Genetic gain in *Passiflora* seed traits from recurrent selection among full-sib families

Cleidiane Alves Rodrigues[1], Henrique Duarte Vieira[1], Rosenilda de Souza[1*], Débora Souza Mendes[1] and Alexandre Pio Viana[1]

Abstract: *The germination potential must be considered in the selection of passion fruit genotypes, since vigorous seeds originate seedlings with a higher growth rate, resulting in superior plants with high agronomic performance. This study proposes to estimate genetic parameters and selection gain for seed traits of full-sib families (FSF) of passion fruit under recurrent selection for resistance to the cowpea aphid-borne mosaic virus (CABMV). Physical and physiological seed traits of 86 FSF were evaluated; genetic parameters, genotypic correlations between traits and genetic gains were estimated using four selection indices. There were significant differences and genetic variability between families and positive genetic correlations between variables. The best distribution of genetic gains was obtained by the Mulamba and Mock index, using the heritability coefficient and arbitrary weights. This index selected the best 26 families in terms of seed characteristics to compose the second cycle of recurrent selection for resistance to CABMV.*

Keywords: *Cowpea aphid-borne mosaic virus, genotypic correlation, passion fruit, seed vigor, selection index*

INTRODUCTION

Brazil is the world's largest producer and consumer of passion fruit (*Passiflora edulis*), with an output of 690,364 t of the fruit in 2020 (IBGE 2021). Due to the versatility of uses, interest in the fruit has increased in several countries. To meet the growing demand for passion fruit around the world, the successful establishment of plants in the field is a key requirement, directly related to the physiological potential of the seeds. Seed quality is determined by germination and vigor tests (accelerated aging, seedling growth, and seedling dry weight) (Brasil 2009, Krzyzanowski et al. 2020). At present, digital image analysis is also used to evaluate and characterize seeds of different species, particularly for selection of promising genotypes in breeding programs, for being a non-destructive, fast and accurate procedure (Torres et al. 2019).

However, one of the great challenges in *Passiflora* breeding is to develop a genotype that encompasses the highest number of desirable agronomic traits, e.g., high-quality fruit, resistance to the main diseases and vigorous seeds and seedlings. Thus, breeders must take the seed-related variables into consideration for the development of new cultivars (Torres et al. 2019).

The study of genetic parameters and application of selection indices are two breeding techniques that allow the selection of superior genotypes. Both have
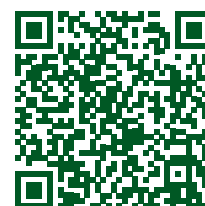
[1] Universidade Estadual do Norte Fluminense Darcy Ribeiro, Avenida Alberto Lamego, 2000, Parque California, 28013-602, Campos dos Goytacazes, RJ, Brazil

been employed in passion fruit breeding focused on fruit yield and disease resistance traits and resulted in promising genetic gains (Cavalcante et al. 2018, Dalbosco et al. 2018).

The breeding program of passion fruit at the State University of Northern Rio de Janeiro (UENF), initiated in 1998, selected the best genotypes for agronomic traits and fruit based on intrapopulation recurrent selection (Ribeiro et al. 2019, Torres et al. 2019). The traits related to seed quality were not included in the selection of superior genotypes. However, Rodrigues et al. (2020) identified the presence of genetic variability for seed traits in progenies of the third recurrent selection cycle and claimed that selection for agronomic fruit traits was effective for seed traits.

Parallel to breeding for agronomic traits at UENF, recurrent selection studies were initiated for resistance to cowpea aphid-borne mosaic virus (CABMV) (Preisigke et al. 2020, Vidal et al. 2021, Mendes et al. 2022). Resistance genes to CABMV were incorporated from the interspecific cross between cv. UENF Rio Dourado and *P. setacea* (wild species with resistance allele for CABMV and seed dormancy) (Santos et al. 2019, Preisigke et al. 2020). However, the seed germination potential was not analyzed after the successive generations of backcrossing and recombination of cv. UENF Rio Dourado with the wild species *P. setacea*.

Therefore, this study was undertaken to: 1) estimate the genetic parameters associated with physical and physiological seed traits of passion fruit full-sib families in recurrent selection; 2) estimate genetic gains in seeds traits by selection indices; and 3) select the best families for seed traits and continue the recurrent selection cycles for CABMV resistance.

MATERIAL AND METHODS

The 86 full-sib families (FSF) evaluated in this study were derived from pairwise intercrosses among 38 superior genotypes extracted from an initial population resulting from crosses among three populations, namely: population 1 (BC_1) (F_1 segregating population (*Passiflora edulis* × *Passiflora setacea*) × the *P. edulis* population (recurrent parent) (Gonçalves et al. 2021); population 2 (*P. edulis* × selected genotypes of the BC_1 population) (Vidal et al. 2021); and population 3 (interspecific hybrids (*P. edulis* × *P. setacea*)) (Santos et al. 2014).

The sample to evaluate physical and physiological quality consisted of a seed mixture from fruits of nine plants of each FSF and was obtained from an experiment in the UENF passion fruit breeding program for resistance to CABMV (Mendes et al. 2022). It consisted of FSF from the first cycle of recurrent selection and two controls (*Passiflora edulis*: cultivar UENF Rio Dourado (Viana et al. 2016); and the wild species *Passiflora setacea*: with the CABMV resistance allele). The field trial, at the Antônio Sarlo State College of Agriculture (lat 21º 42' 48'' S, long 41º 20' 38'' W, alt 14 m asl) in Campos dos Goytacazes, northern region of the state of Rio de Janeiro, Brazil, was laid out in a randomized block design with three replications and three plants per plot (Mendes et al. 2022).

The seeds of 86 full-sib families from the first cycle of recurrent selection for CABMV resistance plus two statistical controls, the parents *P. edulis* and *P. setacea,* were evaluated in a completely randomized design, in a total of 88 treatments. The tests were carried out at the Plant Science Laboratory – Seed Production and Technology Section, UENF.

The seeds were evaluated for the physical trait 1000-seed weight (TSW); the seed biometry variables of area, maximum diameter (Dmax), minimum diameter (Dmin), and circumference (Circ); and the following physiological traits: germination percentage (G), germination speed index (GSI), shoot length (SL), root length (RL), shoot dry weight (SDW), root dry weight (RDW) and accelerated aging test (AA). For genotypic correlation analysis, in addition to the seed traits, four fruit variables (fruit weight, length and diameter and pulp weight) were measured and the area under the mean disease progress curve (AUDPCM) for CABMV resistance was estimated. Data of fruit and AUDPCM were recorded in the evaluations of fruits and leaves of nine plants per genotype, as proposed by Mendes et al. (2022).

A thousand-seed weight was calculated from eight 100-seed replicates, as defined by the Rules for Seed Testing (Brasil 2009). Seed biometry was evaluated using the GroundEye® instrument in four 50-seed replicates.

The physiological traits were assessed in an experiment with four 50-seed replicates. The seeds were placed on a paper substrate moistened with water (2.5 times the paper weight). The rolls were placed in transparent polyethylene bags and these in a germination chamber regulated at temperatures alternating from 30 to 20 ºC, respectively, under a photoperiod of 8 h light and 16 h dark.

Table 1. Variance components estimated for passion fruit full-sib families under recurrent selection for resistance to the cowpea aphid-borne mosaic virus

Parameter description	Formula [1]
Phenotypic variance between genotype means	$\hat{\sigma}_p^2 = \dfrac{GMS}{r}$
Genotypic variance between genotype means	$\hat{\sigma}_g^2 = \dfrac{GMS - RMS}{r}$
Environmental variance between genotype means	$\hat{\sigma}_e^2 = \dfrac{RMS}{r}$
Heritability coefficient at the level of genotype means	$h^2 = \dfrac{\hat{\sigma}_g^2}{\hat{\sigma}_p^2} = \dfrac{\hat{\sigma}_g^2}{GMS/r}$
Coefficient of genetic variation	$CV_g = 100 \sqrt{\hat{\sigma}_g^2}/m$
Coefficient of environmental or experimental variation	$CV_e = 100 \sqrt{RMS}/m$
Variation index	$\hat{I}_v = \dfrac{CV_g}{CV_e}$
Genotypic correlation	$r_g = \dfrac{\hat{\sigma}_{gxy}^2}{\sqrt{\hat{\sigma}_{gx}^2 \, \hat{\sigma}_{gy}^2}}$
Estimator of genotypic covariance between traits x and y	$\hat{\sigma}_{gxy}^2 = \dfrac{MPG_{xy} - MPR_{xy}}{r}$
Estimator of genotypic variance of trait x	$\hat{\sigma}_{gx}^2 = \dfrac{GMS_x - RMS_x}{r}$
Estimator of genotypic variance of trait y	$\hat{\sigma}_{gy}^2 = \dfrac{GMS_y - RMS_y}{r}$

[1] Expressions proposed by Cruz et al. (2014). GMS: genotype mean square; RMS: residual mean square; r: number of replicates; m: genotype mean; MPGxy: mean product associated with the treatment; MPRxy: mean product associated with the residual.

The germination percentage was evaluated 28 days after the beginning of the trial (Brasil 2009). During the germination test, the germination speed index (GSI) was determined based on the formula proposed by Maguire (1962), by counting the number of seeds with a radicle length of 0.5 cm every two days. Shoot and root length of 10 seedlings per treatment were measured. Shoot and root dry weight were measured after drying the 10 seedlings in a forced-air oven at a constant temperature of 65 ºC for 72 h.

To evaluate accelerated aging (AA), another trial was carried out with four 50-seed replicates, which were scattered on a metal screen placed on a plastic germination box with 40 mL of water, and left to stand in a germination chamber at 40 °C for 48 h. Then, seed germination was assessed, as described above.

The data were subjected to analysis of variance at a significance level of 5% probability ($p \leq 0.05$) by the F test, by the random statistical model:

$$Y_{ij} = \mu + G_i + E_{ij}$$

where Y_{ij} = observation regarding effect i in replicate j; μ = general constant; G_i = effect of genotype i (i = 1, 2, ..., 88), with $G_i \sim$ NID (0, σ^2); and E_{ij} = experimental error, with $E_{ij} \sim$ NID (0, σ^2). Based on the mean squares estimates, the following variance components were estimated: phenotypic variance (σ_p^2), genotypic variance (σ_g^2), environmental variance (σ_e^2), heritability (h^2), variation index ($\hat{I}_v$), coefficient of genetic variation (CV_g) and genotypic correlation (r_g), by the expressions proposed by Cruz et al. (2014) (Table 1).

Genetic gains were estimated using the selection indices of Mulamba and Mock (1978), Pesek and Baker (1969), Smith (1936) and Hazel (1943), and Williams (1962). The following economic weights were used, as suggested by Cruz et al. (2014): CV_g, h^2, and arbitrarily assigned weights (of 80, 100, 80, 50, 50, 30, 30, and 50, respectively) for the traits GSI, G, AA, SL, RL, SDW, RDW, and TSW. The seed biometry variables were excluded from the prediction of genetic gains due to their strong genotypic correlation with TSW. The analyses were performed using software Genes (Cruz 2016).

RESULTS AND DISCUSSION

Genetic parameters and correlations between traits

Data analysis detected significant differences (p ≤ 0.05) between the passion fruit FSF for all analyzed variables (Table 2). The coefficients of experimental variation (CV_e %) were low (< 10%) for all traits, indicating good experimental precision, i.e., reliability in the estimation of genetic parameters and gain prediction, indicating high selection efficiency.

Phenotypic variance (σ_p^2), genotypic variance (σ_g^2) and environmental variance (σ_e^2) were estimated at 0.00027 - 136.94; 0.0027 - 126.24; and 0.00001 - 10.70, respectively (Table 2). The values found for σ_g^2 (significant, non-zero and > σ_e^2) indicate the existence of variability in the population, which is the result of genetic differences between families and suggests that the seed traits of progenies can be maximized by selection.

The high genetic variance values resulted in high heritability (h^2) estimates for all variables, which ranged from 92.2, for AA, to 99.7%, for TSW. Similar h^2 results were observed for 1000-seed weight, GSI, RL, and SDW in passion fruit hybrids (Cremasco et al. 2021); and for SDW, RL and TSW in seeds of S2 guava families (Silva et al. 2021). The same families as in this study were evaluated by Mendes et al. (2022), who reported h^2 values of 86.0 and 92.0% for AUDPCM and fruit yield, respectively. The coefficient of genetic variation (CV_g) ranged from 7.24 (Circ) to 24.97 (RDW). This coefficient determines the genetic variation available for selection; i.e., high values as those found are desirable.

Variation indices ($\hat{I}_v$) greater than unity were also found, which ranged from 1.72 (AA) to 9.52 (TSW). The parameter $\hat{I}_v$, which is not influenced by the mean, is used to assist in the selection process and expresses the relationship between genetic and environmental variation. Variation indices equal to or greater than unity are desirable, for having a greater chance of success in selection (Vencovsky 1987), which were identified in this study. The results of Silva et al. (2021) for guava seed traits were comparable, where the high h^2 values contributed to good variation indices.

Table 2. Estimates of mean squares, means, and genetic parameters of physical and physiological seeds traits of passion fruit full-sib families under recurrent selection for resistance to the cowpea aphid-borne mosaic virus

SV	df	Mean square											
		GSI	G	AA	SL	RL	SDW	RDW	Area	Dmax	Dmin	Circ	TSW
T	87	3.7*	639.6*	813.3*	3.6*	3.3*	266.2*	93.4*	0.001*	0.004*	0.001*	0.077*	0.278*
G	85	2.3*	253.8*	547.8*	2.1*	2.1*	169.8*	80.3*	0.001*	0.004*	0.001*	0.075*	0.253*
C	1	78.1*	20000.0*	11704.5*	78.4*	76.8*	4050.0*	364.5*	0.005*	0.004*	0.008*	0.122*	1.777*
G × C	1	51.0*	14075.3*	12494.5*	55.9*	29.8*	4677.3*	939.5*	0.006*	0.004*	0.014*	0.254*	0.895*
R	264	0.07	14.9	42.8	0.12	0.13	5.23	2.07	0.000	0.000	0.000	0.001	0.001
Total	351												
CV_e (%)		4.85	4.22	8.46	6.04	7.26	4.93	8.24	2.37	1.17	1.17	1.63	1.13
Genotype mean		5.68	92.4	78.2	5.81	5.05	47.0	17.71	0.204	0.635	0.415	1.88	23.3
Amplitude		3.94 – 7.37	59.0- 100.0	33.5- 98.5	4.17- 7.53	3.44- 6.49	32.5- 64.0	8.25- 30.75	0.168 – 0.240	0.558 – 0.725	0.375 – 0.460	1.65 – 2.45	16.2 – 28.3
Passiflora edulis		6.25	100.0	76.5	6.26	6.2	45.0	13.5	0.200	0.365	0.405	1.82	24.6
Passiflora setacea		0	0	0	0	0	0	0	0.150	0.588	0.340	1.57	15.2
Genetic parameter[1]													
σ_p^2		0.57	63.45	136.94	0.54	0.53	42.44	20.07	0.0003	0.0009	0.0003	0.0187	0.0632
σ_g^2		0.55	59.72	126.24	0.51	0.49	41.14	19.56	0.0003	0.0009	0.0003	0.0185	0.0630
σ_e^2		0.02	3.73	10.70	0.03	0.03	1.31	0.52	0.0000	0.0000	0.0000	0.0002	0.0002
h^2 (%)		96.7	94.1	92.2	94.4	93.7	96.9	97.4	97.9	98.5	98.0	98.8	99.7
CV_g (%)		13.0	8.36	14.4	12.3	13,93	13.66	24,97	8.02	4.73	4.12	7.24	10.76
$\hat{I}_v$		2.71	2.00	1.72	2.05	1.93	2.80	3.07	3.39	4.04	3.53	4.46	9.52

SV = source of variation; df = degrees of freedom; GSI = germination speed index (%); G = germination (%); AA = accelerated aging (%); SL = shoot length (cm); RL = root length (cm); SDW = shoot dry weight *(mg seedling⁻¹)*; RDW = root dry weight *(mg seedling⁻¹)*; Area = (cm²); Dmax = maximum diameter (cm); Dmin = minimum diameter (cm); Circ. = circumference (cm); TSW = 1000-seed weight (g); CV_e = coefficient of experimental variation; [1]Genetic parameters on a progeny-mean basis; σ_p^2 = phenotypic variance; σ_g^2 = genotypic variance; σ_e^2 = environmental variance; h^2 = heritability; CV_g = coefficient of genetic variation; Iv = variation index. *, ** - significant at 5% and 1% probability, respectively, by the F test.

The estimated genetic parameters indicate a favorable situation for selection regarding the germination potential of families in the first recurrent selection cycle of passion fruit for CABMV resistance. The results allow the conclusion that selection will be efficient, particularly for the variables GSI, SDW, RDW, and TSW.

Genotypic correlations were positive and high between germination and AA (r_g = 0.73), and between 1000- seed weight and SDW and Area (r_g = 0.69 and 0.75) (Table 3). Fruit and seed variables showed positive correlations, which were greater than 0.50 between fruit weight and G, SDW, and TSW (0.52, 0.65, and 0.69, respectively). Pulp weight was significantly and positively correlated with G, AA, SDW, RDW and TSW (0.57, 0.51, 0.73, 0.57 and 0.72, respectively). The AUDPCM had positive and significant correlations (0.45 and 0.40) with SDW and RDW, respectively, as well as correlations below these values with the other seed variables.

Determining the degree of association between variables is important and can be fundamental if a breeder is interested in selecting multiple traits or if the heritability of a desirable trait is low (Borém and Miranda 2013, Cruz et al. 2014). However, few studies on passion fruit have addressed the genetic correlations between seed traits or between seed and fruit traits. Mostly, only the correlation between number of seeds per fruit and the other fruit traits are analyzed. In a study on seed weight, Santos et al. (2009) found that the fresh weight of one seed correlated positively only with the amount of juice per seed. Positive correlations between number of seeds and fruit weight, length and diameter were reported by Sousa et al. (2012). According to Alves et al. (2012), seed dry weight correlated positively with fresh pulp weight (0.62) and pulp percentage (0.44).

Considering that genotypic correlation is the inheritable part of the phenotypic correlation between two traits (Oliveira et al. 2011), the results suggest that (provided care is taken) indirect selection for germination and SDW based on selection for TSW would be possible. In addition, the positive correlation found between pulp weight and TSW and SDW indicates that indirect selection for pulp volume tends to result in the selection of genotypes with heavier seeds and seedlings with greater shoot development. These results are relevant for passion fruit breeding, as they make the use of indirect selection possible to develop more productive genotypes with vigorous seeds.

Genotypes with more vigorous seeds tend to have a better initial field performance, stand establishment and yields (Krzyzanowski et al. 2018). Different factors are involved in seed vigor, e.g., seed weight, germination speed and the ability to form well-developed seedlings. It is known that a high germination speed indicates high rates of metabolic activity, which result in high growth rates and early completion of the germination phase (Krzyzanowski et al. 2018),

Table 3. Estimates of genotypic correlation coefficients between fruit and seed traits of 86 passion fruit full-sib families under recurrent selection for resistance to the cowpea aphid-borne mosaic virus

	GSI	G	AA	SL	RL	SDW	RDW	Area	Circ	TSW	AUDPCM	FW	FL	FD	PW
GSI	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
G	0.48**	1	-	-	-	-	-	-	-	-	-	-	-	-	-
AA	0.48**	0.73**	1	-	-	-	-	-	-	-	-	-	-	-	-
SL	-0.02	0.33**	0.32**	1	-	-	-	-	-	-	-	-	-	-	-
RL	0.31**	0.37**	0.24*	0.35**	1	-	-	-	-	-	-	-	-	-	-
SDW	0.01	0.53**	0.44**	0.25*	0.11	1	-	-	-	-	-	-	-	-	-
RDW	0.07	0.39**	0.30**	-0.10	0.06	0.82**	1	-	-	-	-	-	-	-	-
Area	0.29**	0.19	0.13	0.08	0.18	0.32**	0.14	1	-	-	-	-	-	-	-
Circ	0.08	0.26*	0.16	0.16	-0.05	0.40**	0.20	0.31**	1	-	-	-	-	-	-
TSW	0.23*	0.52**	0.38**	0.35**	0.28**	0.69**	0.41**	0.75**	0.38**	1	-	-	-	-	-
AUDPCM	0.14	0.29**	0.23*	0.12	0.19	0.45**	0.40**	0.16	0.30**	0.37**	1	-	-	-	-
FW	0.13	0.52**	0.44**	0.32**	0.19	0.65**	0.46**	0.37**	0.27*	0.69**	0.40**	1	-	-	-
FL	0.07	0.31**	0.32**	0.20	0.06	0.33**	0.16	0.29**	0.33**	0.49**	0.36**	0.70**	1	-	-
FD	0.10	0.41**	0.41**	0.32**	0.08	0.49**	0.28**	0.30**	0.32**	0.60**	0.40**	0.83**	0.84**	1	-
PW	0.17	0.57**	0.51**	0.38**	0.23*	0.73**	0.57**	0.34**	0.21	0.72**	0.44**	0.91**	0.57**	0.74**	1

GSI = germination speed index (%); G = germination (%); AA = accelerated aging (%); SL = shoot length (cm); RL = root length (cm); SDW = shoot dry weight *(mg seedling⁻¹)*; RDW = root dry weight *(mg seedling⁻¹)*; Circ. = circumference (cm²); TSW = 1000-seed weight (g); AUDPCM = area under the mean disease progress curve; FW = fruit weight (g); FL = fruit length (mm); FD = fruit diameter (mm); PW = pulp weight (g). *, ** - significant at 5% and 1% probability, respectively, by the t test.

and that vigorous seeds produce seedlings with a higher growth rate. Such seedlings have functional advantages, by better exploiting the environmental conditions, which results in superior plants with high agronomic performance (Krzyzanowski et al. 2018).

Overall, the larger or heavier seeds were the best nourished during development. They had larger amounts of reserves, a determining factor for good germination performance, and more vigorous seedlings could be grown from them (Carvalho and Nakagawa 2012). In view of the high heritability values and positive correlations with physiological seed traits (G and SDW) and fruit yield traits (pulp weight), the variable TSW is suggested as an excellent option to be used as basis for the selection of superior passion fruit genotypes for seed quality. Furthermore, 1000-seed weight is an easy-to-measure and non-destructive variable.

Prediction of genetic gains and family selection

Estimates of selection gains based on three economic weight criteria (CV_g, h^2, and arbitrarily assigned weights) and a selection intensity of 30% resulted in positive values for the seed traits of passion fruit FSF under recurrent selection for CABMV resistance (Table 4). However, there were differences regarding the gains, depending on the index used.

The Mulamba and Mock (1978) index provided percentages of positive genetic gains, using all economic weights, for most variables. The gain percentages were best for GSI (6.79%), RL (9.08%) and TSW (8.36%), with h^2 as economic weight; for SDW (11.67%) and RDW (17.65%) using CV_g; and for G (5.94%), AA (10.04%) and SL (6.30%), using arbitrary weights (Table 4). Regardless of the economic weights, the Pesek and Baker (1969) index provided negative and low gains for G, AA, SDW, and RDW (Table 4), which is not interesting for selection for seed traits of genotypes.

The Smith (1939) and Hazel (1943) and Williams (1962) indices, which use CV_g and h^2 as economic weights, resulted in low gains for GSI, G, SL, and RL. Although the gain estimates by the Smith (1939) and Hazel (1943) and Williams (1962) indices were positive, the values are uninteresting compared to those of the Mulamba and Mock (1978) index,

Table 4. Estimates of means of selected families (Xs) and percentage gains (GS) by simultaneous selection based on three economic weight criteria[1] for eight seed variables of passion fruit full-sib families under recurrent selection for resistance to the cowpea aphid-borne mosaic virus

Variable	Mulamba & Mock (1978)						Smith (1939) and Hazel (1943)					
	h^2		CV_g		AW		h^2		CV_g		AW	
	Xs	GS	Xs	GS	Xs	GS	Xs	GS	Xs	GS	Xs	GS
GSI	6.08	6.79	5.99	5.42	6.05	6.36	5.76	1.40	5.72	0.60	5.90	3.65
G	97.90	5.57	97.37	5.02	98.27	5.94	97.60	5.25	97	4.65	98.08	5.74
AA	85.17	8.18	85.87	9.00	86.75	10.04	86.48	9.72	85.06	8.04	88.54	12.14
SL	6.18	6.09	6.13	5.24	6.19	6.30	6.06	4.22	6.01	3.26	6.13	5.22
RL	5.54	9.08	5.44	7.26	5.46	7.60	5.25	3.64	5.18	2.41	5.35	5.58
SDW	52.29	10.99	52.62	11.67	51.37	9.09	53.65	13.81	54.24	15.02	51.60	9.56
RDW	20.02	12.68	20.92	17.65	19.66	10.73	21.43	20.46	22.28	25.11	19.74	11.56
TSW	25.28	8.36	25.05	7.39	24.82	6.39	24.93	6.86	24.81	6.35	24.68	5.81
Variable	Pesek & Baker (1969)						Williams (1962)					
	h^2		CV_g		AW		h^2		CV_g		AW	
	Xs	GS	Xs	GS	Xs	GS	Xs	GS	Xs	GS	Xs	GS
GSI	6.10	7.10	6.05	6.29	6.16	8.21	5.73	0.76	5.74	0.97	5.90	3.65
G	91.54	-0.91	91.75	-0.69	92.85	0.42	97.58	5.23	97.29	4.94	98.08	5.74
AA	76.83	-1.65	77.21	-1.20	78.37	0.16	87.17	10.54	86	9.15	88.54	12.14
SL	6.30	8.06	6.28	7.77	6.31	8.28	6.04	3.79	6.03	3.63	6.13	5.22
RL	5.41	6.62	5.42	6.88	5.42	6.93	5.20	2.78	5.24	3.60	5.35	5.58
SDW	47.02	0.12	47.72	1.57	47.23	0.56	53.45	13.39	53.86	14.22	51.60	9.56
RDW	17.21	-2.75	18	1.58	17.41	-1.64	21.12	18.71	21.84	22.68	19.74	11.15
TSW	23.75	1.84	23.73	1.76	23.64	1.35	24.93	6.86	24.82	6.39	24.68	5.81

[1] Economic weights: h^2 = heritability coefficient; CV_g = coefficient of genetic variation; AW = arbitrarily assigned weights; GSI = germination speed index (%); G = germination (%); AA = accelerated aging (%); SL = shoot length (cm); RL = root length (cm); SDW = shoot dry weight (*mg seedling $^{-1}$*); RDW = root dry weight (*mg seedling $^{-1}$*); TSW = 1000-seed weight (g).

which provided better estimates and a better distribution of gains for the studied variables, based on the heritability coefficient and arbitrary weights.

The Mulamba and Mock (1978) index proved effective in predicting genetic gains in passion fruit (Gonçalves et al. 2007, Neves et al. 2011, Krause et al. 2012, Dalbosco et al. 2018). Similarly, the best gain predictions in passion fruit were also obtained by this index by Gonçalves et al. (2007) and Dalbosco et al. (2018). For Neves et al. (2011), the Mulamba and Mock (1978) index, based on genotypic and phenotypic analyses, provided satisfactory total genetic gains for simultaneous selection in passion fruit. For agronomic traits of passion fruit, Krause et al. (2012) predicted genetic gains with the Mulamba and Mock index (1978).

The high percentage gains estimated for the traits G, AA, SDW, RDW and TSW by the Mulamba and Mock (1978) index represent the possibility of gains with selection in passion fruit, with a view to breeding lines with a higher germination rate and greater vigor. These characteristics would make the plants more tolerant to severe stress under adverse conditions, resulting in better crop stands in the field.

Therefore, the Mulamba and Mock (1978) index with h^2 as economic weight was adopted as strategy to select the best families in this study, since it provided the best gains for GSI, RL, SDW, RDW and TSW. These traits are related to the physiological potential and vigor of seeds and, consequently, the ability to generate plants with good initial development in the field and high yield levels.

The 26 best FSF of passion fruit selected for seed traits were RS3, RS10, RS13, RS24, RS61, RS26, RS31, RS33, RS36, RS40, RS42, RS49, RS51, RS56, RS57, RS58, RS59, RS25, RS62, RS65, RS67, RS69, RS70, RS71, and RS75. For these families, the values of the traits GSI, G, AA, SL, RL, SDW, RDW, and TSW were 6.08, 97.90%, 85.17%, 6.18 cm, 5.54 cm, 52.29 mg, 20.02 mg, and 25.28 g, respectively (Table 4).

Among the selected families, only RS75, RS25 and RS33 coincided with the families selected by Mendes et al. (2022) to form the next selection cycle for resistance to CABMV in passion fruit. It is worth mentioning that these authors selected for resistance to CABMV and fruit yield. These results reinforce the need to evaluate seed traits in passion fruit breeding, since the best families for fruit yield and abiotic stress resistance are not necessarily the best for physical and physiological seed traits.

In this scenario, this study confirmed that the seed germination potential must be taken into consideration in selection for superior passion fruit genotypes. Therefore, in the medium and long term, selection for superior genotypes in the *Passiflora* spp. breeding program should not only focus on agronomic plant and fruit-related traits, but also on the variables germination speed index, shoot and root dry weight and 1000-seed weight.

CONCLUSION

The genetic parameters indicate a favorable situation for selection regarding the germination potential of families in the first cycle of recurrent selection of passion fruit for resistance to CABMV.

The trait 1000-seed weight stood out with high heritability indices, genetic gain prediction and genotypic correlations with seed and fruit traits.

When heritability was used as economic weight, the Mulamba and Mock index provided the best distribution of genetic gains and was employed in the selection of the 26 best *Passiflora* spp. full-sib families to compose the second cycle of recurrent selection.

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