Selection and genetic dissimilarity in S_2 families of guava through seed attributes[1]

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ABSTRACT

This study was developed to carry out selection, estimate genetic parameters and predict individual genetic values of 55 genotypes from S_2 families as well as estimate genetic dissimilarity based on physiological seed attributes. All S_2 genotypes evaluated were obtained from self-pollination of S_1 genotypes from the guava breeding program. The experiment was laid out in blocks with 55 S_2 genotypes and four blocks. Genetic parameters were estimated and the best genotypes were selected based on the genetic value, using the statistical method of mixed models. In addition, genetic divergence was estimated based on the mean Euclidean distance. Although heritability values were considered medium to high magnitude for germination (0.22) and germination speed index (0.35), genetic gains were obtained for all traits. Based on the evaluation of individual BLUPs, the S2 genotypes that contributed to most of the evaluated traits were: 5, 31, 85, 214, 369, 393, 398, 442, 443, 444, 449 and 529, suggesting potential to generate vigorous. Through genetic dissimilarity, it was possible to verify the formation of five distinct groups. Therefore, the selection of divergent genotypes with high average for germination is recommended for the advancement of generation in the guava breeding plant.

Keywords: *Psidium guajava;* mixed models; self-pollination; vigor.

INTRODUCTION

Guava (*Psidium guajava* L.) is a plant widespread in all tropical regions of Brazil, which makes it the third largest producer of the fruit worldwide, only behind India and Mexico (Rajan & Hudedamani, 2019). In 2019, Brazil produced 552,393 t of guava, of which the state of Rio de Janeiro accounted for 20,785 t (IBGE, 2021).

The increase in guava production is related not only to fresh fruit consumption, but also to the great demand from the sweets and juice industry. In addition to increased yields, guava breeding programs aim at the production of fruits with dual purpose. In doing so, they are able to meet the market demand, with fresh fruit for table consumption and for industrial use (Almeida *et al.,* 2019; Mitra, 2010).

Guava can be sexually or asexually propagated, the asexual form being the most used in commercial crops (Campos *et al.,* 2017). However, in breeding programs this fruit bowl is multiplied via seeds, to ensure greater genetic variability in the selection processes. In fact, some studies are being carried out to obtain inbred cultivars (Ambrósio *et al.,* 2021)

The State University of Northern Rio de Janeiro (UENF) developed a breeding program for the species *P. guajava* L. Research began with Pessanha *et al.* (2011), Campos *et al.* (2013), Oliveira *et al.* (2014), Campos *et al.*

(2016) and Quintal *et al.* (2017) and has yielded promising results. Such an example is the work of Ambrósio *et al.* (2021) involving inbred families through self-pollination (S_1), which resulted in quality fruits, enabling the development of varieties through the production of inbred lines.

Therefore, it is necessary to investigate the physiological quality and genetic diversity of individuals obtained by self-pollination using seed attributes, since seeds obtained from the self-pollination process should possess high vigor and physiological quality. In the future, these genotypes will be able to generate a variety (inbred line) that can be commercially propagated through seeds.

The physiological quality of a seed is linked to its metabolic traits, among which germination and vigor stand out. Germination refers to the emergence and development of essential embryonic structures, which expresses the ability of the seed to form a normal seedling under normal conditions. Vigor indicates the ability of a seed to generate high-performance plants under unfavorable conditions. High germination and vigor translate into better plant performance in the field, e.g., higher germination speed and seedling emergence under adverse conditions (Brasil 2009).

Studies with soybean have shown that high vigor seeds provide rapid and uniform germination and emergence of seedlings, resulting in high performance plants, with higher yield potential (França-Neto *et al.,* 2012). Rossi *et al.* (2017) observed that the use of the soybean seeds of high vigor resulted in taller plants, with increased height of the first pod, and a larger number of pods per plant. This information is of great relevance for breeding programs that will be able to select genotypes with better performance in the field based on the physiological quality of the seeds. Identify the genetic control of traits involved with the quality of seeds is essential for understanding the nature of the action of genes involved these traits and evaluating the efficiency of different breeding strategies to obtain genetic gains and maintain an adequate genetic base (Pérez Pelea *et al.,* 2019). Thus, it is important, the use of methods that estimate the components of variance and allow the prediction of individual genetic values of the selected genotypes. In that sense, the REML/BLUP procedure is a suitable and precise tool for the estimation of variance components and prediction of genetic values in perennial plants. In this approach, REML (Restricted Maximum Likelihood) is employed to estimate variance components and BLUP (Best Linear Unbiased Predictor) to predict the genetic values of

individuals by using all genetic and non-genetic information available in a set of observations (Viana & Rezende, 2014). This strategy was used by Ambrósio *et al.* (2021) to select the best S_1 genotypes from guava tree based on the main agronomic traits.

Due to its mixed reproductive system, the selection of S_2 seeds with high physiological quality makes it possible, in the future, to obtain guava cultivars both through the development of inbred varieties (inbred lines), as well as the production of hybrids through the use of heterosis. In view of the above-described scenario, this study was developed to: i) estimate genetic parameters and predict individual genetic values for 55 S_2 guava genotypes using the mixed-model methodology; and ii) estimate genetic dissimilarity based on physiological seed attributes aiming to select the most vigorous and divergent genotypes for the guava breeding program.

MATERIAL AND METHODS

Plant material

The experiment was carried out in the laboratory of the Seed Production and Technology Unit at the State University of Northern Rio de Janeiro (CCTA-UENF), located in Campos dos Goytacazes - RJ, Brazil. The S_2 family guava seeds originated from the 55 most productive genotypes of the S_1 families, according to the results of previous work carried out at the Plant Breeding Laboratory at UENF (Ambrósio *et al.,* 2021). The S_1 families were obtained through the self-fertilization of the best individuals resulting from the 18 families obtained by Pessanha *et al.* (2011) and assessed by Quintal *et al.* (2017) (Table 1).

The population of S_1 families is located in the municipality of Itaocara - RJ, Brazil, at the experimental unit of Ilha Barra do Pomba (21º40' S, 42º04' W, 76 m altitude). The soil in the experimental area is classified as Red-Yellow Argisol (Embrapa, 2006). An experimental randomized block design with 18 S_1 families, three replicates, and ten plants per plot was used. Seeds from the fruits of self-fertilization were sown in tubettes (three seeds each tubette) and maintained in a greenhouse. Seedlings were planted, in July 2014, with spacing of 4-m between rows and 1.5-m between plants. Liming, planting and covering fertilizers were implemented according to soil analysis, following the recommendations of Costa *et al.* (2003). Pests and diseases were controlled using Confidor (Evidence) and Leybacid R pesticides. Drip irrigation was also used.

Table 1: Origin of the S$_2$ genotypes of guava used in this study

Full-sib family	*Parents	**S$_1$ inbred families/Genotypes	Number of self-pollinated genotypes
1	17/5/1	1/ (5; 369)	2
2	7/9/1	2/ (17; 196; 198; 199; 372)	5
3	13/3/1	3/ -	0
4	4/6/1	4/ (31; 214; 393; 398)	4
5	5/8/1	5/ (47; 227; 229)	3
6	4/5/2	6/ (51; 54; 231; 414)	4
7	13/4/1	7/ (241; 424; 429; 430)	4
8	5/10/1	8/ (72; 75; 78; 251)	4
9	3/7/1	9/ (85; 442; 443; 444; 446; 449)	6
10	10/5/1	10/ (276; 279)	2
11	5/4/1	11/ -	0
12	2/6/2	12/ (115)	1
13	8/4/1	13/ (122;123;127;129;302;303;304; 306)	8
14	5/9/1	14/ -	0
15	3/11/1	15/ (144)	1
16	3/5/1	16/ (151;159;160; 334)	4
17	4/9/1	17/ (529)	1
18	4/8/1	18/ (174; 177; 178; 535; 537; 539)	6

* Parents: Family / Genotype / Block: most productive genotypes evaluated and selected by Quintal *et al.* (2017), which were self-pollinated, originating S$_1$ plants. ** S$_1$ Family / Genotypes: in parentheses, the 55 most productive individuals selected by Ambrósio *et al.* (2021), which were self-pollinated, originating the S$_2$ genotypes evaluated in this study.

The selected S$_1$ genotypes were self-pollinated to obtain the S$_2$ families. Self-pollination was achieved by protecting the flowers, by covering them before anthesis. Buds were identified and the fruits later protected with a paper bag. After harvesting the fruits, the seeds were removed by rubbing on a steel mesh sieve under running water.

The removed seeds were left to dry at room temperature for 48 h. Twenty-four hours after the beginning of the drying process, the seeds were turned to dry evenly. After the S$_2$ seeds were dried, the following physical and physiological tests were carried out:

Thousand-seed weight: to calculate the weight of 1000 seeds, eight replicates of 100 seeds were used, following the Rules for Seed Testing (Brasil, 2009).

Germination test: conducted using four replicates of 50 seeds of each of the 55 genotypes and a paper roll as substrate (Table 1). The germination chambers were set to an alternating temperature of 35-25 °C, with a light/dark photoperiod of 8 h/16 h, respectively. Assessments were carried out on alternate days until the 28th day, when germination speed index and the percentages of normal seedlings, abnormal seedlings and non-germinated seeds were recorded (Maitan *et al.,* 2020).

Germination speed index: measured when the germinating seed and its shoot had at least 1 cm, on alternate days. This variable was calculated by the formula proposed by Maguire (1962). Shoot and root lengths: four paper rolls were mounted with 10 seeds and, at the end of the 28th day, the seedlings were measured with a graduated ruler.

Accelerated aging: the seeds were placed evenly on an aluminum screen inside a germination box with 40 mL of water at the bottom. Subsequently, the germination boxes were subjected to a temperature of 41 ºC for 48 h and then for 28 days, inside a germination chamber. After this procedure, the test was performed to assess germination as described above (Brasil, 2009).

Genetic evaluation by mixed-models: Estimate of genetic parameters

Statistical analyses were carried out for seed physio-

logical traits by the REML/BLUP methodology. The significance of random effects was determined by Deviance Analysis, using the REML method, which advantageously replaces analysis of variance (ANOVA) in cases of unbalanced data by the maximum likelihood ratio test (LRT). In this study, the unbalance is due to the different number of individuals within each of the 15 families evaluated, that ranged from one to eight (Table 1). The deviances were obtained as described by Viana & Resende (2014), using the model with and without the respective effects, by subtracting the deviance obtained in the complete model and the model without the effect, and compared using the Chi-square value (χ^2) with one degree of freedom (Viana & Resende, 2014).

Analyses were conducted using Selegen-REML/BLUP software (Resende, 2016), by applying the statistical model proposed for selection in S_2 without repeated measures, in a randomized-block design.

$$Y = X_u + Z_a + W_p + e$$

where y is the data vector; u is the scalar referring to the overall mean effect (fixed effect); a is the vector of individual additive genetic effects within populations (assumed random); p is the vector of population effects (assumed random); e is the vector of errors or residuals (random); and X, Z and W represent the incidence matrices for the u, a and p effects, respectively.

The following variance components and parameters were estimated: σ_g^2: genetic variance between families; σ_f^2: individual phenotypic variance; σ_e^2: residual variance; h_a^2: individual narrow-sense heritability; and overall mean. Individual narrow-sense heritability can be classified as low (h < 0.15), medium (0.15 < h < 0.50) and high (h > 0.50) magnitude, which is represented by the ratio of genotypic to phenotypic variation (Resende, 2002). To check if there were increases in genetic gain, the REML/BLUP procedure was used. The S_2 genotypes were ranked according to the genotypic values found for each trait. From these values, the 20 best genotypes for each trait were selected.

Genetic diversity

The study of genetic divergence was undertaken for 55 S_2 genotypes. With the means of seed physiological traits, a matrix was constructed based on the mean Euclidean distance, using genes software (Cruz, 2013). To identify the cut-off points, the method of Mojena (1977) was adopted with a K value = 1.25, where cuts at 73% and 80% dissimilarity are recommended. Cluster analysis of individuals via dendrogram was performed by applying the UPGMA method (Unweighted Pair Group Method with Arithmetic Mean), using Mega software version 6 (Kumar *et al.,* 2008).

RESULTS AND DISCUSSION

Genetic parameters

According to deviance analysis, there were significant differences for all evaluated traits based on the chi-square test at p < 0.01 probability (Table 2). Therefore, it can be stated that there is genetic variability among the evaluated genotypes, which will enable a successful selection of superior genotypes.

Genetic variance was found to have a smaller contribution over the total variability for all evaluated traits, which culminated in lower estimates of individual narrow-sense heritability (Table 3). The individual narrow-sense heritability for most of the evaluated traits was classified as medium, ranged from 0.22, for germination, to 0.35, for germination speed index. Root length was the only variable to show individual narrow-sense heritability of low magnitude (0.12) (Table 3).

Different results were observed by Silva *et al.* (2021), who found values of heritabilities above 90% for the variables related to seed quality in S_2 families of *Psidium guajava* using the Least squares method (LS).

Heritability is not an immutable parameter, it depends, among other factors, on the method by which the variance components are estimated and the proportion of genetic variance considered, that is, the total genetic effect or just the additive component. In this study, the variance components were estimated by the restricted likelihood method and considering only the additive variance (heritable effect). This model was that best adjusted the data set, considering the unbalance between families (Table 1).

Ambrósio *et al.* (2021) worked with a population of 18 S_1 families of *P. guajava*, using the mixed model methodology (REML/BLUP) for unbalanced data, and also found medium to low values for individual narrow-sense heritability. The researchers explained that low-magnitude individual heritability is common for quantitative traits and, as a rule, they lead to moderate heritability magnitudes at the level of progeny means, for traits such as fruit

Table 2: Deviance analysis for seed physiological traits of S$_2$ individuals in 55 *Psidium guajava* genotypes

| Trait | Deviance | | LTR (χ2) |
	Full model	Genotype	Genotype
Accelerated aging (%)	1502.36	1527.44	25.07*
1000-seed weight (g)	657.74	630.22	27.52*
Germination speed index	-153.38	-98.65	54.73*
Germination (%)	1477.20	1502.80	25.6*
Shoot length (cm)	-8.31	20.68	28.99*
Root length (cm)	89.19	100.06	10.87*

*significant at p < 0.01 by the Chi-square test. LRT (χ2): likelihood ratio test.

Table 3: Estimates of variance components and genetic parameters of S$_2$ individuals in 55 *Psidium guajava* genotypes: σ_g^2: genetic variance between families; σ_f^2: individual phenotypic variance; σ_e^2: environmental variance; h_a^2: individual narrow-sense heritability and overall mean

Trait	σ_g^2	σ_f^2	σ_e^2	h_a^2	Overall mean
Accelerated aging (%)	104.41	412.20	307.79	0.25	85.40
1000-seed weight (g)	1.90	7.64	5.74	0.25	13.32
Germination speed index	0.08	0.24	0.15	0.35	2.11
Germination (%)	80.67	366.14	285.46	0.22	90.80
Shoot length (cm)	0.13	0.44	0.30	0.30	2.87
Root length (cm)	0.07	0.57	0.50	0.12	2.13

weight, total number of fruits, pulp mass, fruit mass and placental mass. Therefore, considering all the mentioned aspects, these heritability values are expected. As stated by Resende (2002), the REML/BLUP methodology has more accurate models than at least squares method when data to be analyzed has some degree of unbalance.

Another reason to explain these low values of heritability would be the mixed reproduction system of guava (allogamous with high rates of self-fertilization), allowing that one generation of self-fertilization is enough to reduce genetic variability, impacting heritability values. Knowledge of genotypic variance is very important for breeding programs, as it indicates the range of genetic variation of a trait, given the possibility of its improvement (Cruz *et al.,* 2014). In the study of genetic traits, heritability has its predictive role, expressing the reliability with which the phenotypic value represents the genetic value (Silva *et al.,* 2013). Although narrow-sense heritability values are classified as medium for most traits, mixed modeling (REML/ BLUP), the population structure allows for excellent esti-

mates and considerable predicted gains in the selection of the best individuals for future crosses or self-pollination.

Genetic gains

The 20 best S$_2$ genotypes were selected for all traits, corresponding to 36.36% of the evaluated individuals. Gains were estimated and the new means were higher than the overall mean for all traits (Table 4).

As regards the selection of genotypes for the evaluated traits, relevant gains could be obtained with selection for most traits. When we compare the mean of the 20 selected genotypes with the overall mean of the population, the best genetic gain estimates are detected for shoot length (28.22%), root length (18.75%), germination speed index (17.06%), 1000-seed weight (16.63%) and accelerated aging (13.54%) (Table 4). Only germination showed low-magnitude gains (7.52%) relative to the other traits ranked (Table 4). The genetic gain estimated by BLUP is equivalent to the predicted genetic values for the selected genotypes, and the new average refers to the general aver-

Table 4: Ranking of the 20 genotypes with the best gain estimates (G%) and estimated new means, by REML/BLUP, in guava families

Rank	Accelerated aging (%)		1000-seed weight		Germination (%)	
	G (%)	New mean*	G (%)	New mean*	G (%)	New mean*
1	13.54	96.96(31/4)	16.63	15.52(529/17)	7.52	97.63(47/5)
2	13.54	96.96(393/4)	16.10	15.45(276/10)	7.52	97.63(227/5)
3	13.54	96.96(398/4)	14.81	15.28(372/2)	7.52	97.63(229/5)
4	13.54	96.96(214/4)	13.61	15.12(17/2)	7.50	97.62(214/4)
5	13.27	96.74(144/15)	12.93	15.03(199/2)	7.49	97.61(393/4)
6	12.69	96.24(5/1)	12.47	14.96(446/9)	7.49	97.61(398/4)
7	12.47	96.05(196/2)	12.02	14.92(198/2)	7.44	97.60(31/4)
8	12.37	95.96(372/2)	11.72	14.87(444/9)	7.39	97.51(151/16)
9	12.28	95.89(17/2)	11.41	14.83(279/10)	7.36	97.50(159/16)
10	12.12	95.75(198/2)	11.11	14.80(449/9)	7.33	97.47(160/16)
11	12.05	95.69(199/2)	10.88	14.77(196/2)	7.31	97.45(334/16)
12	11.86	95.53(369/1)	10.73	14.74(443/9)	7.10	97.25(5/1)
13	10.98	94.78(442/9)	10.51	14.71(442/9)	7.08	97.24(369/1)
14	10.90	94.71(446/9)	10.28	14.68(85/9)	7.07	97.19(442/9)
15	10.82	94.45(444/9)	10.05	14.65(539/18)	7.01	97.18(444/9)
16	10.60	94.39(85/9)	9.83	14.63(537/18)	6.99	97.16(85/9)
17	10.53	93.95(449/9)	9.67	14.60(369/1)	6.98	97.15(443/9)
18	10.01	93.65(529/17)	9.52	14.60(5/1)	6.91	97.09(449/9)
19	9.66	93.32(443/9)	9.30	14.55(177/18)	6.72	96.90(529/17)
20	9.17	93.23(414/6)	9.07	14.63(174/18)	6.68	96.88(78/8)

Rank	Germination speed index		Shoot length		Root length	
	G (%)	New mean*	G (%)	New mean*	G (%)	New mean*
1	17.06	2.48(5/1)	28.22	3.69(529/17)	18.75	2.59(393/4)
2	17.06	2.47(369/1)	24.39	3.60(5/1)	18.75	2.59(398/4)
3	16.59	2.46(529/17)	17.07	3.44(369/1)	18.75	2.58(47/4)
4	15.64	2.44(398/4)	16.38	3.35(393/4)	18.75	2.58(214/4)
5	15.17	2.43(72/8)	15.33	3.30(398/4)	18.33	2.57(229/5)
6	14.22	2.41(251/8)	14.98	3.29(31/4)	18.33	2.57(31/4)
7	14.22	2.39(31/4)	12.89	3.35(199/2)	17.92	2.57(227/5)
8	13.27	2.39(444/9)	12.89	3.24(198/2)	17.50	2.55(529/17)
9	12.80	2.38(78/8)	12.20	3.23(372/2)	16.05	2.52(231/6)
10	12.80	2.38(85/4)	11.85	3.23(214/4)	15.68	2.51(5/1)
11	12.80	2.38(393/4)	10.45	3.20(17/2)	14.05	2.47(115/12)
12	12.80	2.38(75/8)	10.10	3.18(539/18)	14.77	2.46(51/6)
13	12.32	2.37(443/9)	10.10	3.17(537/18)	12.75	2.44(414/6)
14	12.32	2.37(214/4)	9.79	3.17(196/2)	12.08	2.43(54/6)
15	11.85	3.36(446/9)	9.79	3.17(174/18)	10.94	2.40(251/16)
16	11.85	3.36(442/9)	9.41	3.16(535/18)	10.77	2.39(78/8)
17	11.85	3.36(449/9)	9.41	3.15(443/9)	9.86	2.37(75/8)
18	11.37	2.35(227/5)	9.06	3.15(442/9)	9.59	2.37(54/6)
19	10.90	2.34(229/5)	9.79	3.14(85/9)	9.34	2.36(72/8)
20	10.90	2.34(47/5)	9.06	3.13(444/9)	8.76	2.34(369/1)

*(Genotype/Family).

age added to the gain. This results in the improvement of the population average for the assessed traits (Santos *et al.,* 2015).

Allogamous populations, highly heterozygous, when subjected to self-fertilization reduces genetic variability, and this impacts heritability values, which in turn implies lower gain estimates. The genetic structure of the population evaluated may have contributed to the decrease in the gain. Santos *et al.* (2015) reports that divergent crosses originate populations with high genetic variability, favoring high heritability estimates, which, in turn, favor the achievement of greater genetic gain.

In the selection of the 20 best S₂ genotypes, genotypes 5 and 369, from family 1, and genotype 529, representing family 17, were ranked for all evaluated traits. It can be inferred that these genotypes have high potential to be selected for the continuity of self-pollination generations, given the interest in these traits for propagating more vigorous plants (Table 4). Five genotypes of family 9 (85, 442, 443, 444, 449) stood out among the top 20, representing (25%) of the genotypes for the traits of germination, germination speed index, 1000-seed weight, shoot growth and accelerated aging. These were not ranked only for root growth (Table 4).

Four other S₂ genotypes, representatives of family 4 (31, 214, 393, 398), were among the top 20 for the traits of germination, germination speed index, shoot growth and accelerated aging (Table 4). These 12 genotypes are part of four families, namely, 1, 4, 9 and 17, which suggests great potential for selection aiming at seed vigor.

The S₁ population of *P. guajava* originated the 55 S₂ genotypes evaluated in this study. Thus, it is important to stress that families 1 and 4, considered the most vigorous based on seed traits, were also selected for agronomic traits such as fruit weight, pulp weight, total fruit weight and total number of fruits by Ambrósio *et al.* (2021).

When the selection method is effective, satisfactory gains are predicted for the evaluated traits. This fact guides the breeding program to more effectively decide which strategy can be adopted, since it is possible to determine which are the best families and the best individuals within these families. In general, the use of selection procedures based on mixed models is justified, since despite the low-heritability traits, favorable genetic gains were predicted and the genotypes exhibit selection potential (Table 4).

Genetic diversity

Regarding genetic divergence between the 55 S₂ genotypes, five distinct groups were formed (Figure 1).

Group I comprised genotypes 17, 123 and 214. Being the most genetically divergent from the others, this group had the lowest performance for some important traits, e.g., germination (78.83%) and germination speed index (1.78). This finding is explained by the low germination potential of genotype 17 (Figure 1). However, in this group, individual 214 achieved the greatest gains for the traits of germination (97.62%), germination speed index (2.37), shoot growth (3.23 cm) and accelerated aging (96.96%) (Table 4).

Group II consisted of genotypes 231 and 241, both of which exhibited the same 1000-seed weight and similar germination. Group III stood out for having genotypes with higher germination means (98.33%), where genotypes 78, 144, 199, 229, 303 and 442 were allocated (Figure 1). In Group III, genotype 442, from family 9, stood out, as it was ranked for a greater number of evaluated traits, namely, germination, germination speed index, 1000-seed weight, shoot growth and accelerated aging (Table 4).

Group IV, which has only one representative-genotype 85, from family 9-showed the highest average germination speed index (2.48) and shoot growth (3.25 cm) among the groups (Figure 1). This genotype also stood out for showing significant gains and being ranked for the traits of germination, germination speed index, 1000-seed weight, shoot growth and accelerated aging (Table 4).

Lastly, Group V, the largest, comprised the largest number of genotypes (43), corresponding to 78% of the evaluated individuals. This group had a germination mean of 93.59%, which is excellent for seed vigor, a germination speed index of 2.07 and shoot growth of 2.80 cm (Figure 1). Individuals 5, 369 and 529, belonging to Group V, were considered the most promising, ranking among the 20 best for all evaluated traits. The traits of germination, germination speed index and shoot growth are among the most important in the evaluation of seed vigor potential.

Thus, the best-ranked individuals for these traits were genotype 214, allocated to Group I; 444, to Group II; 85, to Group IV; and genotypes 31, 393, 398, 443, 444, 449, allocated to Group V. To achieve success in a breeding program, breeders must always use populations with high genetic variability. To this end, the most divergent and superior parents should be recombined, thereby increasing the
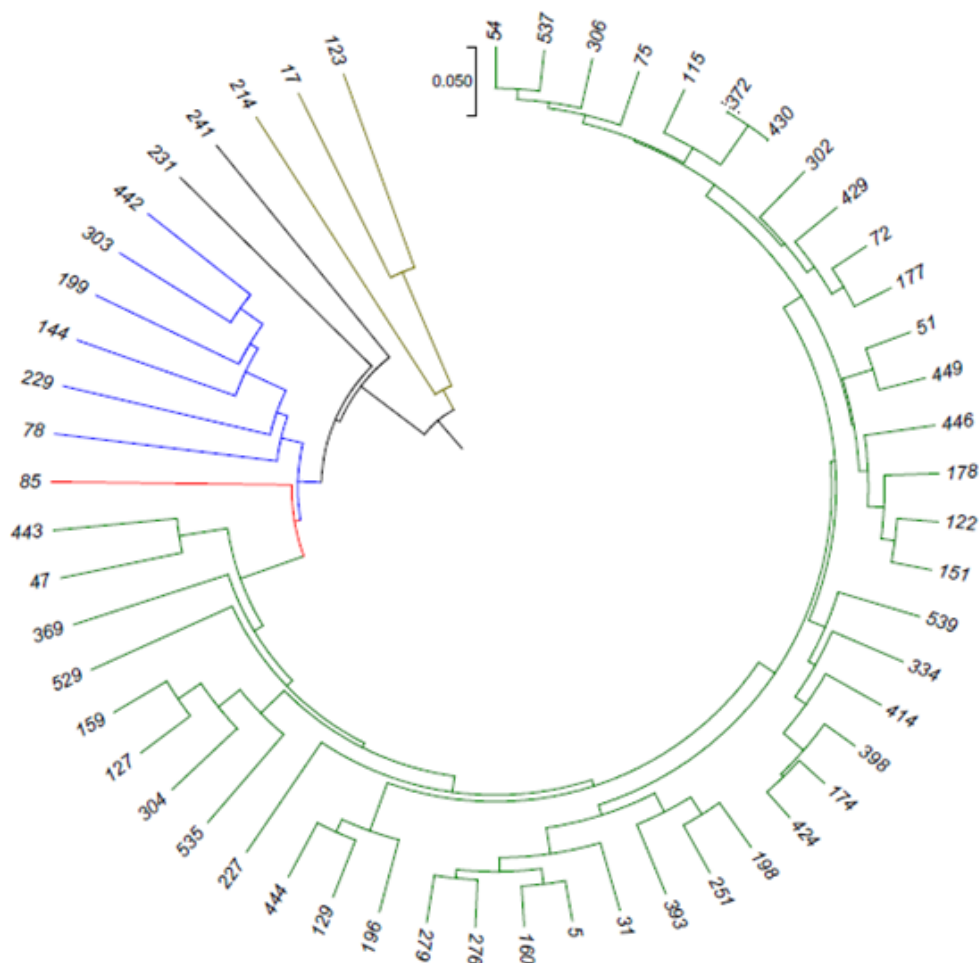
Figure 1: Dendrogram generated by the UPGMA method from the distance matrix obtained based on the Mean Euclidean Distance for the traits evaluated in seeds of selected guava S_2 genotypes.

genetic variability in their segregating populations through favorable allelic combinations (Oliveira *et al.,* 2018).

Therefore, hybridizations are recommended between genotype 214 from Group I and the selected genotypes belonging to Groups IV and V (5, 85, 369, 443, 444, 449, 529) provided they are not from family 4, as they will be members of the same family as genotype 214. Crosses between individuals of Groups I and IV; I and III; and III and IV and are also indicated, as all genotypes belong to different families within all recommended groups.

Another alternative would be to self-pollinate the genotypes selected within the groups for the most important traits. Thus, genotypes 5, 31, 85, 214, 369, 393, 398, 442, 443, 444, 449 and 529 can be self-pollinated to form the S_2 plant population.

CONCLUSIONS

In general, heritability values for all traits were medium, but gains with selection could be estimated by estimating the individual BLUPs. The S_2 seed genotypes 5, 31, 85, 214, 369, 393, 398, 442, 443, 444, 449 and 529, which showed the highest gain estimates for germination, accelerated aging, germination speed index and shoot growth and were genetically divergent, are recommended for future crosses.

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