

Genetic evaluation and selection of cocoa tree clones

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ABSTRACT: The cultivation of cocoa is of great socio-economic importance worldwide. Cocoa beans are the essential raw material for chocolate production. The variability of cacao studied presents only a small fraction of the existing genetic diversity, mainly in the Amazon region. Furthermore, just a small part of this variability has been exploited in cocoa breeding. Thus, the present study processed the genetic evaluation and selection of cocoa clones, based on morpho-agronomical traits. For this, we evaluated 145 clones, during 37 harvests from, four consecutive years. The following traits were evaluated: total number of fruits collected (TNFC), total number of healthy fruits (TNHF), weight of wet seeds from healthy fruits (WWSHF), average weight of wet seeds per healthy fruit (AWWSHF), weight of dry seeds from healthy fruit (WDSHF), percentage of fruits with germinated seeds (PFGS), number of branches with witches' broom disease (NBWB), and number of inflorescence with witches' broom disease (NBWB). Significant differences (P < 0.05) among the clones were observed for all traits, which reveal an expressive variability and possibility of gains with selection. The highest significant correlations (P < 0.05) occurred between traits TNFC and TNHF (0.94), TNHF and AWWSHF (0.86), and TNHF and AWDSHF (0.86). Based on the selection index, the clones POUND 12 and CAB 12, 228, 253, 257, 258, and 422 were the most suitable for selection.

Key words: Theobroma cacao L., genetic resources, germplasm characterization, genetic variability, plant breeding.

Avaliação genética e seleção de clones de cacaueiro

RESUMO: O cultivo do cacau tem grande importância socioeconômica mundial. Os amêndoas de cacau são a matéria-prima essencial para a produção de chocolate. A variabilidade do cacaueiro avaliada representa apenas uma pequena fração da diversidade genética existente, principalmente na região amazônica. Além disso, apenas uma pequena parte dessa variabilidade foi explorada no melhoramento de cacau. Dessa forma, o presente estudo teve como objetivo realizar a avaliação genética e seleção de clones de cacau, com base em características morfo-agronômicas. Para isso, foram avaliados 145 clones, durante 37 colheitas, em quatro anos consecutivos. As seguintes características de frutos e sementes foram avaliadas: número total de frutos colhidos (NTFC), número total de frutos sadios (NTFS), peso de sementes úmidas dos frutos sadios (PSUFS), peso médio de sementes úmidas dos frutos sadios (PMSUFS), peso de sementes secas dos frutos sadios (PSSFS), peso médio de sementes secas dos frutos sadios (PMSSFS), porcentagem de frutos com vassoura-de-bruxa (PFVB), porcentagem de frutos com broca (PFBR), porcentagem de frutos com sementes germinadas (PFSG), número de ramos com vassoura-de-bruxa (NRVB) e número de almofadas florais com vassoura-de-bruxa (NAFVB). Diferenças significativas (P < 0,05) entre os clones foram observadas para todas as características, o que revela uma expressiva variabilidade e possibilidade de ganhos com a seleção. As maiores correlações significativas (P < 0,05) ocorreram entre os caracteres NTFC e NTFS (0,94), NTFS e PMSUFS (0,86) e, NTFS e PMSSFS (0,86). Com base no índice de seleção, os clones POUND 12 e CAB 12, 228, 253, 257, 258 e 422 foram considerados os mais adequados para a seleção.

Palavras-chave: caracterização de germoplasma, melhoramento de plantas, recursos genéticos, Theobroma cacao L., variabilidade genética.

INTRODUCTION

The cultivation of cocoa (*Theobroma cacao* L.) has great socioeconomic relevance worldwide.

The beans, after being fermented and dried, constitute the essential raw material of chocolate, candies, cocoa butter, and several pharmaceutical and cosmetic products (SOUZA et al., 2016). Given

Received 06.02.21 Approved 01.04.22 Returned by the author 05.21.22 CR-2021-0433.R1 Editors: Leandro Souza da Silva D Cicero Almeida such importance, the use of more productive, pestand disease-resistant genotypes is crucial to assure the yield and the economic development of the crop (RUBIYO et al., 2015). This fact has motivated the creation of cocoa breeding programs (RODRIGUES-MEDINA et al., 2019).

The use of genetic resources from native cocoa populations in breeding programs has aroused interest in the scientific community after the exploratory collections carried out by POUND (1938) in Upper Amazon region, Colombia, and Ecuador. In those cases, the objective was to identify cocoa genotypes resistant to the witches' broom disease. However, the significant genetic variability reported and rescued in those populations, their potential for plant breeding, and the necessity of expanding the genetic base of current programs in several countries have motivated numerous further incursions for germplasm collecting.

The Executive Committee of the Cocoa Cultivation Plan (CEPLAC), on the Brazilian institution that researches cocoa, has collected, since 1965 (VELLO & MEDEIROS, 1965), and maintained a large germplasm bank with more than 2,000 accessions (SOUZA et al., 2012). Wild populations are reservoirs of genetic diversity, and they can be bred with cultivated varieties (BROZYNSKA et al., 2016). They are sources of genes that might be exploited in breeding programs, to develop genotypes that guarantee higher resistance to pests and diseases, better adaptability to the cultivation areas, and increased yield, among other purposes (GOVINDARAJ et al., 2015).

Despite the economic importance and the long history of use and selection of T. cacao cultivars, modern breeding programs have existed for less than a century and have advanced only a few generations (TOXOPEUS, 1985; DUVAL et al., 2017; WIBAUX et al., 2017; RODRIGUEZ-MEDINA et al., 2019, DOARÉ et al., 2020). There is an expressive genetic variability available, but just a small fraction of it has been exploited in breeding programs conducted by the producing countries. Also, most of these initiatives employed a restricted number of genotypes with narrow genetical basis, in order to obtain high gains in the short term, which aggravates the overall genetical vulnerability of the crop (SANTOS et al., 2015). It is important to bear in mind that genetic resources of cocoa are conserved ex-situ and in-field germplasm bank, since this species has recalcitrant seeds to desiccation and long-term storage.

The analysis of genetic diversity has helped to identify unique phenotypes and genotypes

(BALLESTEROS et al., 2015; COSME et al., 2016). The collection, evaluation, and characterization of germplasm allow attaining, via proper processes and methods, information on the genetic resources assembled in the bank. Breeders may use such data to guide breeding programs with the species. It is necessary to know, investigate, and characterize the morpho-agronomical traits of the whole T. cacao genepool, so that it becomes possible to reason about its breeding potential (ALMEIDA & DIAS, 2001). Several traits, considered either individually or in combination, have proven to be of great value for the selection of superior genotypes in bean yield (DOARÉ et al., 2020). The present study aimed to process the genetic evaluation and selection of cocoa clones, based on morpho-agronomical traits.

MATERIALS AND METHODS

Study site

The study used accessions from the cocoa germplasm bank of the Experimental Station at Ouro Preto (Estex-OP) (latitude 10° 44' 30" S, longitude 62° 13' 30" W, and altitude 280 m above sea level), belonging to CEPLAC, located in the city of Ouro Preto do Oeste, at 340 km from Porto Velho, Rondônia (RO), Brazil. According to the Köppen's classification, the region is under the Aw climate type (tropical wet and dry), with temperatures around 18 °C in the coldest month, and a well-defined dry season. The average annual rainfall is 1940 mm, more intense from November to April, with 80.3% of the total precipitation concentrated in this period. The average annual temperature is 24.6 °C, with October scoring the highest value (25.7 °C) and July the lowest one (22.9 °C). The annual relative humidity (RH) rounds 81%, with lower values from July to September. The insolation is more intense in July, and the lowest evaporation rate occurs in August. The predominant soil of Estex-OP's cocoa genebank is Argisol Red-Yellow, of medium natural fertility and presents water deficit from June to September (BARBOSA & NEVES, 1983; SCERNE et al., 2000).

Plant material

The Estex-OP cocoa genebank contains 615 clonal accessions from multiple provenances, especially from wild populations from Rondônia. The clones were produced by patch budding, with rootstocks from different genetic matrices, ranging from four to six months old. The genebank was planted between 1977 and 1984. All accessions were established in a space dimensioned 3.0 x 3.0 m

and planted in 40 x 40 x 40 cm pits. Banana (*Musa sp.*) was used in association to provide provisory shading, at the same spacing as that employed for the cocoa trees. In the first implementation blocks, permanent shading had been provided by *Clitoria racemose*, a legume tree that had stood out among other alternatives. Subsequently, a mix of local tree species was adopted. They were spaced differentially, varying from 12 x 12 m to 24 x 24 m, with one plant positioned diagonally. The clones were placed in the field in one of these plot schemes: ten to fourteen plants, organized in two adjoining lines; five or six plants, arranged in a single line; four, five, or six, also in a single line; and fourteen to thirty-six plants, in either one or two lines.

For the purposes of this research, 145 accessions were selected (Table 1), bearing in mind the following characteristics: physiological maturity (accessions older than ten years in the field); number of plants of the same field age per accession (minimum of three); agronomical state suitable for analysis (considering size and architecture of the trees); yield control and competitivity among plants within a plot (appraised via the number of dead plants in the surroundings). The number of repetitions varied according to the clone evaluated. The number of plants evaluated varied between 3 and 14 plants per clone. The study was performed at 37 harvests, during four consecutive years. Altogether, eleven traits were

evaluated: total number of fruits collected (TNFC); total number of healthy fruits (TNHF); weight of wet seeds from healthy fruits (WWSHF, in g); average weight of wet seeds per healthy fruit (AWWSHF, in g); weight of dry seeds from healthy fruit (WDSHF, in g), estimated by multiplying the AWWSHF by the correction factor of 40%; average weight of dry seeds per healthy fruit (AWDSHF, in g), percentage of fruits with witches' broom disease (PFWB), percentage of fruits with borer (PFBR), percentage of fruits with germinated seeds (PFGS), number of branches with witches' broom disease (NBWB), and number of inflorescence with witches' broom disease (NIWB). Only eight of these traits were considered for processing the selection index. TNFC was not included because choosing the genotypes is conditioned to the TNHF, as the commercial seeds are exclusively extracted from healthy fruits. WDSHF was withal disregarded once its calculation depends on a correction factor of 40%. Eventually, the AWDSHF was not considered because it is estimated by dividing the WDSHF by the TNHF.

Statistical procedures

The data from all accessions were amounted by year and traits. Then, the average values corresponding to a four-year span were calculated, and the results were subjected to the normality test. Since most of the traits exhibited

Table 1 - List of the 145 cocoa clones evaluated in Ouro Preto do Oeste, RO, Brazil.

| Clones | Clone code source | Provenance | Nr. of clones |
|----------------------------------|------------------------------|--|---------------|
| BE 9 and 10 | Belém | Belém (PA) surroundings | 2 |
| CAB 008 to 013 CAB 417 to 474 | Cacau da Amazônia Brasileira | Presidente Médici (RO) region Ouro Preto do Oeste, Jaru, Mirante da Serra and Ji- Paraná (RO) region | 44 |
| CAB 035 to 042 | | Santarém (PA) region | 6 |
| CAB 218 to 414 | | Ariquemes (RO) region | 63 |
| ICS 9 and 100 | Imperial College Selection | Farms in Trinidad and Tobago | 2 |
| IMC 67 | Iquitos mixed calabacillo | Iquitos region (Peru) | |
| PA 150 | Parinari | Parinari region (Peru) | 4 |
| Pound 7 and 12 | Pound | the Nanay river (Loreto, Peru) | |
| MA 11 to 15 | Manaus | Careiro Island (surroundings of Manaus, AM) | 4 |
| RB 39 | Rio Branco | Rio Branco (AC) surroundings | 1 |
| SA 002 to 020 SA 046 to 047 | Amazonian selection | Commercial plantations (RO) Commercial plantations (RO) | 19 |

a slight deviation from normality, the analyses of variance (ANOVA) were applied to the original data. Data (*x*) referring to NBWB and NIWB, expressed in percentage, showed significant deviation from normality. Thus, they were transformed through the following function Y:

$$Y = \sqrt{x + 0.5}$$

The analyses of variance using the average data of all four years were done according to the following mathematical model considering a hierarquical classification scheme (DIAS & BARROS, 2009):

$$Y_{ij} = \mu + C_i + \varepsilon_{ij}$$

Where:

 Y_{ii} is the observation of clone *i* in plant *j*;

 μ is the overall average;

 C_i is the effect of clone *i*, with i = 1, 2, ..., C;

 ε_{ij} is the sampling error associated with the observation Y_{ij} , represented by the plant/clone variation.

The Pearson correlation analysis, which quantifies the association between pairs of traits was also calculated. All these statistical procedures were performed using software SAS (SAS INSTITUTE INC., 1989) using proc GLM. The rank summation index proposed by MULAMBA & MOCK (1978) was used to assess the index of selection, as previously done by CRUZ et al. (2012). In this case, the software Selegen-Reml/Blup (RESENDE, 2016) was employed.

RESULTS AND DISCUSSION

The analyses of variance revealed significant differences (P < 0.05) among the clones, for all traits studied (Table 2), confirming the existence of genetic variability among them. A similar outcome was obtained by OKABE et al. (2004) and ALMEIDA et al. (2009), who considered accessions from the Estex-OP cocoa genebank. Likewise, other authors verified genetic diversity among wild cocoa populations via morphological traits and molecular markers (BOZA et al., 2013; MARTÍNEZ et al., 2017; OSORIO-GUARÍN et al., 2017; IZZAH et al., 2018). The existence of variability is an essential requisite for cocoa breeding (ALMEIDA & DIAS, 2001).

Concerning the yield components, the values of the coefficient of variation (CV) ranged from 9.25% (AWWSHF) to 99.31% (PFGS). In-

| | Sources of | Sources of variation | | | | |
|---------------------|------------------|----------------------|----------|-------|--|--|
| Traits | Mean so | Average | CV (%) | | | |
| | Clone | Error | | | | |
| TNFC ¹ | 1,753.60* | 371.29 | 41.57 | 46.35 | | |
| TNHS ² | 996.34* | 164.08 | 25.66 | 49.92 | | |
| WWSHF ³ | 3,571,906.60* | 904.634 | 1,869.98 | 50.86 | | |
| AWWSHF ⁴ | $4,\!202.90^{*}$ | 55.24 | 80.31 | 9.25 | | |
| WDSHF ⁵ | 571,502.28* | 144,740.50 | 747.98 | 50.86 | | |
| AWDSHF ⁶ | 672.42^{*} | 8.84 | 32.12 | 9.26 | | |
| PFWB ⁷ | 307.72* | 37.89 | 19.39 | 31.75 | | |
| PFBR ⁸ | 178.42^{*} | 37.30 | 14.16 | 43.12 | | |
| PFGS ⁹ | 6.90^{*} | 2.22 | 1.50 | 99.31 | | |
| NBWB ¹⁰ | 2.63^{*} | 0.29 | 1.86 | 28.84 | | |
| NIWB ¹¹ | 1.18^{*} | 0.17 | 0.99 | 41.24 | | |
| df | 144 | 618 | | | | |

Table 2 - Summary of the analyses of variance of 11 traits evaluated in 145 cocoa clones in Ouro Preto do Oeste, RO, Brazil.

¹Total number of fruits collected; ² Total number of healthy fruits; ³ Weight of wet seeds from healthy fruits, in g; ⁴ Average weight of wet seeds per healthy fruit, in g; ⁵ Weight of dry seeds from healthy fruits, in g; ⁶ Average weight of dry seeds per healthy fruit, in g; ⁷ Percentage of fruits with witches' broom disease; ⁸ Percentage of fruits with borer; ⁹ Percentage of fruits with germinated seeds; ¹⁰ Number of branches with witches' broom disease; ¹¹ Number of inflorescence with witches' broom disease. ^{*} Significant at a 5% probability level, according to the F test.

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field disease resistance traits varied from 28.84% (NBWB) to 41.24% (NIWB). The coefficient of variation is a measure of dispersion used to estimate the precision of experiments and represents the standard deviation expressed as a percentage of the mean (MOHALLEM et al., 2008). ALMEIDA et al. (2009), when evaluating the agronomic behavior of 140 accessions of cocoa from different origins, found coefficients of variation (CV) values between 8.9% in AWWSHF and 40.1% in TNHF, in terms of production components. As for field resistance components, values ranging from 37.6% in NBWB to 57.9% in PFBR were observed.

PIMENTEL-GOMES (1985) classified the experimental coefficient of variation as: low (less than 10%); medium (10% to 20%); high (20% to 30%) and very high (greater than 30%), but this classification also depends on the culture and evaluation conditions. The high coefficients of variation obtained in this study can be attributed to not only the expressive natural variation of wild cocoa, but also due to the gathering of data under non-experimental conditions, so the CVs found can be considered acceptable (OKABE et al., 2004).

Based on the coefficients of correlation (Table 3), the most significant linear associations occurred between TNFC and TNHF (0.94), TNHF and WWSHF (0.86), and TNFC and WWSHF (0.85). Phenotypic correlations allow quantifying the association between two traits related to yield and in-field disease resistance, for example, disregarding, however, what has caused them (DIAS & RESENDE, 2001). The phenotypic correlation between TNFC and TNHF (r = 0.94) is particularly interesting for breeding programs, since excluding nonviable fruits from the harvested set is a time-consuming task. This finding is supported by that of ALMEIDA et al. (2009), who equally obtained a highly significant correlation value (r = 0.93) between these two traits, when studying accessions from the same genebank. Nevertheless, it is advisable to use these components sparingly, as an increase in the number of fruits might imply in reductions in the amount of seeds, in the weight of fermented and dried beans per fruit, and in the mass of the whole fruit (DIAS & RESENDE, 2001).

The TNFC, which includes both healthy and unhealthy seeds, gives an idea on the potential yield of the plant, whereas the TNHF represents the real yield. The selection of genotypes is; therefore, better performed by adopting the TNHF once commercial beans are extracted only from healthy fruits (CARVALHO et al., 2001). On that account, the direct selection targeting the TNHF can ultimately maximize the yield selection gain, as this trait is genetically correlated to the mass of both fermented and dried beans produced per plant (DIAS & RESENDE, 2001).

The relevance of the TNHF increases as a result of its significant positive correlation with the weight of wet seeds (ESQUIVEL & SORIA, 1967). This fact was observed in the present study (r = 0.86), as well as in those carried out by CARVALHO et al. (2001) (r = 0.95) and ALMEIDA et al. (2009) (r = 0.83).

Table 3 - Linear correlations between 11 traits evaluated in 145 cocoa clones in Ouro Preto do Oeste, RO, Brazil.

| Traits ¹ | TNHF | WWSHF | AWWSHF | WDSHF | AWDSHF | PFWB | PFBR | PFGS | NBWB | NIWB |
|---------------------|------------|------------|--------|------------|------------|-------------|-------------|--------|------------|------------|
| TNFC | 0.94^{*} | 0.84^{*} | -0.33* | 0.84^* | -0.33* | -0.04 | -0.26^{*} | 0.04 | 0.37^{*} | 0.26^{*} |
| TNHF | | 0.86^{*} | -0.36* | 0.86^{*} | -0.36* | -0.26* | -0.38* | 0.04 | 0.28^{*} | 0.15^{*} |
| WWSHF | | | 0.05 | 1.00^{*} | 0.05 | -0.18^{*} | -0.36* | -0.04 | 0.30^{*} | 0.22^{*} |
| AWWSHF | | | | 0.05 | 1.00^{*} | 0.18^{*} | 0.07^* | -0.13* | -0.01 | 0.04 |
| WDSHF | | | | | 0.05 | -0.18^{*} | -0.36* | -0.04 | 0.30^{*} | 0.22^{*} |
| AWDSHF | | | | | | 0.18^{*} | 0.07^* | -0.13* | -0.01 | 0.04 |
| PFWB | | | | | | | 0.04 | 0.02 | 0.26^{*} | 0.26^{*} |
| PFBR | | | | | | | | -0.14* | -0.24* | -0.13* |
| PFGS | | | | | | | | | 0.14^{*} | 0.04 |
| NBWB | | | | | | | | | | 0.54^{*} |

¹See code in Table 2. ^{*}Significant at a 5% probability level, according to t test.

The weight of wet seeds per fruit is a crucial aspect for farmers, once it is linked straight to the amount of raw material that will undergo fermentation and drying before being commercialized (ALMEIDA et al., 2009). In this research, a perfect correlation (r= 1) was detected between WWSHF and WDSHF, since the latter trait was estimated by multiplying the former by a correction factor of 0.4 - a regular method for converting the weight of wet seeds into weight of dry seeds, which relies on a moisture reduction of 60% after the drying process. High correlations were observed between TNFC and WDSHF (r = 0.84), TNFC and WWSHF (r = 0.84), TNHF and WDSHF (r = 0.86) and TNHF and WWSHF (r = 0.86).

Another trait that must be contemplated in cocoa breeding is the AWWSHF, commonly employed for indirectly assess of production (DIAS & KAGEYAMA, 1995). It potentially reduces the costs due to harvesting and breaking of the pods, in addition to increase the commercial value of the final product, as chocolate industries demand seeds with average dry weight above 1 gram (DIAS & RESENDE, 2001). However, the small magnitude of the correlations revealed here for the traits TNFC, TNHF, WWSHF, WDSHF, and AWDSHF ($r \le 0.052$) indicates the difficulty in selecting clonal accessions for high productivity based on the AWDSHF. CARVALHO et al. (2001) and ALMEIDA et al. (2009) also verified a similar limitation.

The percentages of fruits with germinated seeds (PFGS), borer (PFBR), and witches' broom disease (PFWB), as well as the number of branches and inflorescence with witches' broom disease (NBWB and NIWB, respectively) are factors that interfere with the production. These traits can play a vital role in discriminating tolerant and better-adapted genotypes. The overall average number of healthy fruits per plant, considering the four-year cultivation, was of 25.66 and a yield loss of 38.27% occurred due to witches' broom disease (*Moniliophthora perniciosa*), borer (*Conotrachelus humeropictus*), animal predation, and harvest delays (mummified pods and germinated seeds).

Witches' broom disease has a high incidence in the cocoa-producing region of the state of Rondônia, where the climatic condition favors its development (SÁNCHEZ, 2011). The absence or weak manifestation of symptoms might be the result of environmental conditions or resistance genetic factors. In this study, the location where the accessions had been cultivated had a substantial concentration of the pathogen, as hybrid varieties were raised nearby without any pest management system (ALMEIDA et al., 2009). Rainfall, temperature, and relative humidity (RH) of the air could also have affected the release of basidiocarps causing of witches' broom disease. They are mostly disseminated by wind and rain, when the RH is between 80% and 85%, and temperatures between 20 °C and 25 °C (ROCHA & WHEELER, 1985). The environmental conditions might also have influenced the borer infestation, which is favored at 27 °C and 80% RH (MENDES et al., 1997) and in periods of intense precipitation (THOMAZINI, 2002). The manifestation of the pest ultimately depends on cultivation practices, age, density, and system of plantation (ALMEIDA et al., 2009).

The weak associations between PFWB and NBWB (r = 0.26), PFWB and NIWB (r = 0.26), and NBWB and NIWB (r = 0.54) indicated that the witches' broom infection can spread, at some level, from the treetops to the inflorescence. The low correlations between PFBR, PFWB, NBWB, and NIWB ($r \le 0.37$) and the remaining traits evidence the difficulty in conducting a selection that simultaneously contemplates both in-field resistance and yield components, as previously reported by ALMEIDA et al. (2009).

By applying the rank summation index proposed by MULAMBA & MOCK (1978), the 145 genotypes were sorted, according to the traits TNHF, WWSHF, AWWHF, PFWB, PFBR, PFGS, NBWB, and NIWB, in order of their contribution to breeding. Initially, the genotypes were organized within each trait, by giving lower absolute values to the betterperforming ones. After that, the scores attributed to the elements were amounted, thus obtaining the average of the ranks. An inferior status represented a more favorable combination among traits, whereas a high value implied an unfavorable condition (CORRÊA et al., 2015). In the aftermath, the genotypes POUND 12, CAB 12, 253, 422, 257, 258, and 228 were placed in the seven first positions, so they can be considered the best options for selection purposes, as they possess the ideal traits for both yield and in-field resistance (Table 4). The clones adjudged suitable for selection by this study can be used as genitors in intra- and interpopulational hybridization programs. Future actions should contemplate issues of productivity and resistance to diseases, to secure a base-population adapted to adverse conditions.

ALMEIDA et al. (2009) analyzed the agronomical performance of eight yield components and resistance traits of 140 accessions. They reported out that the accession POUND 12 had the best performance regarding the weight of wet

| Order | Clone | TNHF ¹ | WWSHF | AWWSHF | PFWB | PFBR | PFGS | NBWB | NIWB | Rank |
|-------|----------|-------------------|-------|--------|------|------|------|------|------|------|
| 1 | POUND 12 | 29 | 5 | 47 | 93 | 79 | 10 | 16 | 49 | 41.0 |
| 2 | CAB 12 | 21 | 87 | 16 | 33 | 126 | 14 | 22 | 10 | 41.1 |
| 3 | CAB 253 | 11 | 79 | 109 | 64 | 18 | 35 | 26 | 9 | 43.8 |
| 4 | CAB 422 | 4 | 85 | 89 | 23 | 60 | 45 | 24 | 23 | 44.1 |
| 5 | CAB 257 | 23 | 15 | 108 | 69 | 54 | 24 | 2 | 59 | 44.2 |
| 6 | CAB 258 | 30 | 7 | 76 | 105 | 30 | 88 | 5 | 16 | 44.6 |
| 7 | CAB 228 | 20 | 13 | 24 | 132 | 118 | 18 | 25 | 13 | 45.3 |
| 8 | CAB 248 | 27 | 88 | 70 | 52 | 67 | 36 | 4 | 21 | 45.6 |
| 9 | CAB 250 | 7 | 63 | 57 | 19 | 43 | 43 | 23 | 113 | 46.0 |
| 10 | CAB 373 | 46 | 8 | 127 | 54 | 1 | 38 | 99 | 11 | 48.0 |
| 11 | CAB 419 | 37 | 33 | 105 | 58 | 44 | 50 | 37 | 36 | 50.0 |
| 12 | CAB 13 | 10 | 20 | 19 | 66 | 123 | 59 | 30 | 75 | 50.2 |
| 13 | CAB 218 | 19 | 48 | 1 | 85 | 125 | 39 | 56 | 32 | 50.6 |
| 14 | SA 20 | 50 | 54 | 52 | 122 | 109 | 1 | 12 | 12 | 51.5 |
| 15 | CAB 229 | 24 | 112 | 81 | 92 | 56 | 12 | 14 | 28 | 52.3 |
| 16 | SA 9 | 104 | 68 | 48 | 14 | 5 | 44 | 122 | 17 | 52.7 |
| 17 | CAB 432 | 31 | 72 | 100 | 43 | 52 | 115 | 13 | 6 | 54.0 |
| 18 | CAB 447 | 25 | 60 | 60 | 31 | 29 | 103 | 45 | 82 | 54.3 |
| 19 | CAB 10 | 6 | 36 | 20 | 89 | 129 | 20 | 39 | 98 | 54.6 |
| 20 | CAB 411 | 60 | 31 | 74 | 4 | 82 | 113 | 15 | 61 | 55.0 |

Table 4 - Classification, based on the summation of ranks, of eight traits evaluated in 145 cocoa clones, in Ouro Preto do Oeste, RO, Brazil.

¹See code in Table 2.

seeds from healthy fruits, average weight of wet seeds per fruit, and number of fruits with witches' broom symptoms per plant. CAB 253 and CAB 422, in their turn, showed better results of weight of wet seeds from healthy fruits, total number of harvested fruits, and total number of healthy fruits per plant. The genotypes CAB 228 and CAB 12 were prominent in weight of wet seeds from healthy fruits and number of fruits with witches' broom symptoms, respectively. Lastly, they concluded that the accessions CAB 9, 13, 40, 218, 226, 417, and 452 were tolerant of both the witches' broom disease and borer. They exhibited an intermediate to high yield, thereby being good options for creating superior varieties.

CONCLUSION

The present research introduced new facts on cocoa clones from wild populations and their agronomical potential as a source of genetic

variability. This information expands the possibility of genetic gains by selection. The evaluation of linear correlations between morpho-agronomical traits is also noteworthy due to their applicability in plant breeding. It was also possible to identify and classify clones more suitable to selection, by employing the selection index, highlighting the clones POUND 12 and CAB 12, 228, 253, 257, 258, and 422.

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DECLARATION OF CONFLICT OF INTEREST

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AUTHORS' CONTRIBUTIONS

All authors contributed equally for the conception and writing of the manuscript. All authors critically revised the manuscript and approved of the final version.

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