



Early selection of resilient progenies to seed yield in soybean populations

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ABSTRACT: This study carried out early selection of soybean progenies that are productive and resilient to environmental conditions. The experiment took place at the Genetic Breeding Program of UNIJUI (University of the Northwest of the State of Rio Grande do Sul), located in Ijuí - RS, Brazil. The experiment used augmented blocks design with interim checks. The regular treatments correspond to 24 soybean F₂ populations and the common treatments were 18 commercial checks, arranged in four replications. At full physiological maturity, in each experimental unit, five plants were randomly collected to obtain seed weight per plant (SWP, g). The Jinks and Pooni methodology was used to calculate the probability of extracting superior lineages from the evaluated populations. The best control and promising cultivars to compose the parent bank are BMX FORÇA RR, FUNDACEP 66 RR and TMG 7062 IPRO. Jinks and Pooni's methodology identified populations IRC₀₀₁, IRC₀₀₂, IRC₀₁₇, IRC₀₁₉, IRC₀₂₈, IRC₀₃₀, IRC₀₃₂, IRC₀₃₃, IRC₀₃₅, IRC₀₃₆, IRC₀₃₉ and IRC₀₄₀ as having high potential for extraction of superior lineages.

Key words: *Glycine max*, genetic parameters, Jinks and Pooni method, plant breeding.

Seleção precoce de progênies resilientes para produtividade de sementes em populações de soja

RESUMO: O objetivo desse estudo foi realizar a seleção precoce de progênies de soja produtivas e resilientes às condições ambientais. O experimento foi realizado no Programa de Melhoramento Genético da Universidade do Noroeste do Estado do Rio Grande do Sul (UNIJUI), localizado em Ijuí, Rio Grande do Sul, Brasil. Foi utilizado o delineamento incompleto de blocos aumentados com testemunhas intercalares. Os tratamentos regulares correspondem a 24 populações de soja F₂ e os tratamentos comuns foram 18 testemunhas comerciais, arranjadas em quatro repetições. Em plena maturidade fisiológica, em cada unidade experimental, cinco plantas foram coletadas aleatoriamente para obtenção do peso de sementes por plantas. Utilizou-se a metodologia de Jinks e Pooni para calcular a probabilidade de extração de linhagens superiores das populações avaliadas. As cultivares de melhor controle e promissoras para compor o banco parental foram BMX FORÇA RR, FUNDACEP 66 RR e TMG 7062 IPRO. A metodologia de Jinks e Pooni identificou as populações IRC₀₀₁, IRC₀₀₂, IRC₀₁₇, IRC₀₁₉, IRC₀₂₈, IRC₀₃₀, IRC₀₃₂, IRC₀₃₃, IRC₀₃₅, IRC₀₃₆, IRC₀₃₉ e IRC₀₄₀ como de alto potencial para extração de linhagens superiores.

Palavras-chave: *Glycine max*, parâmetros genéticos, método de Jinks e Pooni, melhoramento de plantas.

INTRODUCTION

Soybean (*Glycine max* L.) are an important source of protein for human and animal nutrition (OLIVEIRA et al., 2017). Projections of population growth associated with environmental variations require the development and selection of resilient soybean progenies in terms of grain yield (ONU, 2019). The objectives of breeding programs should be based on the selection of genotypes that have high productive potential, stability and adaptability to adverse environmental conditions (GIORDANI et al., 2019; SZARESKI et al., 2015).

Developing genotypes with a superior phenotypic response in adverse environmental conditions is the strategy to guarantee productivity in conditions with less availability of environmental resources (DARONCH et al., 2019). The success of this strategy is associated with the availability of genetic variability. The formation of segregating populations with the potential to produce superior lines is dependent on the concentration of favorable alleles in the parents involved (RAMALHO et al., 2012). Early evaluation of these populations makes it possible to identify and select potential progenies, while discarding less promising ones. This strategy optimizes resources and speeds up the process in breeding programs.

For that, the REML/BLUP methodology has helped to select genotypes in crops such as soybeans (PRADEBON et al., 2023; KEHL et al., 2022; KNEBEL et al., 2021), wheat (LORO et al., 2023), white oats (SCHMIDT et al., 2023) and corn (CARVALHO et al., 2017). This methodology makes it possible to estimate variance components and genetic parameters that indicate the proportion of the phenotype that is determined by the genetic makeup. This makes it possible to check whether the selection of the best genotypes can be carried out based on phenotypic information from the field (RESENDE, 2007).

Some methodologies make it possible to estimate the probability of extracting superior lines from segregating populations that outperform a standard genotype, such as the Jinks and Pooni method (JINKS & POONI, 1976). This makes genotype selection efficient, since there is a probability associated with selection (MEZZOMO et al., 2021). Based on this, the combined use of methodologies for genotype selection results in greater assertiveness in the estimation of genetic parameters, prediction of genotypic values and the identification of the best genotypes; consequently, the greatest simultaneous gain for the traits of interest (RESENDE, 2016; SANTOS et al., 2019).

The need to mitigate negative environmental effects and satisfy the growing demand for food is driving research into resilient and productive soybean genotypes. Improving the efficiency and dynamics of breeding programs is essential. In order to do this, selection efficiency must be increased so that only populations with high potential are selected, in order to optimize the development of superior genotypes and reduce operating costs. Therefore, the aim of this study was to carry out early selection of soybean progenies that are productive and resilient to environmental conditions.

MATERIALS AND METHODS

The experiment took place at the Genetic Improvement Program of UNIJUI (Universidade Regional do Noroeste do Estado do Rio Grande do Sul), located in Ijuí - RS, Brazil, under the

geographical coordinates: 28°53'10" S and 52°59'55" W. The experiment used augmented blocks design with interim checks. The regular treatments correspond to 24 soybean F₂ populations and the common treatments were 18 commercial checks, arranged in four replications. The cultivars, maternal and paternal parents and the cultivars used are in table 1. Growth habit qualitatively characterized the seeds of the cultivars (Table 2).

Each experimental unit was formed by five rows of five meters in length, spaced at 0.45 m, totaling 2.25 square meters, sowing took place in the second half of October 2018 and fertilization with 200 kg ha⁻¹ in the 05-20-20 NPK formulation. Management to control insect pests and diseases took place in order to avoid damage during the conduct of the experiments. Fungicides and insecticides were applied to control pathogens and insect pests in order to avoid any damage to the experiments. At full physiological maturity, every experimental unit randomly collected five plants. Each experimental unit manually threshed the seeds of the five plants. Thus, obtaining the seed weight per plant (SWP, g).

Subsequently, the method based on Restricted Maximum Likelihood (REML) was used in order to estimate the variance components and genetic parameters, according to the following statistical model: $y = Xb + Za + Wi + e$, where y is the data vector; b is the vector of the block effects (assumed as fixed) added to the general average; a is the vector of individual genotypic effects (assumed as random); i is the vector of the effects of the genotype/environment interaction (with the environment corresponding to years); e is the vector of errors (random); and X , Z , and W represent the incidence matrices for the referred effects. The significance was obtained through the Deviance analysis at 5% probability by the Chi-square test. This approach allowed of the following estimations: phenotypic variance (PV), genotypic variance (GV), residual variance (EV), broad sense heritability (H^2), accuracy (Acc), coefficient of genotypic variation (CVg), residual coefficient of variation (CVe) and coefficient of variation of the proportion between genotypic and residual coefficient of variation (CVr). To predict genetic values, BLUP (best linear unbiased prediction) was used, through estimates of variance components

Table 1 - Morphological description of cultivars, inbred lines (common treatments), maternal and paternal parents base for segregating F2 populations.

Cultivars	FC	HC	GH	PC	VC	Maternal parents	Paternal parents	F2 (Pop)
NS 4823	P	Black	I	Medium Brown	Light Brown	BMX MAGNA RR	FUNDACEP 66 RR	IRC001
NA 5909 RG	P	Imperfect Black	I	Gray	Light Brown	BMX APOLO RR	FUNDACEP 66 RR	IRC002
5958 RSF IPRO	P	Light Brown	I	Gray	Light Gray	BMX MAGNA RR	MONASCA RR	IRC003
BMX ATIVA RR	P	Imperfect Black	D	Gray	Light Gray	ROOS CAMINO RR	FPS PARANAPANEMA RR	IRC005
BMX POTÊNCIA RR	W	Light Brown	I	Gray	Light Gray	BMX APOLO RR	MAR.M4 C B	IRC006
ROOS CAMINO RR	W	Yellow	I	Gray	Light Brown	BMX APOLO RR	MAR.M4 C B	IRC007
BMX APOLO RR	W	Yellow	I	Gray	Dark Brown	BMX APOLO RR	FPS URANO RR	IRC008
BMX MAGNA RR	W	Light Brown	I	Gray	Light Gray	FPS NETUNO RR	BMX APOLO RR	IRC012
BMX FORÇA RR	W	Light Brown	I	Gray	Light Gray	BMX MAGNA RR	BMX APOLO RR	IRC013
FPS NETUNO RR	W	Light Brown	I	Gray	Light Gray	ROOS CAMINO RR	FPS URANO RR	IRC016
FUNDACEP 66 RR	P	Imperfect Bown	I	Gray	Light Gray	FPS JÚPITER RR	MONASCA RR	IRC017
FPS JUPITER RR	W	Light Brown	I	Gray	Light Gray	FUNDACEP 66 RR	NK 7059 RR	IRC019
NS 6700 IPRO	P	Imperfect Black	I	Gray	Light Gray	M	M4	IRC027
FPS PARAPANEMA RR	P	Brown	SD	Light Brown	Medium Brown	M	M5	IRC028
ROTA 54	P	Black	I	Medium Brown	Medium Brown	M	M6	IRC029
TMG 7062 IPRO	W	Light Brown	SD	Gray	Light Gray	BMX FORÇA RR	MAR.M4 C B	IRC030
TMG 7161 RR	W	Light Brown	I	Gray	Light Gray	5958 RSF IPRO	MAR.M2 CHAPADA	IRC031
FPS URANO RR	P	Light Brown	D	Gray	Light Gray	BMX MAGNA RR	NA 5909 RG	IRC032
BMX TURBO RR	P	Light Brown	I	Gray	Dark Gray	MAR.M4 C B	NA 5909 RG	IRC033
						5958 RSF IPRO	NS 6700 IPRO	IRC034
						BMX FORÇA RR	MAR.M4 C B	IRC035
						BMX APOLO RR	TMG 7161 RR	IRC036
						TMG 7161 RR	NA 5909 RG	IRC039
						BMX TURBO RR	TMG 7161 RR	IRC040

FC: flower color, HC: hilum color, GH: growth habit, PC pubescence color, VC: vegetable color, P: purple, W: white, I: indeterminate, D: determinate, SD: semi-determinate.

Table 2 - Variance components and estimated genetic parameters by the REML methodology and prediction of the best unbiased value for commercial checks.

Cultivars	Order	g	u + g	Gain	New Mean	Parameters	
NS 4823	1	8.036	26.678	8.036	26.678	GV	21.187
NA 5909 RG	2	5.780	24.422	6.908	25.550	EV	15.345
5958 RSF IPRO	3	4.769	23.411	6.195	24.837	PV	36.536
BMX ATIVA RR	4	4.696	23.337	5.820	24.462	H ²	0.579
BMX POTÊNCIA RR	5	3.741	22.383	5.405	24.046	Ac	0.920
ROOS CAMINO RR	6	3.364	22.006	5.064	23.706	CVg%	24.691
BMX APOLO RR	7	1.9226	20.564	4.616	23.257	CVe%	21.013
BMX MAGNA RR	8	0.261	18.903	4.071	22.713	CVr%	1.175
BMX FORÇA RR	9	-0.723	17.918	3.538	22.180	Overall Mean	18.642
FPS NETUNO RR	10	-1.306	17.336	3.054	21.696		
FUNDACEP 66 RR	11	-2.272	16.369	2.569	21.212		
FPS JUPITER RR	12	-2.282	16.359	2.165	20.807		
NS 6700 IPRO	13	-2.706	15.934	1.791	20.432		
FPS PARAPANEMA RR	14	-3.553	15.089	1.4092	20.0510		
ROTA 54 IPRO	15	-3.948	14.694	1.0520	19.6939		
TMG 7062 IPRO	16	-4.594	14.048	0.6992	19.3411		
TMG 7161 RR	17	-4.791	13.851	0.3762	19.0181		
FPS URANO RR	18	-6.396	12.246	0.0000	18.6419		

g: Predicted Genetic Value; u+g: Predicted Genetic Value + Additive; G: Pure Genetic Gain; u+g, GV: Genotypic Variance, EV: Residual Variance; PV: Phenotypic Variance; H²: Broad Sense Heritability for Total Genotypes; Ac: Accuracy; CVg%: Genotypic Variation Coefficient; CVe%: Coefficient of Residual Variation, CVr%: Coefficient of Variation between genotypic and residual coefficient of variation.

obtained by the restricted maximum likelihood method (REML).

Subsequently, the method of partitioning genetic trends based on genealogy and selection strategies was listed (OLIVEIRA et al., 2022). To predict the potential of populations to generate superior lineages, the methodology of JINKS & POONI (1976) was used. This technique estimates the probability of obtaining lineages that exceed a defined standard in the generation under study. When evaluating this probability, it was considered that the productivity of the lines follows a normal distribution, using the properties of a standardized normal distribution, that is:

$$Z = \frac{(SWPPG + 20\%) - SWPPG_i}{\sqrt{GV}}$$

Where: Z: is the approximation of the normal curve/standardized probability; SWPPG + 20%: is the predicted genetic seed mass per plant from the best control plus 20%; SWPPGi: is the predicted genetic seed mass per plant of each population; and GV: is the genetic variance of each population. From this, the

probabilities of obtaining strains that exceed SWPPG + 20% were calculated. Lineages with a probability greater than 50% were selected. The analyzes were carried out using the following R Packages: ExpDes.pt (FERREIRA et al., 2021) to verify the assumptions of the analyses; metan (OLIVOTO & LUCIO, 2020) to apply REML/BLUP; ggplot2 (WICKHAM, 2016) to develop the graphs and AlphaPart (OLIVEIRA et al., 2022) to partition the genetic trend of the population. All analyzes were performed using the software R (R CORE TEAM, 2022).

RESULTS AND DISCUSSION

The group of cultivars (Table 2) with indeterminate growth habit revealed that the NS 4823 cultivar had the best mean SWP performance (26.678 g) and inferiority obtained by the TMG 7161 RR cultivar (19.018 g). In comparison with these controls, it was identified that the populations IRC₀₄₀, IRC₀₁₉, IRC₀₂₈, IRC₀₃₀, IRC₀₃₃, IRC₀₃₅, IRC₀₀₂ and IRC₀₁₇ were superior to the described cultivar group (Figure 1), that is, they exhibited averages

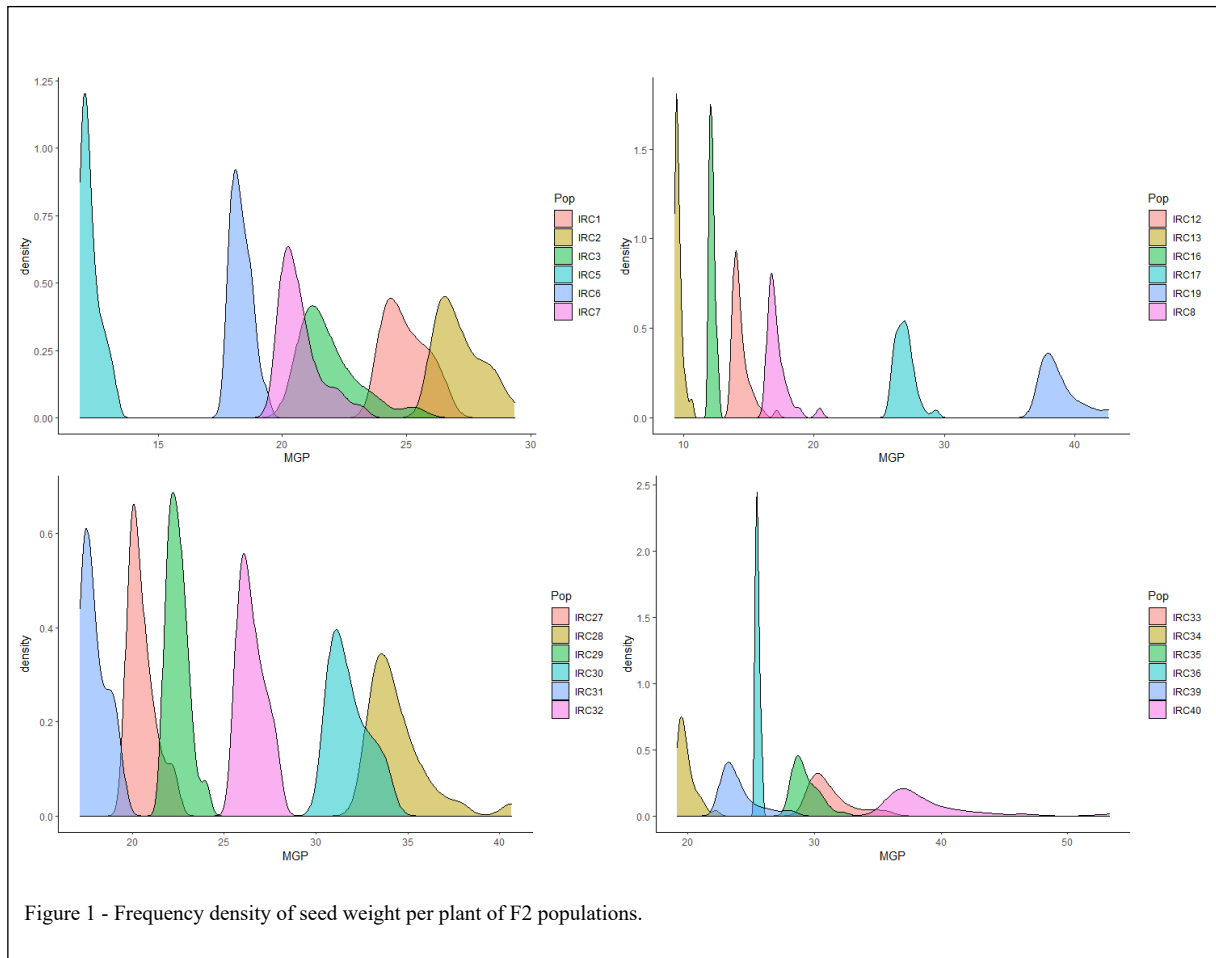


Figure 1 - Frequency density of seed weight per plant of F₂ populations.

greater than 26.678 g. Regarding the cultivars with semi-determined growth habit, the cultivar TMG 7062 IPRO as superior to the group of cultivars with the same habit, with grain weight per plant of 24.046 g. The populations IRC₀₄₀, IRC₀₁₉, IRC₀₂₈, IRC₀₃₀, IRC₀₃₃, IRC₀₃₅, IRC₀₀₂, IRC₀₁₇, IRC₀₃₂, IRC₀₃₆ and IRC₀₀₁ were superior to that check.

When observing the checks of determinate growth habit, to cultivate BMX ATIVA obtained an average of 24.462 g of seed weight, considered superior; therefore, the populations that expressed means greater than the value found were IRC₀₄₀, IRC₀₁₉, IRC₀₂₈, IRC₀₃₀, IRC₀₃₃, IRC₀₃₅, IRC₀₀₂, IRC₀₁₇, IRC₀₃₂, IRC₀₃₆ and IRC₀₀₁. According to SANTOS et al. (2019), plants with determinate growth habit are contrasting to indeterminate cultivars, mainly for quantitative characteristics.

Therefore, it was possible to identify soybean F₂ populations that express average grain

per plant performance superior to certain control cultivars. This indicated that in the specific crossing that built this heterozygous population, there was success in increasing genetic variability, which is manifested as a function of grain weight. For PELUZIO et al. (2014), genetic variability between parents makes it possible to obtain increases in heterozygosity and an increase in favorable genes and alleles, a fact that well-directed selections will favor the obtainment of elite lines and subsequently promising cultivars.

The Deviance analysis revealed a significant effect for the seed weight per plant by the Chi-square test at 5% probability (Table 3). This indicated that there is genetic variability among the control soybean cultivars. MATHEW et al. (2018), highlighted in their studies the importance of genetic variability for the selection of superior genotypes.

Table 3 - Descriptive analysis of maximum (Max), medium (Med) and minimum (Min) values of seed weight per plant (g) of control populations and cultivars.

Cultivar	-----GH-----	----Mean----	-----Pop-----	----Max----	----Med----	-----Min-----
NS 4823	I	26.678	IRC40	53.288	38.921	35.89
NA 5909 RG	I	25.550	IRC19	42.628	38.789	37.161
5958 RSF IPRO	I	24.837	IRC28	40.658	34.489	32.839
BMX ATIVA RR	D	24.462	IRC30	34.057	31.808	30.479
BMX POTÊNCIA RR	SD	24.046	IRC33	35.753	31.225	29.517
ROOS CAMINO RR	I	23.706	IRC35	32.304	29.314	28.203
BMX APOLO RR	I	23.257	IRC2	29.334	27.154	26.014
BMX MAGNA RR	I	22.713	IRC17	29.325	26.963	25.979
BMX FORÇA RR	D	22.180	IRC32	28.015	26.508	25.536
FPS NETUNO RR	SD	21.696	IRC36	25.901	25.511	25.316
FUNDACEP 66 RR	I	21.212	IRC1	26.612	24.962	23.846
FPS JUPITER RR	I	20.807	IRC39	28.277	24.023	22.538
NS 6700 IPRO	I	20.433	IRC29	23.984	22.466	21.741
FPS PARAPANEMA RR	I	20.051	IRC3	25.265	21.892	20.623
ROTA 54 IPRO	I	19.694	IRC7	23.128	20.707	19.815
TMG 7062 IPRO	I	19.341	IRC27	22.275	20.518	19.769
TMG 7161 RR	I	19.018	IRC34	22.221	19.903	19.167
FPS URANO RR	D	18.642	IRC6	19.304	18.338	17.786

Pop: Population; GH: growth habit; I: Indeterminate; D: Determinate, SD: Semi-determinate.

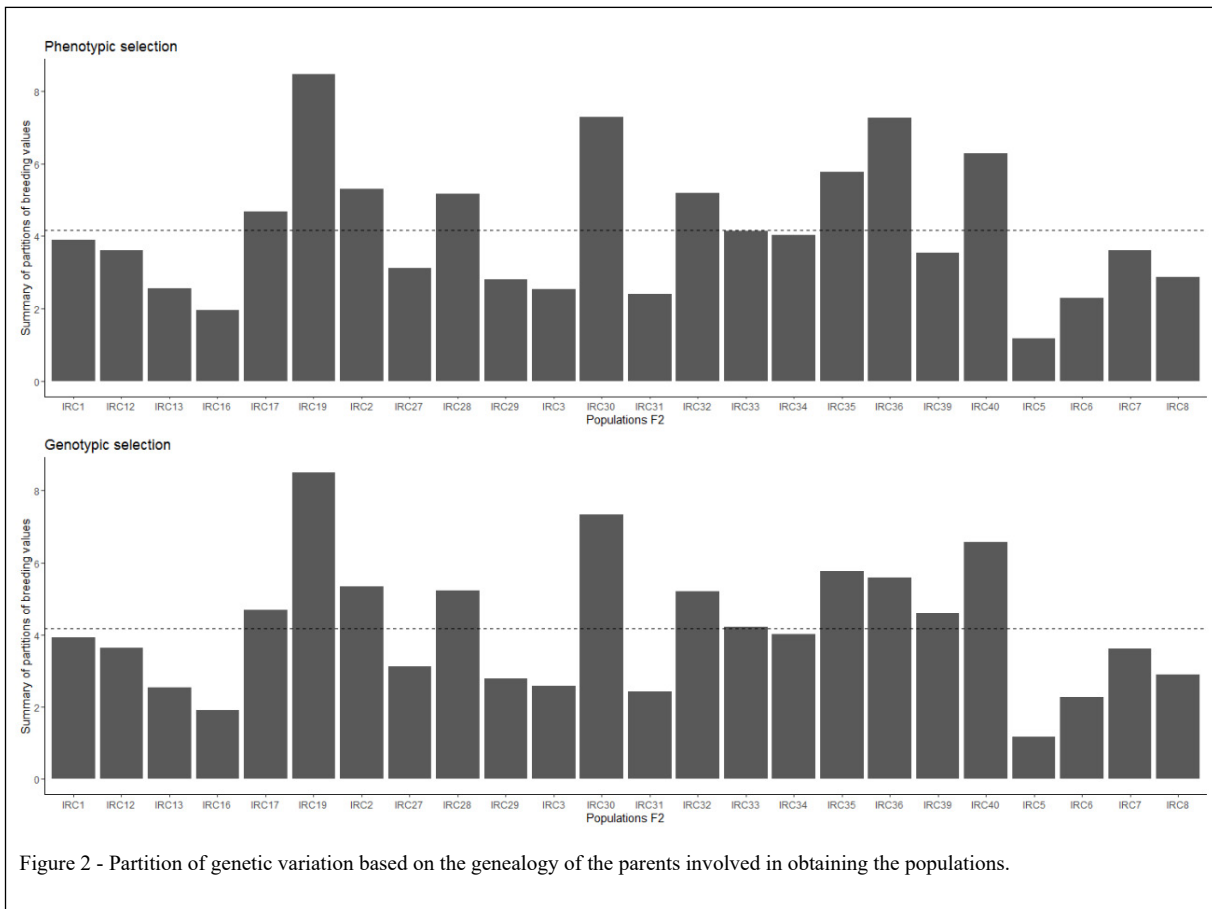
Regarding the controls (Table 3), the seed weight per plant was due to 57% of genotypic variance (GV), NARDINO et al. (2016), describes that this is a measure that allows to determine the size of the genetic variability present in the population for the traits under study. However, phenotypic variation (PV) contributed 43% to trait expression. SANTOS et al. (2019) estimated the phenotypic, environmental and genetic variance in a soybean F₂ population, this study revealed a smaller contribution of genetic variation in the phenotypic manifestation of the seed weight per plant character.

The heritability reveals the fraction of the genetic variance that exists in the phenotypic variance, and may indicate reliability and experimental precision for the phenotype (RAMALHO et al., 2012). In this study, H²:0.57 was obtained, characterizing average heritability. Accuracy (Acc) was expressed as high (0.92) which results in experimental precision, as accuracies close to indicate greater efficiency in selection strategies and genetic gains to the characters (COSTA et al., 2000). The genotypic coefficient of variation (CVg%) exhibited magnitudes of

24.69%, and the residual (CVe%) of 21.01%, thus the ratio of the genotypic and residual coefficient of variation (CVr) was 1.17, which determines high genetic variability and high probability of selection of populations for seed weight, for VECONVSKI & BARRIGA (1992), the occurrence of values greater than 1 indicates promising selection for the character in question.

For TEIXEIRA et al. (2017), estimating and understanding the genetic parameters provides breeders with knowledge of the genetic structure of the population, better decision-making at the time of selection, choice of methods that are most suitable and resulting in better results for selection. Thus, the control cultivars with the highest genetic value were NS 4823, NA 5909 RG, 5958 RSF IPRO, BMX ATIVA RR, BMX POTÊNCIA RR, ROOS CAMINO RR, BMX APOLO RR and BMX MAGNA RR.

The phenotypic and genotypic selection parameters were estimated (Figure 2 and Table 4). The method used was the partitioning of genetic trends, which aims to highlight the sources of genetic gains and the relationship between the sources and the parameters that affect them (OBSTETER et al., 2021; OLIVEIRA et al., 2022).



The populations IRC₀₀₁, IRC₀₀₂, IRC₀₁₇, IRC₀₁₉, IRC₀₂₈, IRC₀₃₀, IRC₀₃₂, IRC₀₃₃, IRC₀₃₅, IRC₀₃₆, IRC₀₃₉ and IRC₀₄₀ expressed additive contribution potential, as they are above the mean index (≥ 4.17). However, populations IRC₀₀₃, IRC₀₀₅, IRC₀₀₆, IRC₀₀₇, IRC₀₀₈, IRC₀₁₂, IRC₀₁₃, IRC₀₁₅, IRC₀₂₇, IRC₀₂₉, IRC₀₃₁, and IRC₀₃₄ exhibited the lowest potential additive gains, since they are below the index. These results indicated that among the populations, it is possible to find those with the highest seed weight per plant, and these should be selected to continue in the improvement process. Studies by CRUZ et al. (2014), corroborates the results of selection gains, making it possible to identify whether selection was successful or not, discarding populations with low additive genetic effects that would be costly for the breeding program. Thus, progenies with a higher additive potential are more likely to transmit their characteristics to subsequent generations.

The genetic variance used in the estimates established the direction of heritability (HALLAUER et al., 1988). In view of this, heritability in the broad sense (H^2) comes from the ratio between the total genetic variance (additive, dominance and epistatic effects) and the phenotypic variance of the trait (MATHER & JINKS, 1984).

By adopting the classification of heritability (H^2), in which values > 0.7 (70%) are considered high, medium or intermediate values of 0.30 (30%) and 0.69 (69%) and low values below 0.30, the values demonstrated by the populations for seed weight per plant can be classified as low, as the populations presented a heritability of 0.20, with the exception of IRC₀₃₆ (H^2 : 0.01) (Table 3). LEITE et al. (2016) point out that the selection of progenies with greater potential is complex, as most exhibit low heritability.

Table 4 - Probability of extracting superior lineages from soybean segregating populations calculated by the Jinks and Pooni method, based on unbiased linear prediction (BLUP).

MATERNAL PARENT	PATERNAL PARENT	F1	F2 (Pop)	SWPPM	SWPPG	PV	GV	H ²	Z (L:23, 52g + 20% T)	P (%)	Sel
BMX MAGNA RR	FUNDACEP 66 RR	169	IRC001	23.846	24.962	166.498	33.299	0.2	-0.2	57.194	High
BMX APOLO RR	FUNDACEP 66 RR	173	IRC002	26.014	27.154	164.897	32.979	0.2	-0.5	67.622	High
BMX MAGNA RR	MONASCA RR	153	IRC003	20.623	21.892	221.352	44.270	0.2	0.2	41.886	Low
ROOS CAMINO RR	FPS PARANAPA NEMA RR	132	IRC005	11.867	12.286	25.757	5.152	0.2	1.413	7.883	Low
BMX APOLO RR	MAR.M4 C B	154	IRC006	17.786	18.337	44.283	8.857	0.2	0.7	25.725	Low
BMX APOLO RR	MAR.M4 C B	124	IRC007	19.815	20.707	101.935	20.387	0.2	0.4	36.175	Low
BMX APOLO RR	FPS URANO RR	140	IRC008	16.447	17.191	80.923	16.185	0.2	0.8	21.298	Low
FPS NETUNO RR	BMX APOLO RR	152	IRC012	13.768	14.403	50.585	10.117	0.2	1.147	12.575	Low
BMX MAGNA RR	BMX APOLO RR	122	IRC013	9.334	9.651	12.124	2.425	0.2	1.745	4.054	Low
ROOS CAMINO RR	FPS URANO RR	155	IRC016	11.929	12.196	9.535	1.907	0.2	1.424	7.717	Low
FPS JÚPITER RR	MONASCA RR	176	IRC017	25.979	26.963	137.578	27.516	0.2	-0.4	66.751	High
FUNDACEP 66 RR	NK 7059 RR	190	IRC019	37.161	38.789	329.758	65.952	0.2	-1.921	97.261	High
M	M4	M4	IRC027	19.769	20.518	73.855	14.771	0.2	0.4	35.286	Low
M	M5	M5	IRC028	32.839	34.489	382.144	76.428	0.2	-1.379	91.616	High
M	M6	M6	IRC029	21.741	22.466	74.889	14.978	0.2	0.1	44.727	Low
BMX FORÇA RR	MAR.M4 C B	239	IRC030	30.479	31.808	218.878	43.776	0.2	-1.043	85.142	High
5958 RSF IPRO	MAR.M2 CHAPADA	250	IRC031	17.150	17.965	91.404	18.281	0.2	0.7	24.235	Low
BMX MAGNA RR	NA 5909 RG	220	IRC032	25.536	26.509	129.127	25.825	0.2	-0.4	64.652	High
MAR.M4 C B	NA 5909 RG	235	IRC033	29.517	31.225	394.808	78.962	0.2	-0.9	83.377	High
5958 RSF IPRO	NS 6700 IPRO	224	IRC034	19.167	19.903	66.887	13.377	0.2	0.5	32.459	Low
BMX FORÇA RR	MAR.M4 C B	216	IRC035	28.203	29.314	153.377	30.675	0.2	-0.7	76.691	High
BMX APOLO RR	TMG 7161 RR	248	IRC036	25.316	25.511	441.994	7.801	0.0	-0.3	59.888	High
TMG 7161 RR	NA 5909 RG	255	IRC039	22.538	24.023	280.864	56.173	0.20	-0.1	52.524	High
BMX TURBO RR	TMG 7161 RR	256	IRC040	35.890	38.921	1416.267	283.254	0.20	-1.937	97.364	High

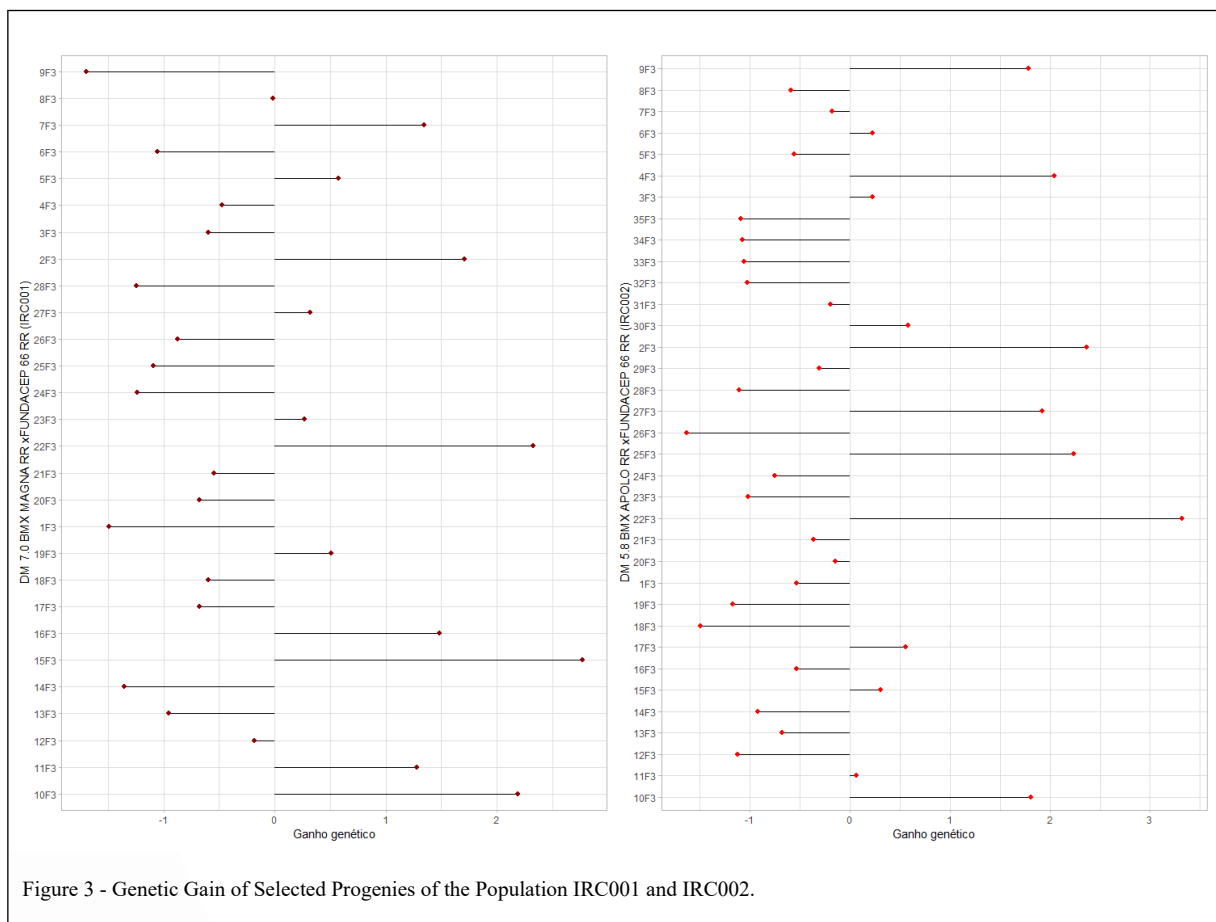
SWPPM: Seed Weight per Plant Phenotypic Mean; SWPPG: Seed Weight per Plant Predicted Genetic; PV: Phenotypic Value; GV: Genotypic Value; H²: Broad Sense Heritability; Z: Normal Curve Approximation/Studentized Probability; P: Probability of Obtaining a New Lineage; Sel: Selection Index.

The highest selection probabilities found are for IRC₀₄₀ with 97.364% and IRC₀₁₉ with 97.261%. Percentages greater than 50% are considered high, therefore, populations IRC₀₀₁, IRC₀₀₂, IRC₀₁₇, IRC₀₂₈, IRC₀₃₂, IRC₀₃₃, IRC₀₃₅, IRC₀₃₆ and IRC₀₃₉ tend to express SWP superiority. The JINKS & PONNI (1976) method is shown to be efficient in a study carried out by MEZZOMO et al. (2021), in the wheat crop, which identified promising populations. Thus, it can be inferred that these populations have potential for selection and prominence in the context of genetic improvement programs, since they have a high probability of surpassing the average of the best control cultivar by 20%.

The lines (Figure 3), which showed positive in relation to selection gains will be selected, on the other hand, those that showed gains below zero should be discarded. From the population IRC₀₀₁, derived from the cross between BMX MAGNA RR x FUNDACEP 66 RR, a higher SWP potential was observed in the strain 15F_{3-IRC001}.

Through this, you can obtain a selection gain of 8.9% in relation to the seed weight per plant, which may result from the recombination of the different characteristics of the genitors (Figure 3). Such as morphological genetic markers, flower color and hilum color (Table 1), the paternal parent being disease tolerant: frog-eye spot (*Cercospora sojina*) and bacterial growth (*Pseudomonas savastanoi* pv. *Glycinea*.), while the maternal parent is susceptible, these gains are explained by genetic recombination that resulted in transgressive progenies to these traits (RESENDE & ALVES, 2021).

The lineage 22F_{3-IRC002} has the possibility of exhibiting superiority of 8.3% in relation to the population IRC₀₀₂ which comes from the cross between BMX APOLO RR x FUNDACEP 66 RR, the lineage 9F_{3-IRC003} of the population IRC₀₀₃ (BMX MAGNA RR x NK 7059 RR) expressed the highest genetic gain among all with 17,4%. The population IRC₀₀₅ from the intersection (ROOS CAMINO RR x FPS PARANAPANEMA RR)



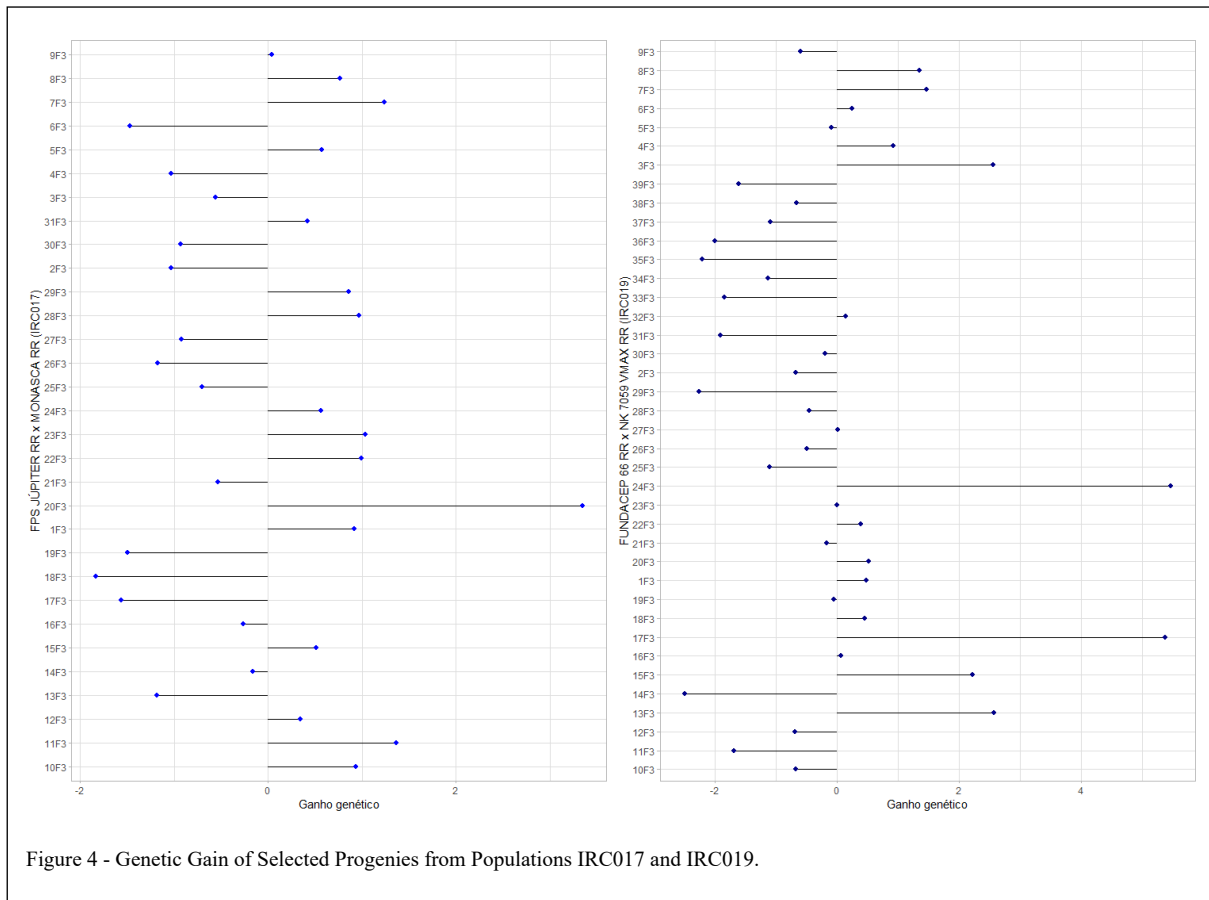
generated the progeny $17F_{3-IRC005}$ which reveals increases of 18.8%. This was obtained by the allelic complementarity related to the contrasting growth habit between the parents.

The populations IRC_{006} and IRC_{007} considered full sisters and derived from the cross between BMX APOLO RR x MAR.M4 C B, expressed high gains through lineage $12F_{3-IRC006}$ (12,5%) and $17F_{3-IRC007}$ (12%), as well as IRC_{008} (BMX APOLO RR x FPS URANO RR) who revealed the lineage $4F_{3-IRC008}$ with gains of 17.9%, with this additive genetic increment resulting from the contrast of the parents regarding the maturation group 5.5 and 6.2. The population IRC_{012} was obtained by recombination FPS NETUNO RR x BMX APOLO RR who highlighted the progeny $36F_{3-IRC012}$ (11.9%). in the population IRC_{013} (BMX MAGNA RR x BMX APOLO RR), shows possible additive genetic gains through the $12F_3$ with 9.2%. The population IRC_{016} (ROOS CAMINO RR x FPS URANO RR) highlights the lineage $23F_{3-IRC016}$ with

gains of 10.2% this being promising to potentiate grain weight per plant with less resources from the production environment.

The progeny $20F_{3-IRC017}$ was superior in the internal selection to the population IRC_{017} (FPS JÚPITER RR x NK 7059 RR) expressing 11% of additive effects, for IRC_{019} (FUNDACEP 66 RR x NK 7059 RR) highlights the lineage $24F_{3-IRC019}$, with 8.6% gain when selected (Figure 4). According to Ramalho et al. (2012), in the initial generations of the breeding program, a large proportion of non-additive genes are present, these can compromise the selection gain, in this way the breeder's skill, method, direction and selection pressure must be assertive to maximize genetic advances in an improvement program.

The population IRC_{027} (MASSAL) highlights the lineage $12F_{3-IRC027}$ with gain of 12.4%, for IRC_{028} (MASSAL) expresses superiority to $22F_{3-IRC028}$ with 17.6% (Figure 5). In the population IRC_{029} (MASSAL), the selection gain



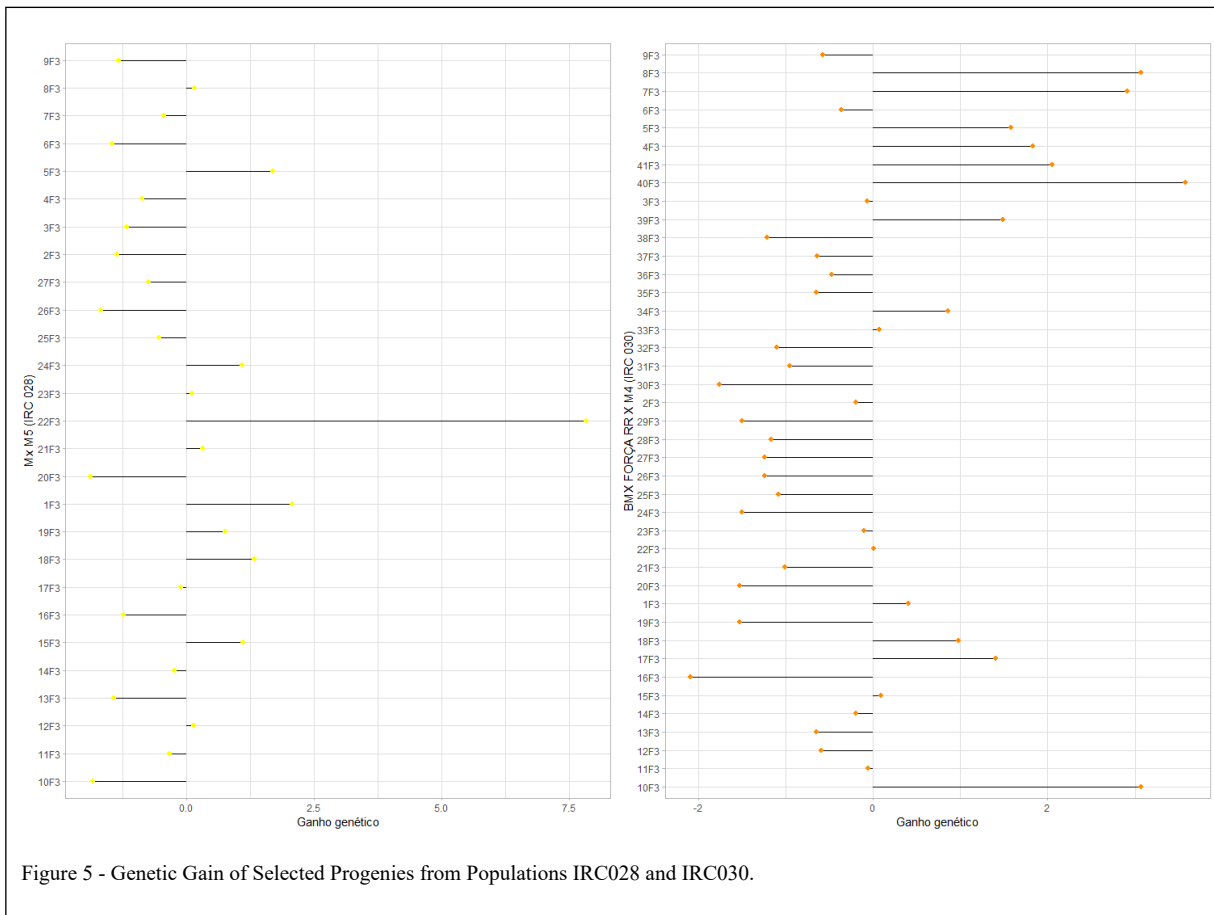


Figure 5 - Genetic Gain of Selected Progenies from Populations IRC028 and IRC030.

could be 14.1% in the lineage selection $2F_{3-IRC029}$, in contrast, smaller selection gains are obtained by the population IRC_{030} (BMX FORÇA RR x MAR. M₄ C B) through lineage $40F_{3-IRC030}$.

When analyzing the population IRC_{031} (5958 RSF IPRO x MAR.M2 C), it can be inferred that in the progeny $12F_{3-IRC031}$ there will be 11.5% of genetic gains, for IRC_{032} (BMX MAGNA RR x NA 5909 RG) only 7.3% of genetic gain can be obtained when selecting the lineage $18F_{3-IRC032}$ (Figure 6). The population IRC_{033} (MAR.M4 C B x NA 5909 RG) expresses gains through progeny $14F_{3-IRC033}$ with 15.2%, IRC_{034} (5958 RSF IPRO x 6700 RR) reveals 15.5% gains when selecting lineage $16F_{3-IRC034}$ as well as the lineage $32F_{3-IRC035}$ obtain 10.5% genetic gains for being from the population IRC_{035} (BMX FORÇA RR x MAR.M4 C B).

The population IRC_{036} (BMX APOLO RR x TMG 7161 RR) will have satisfactory gains when selecting the lineage $1F_{3-IRC036}$ with 7.7% (Figure 7). For IRC_{039} (TMG 7161 RR x NA 5909 RG)

the progeny $11F_{3-IRC039}$ expressed 11.4% of genetic gains, however, among all populations IRC_{040} (BMX TURBO RR x TMG 7161 RR) showed that the possible lineage with the highest genetic gain resulting from selection was $22F_{3-IRC040}$ with 19.1% increment (Figure 8). All segregating populations obtained lines with genetic potential to generate lineages with high productivity, in addition to the additive genetic gain, knowledge of the genealogy involved in building the lineage becomes crucial for the success of the selections and the breeding program (PINHEIRO et al., 2013).

CONCLUSION

The best control and promising cultivars to compose the parent bank are BMX FORÇA RR, FUNDACEP 66 RR and TMG 7062 IPRO.

Jinks and Pooni's methodology identified populations IRC_{001} , IRC_{002} , IRC_{017} , IRC_{019} , IRC_{028} , IRC_{030} , IRC_{032} , IRC_{033} , IRC_{035} , IRC_{036} , IRC_{039} and

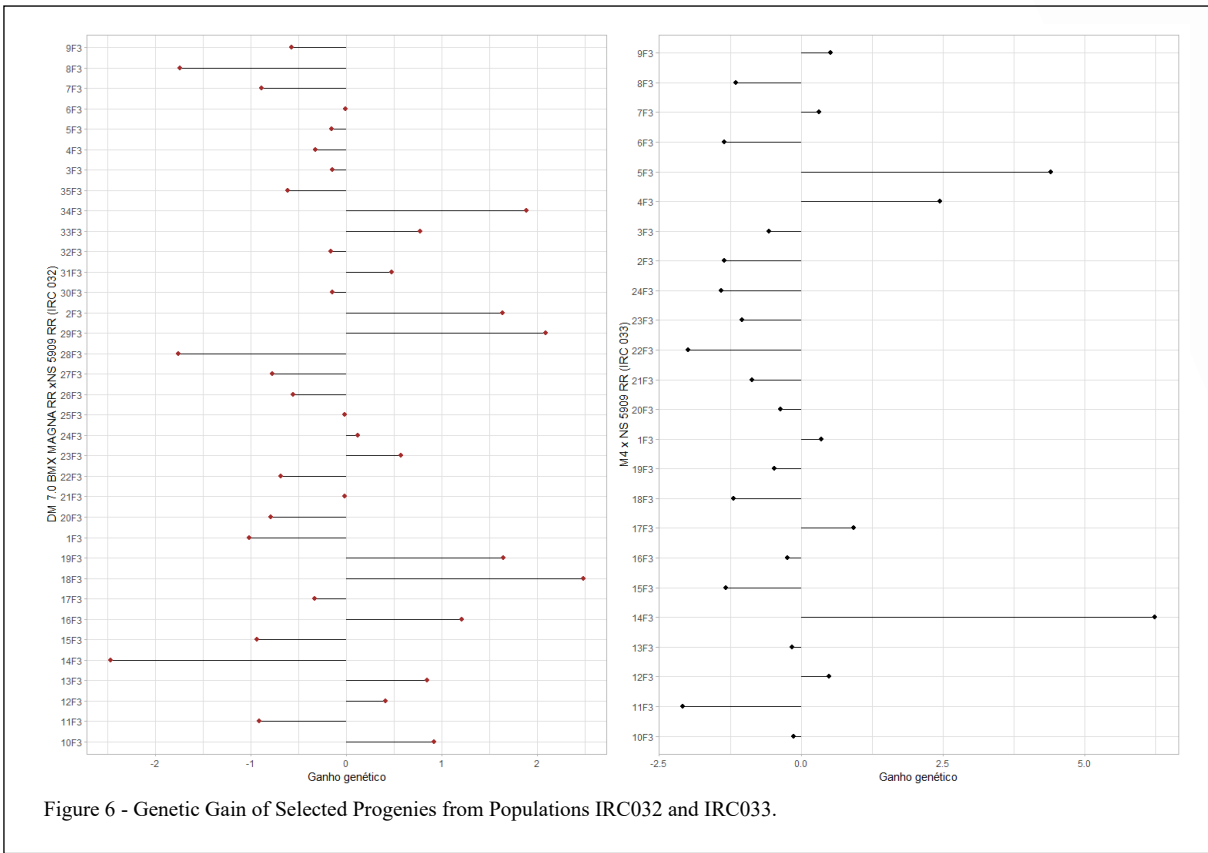


Figure 6 - Genetic Gain of Selected Progenies from Populations IRC032 and IRC033.

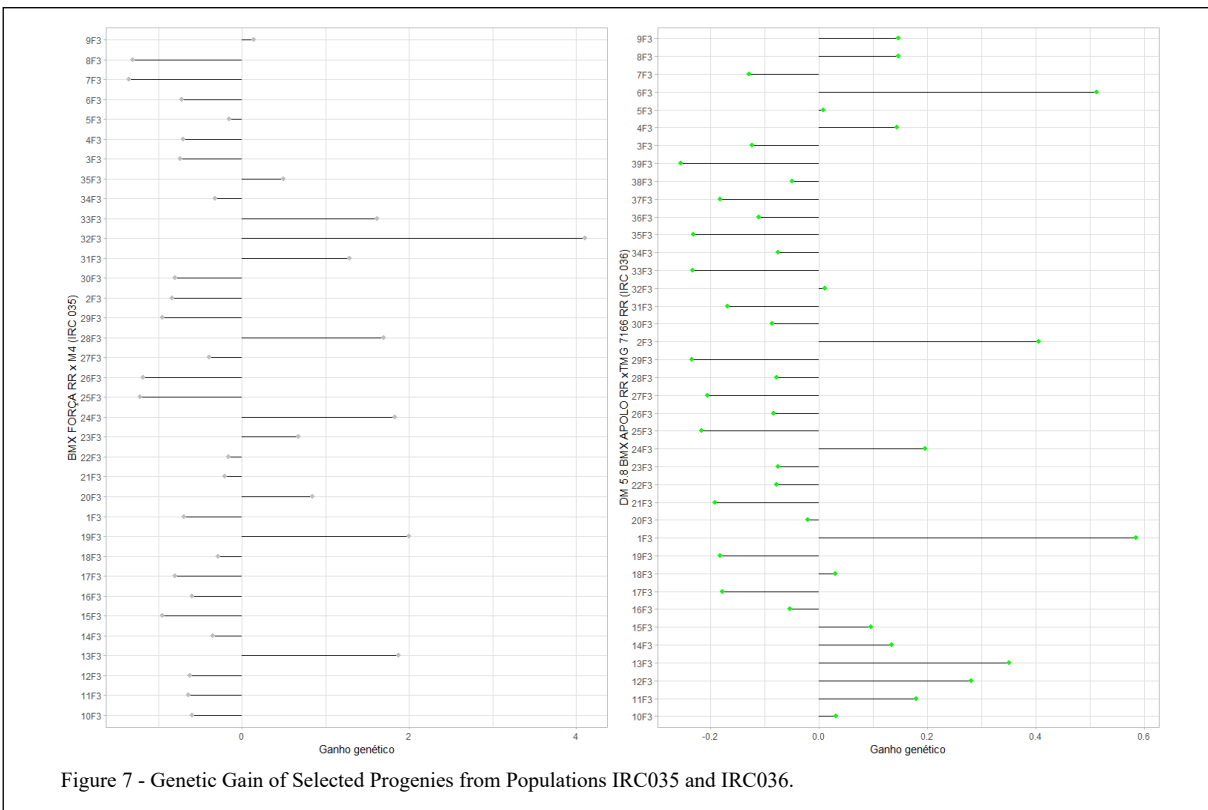


Figure 7 - Genetic Gain of Selected Progenies from Populations IRC035 and IRC036.

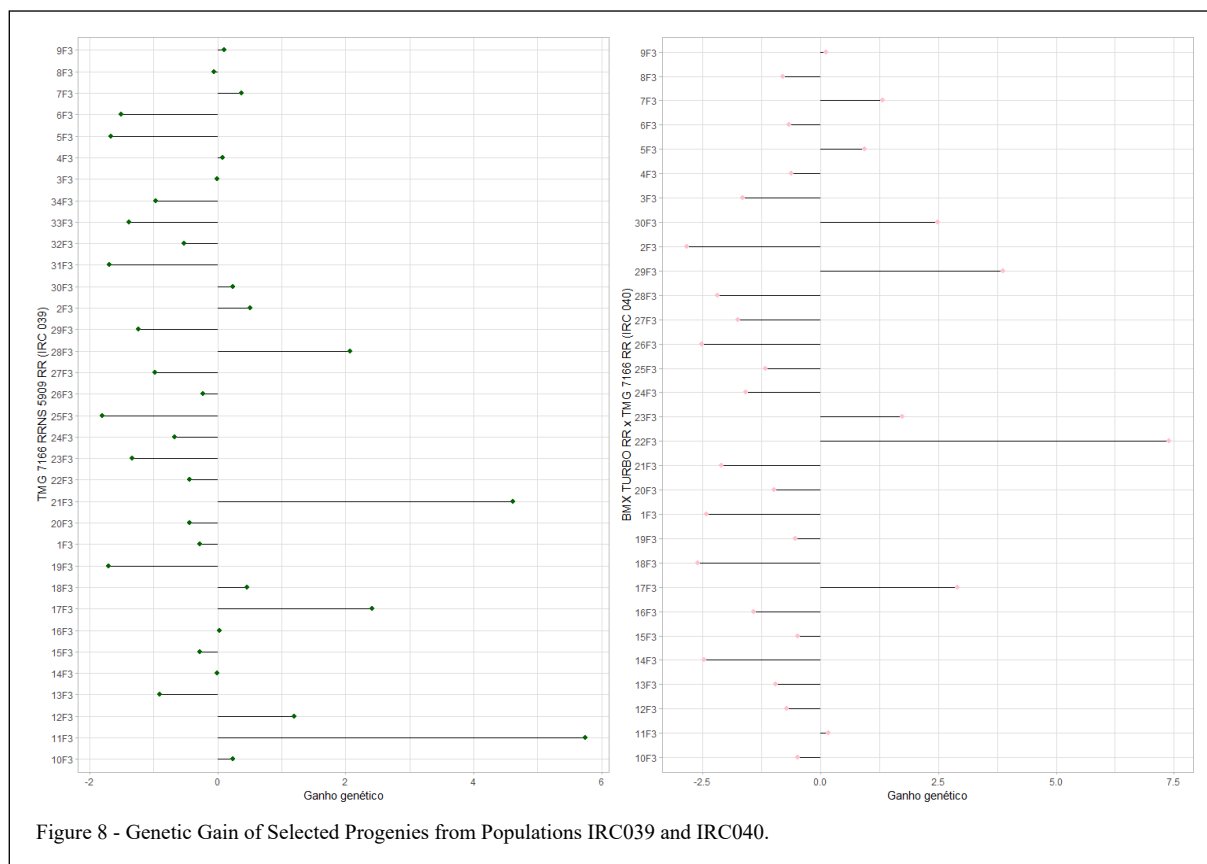


Figure 8 - Genetic Gain of Selected Progenies from Populations IRC039 and IRC040.

IRC₀₄₀ as having high potential for extraction of superior lineages.

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DECLARATION OF CONFLICT OF INTEREST

The authors declare no conflict of interest.

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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