

Stratified mass selection, individual selection between and within, and genetic gains in native maize varieties¹

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ABSTRACT

Maize is an important cereal that is grown and consumed all over the world. Among the selection methods that contribute to increasing the frequency of favorable alleles in native maize populations, selection between and within and stratified mass selection in half-sibling families has proven efficient. This study aimed to conduct an individual selection between and within and stratified mass selection in ten half-sibling families of native maize and to estimate the variance components, genetic parameters, and selection gains for them. Ten half-brother families of families were evaluated. The experimental design was DBC, with two replications totaling 20 experimental units, evaluating four plants per plot. The spacing used was 0.8 by 0.3 m. The following were evaluated: stalk diameter (SD), ear length (EL), ear diameter (ED), number of rows (NF), number of grains per row (NGR), ear mass (EM), and total grain mass (TGM) were evaluated. Individual analyses were carried out for all the traits evaluated, selected to increase the original means with a selection intensity of 50% between/50% within. Stratified mass selection yielded higher selection gains than selection between and within families. The selection of the character's ear mass and total grain mass showed the highest estimates of genetic gain, 54.45 and 48.37%, respectively.

Keywords: variance components; half-sib families; genetic variability.

INTRODUCTION

Maize (*Zea mays* L.) is one of the most important cereals grown and consumed worldwide due to its productive potential, chemical composition, nutritional value, and multiplicity of applications.⁽¹⁾ Approximately 60% of the maize produced in the world is used for animal feed, in the form of grains, bran, silage, and feed.^(2,3)

Zea mays L. is characterized by wide genetic variability, confirmed by its adaptation to large variations in latitude, altitude, temperature, biotic and abiotic stresses, and even small environmental variations in localized regions.⁽⁴⁾ In Brazil, maize germplasm is also characterized by wide variability, including breeds, local varieties, and exotic or semi-exotic germplasm introduced from other countries.^(5,6)

From the 1950s onwards, a series of transformations took place in world agriculture, among which genetic changes were perhaps the ones that most affected the lives of farmers, who need large quantities of fertilizers, agrochemicals, machinery, and equipment to maintain them.^(7,8) As a result, it is becoming increasingly necessary to search for maize germplasm available in the country and among plant populations traditionally used in agriculture with few modern technological elements.⁽⁹⁾

In this sense, landraces of corn emerge as a precious source of favorable alleles, as they require low levels of investment in inputs to achieve satisfactory productivity.⁽¹⁰⁾ These breeds are less productive than commercial cultivars but have great genetic variability and resistance, making it possible for farmers to obtain the seeds themselves.⁽¹¹⁾ Once cultivated by communities, such as indigenous peoples and family farmers, they are usually subjected to selection for characteristics related to production in each harvest, providing good performance in the conditions in which they are grown.⁽¹²⁾

Normally, farmers who grow native maize use little or no agrochemicals on their fields, making it easier to maintain environmental balance and generate a pattern of ecological sustainability.⁽¹³⁾ These materials result from the accumulation of collectively constructed and reconstructed knowledge, which, even in the face of the hegemonic practice of GM cultivation, are present in countless experiences that represent the conditions for sustainable development.⁽¹⁴⁾

Among the intrapopulation selection methods that contribute to increasing the frequency of favorable alleles in creole corn populations, individual selection between and

within and stratified mass in half-sib families have proven to be efficient, as they allow genetic progress to be made faster, due to the possibility of carrying out more than one cycle per year.^(4,15) While individual selection between and within consists of selecting or rejecting families taking into account the deviation of their value in relation to the average phenotypic value of the population, considering only a single character of interest, stratified mass selection is based on the individual selection of plants into strata, with each of these representing an independent selective unit.⁽¹⁶⁻¹⁸⁾

Carvalho *et al.*⁽¹⁹⁾, when evaluating the genetic parameters in the CMS-52 corn population in Sergipe, subjected to three cycles of individual selection between and within half-sib progenies, they observed broad potential for selection gains, with an average progress of 12.3% and greater selection efficiency with progeny averages when compared to mass selection. Carvalho & Souza,⁽²⁰⁾ estimating the genetic parameters in the BR 5011 Sertaneja corn variety, carried out 17 cycles of selection between and within half-sib progenies and three cycles of stratified mass selection in the period from 1985 to 2005, observing wide variability genetics in these, both free and potential.

The estimation of genetic parameters is very important in plant breeding, as it allows the nature of the action of genes involved in the control of quantitative traits to be identified.⁽²¹⁾ It also makes it possible to evaluate the efficiency of different breeding strategies by obtaining genetic gains and maintaining the appropriate genetic base. In this way, estimates of genetic parameters such as genetic variance, heritability and selection gains between the characters of the production components make it possible to know the potential of populations for improvement.

Given the great genetic diversity of creole corn genotypes present in the Brazilian Amazon and cultivated by traditional populations, it is essential to carry out work aimed at understanding and exploring the rich existing genetic variability, contributing to the studies and preservation of these native corn populations. As they are a rich source of favorable alleles, it is expected that these traditional materials present valuable morphoagronomic characteristics for future breeding programs.

In this context, the objective of this work was to carry out stratified and individual mass selections between and within ten families of half-sibs of Creole corn from Acre, originating from plants obtained by mass selection in the previous cycle, as well as to estimate the variance com-

ponents, genetic parameters and selection gains of these genotypes.

MATERIAL AND METHODS

The experiment was set up and conducted in the experimental area of the Federal University of Acre, located in the municipality of Rio Branco, under the geographical coordinates 67° 42' 18" O and 10° 01' 30" S and elevation of approximately 136 meters. According to the Koppen and Geiger classification, the local climate is tropical, hot, and rainy; Am has an average temperature of 25.5 °C and annual rainfall of 1806 mm.⁽²²⁾

The experiment was carried out between December 2020 and March 2021. It used a randomized block design with ten treatments and two replications (10 x 2). The plots consisted of three planting lines, each 5 meters long and spaced 0.8 m by 0.3 m, with a useful area 10m².

The treatments consisted of ten native maize families whose seeds came from plants belonging to four local varieties. $i = 10\%$ was applied among 106 genotypes obtained by mass selection. The native maize seeds used have been registered in the National System of Genetic Heritage and Associated Traditional Knowledge under A6A46CC and CGEN registration no. 201/2014.

The harvest took place in March 2021. All the plants that had produced ears at the end of the experiment were evaluated. The characters evaluated were stalk diameter (SD), ear length (EL), ear diameter (ED), number of grain rows (NF), number of grains per row (NGR), ear mass (EM), and total grain mass (TGM).

The analysis of variance was carried out following the statistical model for randomized blocks proposed by Cruz et al.⁽²³⁾

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

In which: Y_{ijk} is the value observed in the k -th individual, evaluated in the i -th genotype of the j -th block; μ is the overall mean of the experiment; G_i is the fixed effect of the i -th genotype; B_j is the effect of the j -th block; D_{ij} is the effect of plot ij ; E_{ijk} is the effect of individual k , of the i -th genotype in the j -th block.

The variance components were estimated from the analysis of variance using the following expressions:⁽²³⁾

Block variance: $\sigma_b^2 = \frac{QMB - QME}{ng}$; genetic variance between plot averages: $\sigma_g^2 = \frac{QMG - QME}{nr}$; environmental variance between plots: $\sigma_e^2 = \frac{QME - QMD}{n}$; genetic variance within families or between plants within plots: $\sigma_d^2 = QMD$.

Heritability coefficients were estimated at the level of individual plants within families and at the family average level for use in the selection schemes used:⁽²³⁾

Heritability at the level of families (selection between family means): $h_{\text{between}}^2 = \frac{\sigma_g^2}{QMG/nb}$; heritability at the level of individual plants (selection within families): $h_{\text{within}}^2 = \frac{\sigma_g^2}{QMD}$; heritability at the level of individual plants in the block: $h_d^2 = \frac{(\frac{1}{n})\sigma_g^2}{\sigma_e^2 + \sigma_d^2 + \sigma_g^2}$; heritability at the level of individual plants in the experiment: $h_e^2 = \frac{(\frac{1}{n})\sigma_g^2}{\sigma_e^2 + \sigma_d^2 + \sigma_g^2 + \sigma_b^2}$.

The coefficients of variation were estimated as proposed by Vencovsky & Barriga:⁽²⁴⁾ experimental coefficient of variation (CV_1): $CV_{\text{exp}\%} = \frac{100\sqrt{QME/n}}{\widehat{m}}$; coefficient of environmental variation (CV_2): $CV_{\text{e}\%} = \frac{100\sqrt{\sigma_e^2}}{\widehat{m}}$; genetic coefficient of variation between families (CV_3): $CV_{\text{ge}\%} = \frac{100\sqrt{\sigma_{gm}^2}}{\widehat{m}}$; genetic coefficient of variation within families (CV_4): $CV_{\text{gd}\%} = \frac{100\sqrt{\sigma_{gd}^2}}{\widehat{m}}$. Where \widehat{m} is the overall experimental average.

Selection gains were estimated using ten genotypes from half-brother families (HBF), with selection intensity = 50% between and 50% within families. All characters were selected in the positive direction, i.e., to increase their original means. The selection intensity of 50% between and 50% within families ($k=0.8$) was chosen to ensure an adequate number of genotypes selected for the following selection cycle. Selection gains between and within were estimated using the method that takes selection differentials into account, according to Cruz et al.⁽²³⁾

After collecting the experimental data, two analyzes were carried out: Selection between and within stratified - direct and indirect (for individual selection between and within) and Selection between and within mass - direct and indirect (for stratified mass selection), aiming to estimate genetic gains and select the best genotypes. All statistical analyses were carried out using Genes software.⁽²⁵⁾

RESULTS AND DISCUSSION

Table 1, referring to the analysis of variance, shows significant results by the F test at 1% probability for the seven characters analyzed in the families studied. Results such as these are desirable in plant breeding, as they indicate the existence of ample genetic variability between or within families and their great potential for future genetic gains through selection.

The experimental coefficients of variation ($CV_{\text{e}\%}$) were very high (>30%), according to Pimentel Gomes & Garcia⁽²⁶⁾ ranging from 35.37% to 56.88%. According to

Carpentieri-Pípolo *et al.*,⁽²⁷⁾ high $CV_{e\%}$ values in native maize, as observed in this study, indicate that the experiment did not have the environmental factors adequately controlled, which may have influenced the variance analysis. According to the authors, these results can be explained by the adverse environmental conditions at the experiment site and the great genetic variability within the populations, an important element for selection.

The high $CV_{e\%}$ values observed can be explained by the environmental conditions during the trial period, characterized by long periods of drought and low rainfall for the 2020/2021 agricultural year in Baixo Acre, with greater impact in the months of January and February, during the flowering and grain filling phases, respectively. The wide genetic variability of the landrace's genotypes tested may also have influenced $CV_{e\%}$ estimates, since this is a population in the initial stages of selection, characterized in this way by high segregation between the plants that make up it. Even with high $CV_{e\%}$, significant family effects were obtained for all variables studied at 1% (Table 1), in line with the results observed by Cargnelutti Filho & Storck⁽²⁸⁾, who evaluated statistics for classifying experimental precision of corn cultivar trials, found that of the 101 experiments studied, 7 showed $CV_{e\%} > 20\%$, and of these, 5 (71%) showed a difference between cultivars, and their results should not be disregarded.

The genetic variances within families (σ_{gd}^2) were higher than those between families (σ_{ge}^2) for all the characters studied (Figure 1). This result indicates that selection within families is more efficient than between families. The most pronounced within-family genetic variability (σ_{gd}^2) was observed for the ear mass (EM) and total grain mass

(TGM) characters, with 3779.8 and 2569.91, respectively, reflecting a greater probability of success with selection for these characters within the families studied.

Similar results were observed by Matta & Viana⁽²⁹⁾ in popcorn, who obtained genotypic variances within families in the order of 50.35 and 790.58 for the variables expansion capacity and grain production, respectively, much higher than 3.74 and 159.64 of the genotypic variance between families for the same variables. According to the authors, in the case of unimproved populations, results like this demonstrate the existence of variability, influencing the quality of the genotypes under study.

The block (σ_b^2) and environmental (σ_{ee}^2) variances were relatively low compared to the others, indicating less influence from the blocks and the environment than the effect of the genotype on phenotypic determination for the characters studied. The negative is due to the estimation method, which allows us to extract superior individuals.

In general, the coefficients of heritability at the family level (h_m^2) were high, with values above 0.83 for all the variables studied (Table 2). Results suggest high genetic control over phenotypic determination, indicating great selection potential for all the genotypes evaluated based on family averages. Soares *et al.*,⁽³⁰⁾ estimating the genetic parameters in a population of recombinant inbred lines of tropical maize, obtained an average heritability coefficient of 0.80 for ear weight. The result is close to that obtained in this study for the variable in question ($h_m^2 = 0.85$).

The heritability coefficients at family average level (>0.83) obtained in the present study were higher than the h^2 values obtained by Magar *et al.*⁽³¹⁾ for number of rows (0.73), number of grains per row (0.14), mass (0.44), diam-

Table 1: Summary of the analysis of variance for the characters evaluated in families of native maize varieties in Rio Branco, 2021

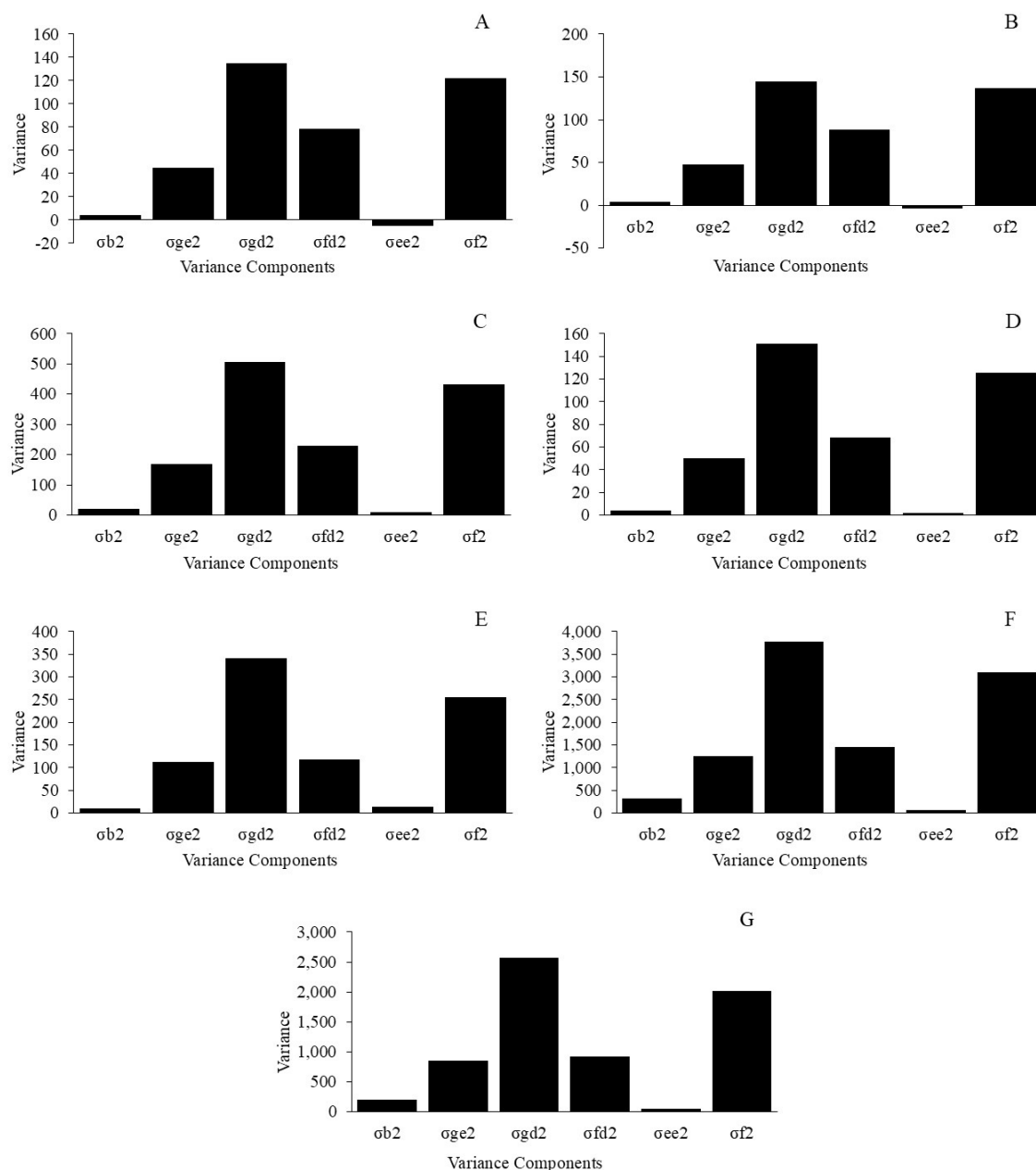
| FV | QM | | | | | | |
|------------|----------|-----------|------------|-----------|-----------|-------------|------------|
| | SD | EL | ED | NF | NGR | EM | TGM |
| Blocks | 224.45 | 249.22 | 1140.81 | 248.51 | 594.05 | 14413.35 | 8966.34 |
| Families | 417.33** | 4114.02** | 14615.11** | 4318.76** | 9710.70** | 106411.41** | 71744.89** |
| Between | 520.863 | 648.41 | 2432.77 | 692.86 | 1535.70 | 15696.24 | 10067.07 |
| Inside | 4700.13 | 5296.72 | 13814.15 | 4108.25 | 7119.50 | 87801.93 | 55232.24 |
| Average | 7.21 | 8.498 | 21.60 | 7.71 | 13.53 | 59.03 | 44.57 |
| CV_e (%) | 52.74 | 49.94 | 38.06 | 56.88 | 48.29 | 35.37 | 37.52 |

SD = Stalk diameter; EL = Ear length; ED = Ear diameter; NF = Number of rows; NGR = Number of grains per row; EM = Ear mass; TGM = Total grain mass; FV = Source of variation; QM = Mean square; ** significant at 1% significance by the F test.

eter and length of ears (0.41 and 0.43), and those of Costa et al.⁽³²⁾ in green corn and Abe & Adelegan⁽³³⁾ in super sweet corn for number of rows (0.48 and 0.77), diameter (0.26 and 0.66) and length of ears (0.46 and 0.67, respectively). These results suggest a strong genetic influence on phenotypic determination, with low environmental interference and conditions broadly favorable to selection in these traditional genotypes.

The coefficients of heritability of individuals within

families (h_d^2) were higher than 1 for all the characters studied, with the highest value observed for total grain mass (2.79). These results can be explained by the wide genetic variation observed within families compared to between families. The heritability estimates based on the individuals in the block (h_b^2) and the experiment (h_e^2) were very close, indicating that the blocks contributed less to the phenotypic variance, allowing for more efficient selection between and within families.



σ_b^2 = Variance due to the block effect; σ_{ge}^2 = Genetics between family averages; σ_{gd}^2 = Genotypic within families; σ_{fd}^2 = Phenotypic within families; σ_{ee}^2 = environmental between plots; σ_f^2 = Total phenotypic.

Figure 1: Estimates of variances for the characters stalk diameter (A), ear length (B), ear diameter (C), number of grain rows (D), number of grains per row (E), grain mass ear (F) and total grain mass (G) in families of creole corn varieties in Rio Branco, 2021.

Table 2: Estimates of the coefficients of heritability at the level of family means (h_m^2), of individuals within families (h_d^2), of individuals in the block (h_b^2) and in the experiment (h_e^2), estimated for variables in families of native maize varieties in Rio Branco, 2021

| Heritability coefficients | Variable | | | | | | |
|---------------------------|----------|------|------|------|------|------|------|
| | SD | EL | ED | NF | NGR | EM | TGM |
| h_m^2 | 0.86 | 0.84 | 0.83 | 0.84 | 0.84 | 0.85 | 0.86 |
| h_d^2 | 1.72 | 1.64 | 2.20 | 2.20 | 2.87 | 2.58 | 2.79 |
| h_b^2 | 1.46 | 1.41 | 1.65 | 1.67 | 1.85 | 1.80 | 1.88 |
| h_e^2 | 1.41 | 1.38 | 1.57 | 1.61 | 1.78 | 1.62 | 1.69 |

SD = Stalk diameter; EL = Ear length; ED = Ear diameter; NF = Number of rows; NGR = Number of grains per row; EM = Ear mass; TGM = Total grain mass.

Table 3 shows the genetic and environmental coefficients of variation and the CV_{ge}/CV_e and CV_{gd}/CV_e ratios for the characters studied. The genetic coefficient of variation is essential for determining the presence of genetic variability in a population; it expresses the magnitude of the genetic variation in relation to the character's mean.

The CV_{ge}/CV_e ratio, proposed by Vencovsky & Barriga⁽²⁴⁾, gives the proportion of genetic variance about residual error, with no influence from the population mean. The estimates of this index were generally high, indicating sufficient genetic variability for the agronomic traits evaluated. Except for the variables stalk diameter (SD) and ear length (EL), all the characters showed values greater than 1 for the CV_{ge}/CV_e ratio, indicating the superiority of genetic variance over environmental variance, as well as the existence of favorable conditions for selection.⁽²⁴⁾

The CV_{gd}/CV_e relationships in the present study were superior to those found by Candido *et al.*⁽³⁴⁾ in green corn for the variables grain mass (0.41), ear diameter (0.48) and

number of grain rows (0.38). The CV_{gd}/CV_e relationships in this work were also demonstrated to be superior to those found by Rigon *et al.*⁽³⁵⁾ who, estimating genetic diversity in 25 corn hybrids in Rio Grande do Sul, Brazil, found CV_{ge}/CV_e relationships in the order of 1.26 for ear size and 0.82 for grain mass per ear.

According to Cruz *et al.*,⁽²³⁾ when the estimate of this ratio is ≥ 1 , it indicates experimental precision in data collection and a very favorable situation for artificial selection. This favors the phenotypic selection of traits since genetic variation is largely responsible for the differences between and within families.^(23,36)

CV_{gd} was higher than CV_{ge} for all the traits studied, confirming that the chances of obtaining greater gains from selection are potentially greater from individuals within families. For all the variables, the CV_{gd} and CV_{ge} values were higher than 7%, the minimum threshold to be considered high, according to Sebbenn *et al.*,⁽³⁷⁾ indicating the existence of vast genetic variability between and within the native maize families studied.

Table 3: Estimates of the genetic coefficients of variation between families (CV_{ge}), genetic within families (CV_{gd}), environmental (CV_{va}), and the relationship between the genetic coefficients of variation between families and environmental (CV_{ge}/CV_{va}) and within families and environmental (CV_{gd}/CV_{va}), for families of native maize varieties in Rio Branco, 2021

| Parameter | Variable | | | | | | |
|-------------------|----------|--------|--------|--------|--------|--------|--------|
| | SD | EL | ED | NF | NGR | EM | TGM |
| CV_{ge} | 92.94 | 81.65 | 60.22 | 92.01 | 78.78 | 60.13 | 65.67 |
| CV_{gd} | 160.97 | 141.41 | 104.31 | 159.37 | 136.46 | 104.15 | 113.74 |
| CV_{va} | 0 | 0 | 14.65 | 18.92 | 26.65 | 14.19 | 15.79 |
| CV_{ge}/CV_{va} | 0 | 0 | 4.11 | 4.86 | 2.96 | 4.24 | 4.16 |
| CV_{gd}/CV_{va} | 0 | 0 | 7.12 | 8.43 | 5.12 | 7.34 | 7.20 |

SD = Stalk diameter; EL = Ear length; ED = Ear diameter; NF = Number of rows; NGR = Number of grains per row; EM = Ear mass; TGM = Total grain mass.

Table 4: Gains by selection between (GS_e), within (GS_d), and between and within (GS_{ed}) estimated by the methods of selection between and within (ED) and stratified mass (EM) in traits of families of native maize varieties in Rio Branco, 2021

| Method | Variable | | | | | | | |
|--------------|-----------|------|------|-------|------|-------|-------|-------|
| | GS | SD | EL | ED | NF | NGR | EM | TGM |
| ED selection | GS_e | 0.56 | 0.78 | 1.51 | 0.53 | 2.89 | 13.19 | 12.38 |
| | GS_d | 2.31 | 1.23 | 5.79 | 3.75 | 7.89 | 41.26 | 35.99 |
| | GS_{ed} | 2.87 | 2.01 | 7.3 | 4.28 | 10.78 | 54.45 | 48.37 |
| EM Selection | GS_e | 0.53 | 0.78 | 1.51 | 0.53 | 2.89 | 13.19 | 12.37 |
| | GS_d | 4.67 | 2.69 | 9.65 | 4.63 | 13.56 | 73.36 | 58.20 |
| | GS_{ed} | 5.2 | 3.47 | 11.16 | 5.16 | 16.45 | 86.55 | 70.57 |

SD (mm) = Stalk diameter; EL (cm) = Ear length; ED (mm) = Ear diameter; NF = Number of rows; NGR = Number of grains per row; EM (g) = Ear mass; TGM (g) = Total grain mass; GS = Selection gain.

The highest CV_{gd} values were for SD (160.97 and 92.94), NF (159.37 and 92.01), EL (141.41 and 81.65), and NGR (136.46 and 78.78 respectively). The lowest CV_{gd} values were observed for EM (104.15 and 60.13), ED (104.31 and 60.22), and TMG (113.74 and 65.57, respectively).

Table 4 shows the gains from selection between, within, and between families, calculated from the selection differentials, applying a selection intensity of 50% between and 50% within the native maize families evaluated.

The GS_d was higher than the GS_e for all the characters evaluated in both selection methods (individual between and within and stratified mass). These results contrast with those obtained by Carvalho et al.⁽¹⁹⁾, who, working with three selection cycles between and within maize for the CMS-52 population, obtained GS_e higher than GS_d for all cycles studied, indicating that gains between or within families may vary according to the characteristics of the population being improved. The gains from stratified mass selection were higher than those observed for individual selection between and within all the characters studied. This indicates that the former is more efficient at exploiting

the genetic variability in the genotypes under study.

Results like these can be explained by the heritability values used in the gain-by-selection (GS) calculations. For individual selection between and within families, use is made of the heritabilities at the level of family means (h_m^2) and of individuals within families (h_d^2). In stratified mass selection, the individual heritabilities in the block (h_b^2) and the experiment (h_e^2) are used, thus making it possible to exploit the genetic variability existing within families with greater efficiency and intensity since each stratum in this method represents an individual selective unit, with a consequent reduction in the environmental effect in determining the phenotype.

The greatest gains from stratified mass and individual selection between and within were observed for total grain mass (90.91 and 63.36%, respectively), ear mass (87.21 and 55.72%), and number of grains per row (64.86 and 43.09%). The smallest gains for both methods were observed for ear length (21.37 and 12.52%), ear diameter (31.46 and 20.65%), and stalk diameter (36.39 and 19.97%).

Table 5: Creole corn families selected by the selection between and within (ED) and stratified mass (EM) methods, with selection intensity (i) = 50% in Rio Branco, 2021

| Method | Selected families | | | | | | |
|---------------------|-------------------|----|----|----|-----|----|-----|
| | SD | EL | ED | NF | NGR | EM | TGM |
| ED and EM Selection | 1 | 2 | 2 | 2 | 3 | 2 | 2 |
| | 2 | 3 | 3 | 4 | 4 | 3 | 3 |
| | 3 | 5 | 4 | 6 | 6 | 4 | 4 |
| | 5 | 6 | 6 | 8 | 8 | 6 | 6 |
| | 10 | 10 | 10 | 10 | 10 | 10 | 10 |

SD (mm) = Stalk diameter; EL (cm) = Ear length; ED (mm) = Ear diameter; NF = Number of rows; NGR = Number of grains per row; EM (g) = Ear mass; TGM (g) = Total grain mass.

Suhaisini *et al.*,⁽³⁸⁾ working with 15 elite varieties of sweet corn in Tamil Nadu, India, during the summer of 2015, obtained selection gains in the order of 9.55% for ear length, 10.24% for width/diameter of ear and 27.34% for number of grains per row, results lower than those obtained in the present study. Silva *et al.*,⁽³⁹⁾ in turn, obtained genetic gains using the direct selection method in the order of 6.12% for number of rows, 7.97% for ear length and 5.68% for ear diameter, values also lower than those obtained in this work. Results like this demonstrate the great selection potential for Amazonian landraces genotypes, which could be converted into important selection gains as the breeding program progresses over time.

Carvalho *et al.*,⁽⁴⁰⁾ working with five selection cycles of the BRS 5033-Asa Branca maize cultivar, obtained gains ranging from 0.6 to 27.9% between and 0.8 to 26.6% within progenies for the ear weight variable. Lower than in this study. Guimarães *et al.*,⁽⁴¹⁾ estimated gains of 9.62, 3.93, and 9.79% for the number of rows, grains per row, and ear weight, respectively. In this study, the estimated gains were 28.51, 43.09 and 55.72% for selection between and within families for the same traits.

Table 5 shows the Creole corn families selected for each character, from a total of 10 tested, applying $i=50\%$. Genotype 10 was evident, as it was selected for all characters in both selection methods (between and within and stratified mass). Families 2, 3 and 6 stood out for 6 of the 7 variables studied, indicating broad potential for these materials to continue in future selection cycles. Family 4 was selected for 5 of the 7 characters under study. 5 families (50% between), and within these, 8 genotypes (50% within) were selected for the next selection cycle, using both methods, which coincided in relation to the families and plants selected.

The results obtained in this study showed that Amazonian Creole corn genotypes have great potential for selection, constituting a rich source of genetic variability for the improvement of the species. Given the scarcity of works of this type in the literature, more studies like this are necessary to contribute to the knowledge and preservation of existing genetic variability, as well as to the formation of productive cultivars based on these genotypes, which will benefit small producers and populations traditional.

CONCLUSIONS

The native maize families evaluated show genetic variability for all the studied characters. Heritabilities based on

family averages show high genetic control and favorable and promising conditions for selection. The character's number of grains per row, ear mass, and total grain mass show high gain values, which are favorable for use in the selection of native maize families.

Creole families 2, 3, 4, 6 and 10 are the most productive and promising for the selection of the characters under study. Stratified mass selection provided greater gains than individual selection between and within families. This makes it necessary to conduct new experiments to obtain productive cultivars in advanced selection cycles.

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