_i + B_j + \varepsilon_{ij} + \delta_{ijk} \quad (1)$$

Where Y_{ijk} is the observation obtained in the k^{th} individual of the i^{th} family evaluated in the j^{th} block; μ is the overall mean of the experiment; G_i is the random effect of the i^{th} family; B_j is the random effect of the j^{th} block; ε_{ij} is the random effect of the variation between families; and δ_{ijk} is the random effect of the variation between plants, within the family.

Based on the analysis of variance, the estimates of the following parameters were calculated:

Phenotypic variance within family:

$$\sigma_d^2 = MSE_{within} \quad (2)$$

Genotypic variance between and within families:

$$\sigma_g^2 = \frac{MS_{family} - MSE_{between}}{nb} \quad (3)$$

Environmental variance between family means:

$$\sigma_e^2 = \frac{MSE_{between} - MSE_{within}}{n} \quad (4)$$

Broad-sense heritability between family:

$$h_b^2 = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_f^2} \quad (5)$$

Broad-sense heritability within family:

$$h_w^2 = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_d^2} \quad (6)$$

Broad-sense heritability at the level of individual in the block:

$$h_{ib}^2 = \frac{2\hat{\sigma}_g^2}{\hat{\sigma}_g^2 + \hat{\sigma}_e^2 + \hat{\sigma}_d^2} \quad (7)$$

Broad-sense heritability at the level of the individual in the experiment:

$$h_{ie}^2 = \frac{2\hat{\sigma}_g^2}{\hat{\sigma}_g^2 + \hat{\sigma}_e^2 + \hat{\sigma}_d^2 + \hat{\sigma}_b^2} \quad (8)$$

Experimental coefficient of variation:

$$CV_e(\%) = \frac{100 \cdot \hat{\sigma}_e}{\bar{X}} \tag{9}$$

Genetic coefficient of variation:

$$CV_g(\%) = \frac{100 \cdot \hat{\sigma}_g}{\bar{X}} \tag{10}$$

CV_g/CV_e relation; in which MS_{family} is the mean square of families, $MSE_{between}$ is the mean square of error between the families, n is the number of individuals in a family and b is the number of families. For scenarios with unbalance due to loss of information in the parcel, it was considered the value of \bar{n} , taken by:

$$\frac{1}{\bar{n}} = \frac{1}{\bar{g}r} \sum_{i=1}^g \sum_{j=1}^r \left(\frac{1}{n_{ij}} \right) \tag{11}$$

to obtain the estimates.

Estimates of the genetic and phenotypic parameters were considered the true values of the parameter, since the data set studied was considered as the known population. Once full-sib families were used, there is only one genotypic variance estimate, since the estimates of the genotypic variance between and within families, for this family structure, have the same estimator, without considering the effects of dominance deviations. To evaluate the influence loss of experimental data, were simulated failure percentages: 5%, 10%, 15%, 20%, 25%, 30%, 35% and 40%. For each percentage, 20000 resamplings were evaluated, generated from the original data set. Analytic algorithms were developed using the R programming language [23] integrated to GENES software [4] [5] to automate the simulation procedures, analysis and estimation of the parameters presented, and also to apply the method proposed, and design the graphs.

3. Results and Discussion

In the variance analysis, it was noticed that the progeny effect was significant ($p < 0.05$) for traits of diameter at breast height (DBH) and plant height (PH), for both experiments (Table 1). This implies the existence of genetic variability between and within progenies, and the possibility of obtaining genetic gains by selecting the most productive progenies for these traits [29], or by selecting the most productive individuals within the best progenies.

Table 1. Summary of variance analysis of experiments assessed at mean level of plot. Mean squares, coefficient of experimental (CV_e) and genetic (CV_g) variation, corrected mean, genetic parameters are showed.

FV	gl	(I) Mean Square		gl	(II) – Mean Square	
		DBH	PH		DBH	PH
Blocks	2	80.93***	84.22**	3	6.06	1.76
Progeny	31	76.43***	145.67***	27	66.05***	62.98***
Between	62	43.24***	81.35***	81	9.15*	10.24***
Within	864	9.49	12.45	560	6.72	6.23
$CV_e(\%)$		22.3867	20.1468		5.9780	5.4563
\bar{X}		14.9845	23.7870		13.0458	18.3648
$\hat{\sigma}_g^2$		1.1061	2.1439		2.3709	2.1973

$\hat{\sigma}_d^2$	9.4862	12.4536	6.7153	6.2306
$\hat{\sigma}_e^2$	11.2529	22.9664	0.6082	1.0035
\hat{h}_b^2	0.4342	0.4415	0.8615	0.8373
\hat{h}_w^2	0.1166	0.1722	0.3531	0.3527
\hat{h}_{ib}^2	0.1013	0.1141	0.4891	0.4660
\hat{h}_{ie}^2	0.1007	0.1141	0.4901	0.4685
CV_g	7.0188	6.1555	11.8030	8.0716
CV_e	22.3867	20.1468	5.978	5.4546
CV_g/CV_e	0.3135	0.3055	1.9744	1.4798

According to [13], *Eucalyptus* breeding programs in Brazil are based mainly on the selection between and within half-sibling progenies, based on phenotypic measures such as family averages. Regardless of the selection strategy, whose discussion is beyond the scope of this paper, it will depend on the accurate estimation of genetic parameters, which in turn is dependent on the integrity of the experiment. In this sense, an experiment with fewer failures should lead to more accurate estimates of genetic values, and consequently, gains from the selection process.

Estimators for population-genetic parameters of a same trait usually differ between experiments. They depend on the population, but also reflect the environment in which the experiment was conducted. Estimates of variances showed that the two characters under study had similar but not identical genetic control, with estimates of h_b^2 , h_w^2 , h_{ib}^2 and h_{ie}^2 varying for the same trait between experiments.

Heritability estimates for DBH and PH in experiment II were higher than those found in experiment I in all selection units. In both cases, the highest estimates obtained were for broad-sense heritability between family (h_b^2). These results indicate that selection based on progeny means should be more efficient than selection within progenies, considering the same selection intensity. These findings are consistent and similar to those obtained by [19], [27] and [2]. Higher estimates of h_w^2 would indicate a selection within families, as highlighted by [20] and [22].

The experimental coefficient of variation (CV_e) was higher than 20% for DBH and PH in experiment I, being considered high. In the experiment II, both traits showed CV_e below 10%, which denotes high experimental precision (11). The coefficient of genetic variation CV_g is a commonly used parameter to compare genetic variability [26]. According to the authors, estimates of CV_g higher than CV_e lead to favorable conditions for selection among and within families, that should provide higher genetic gains than selection only between families. Also, according to [32] and [18], when the ratio CV_g/CV_e tends to 1.0 or higher values, there is a favorable situation for obtaining gains with the selection. In this context, experiment II should provide greater gains than experiment I by presenting higher CV_g/CV_e , of the order of 1.97 and 1.47, for DBH and PH respectively.

A factor that affects the performance of the experiments and is often outside the control of the researcher is the loss of plants or experimental units. This can happen due to insect attack, pests, mechanical damage caused by animals, competition with weeds or by simple competition with other plants of the experiment itself. These facts are more aggravating in perennial crops that pass through the long period in the experimental units. This loss of plants is usually random and leads to differences in the plant stand, which contributes to the reduction of experimental precision [34] and the correct interpretation of the results [1].

In relation to cultivated annual species, [8] and [28], working respectively with beans and corn, reported stand effect and methods for correcting such effect. However, in perennial species in which the experimental plots usually involve fewer individuals and the losses of some plants may have the most expressive effect, the information is scarce, and the correction methods involve the inclusion of number of failures adjacent to the plant as a covariate for correcting its genotypic value [25]. In such species, according to [1], this factor is further exacerbated by the fact that errors can be cumulative and perpetuate throughout the conduction of the experiment, which can take decades.

Tables 2 to 5 show the results of the mean estimates with standard deviation of the genetic-population parameters for the two characteristics of experiments I and II, complete and with simulated failures that ranged from 5% to 40% in 20000 resamplings. The analysis of the genetic parameters of the experiments when subjected to simulated failures presented distinct and peculiar behaviors, evidenced by the graphic analysis presented in the boxplots of figure 1.

Table 2. Estimates of the genetic and phenotypic parameters in *Eucaliptus* full-sib families for trait diameter at breast height, considering the original experiment (I) and 8 scenarios with different percentages of lost data (5 to 40%), in 20000 simulated experiments.

	(I)	5%	10%	15%	20%	25%	30%	35%	40%
σ_d^2	9.4862	9.4865 ± 0.15	9.4876 ± 0.2192	9.4843 ± 0.2754	9.4822 ± 0.3292	9.4916 ± 0.3822	9.4839 ± 0.4347	9.4888 ± 0.4904	9.493 ± 0.5457
σ_g^2	1.1061	1.0566 ± 0.0876	1.0074 ± 0.121	0.9571 ± 0.1444	0.9076 ± 0.1628	0.8585 ± 0.1764	0.8067 ± 0.1881	0.7576 ± 0.1974	0.7059 ± 0.2022
σ_e^2	11.2529	10.6693 ± 0.3654	10.0826 ± 0.5074	9.5052 ± 0.6106	8.9177 ± 0.6856	8.3257 ± 0.7495	7.7538 ± 0.8037	7.1695 ± 0.8454	6.5827 ± 0.8758
h_b^2	0.4342	0.4325 ± 0.024	0.4307 ± 0.0348	0.4284 ± 0.044	0.4262 ± 0.0523	0.424 ± 0.0601	0.4202 ± 0.0683	0.4171 ± 0.0763	0.413 ± 0.0841
h_w^2	0.1166	0.1114 ± 0.0096	0.1063 ± 0.0132	0.101 ± 0.0158	0.0959 ± 0.0178	0.0906 ± 0.0193	0.0853 ± 0.0206	0.0801 ± 0.0216	0.0747 ± 0.0222
h_{ib}^2	0.1013	0.0997 ± 0.0088	0.098 ± 0.0125	0.0961 ± 0.0154	0.0942 ± 0.018	0.0922 ± 0.0201	0.0898 ± 0.0221	0.0874 ± 0.0241	0.0846 ± 0.0256
h_{ie}^2	0.1007	0.0991 ± 0.0087	0.0975 ± 0.0124	0.0956 ± 0.0153	0.0938 ± 0.0178	0.0918 ± 0.02	0.0893 ± 0.022	0.087 ± 0.0239	0.0842 ± 0.0254
CV_e	22.3867	21.7955 ± 0.3799	21.1841 ± 0.5422	20.5638 ± 0.6725	19.9145 ± 0.7806	19.2373 ± 0.8833	18.5593 ± 0.9815	17.8375 ± 1.0736	17.0856 ± 1.162
CV_g	7.0188	6.8539 ± 0.2839	6.6858 ± 0.4025	6.5096 ± 0.4956	6.3312 ± 0.5754	6.1494 ± 0.6438	5.9512 ± 0.7139	5.7559 ± 0.7748	5.5455 ± 0.8282
CV_g/CV_e	0.3135	0.3147 ± 0.0162	0.316 ± 0.0238	0.3172 ± 0.0302	0.3189 ± 0.0364	0.3211 ± 0.0424	0.3225 ± 0.0487	0.3251 ± 0.0553	0.3276 ± 0.0620

σ_d^2 phenotypic variance within family; σ_g^2 genotypic variance between and within families; σ_e^2 environmental variance between family means; h_b^2 broad-sense heritability between family; h_w^2 broad-sense heritability within family; h_{ib}^2 broad-sense heritability of the individual in the block; h_{ie}^2 broad-sense heritability in the level of the individual in the experiment; CV_e experimental coefficient of variation; CV_g genetic coefficient of variation; CV_g/CV_e genetic and experimental variation coefficient relation.

Table 3. Estimates of the genetic and phenotypic parameters in *Eucaliptus* full-sib families for trait plant height, considering the original experiment (I) and 8 scenarios with different percentages of lost data (5 to 40%), in 20000 simulated experiments.

	(I)	5%	10%	15%	20%	25%	30%	35%	40%
σ_d^2	12.4536	12.4532 ± 0.2414	12.453 ± 0.351	12.4532 ± 0.4446	12.4638 ± 0.529	12.4524 ± 0.6173	12.4507 ± 0.7049	12.463 ± 0.7881	12.4574 ± 0.874
σ_g^2	2.1439	2.0473 ± 0.1526	1.9503 ± 0.2109	1.8524 ± 0.2479	1.7571 ± 0.2846	1.6622 ± 0.3055	1.57 ± 0.3238	1.476 ± 0.3399	1.3757 ± 0.3494
σ_e^2	22.9664	21.7703 ± 0.6459	20.5926 ± 0.895	19.3937 ± 1.0599	18.2065 ± 1.2039	17.0191 ± 1.3012	15.8253 ± 1.3812	14.6131 ± 1.4567	13.4535 ± 1.4945
h_b^2	0.4415	0.4408 ± 0.0217	0.4397 ± 0.0316	0.4387 ± 0.0393	0.4376 ± 0.0476	0.4368 ± 0.0542	0.4362 ± 0.0612	0.4354 ± 0.0684	0.4328 ± 0.0759
h_w^2	0.1722	0.1645 ± 0.0131	0.1568 ± 0.0181	0.149 ± 0.0213	0.1413 ± 0.0245	0.134 ± 0.0265	0.1267 ± 0.0281	0.1191 ± 0.0296	0.1112 ± 0.0304
h_{ib}^2	0.1141	0.113 ± 0.009	0.1116 ± 0.013	0.1101 ± 0.0158	0.1086 ± 0.0189	0.1071 ± 0.0211	0.1056 ± 0.0234	0.1039 ± 0.0257	0.1015 ± 0.0277
h_{ie}^2	0.1141	0.1129 ± 0.009	0.1115 ± 0.0129	0.1101 ± 0.0158	0.1086 ± 0.0189	0.1071 ± 0.0211	0.1056 ± 0.0233	0.1038 ± 0.0256	0.1014 ± 0.0276
CV_e	20.1468	19.6131 ± 0.2971	19.0732 ± 0.4231	18.5066 ± 0.5165	17.9291 ± 0.6049	17.3313 ± 0.6761	16.7083 ± 0.7437	16.0515 ± 0.8185	15.3969 ± 0.8755
CV_g	6.1555	6.0111 ± 0.2254	5.8626 ± 0.3198	5.7087 ± 0.3867	5.5542 ± 0.4577	5.3967 ± 0.5064	5.2386 ± 0.5548	5.0724 ± 0.6015	4.8896 ± 0.6448
CV_g/CV_e	0.3055	0.3066 ± 0.014	0.3077 ± 0.0204	0.3089 ± 0.0256	0.3105 ± 0.0313	0.3123 ± 0.0358	0.3148 ± 0.041	0.3176 ± 0.0465	0.3196 ± 0.0522

σ_d^2 phenotypic variance within family; σ_g^2 genotypic variance between and within families; σ_e^2 environmental variance between family means; h_b^2 broad-sense heritability between family; h_w^2 broad-sense heritability within family; h_{ib}^2 broad-sense heritability of the individual in the block; h_{ie}^2 broad-sense heritability in the level of the individual in the experiment; CV_e experimental coefficient of variation; CV_g genetic coefficient of variation; CV_g/CV_e genetic and experimental variation coefficient relation.

Table 4. Estimates of the genetic and phenotypic parameters in *Eucaliptus* full-sib families for trait diameter at breast height, considering the original experiment (II) and 8 scenarios with different percentages of lost data (5 to 40%), in 20000 simulated experiments.

	(II)	5%	10%	15%	20%	25%	30%	35%	40%
σ_d^2	6.7153	6.7155 ± 0.1164	6.7159 ± 0.1712	6.7194 ± 0.2151	6.7194 ± 0.2562	6.7208 ± 0.3016	6.7176 ± 0.3499	6.7241 ± 0.3953	6.7208 ± 0.4409
σ_g^2	2.3709	2.2548 ± 0.0785	2.1346 ± 0.1107	2.0194 ± 0.1311	1.8977 ± 0.1472	1.7796 ± 0.1586	1.6613 ± 0.1684	1.5429 ± 0.1774	1.4262 ± 0.1834
σ_e^2	0.6082	0.5772 ± 0.106	0.544 ± 0.1485	0.5101 ± 0.1796	0.4776 ± 0.205	0.4446 ± 0.229	0.413 ± 0.2501	0.3808 ± 0.2685	0.3491 ± 0.2824
h_b^2	0.8615	0.8569 ± 0.0075	0.8518 ± 0.0112	0.8464 ± 0.0143	0.84 ± 0.0174	0.8331 ± 0.0205	0.8253 ± 0.0238	0.8162 ± 0.0277	0.8062 ± 0.0316
h_w^2	0.3531	0.3359 ± 0.0139	0.3181 ± 0.0197	0.3009 ± 0.0233	0.283 ± 0.026	0.2655 ± 0.0282	0.2482 ± 0.0302	0.2305 ± 0.032	0.2134 ± 0.0329

h_{ib}^2	0.4891	0.4723 ± 0.0154	0.4544 ± 0.0223	0.4367 ± 0.027	0.4173 ± 0.0309	0.398 ± 0.0344	0.378 ± 0.0376	0.357 ± 0.0408	0.336 ± 0.0432
h_{ie}^2	0.4901	0.4732 ± 0.0154	0.4552 ± 0.0223	0.4373 ± 0.027	0.4179 ± 0.0309	0.3984 ± 0.0344	0.3784 ± 0.0375	0.3573 ± 0.0408	0.3362 ± 0.0432
CV_e	5.978	5.7987 ± 0.5404	5.5974 ± 0.7966	5.3859 ± 1.0079	5.1821 ± 1.1936	5.0064 ± 1.3287	4.8522 ± 1.4447	4.7327 ± 1.52	4.6231 ± 1.5621
CV_g	11.803	11.5086 ± 0.2034	11.1953 ± 0.2947	10.8876 ± 0.3593	10.5518 ± 0.4162	10.2162 ± 0.4633	9.8674 ± 0.5084	9.5063 ± 0.5561	9.1352 ± 0.5984
CV_g/CV_e	1.9744	2.0033 ± 0.2057	2.0484 ± 0.3587	2.1249 ± 0.8993	2.2274 ± 1.5277	2.3202 ± 1.961	2.414 ± 2.458	2.4503 ± 2.5065	2.4662 ± 2.7838

σ_d^2 phenotypic variance within family; σ_g^2 genotypic variance between and within families; σ_e^2 environmental variance between family means; h_b^2 broad-sense heritability between family; h_w^2 broad-sense heritability within family; h_{ib}^2 broad-sense heritability of the individual in the block; h_{ie}^2 broad-sense heritability in the level of the individual in the experiment; CV_e experimental coefficient of variation; CV_g genetic coefficient of variation; CV_g/CV_e genetic and experimental variation coefficient relation.

Table 5. Estimates of the genetic and phenotypic parameters in *Eucaliptus* full-sib families for trait plant height, considering the original experiment (II) and 8 scenarios with different percentages of lost data (5 to 40%), in 20000 simulated experiments.

	(II)	5%	10%	15%	20%	25%	30%	35%	40%
σ_d^2	6.2306	6.23 ± 0.1744	6.2332 ± 0.2562	6.2259 ± 0.3255	6.231 ± 0.3865	6.2388 ± 0.4521	6.2336 ± 0.5109	6.2273 ± 0.5801	6.2293 ± 0.6531
σ_g^2	2.1973	2.0901 ± 0.0841	1.9802 ± 0.1171	1.8706 ± 0.1408	1.7619 ± 0.1562	1.652 ± 0.17	1.5419 ± 0.181	1.4324 ± 0.1914	1.3253 ± 0.1969
σ_e^2	1.0035	0.9509 ± 0.1057	0.8986 ± 0.1484	0.8491 ± 0.1806	0.7937 ± 0.2072	0.74 ± 0.2332	0.6908 ± 0.256	0.6398 ± 0.2776	0.59 ± 0.2989
h_b^2	0.8373	0.8331 ± 0.0086	0.8282 ± 0.0128	0.8228 ± 0.0165	0.8171 ± 0.0199	0.8104 ± 0.0237	0.8027 ± 0.0278	0.7942 ± 0.0324	0.7846 ± 0.037
h_w^2	0.3527	0.3358 ± 0.0172	0.3183 ± 0.0239	0.3014 ± 0.0289	0.284 ± 0.032	0.2664 ± 0.0352	0.2492 ± 0.0374	0.2323 ± 0.0397	0.2153 ± 0.0407
h_{ib}^2	0.466	0.451 ± 0.0175	0.4348 ± 0.025	0.4184 ± 0.031	0.4014 ± 0.0352	0.3833 ± 0.0397	0.3649 ± 0.0435	0.346 ± 0.0475	0.3265 ± 0.0501
h_{ie}^2	0.4685	0.4533 ± 0.0176	0.4369 ± 0.025	0.4203 ± 0.031	0.403 ± 0.0353	0.3848 ± 0.0398	0.3662 ± 0.0436	0.3471 ± 0.0476	0.3275 ± 0.0501
CV_e	5.4546	5.3014 ± 0.2983	5.1438 ± 0.4325	4.9879 ± 0.5446	4.8073 ± 0.6508	4.622 ± 0.768	4.4469 ± 0.8727	4.2619 ± 0.9801	4.0863 ± 1.0755
CV_g	8.0716	7.8708 ± 0.1624	7.6594 ± 0.2326	7.4422 ± 0.2874	7.2207 ± 0.3288	6.9901 ± 0.3693	6.7503 ± 0.4075	6.5031 ± 0.4469	6.2521 ± 0.4787
CV_g/CV_e	1.4798	1.4897 ± 0.0962	1.5007 ± 0.1473	1.5124 ± 0.1983	1.5346 ± 0.2578	1.5681 ± 0.4078	1.6021 ± 0.5312	1.6581 ± 0.7737	1.7369 ± 1.4438

σ_d^2 phenotypic variance within family; σ_g^2 genotypic variance between and within families; σ_e^2 environmental variance between family means; h_b^2 broad-sense heritability between family; h_w^2 broad-sense heritability within family; h_{ib}^2 broad-sense heritability of the individual in the block; h_{ie}^2 broad-sense heritability in the level of the individual in the experiment; CV_e experimental coefficient of variation; CV_g genetic coefficient of variation;

CV_g/CV_e genetic and experimental variation coefficient relation.

In experiment I, for the characteristic DBH, the increase in the number of failures in the experiment did not alter the mean of h_b^2 (Figure 1A) and led to a large increase in the amplitude of the estimates. In experiment II, the increase in the number of failures resulted in a slight decrease in h_b^2 and similar increase in the amplitude of estimates.

According to [29], heritability is one of the most important genetic-population parameters for the genetic study of quantitative character, and whose role is to express the confidence of the phenotypic value as a guide to the genetic value or degree of phenotypic value and genetic value. According to [7] heritability is a property not only of a character but also of the population, of the environmental circumstance to which the individuals are subjected, and of the way in which the phenotype is measured, and since its value depends on the magnitude of all the components of variance, a change in any one of these will affect it. According to [2], variations in this genetic parameter are common and may be associated with the age of evaluation, the site and experimental precision of the experiment.

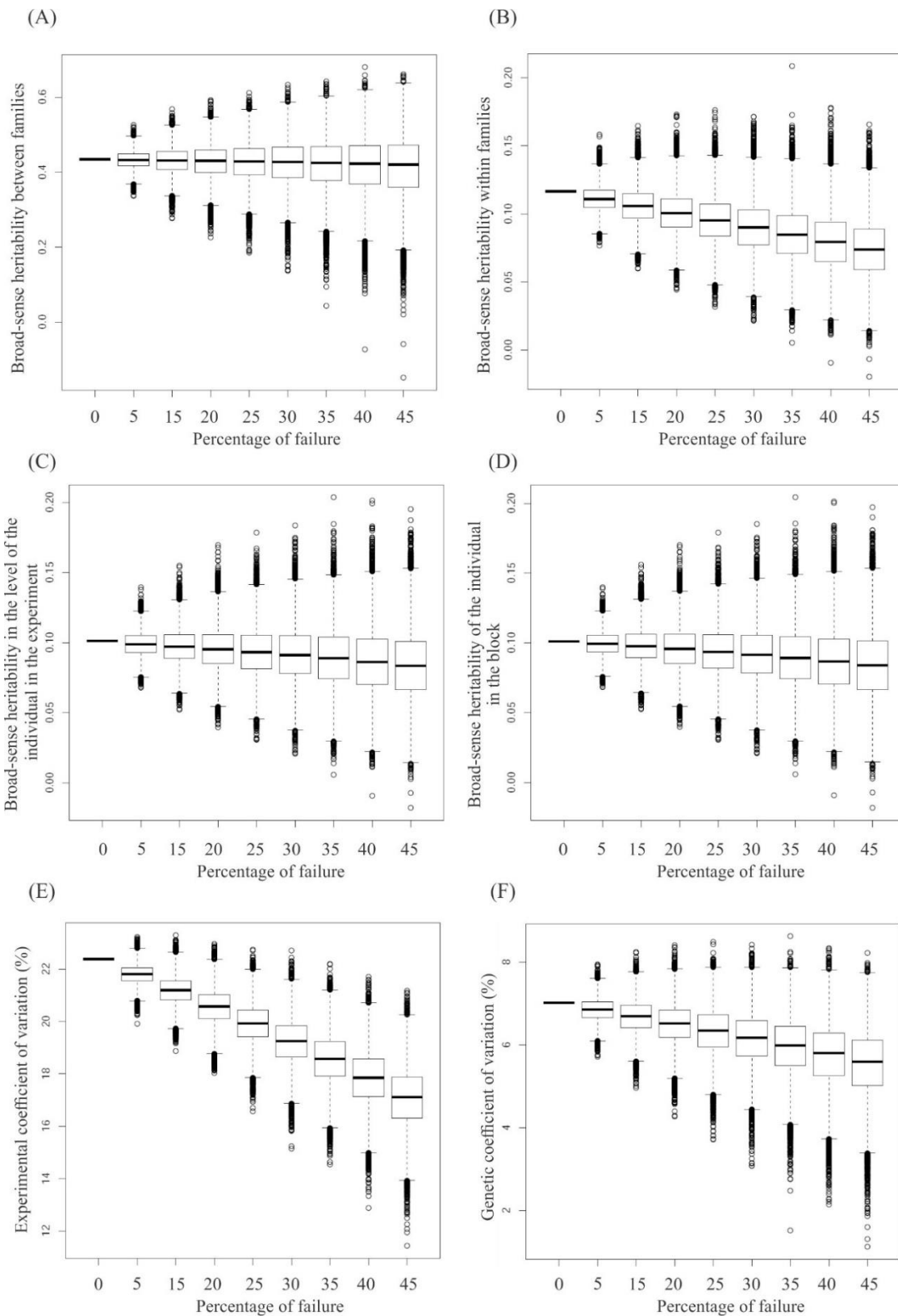


Figure 1. Dispersion of the 20000 parameters estimates of (A) broad-sense heritability between families, (B) broad-sense heritability within families, (C) broad-sense heritability in the level of the individual in the experiment, (D) broad-sense heritability of the individual in the block, (E) experimental coefficient of variation (F) and genetic coefficient of variation.

For all the investigated genetic parameters, an increase in the amplitude of the estimates was verified. Also in the boxplots (Figure 1), the increase of simulated failures caused even an increase in the amount of outliers. In extreme cases, negative variances and heritabilities were detected, indicating that in such cases, this proportion of failure may be extremely harmful for estimating genetic values, to estimate the gain with the selective process and for decision making. The obtaining of negative variances stems from the method used, and its obtaining an indicative of problems in the estimation process. These results, together with those of [1] corroborate the fact that, at the very least, failures in the plant stand impair the identification of the best materials, and that of large amounts of failures are able to make experimentation impossible to breeding purposes and selection of superior genetic materials.

For the estimates of h_w^2 , in all cases, it decreased with the increase in the number of failures in the experiment. Furthermore, they presented estimates lower than those of heritability at the level of family mean, which according to [19], implies that the selection in this selection unit should provide greater genetic gains. In Figures 1-4, 1-F are also presented the behavior for parameter estimates h_{ib}^2 , h_{ie}^2 , CV_e and CV_g , which were similar to h_w^2 .

The results indicated that, in general, the increase of failures in the experiment led to a variety of estimates of genetic parameters, sometimes higher, sometimes inferior, or innocuous. The experiment's behavior with experimental failures should be investigated on a case-by-case basis, since each experiment has a genetic structure unknown to a priori, usually with intricate kinship relationships among the genotypes. A possible criticism that could be raised, is that in the scenarios evaluated, it was not considered that the development of plants adjacent to experimental failures, which should stand out to others. We emphasize that this was not the focus of the work, given the intense work of computational modeling necessary, but that will certainly be investigated in the future.

4. Conclusions

The increase in the number of experimental failures led to an increase in the amplitude of the estimates of genetic parameters.

Experimental failures equal to or greater than 35% of the experiment provided unrealistic estimates of heritabilities. Similar percentage experiments are potentially problematic to estimate genetic parameters and gain with selection.

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