Australian Journal of
Crop Science
AJCS

Aust J Crop Sci. 19(07):800-808 (2025) |
https://doi.org/10.21475/ajcs.25.19.07.p335
ISSN:1835-2707

Genetic parameters and selection of genotypes in rapeseed (*Brassica napus*) populations segregants by REML/BLUP in the Brazilian Cerrado

Willame dos Santos Candido[1,*], Bruno Galvêas Laviola[2], Cíntia Gonçalves Guimarães[2], Erina Vitório Rodrigues[3]; Vitor Rodrigues Nunes[2]; João Pedro de Paula Aires Camargo[2]

[1]Universidade Federal de Santa Catarina – UFSC, Departamento de Fitotecnia, Florianópolis – SC, Brazil
[2]Empresa Brasileira de Pesquisa Agropecuária – Embrapa Agroenergia, Brasília – DF, Brazil
[3]Universidade de Brasília - UnB, Faculdade UnB Planaltina, Planaltina - DF, Brazil

***Corresponding author: Willame dos Santos Candido candidows.will@gmail.com**
ORCID ID: https://orcid.org/0000-0002-3235-0043

Submitted:
10/02/2025

Revised:
22/03/2025

Accepted:
30/04/2025

Abstract: The objective of this study was to estimate genetic parameters in rapeseed populations, as well as to select individuals and families in populations with the potential for developing lines. Four experiments were conducted in the experimental field of Embrapa in 2022, evaluating populations of F_2 progenies. We used a randomized block design for the experiments. Evaluations were carried out 110-120 days after planting. The traits were assessed: silique length (SL), number of siliques per plant (NSP), 1000-seed weight (W1000S), and yield (SY). Estimations of genetic parameters and the selection of individuals were carried out using the REML/BLUP method. The genetic gain through selection was estimated using the Mulamba and Mock index. Significant differences were observed among genotypes across all populations only for the NSP trait. For the W1000S and SY traits, significant differences were also found in the evaluated populations, except in the NACE-D and NACE-50 populations, respectively. However, for SL, no significant differences among genotypes were observed in the evaluated populations. The heritability ranged from 21.99% for the W1000S trait to 78.29% for NSP, in the NACE-D and NACE-61 populations, respectively. Genetic gains were high for SY and NSP in all populations, indicating that these genotypes exhibited high means for the traits. Most superior genotypes originated from the NACE-D (24.15%) and NACE-61 (22%) populations. This suggests that selection within these populations contributes to developing promising lines. The information from this study contributes to the efficiency of breeding programs conducted under tropical conditions.

Keywords: *Brassica napus* L.; Genetic selection; Heritability; Mixed models; Plant breeding.
Abbreviation: silique length (SL), number of siliques per plant (NSP), 1000-seed weight (W1000S), and yield (SY).

Introduction

Rapeseed (*Brassica napus* L. var. oleifera) is the third most widely used oilseed globally as a raw material for oil production, accounting for 14.96% of the total supply, surpassed only by palm oil (*Elaeis guineensis*) (35.84%) and soybean (*Glycine max*) (27.25%) (USDA, 2023). Its production is primarily aimed at edible oils due to the high oil content in the seeds (40-50%) and its favorable composition of fatty acids, making it suitable for human consumption, animal feed, and biofuels. Furthermore, it has potential applications in lubricating oils, polyamide fibers, resins, detergents, emulsifying agents, and as a substitute for vegetable wax (Channaoui et al., 2022; Ghafoor et al., 2023). Given the significance of rapeseed in the biofuel market, it is essential to implement breeding programs to develop new cultivars adapted to different climatic conditions.

A plant breeding program can be divided into three main stages: i) the development of germplasm containing various sources of genetic resources; ii) the selection of superior individuals; and iii) the utilization of the selected individuals to develop an appropriate and superior variety (Nur-E-Nabi et al., 2019). The development of rapeseed lines with higher seed yield requires the establishment of a robust breeding program, initially focused on the formation of a base population with broad genetic diversity for morphological, agronomic, and yield traits.

Moreover, it is important to estimate genetic parameters to understand the genetic basis of the main traits of interest, guiding selection strategies (Hallauer et al., 2010; Borém et al., 2017). Knowledge of genetic variability (Rahman et al., 2011), heritability, and genetic gain through selection (Sarwar et al., 2015) are essential steps for defining more efficient breeding strategies, serving as prerequisites for initiating a breeding program with concrete potential to develop highly productive cultivars (Parveen et al., 2013; Resende, 2015).

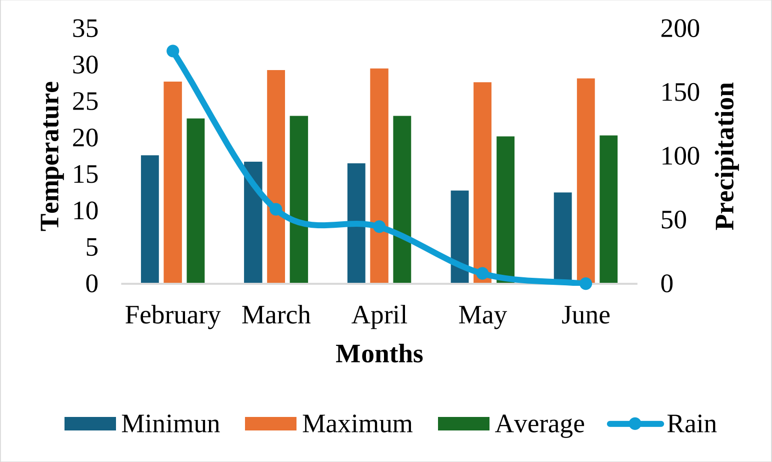

Fig 1. Precipitation and maximum, average, and minimum temperatures recorded during the conduction of the rapeseed experiment. Embrapa Cerrados, Planaltina-DF, 2022. Source: http://clima.cpac.embrapa.br/clima/dados-climaticos/#

The use of mixed linear models in plant genetic improvement to estimate parameters and predict genetic values, particularly with the REML/BLUP methodology, has become routine. This approach allows for accurate and unbiased prediction of genetic values, even under imbalance (Resende, 2016). It also facilitates the simultaneous use of information from both the individual and the family, providing more precise estimates of genetic variance components and individual genetic values (Resende, 2002, 2007; Bergo et al., 2019; Carvalho et al., 2020; Lustri et al., 2021). It is noteworthy that, to date, the literature reports only one study utilizing this method in rapeseed (Bocianowski and Liersch, 2021); thus, it is essential to explore robust statistical methods aimed at enhancing selection efficacy.

The simultaneous selection of multiple traits offers a greater chance of success in selecting promising genotypes for the market (Rodrigues et al., 2011) and can be carried out using various methodologies, notably the rank sum index developed by Mulamba and Mock (1978). In addition to the use of selection indices, a widely adopted and highly accurate alternative in the selection process is the REML/BLUP procedure (Resende, 2007), as it provides additional relevant parameters for the identification of superior genotypes (Gomes et al., 2018; Candido et al., 2020).

The objective of this study was to estimate genetic parameters for the production components in rapeseed populations by selecting individuals and families within populations with the potential for the development of lines adapted to the edaphoclimatic conditions of tropical regions.

Results

Genetic parameters

Statistically significant differences were observed among the genotypes in all populations only for the trait number of siliques per plant (NSP) (Table 1). This indicates a predominance of genetic variability, facilitating the successful selection of promising genotypes with genetic gain potential. For the traits weight of 1000 seeds (W1000S) and yield (SY), significant differences were found in the evaluated populations, except for the NACE-D and NACE-50 populations, respectively. However, for silique length (SL), no significant differences were noted among the genotypes in the evaluated populations, indicating similar performance among the aforementioned traits, and selection can be conducted in any of the populations.

Estimates of genotypic variance and heritability are important for quantifying the improvement potential of the population. The average heritability ranged from 21.99% for the trait weight of 1000 seeds (W1000S) to 78.29% for the number of siliques per plant in the NACE-D and NACE-61 populations, respectively (Table 2). The magnitude of heritability was considered to range from low to high, with high values above 70% indicating that the traits were minimally influenced by environmental factors. Regarding selective accuracy, we observed values of moderate to high magnitude. This parameter indicates the precision of selection and corresponds to the correlation between the predicted genetic values and the true genetic values of the individuals (Resende, 2007).

Genetic gains and family selection

The predicted percentage genetic gains for the Mulamba and Mock selection index yielded positive values for most traits, except for the weight of 1000 seeds in the NACE-61 population. We observed high gains for yield and the number of siliques per plant across all populations, indicating that these genotypes exhibited elevated means for the reported traits (Table 2).

We ranked the individuals based on the predicted additive genetic value (μ + a) for seed yield. It was observed that the majority of superior genotypes originated from the NACE-D population (24.15%) and the NACE-61 population (22%) (Table 3). This suggests that selection within these populations contributes to the development of promising lines. However, although in smaller quantities, individuals from the other populations also displayed high genetic values, making it important to select them to maintain the high variability of the population.

Table 1. Deviance Analysis in populations of rapeseed for the traits silique length (SL), number of siliques per plant (NSP), 1000 seed weight (W1000S), and seed yield (SY, g/plant). Embrapa Cerrados, Planaltina-DF, 2022.

Traits		Effects							
		NACE-D		NACE-50		NACE-61		NACE-76	
		Genotypes	Population	Genotypes	Population	Genotypes	Population	Genotypes	Population
SL	Deviance	53.83	51.65	35.25	35.07	7.76	5.59	29.25	25.89
	LRT	2.18^{ns}		0.18^{ns}		2.17^{ns}		3.36^{ns}	
W1000S	Deviance	41.89	41.25	584.98	47.25	54.87	48.16	556.6	30.05
	LRT	0.64^{ns}		537.73**		6.17**		526.55**	
NSP	Deviance	1341.98	1328.83	633.23	623.84	897.72	882.24	604.23	599.24
	LRT	13.15**		9.39**		15.48**		4.99*	
SY	Deviance	768.89	762.34	337.42	335.98	540.56	535.6	331.93	325.72
	LRT	6.55*		1.44^{ns}		4.96*		6.21*	

* , ** significant at 5% and 1%, respectively.

Table 2. Estimates of genetic parameters for silique length (SL), number of siliques per plant (NSP), 1000 seed weight (W1000S), and seed yield (SY, g/plant). Embrapa Cerrados, Planaltina-DF, 2022.

Genetic Parameters	**NACE-D**				**NACE-50**			
	SL	W1000S	SY	NSP	SL	W1000S	SY	NSP
V_g	0.14	0.07	1207.55	1513218.73	0.10	0.38	387.33	1481762.03
V_e	0.49	0.49	1970.12	1404878.24	0.67	0.71	1062.06	852475.81
V_f	0.64	0.55	3177.67	2918096.97	0.76	1.09	1449.39	2334237.84
h^2_{mp} (%)	36.72	21.99	55.07	68.30	22.21	51.57	42.18	77.66
Acprog (%)	60.60	46.90	74.21	82.64	47.12	71.82	64.94	88.13
Overall mean	4.45	4.45	65.33	2199.07	4.82	3.90	46.66	1519.74
Genetic gain (M&M)	4.73	2.08	49.23	41.10	0.00	5.37	26.03	52.46

Genetic Parameters	**NACE-61**				**NACE-76**			
	SL	W1000S	SY	NSP	SL	W1000S	SY	NSP
V_g	0.10	0.38	1448.38	1109494.83	0.30	0.114674	990.08	1313466.16
V_e	0.27	0.46	2202.57	615471.64	0.38	0.585779	894.89	1201797.87
V_f	0.37	0.84	3650.96	1724966.47	0.68	0.700453	1884.97	2515264.03
h^2_{mp} (%)	42.31	62.48	56.81	78.29	60.82	28.14	68.87	68.61
Acprog (%)	65.05	79.04	75.37	88.48	77.99	53.04	82.99	82.83
Overall mean	4.68	4.05	59.92	1511.15	4.50	4.322627	44.63	1642.14
Genetic gain (M&M)	4.70	-3.71	58.20	77.02	7.35	1.83	46.30	29.32

V_g = genotypic variance; V_e = environmental variance; V_f = phenotypic variance; h^2_{mp} = heritability; Acprog = selection accuracy

Discussion

Research conducted by Shafey et al. (2023), evaluating yield traits and genetic diversity in *Brassica napus* genotypes, reported statistical significance for all assessed yield component traits, such as seed weight (g/plant) and number of siliques per plant. However, no significant differences were found for the trait weight of 1000 seeds. Similarly, Muhammad et al. (2014) and Rameeh (2015) also found significant differences in yield traits, including the number of siliques per plant, weight of 1000 seeds, and seed production in *Brassica napus*. The results presented by these authors support those found in the current study, indicating the potential to select genotypes with superior performance for the aforementioned traits.

Estimates of heritability and genetic variance are crucial in plant breeding, including rapeseed, as they provide insights into the efficiency of genetic improvement. Heritability, which measures the proportion of phenotypic variation attributable to genetic variation, is essential for understanding how traits will behave in future selections.

The heritability values for silique length ranged from 22.21% to 60.82%. The NACE-76 population exhibited the highest heritability (60.82%), suggesting a greater proportion of phenotypic variation attributable to genetic variation. In contrast, the NACE-50 population, with a heritability of 22.21%, indicates that selection for this trait may be more challenging due to a higher influence of environmental factors.

Table 3. Selection of superior individuals in rapeseed populations for the characters silique length (SL), number of siliques per plant (NSP), weight of 1000 seeds (W1000S), and seed Productivity (SY, g/plant). Embrapa Cerrados, Planaltina-DF, 2022.

Population	Family	Indiv	f	u+a	Population	Family	Indiv	f	u+a
NACE-61	6	116	275.80	179.40	NACE-D	3	53	132.10	92.13
NACE-D	6	116	275.80	176.34	NACE-D	25	4925	94.00	92.13
NACE-D	6	126	142.60	143.22	NACE-D	23	4523	90.49	91.09
NACE-61	6	126	142.60	142.61	NACE-D	7	137	46.90	88.34
NACE-D	27	5327	188.90	137.08	NACE 50	6	126	168.00	87.25
NACE-76	19	3819	164.00	131.85	NACE-61	7	137	46.90	87.20
NACE-61	5	105	192.40	127.59	NACE-76	5	95	104.00	87.12
NACE-D	5	105	192.40	127.58	NACE 50	3	63	152.00	86.46
NACE-61	7	147	209.50	125.11	NACE-76	6	116	64.00	84.38
NACE-D	7	147	209.50	124.87	NACE-D	29	5829	102.70	83.60
NACE-D	27	5427	140.20	123.86	NACE-D	24	4724	96.50	83.18
NACE-76	19	3719	126.00	122.22	NACE 50	3	53	88.00	80.61
NACE-76	6	126	168.00	122.06	NACE-D	4	74	123.90	80.15
NACE-76	3	63	152.00	116.85	NACE-61	4	74	123.90	80.11
NACE-D	9	189	190.90	111.75	NACE-D	29	5729	77.10	79.33
NACE-61	9	189	190.90	111.61	NACE-D	31	6131	106.55	78.50
NACE-61	1	11	143.80	109.61	NACE-61	16	3216	126.40	78.08
NACE-D	1	11	143.80	109.11	NACE-D	24	4824	79.90	77.51
NACE-D	5	95	96.00	106.64	NACE-D	10	2010	86.80	76.34
NACE-61	5	95	96.00	106.39	NACE 50	6	116	64.00	75.80
NACE-61	15	2915	132.20	105.05	NACE-D	10	1910	76.30	75.62
NACE-D	15	2915	132.20	104.76	NACE-61	10	1910	76.30	74.82
NACE-D	13	2613	136.70	101.96	NACE-61	10	2010	86.80	74.32
NACE-61	13	2613	136.70	100.91	NACE-D	9	179	24.00	74.21
NACE-D	23	4623	130.20	98.68	NACE-D	42	8342	39.16	73.17
NACE-D	42	8442	153.82	98.41	NACE-61	9	179	24.00	72.61
NACE-D	25	5025	127.70	98.30	NACE-D	39	7839	98.19	72.15
NACE-D	1	21	102.90	97.73	NACE-D	34	6734	79.31	72.05
NACE-D	15	3015	106.80	97.02	NACE-61	19	3819	88.90	71.94
NACE-76	3	53	88.00	96.17	NACE-D	3	63	47.00	70.34
NACE-61	1	21	102.90	96.13	NACE-D	20	4020	102.00	69.97
NACE-61	15	3015	106.80	95.48	NACE 50	5	95	104.00	68.34
NACE-D	13	2513	92.30	93.26	NACE-61	19	3719	60.50	67.92
NACE-61	13	2513	92.30	92.85	NACE-61	3	63	47.00	67.66
NACE-61	3	53	132.10	92.31					

The results for the weight of 1000 seeds showed variation from 21.99% to 62.48%, while for the trait number of siliques per plant, heritability values ranged from 68.30% to 78.29%. For both traits, the NACE-61 population exhibited the highest heritability, suggesting that selection for these traits may be efficient, as the variation is largely of genetic origin. Seed weight is an important trait related to the productivity and quality of rapeseed (Harker et al., 2015; Sabbahi et al., 2023), highlighting the importance of understanding the heritability parameter for this trait.

The high heritability observed in the NACE-61 population (78.29%) for the trait number of siliques per plant may indicate that this population possesses a more diverse or better-adapted genetic base for the expression of this trait, allowing for a faster and more efficient response to selection. Results similar to those obtained in the present study for the trait number of siliques per plant were reported by Krüger et al. (2011) and Nur-E-Nabi et al. (2019).

For yield, heritability values ranged from 42.18% to 68.87%, with the NACE-76 population showing the highest value. These results indicate that yield is a trait that can be improved through selection, especially in populations with higher heritability. Similar results were obtained in studies by Krüger et al. (2011) and Bocianowski and Liersch (2021), corroborating the findings of this work.

Selection accuracy in genetic improvement programs is a crucial factor that influences the success of selecting desirable traits in crops such as rapeseed. According to research conducted by Resende and Alves (2022), selection accuracy is often influenced by genetic inheritance represented by the heritability of the trait, the total number of replications for each genotype and environment (total sample size), and the genotypic correlation between environments.

In the present study, we observed variation in accuracy for the trait siliques length, with values ranging from 47.12% to 77.99% for the NACE-50 and NACE-76 populations, respectively. For the trait yield, accuracies ranged from 64.94% to 82.99% for the NACE-50 and NACE-76 populations, suggesting that the NACE-76 population exhibits superior estimates for genetic gains, facilitating the selection of superior individuals. According to Resende and Duarte (2007), to achieve genetic progress through selection in breeding programs, the accuracy for traits should exceed 70%. Research such as that by Pimentel et al. (2014) emphasizes the importance of robust statistical models that can improve the precision of genetic parameter estimates and, consequently, selection accuracy.

For the traits weight of 1000 seeds and number of siliques, we observed accuracy variations of 46.9% to 79.04% and 82.64% to 88.48%, respectively, between the NACE-D and NACE-61 populations. The high accuracy observed in the NACE-61 population suggests that this population possesses considerable genetic variability for the traits under study. Genetic variability provides a gene pool that can be exploited for the development of more efficient, productive, and stress-resistant cultivars, which are essential in the context of climate change and increasing food demand (Govindaraj et al., 2015; Salgotra and Chauhan 2023).

The genetic gains obtained through the selection index for the trait silique length indicate significant variability among the studied populations. The variation from 0.0% to 7.35% in gains suggests that the NACE-76 population has superior genetic potential for this trait compared to the NACE-50 population. This difference may be related to gene inheritance, the genetic variability available within the populations, and the efficiency of the selection index used.

For the trait weight of 1000 seeds, genetic gains ranged from -3.71% to 5.37% in the NACE-61 and NACE-50 populations, respectively, providing an interesting perspective on the efficiency of the Mulamba and Mock (1978) selection index in the genetic improvement of rapeseed. The variation in gains may be related to several factors, such as the genetic basis of the populations, genotype-environment interaction, and the effectiveness of the selection method employed. In the case of the NACE-61 and NACE-50 populations, the difference in genetic gains can be attributed to the existing genetic variability and the population's response to the applied selection method. According to the literature, selection indices like that of Mulamba and Mock are widely used to maximize genetic progress for various yield traits across multiple crops (Leite et al., 2018; Candido et al., 2020; Casagrande et al., 2022).

The genetic gains obtained through the Mulamba and Mock (1978) selection index indicate significant potential for improving productivity in rapeseed populations, with variations reflecting genetic heterogeneity and environmental response. We observed gains ranging from 26.03% to 58.20% for the NACE-50 and NACE-61 populations, respectively, demonstrating that selection can be highly effective, particularly for the NACE-61 population, which shows superior gain. According to Bernardo (2020) and Batista et al. (2021), the use of selection indices is an effective tool for maximizing selection efficiency, allowing breeders to consider multiple traits simultaneously, such as yield and agronomic characteristics. This approach can lead to significant productivity gains, as evidenced by the results obtained in this experiment.

For the trait number of siliques per plant, genetic gains obtained using the selection index ranged from 29.32% to 77.02% in the NACE-76 and NACE-61 populations, respectively, indicating significant potential for genetic improvement for this characteristic. The number of siliques per plant directly impacts rapeseed productivity, as it is related to grain formation and, consequently, oil production. Previous studies support the importance of the number of siliques as a high-value trait in the selection of rapeseed cultivars with high productivity (Li et al., 2020).

In a genetic improvement program, selection is typically conducted among many genotypes, estimating genetic values essential for this practice (Piepho et al., 2008). As the BLUP estimates indicate, it maximizes the correlation between true genotypic values and predicted genotypic values (Searle et al., 1992; Resende, 2002). Therefore, we selected superior individuals for productivity based on the predicted genetic value in four populations of *Brassica napus* L. We focused on selecting individuals within the superior families, as the literature suggests that this increases the likelihood of identifying families with high genotypic values.

We observed that the individuals occupying the top positions belonged to family 6 of the NACE-61 and NACE-D populations (Table 3). It is noteworthy that families 6, 27, 5, 7, 9, and 15 occupied the top ten positions (data not shown). This supports the previous assertion regarding the effectiveness of selection based on families, as the environmental effects on individual deviations tend to cancel each other out. Consequently, the average phenotypic value of the family approaches the average genotypic value, and the advantages gained will be greater when environmental deviations constitute a significant portion of the phenotypic variance. This is particularly true for quantitative traits, such as productivity, which generally exhibit low heritability (Falconer and Mackay, 1996).

Individuals 116 from family 6 of the NACE-61 and NACE-D populations exhibited the highest predicted genetic value (Table 3). Although the NACE-61 and NACE-D populations contain the greatest number of superior individuals, it is essential to select individuals from the other populations to maintain genetic variability in the subsequent phases of the breeding program. From the 69 selected individuals, we believe that they will constitute populations with high variability and significant potential for developing superior genotypes for productivity.

The procedure for estimating genetic values via BLUP has been employed in various annual crops, such as maize (Almeida et al., 2024; Ferreira et al., 2020; Pedro et al., 2023), soybean (Bezerra et al., 2023), and beans (Akinyosoye et al., 2021), yielding superior gains. However, it is still rarely used in the selection of individuals from the species *Brassica napus* L. Bocianowski and Liersch (2021) assessed the genotypic performance of 25 winter *Brassica napus* L. genotypes using mixed models. According to the authors, mixed models can be recommended as a potential selection method for the development of genotypes in different rapeseed breeding programs aimed at creating new winter rapeseed cultivars.

In the literature, it is common to combine different selection methods to achieve genetic gains in future generations. Bezerra et al. (2023) applied selection indices in segregating (F_2) soybean populations to predict genotypic values and select the superior populations. In our study, we observed that the use of selection indices and estimates of genetic values via BLUP enabled the selection of individuals that will compose the next generations of improvement. The selected progenies will

Table 4. Genetic origin of canola progenies (*Brassica napus* var. oleifera) from four breeding populations and the number of progenies evaluated in the experiments. Embrapa Cerrados, Planaltina-DF, 2022.

Experiments	Breeding populations	Genetic origin (Hybrids)	Number of progenies F_2
1	NACE-D	'DIAMOND'	43
2	NACE-50	'HYOLA 50'	21
3	NACE-61	'HYOLA 61'	30
4	NACE-76	'HYOLA 76'	20

HYBRID: 'DIAMOND'(NUSEED); 'HYOLA 50', 'HYOLA 61', 'HYOLA 76' (ADVANTA).

proceed to the next stages, and when they reach the desired degree of homozygosity, we will select the lines that will form the crossing blocks of the rapeseed breeding program.

Materials and methods

Description of the experimental site

Four experiments were conducted in experimental areas of Embrapa Cerrados, located in Planaltina, DF, at coordinates 15°36'16" S and 47°43'16" W, and at an altitude of 1,034 meters, in February 2022. The genotypes were evaluated under a rainfed cultivation system during the off-season, with a total accumulated rainfall of 293.1 mm. Air temperature and rainfall data for the evaluation months are presented in Figure 1.

The soil in the experimental area exhibited the following chemical characteristics: pH in H_2O - 6.2; organic matter - 29.2 g kg^{-1}; P - 3.3 mg dm^{-3}; K - 0.40 cmolc dm^{-3}; Ca - 4.4 cmolc dm^{-3}; Mg - 1.4 cmolc dm^{-3}; H + Al - 3.0 cmolc dm^{-3}; SB - 6.3 cmolc dm^{-3}; CTC - 9.3 cmolc dm^{-3}; and V% - 67%. Soil preparation involved the use of a primary tillage implement, followed by a medium harrow for soil loosening, and then a leveling harrow to ensure uniformity across the experimental area. The planting and top-dressing fertilizations were carried out according to soil analysis and fertilization recommendations for rapeseed cultivation (SBCS, 2016).

Pest insect control was conducted following conventional recommendations, with insecticides applied as needed for the crop. Weed control was carried out manually using hoes.

Plant materials and experimental design

Four experiments were established, each consisting of F_2 progenies that formed the populations: NACE-D, NACE-50, NACE-61, and NACE-76, derived from 'DIAMOND', 'HYOLA 50', 'HYOLA 61', and 'HYOLA 76', respectively (Table 4). The experimental design employed was a randomized complete block design with two replications, with the treatments consisting of the F_2 progenies. Each experimental plot consisted of a single plant, spaced 1.0 meters apart, which was used for evaluation.

Traits measured

Evaluations were conducted approximately 110-120 days after planting. The following traits were assessed: siliques length (SL, cm), measured using a graduated ruler; the number of siliques per plant (NSP), determined by counting the individual siliques on the plant; the weight of 1000 seeds (P1000S, g), obtained by counting 1000 seeds and weighing them on a balance; and seed yield (SY, g/plant), determined by weighing the total seeds from the plant.

Statistical analysis

The analysis of the data obtained for each trait was conducted using the SELEGEN software (Resende 2016), employing the REML/BLUP methodology. The following statistical model was used: $y = Xr + Za + e$ (Resende, 2007), where y is the data vector, r is the vector of replication effects (assumed to be fixed) added to the overall mean, a is the vector of individual additive genetic effects (assumed to be random), and e is the vector of errors or residuals (random). The uppercase letters represent the incidence matrices for the respective effects.

The significance of the model effects was estimated using Deviance Analysis (ANADEV) of model 111, as outlined by Resende (2007). Subsequently, the likelihood ratio test (LRT) was applied by fitting both the full and reduced models. In the latter, the effect to be tested is omitted, and the results are then compared against the chi-square value with one degree of freedom at the 1% and 5% probability levels.

Using REML, the following genetic parameters were obtained: Vg: genetic variance among families; Ve: residual variance; Vf: individual phenotypic variance; h^2mp: heritability of the progeny mean, assuming complete survival; and Acprog: progeny selection accuracy, assuming complete survival.

The genetic gain from selection was estimated using the selection index developed by Mulamba and Mock (1978), and the selection of individuals and families was based on the ranking obtained from the REML/BLUP analyses (Resende, 2007). Individuals were ranked for yield based on the predicted additive genetic value ($\mu + a$), applying a selection intensity of 30%. Statistical analyses were conducted using the SELEGEN (Resende, 2016) and GENES (Cruz, 2013) software.

Conclusion

The rapeseed genotypes exhibit genetic variability among populations for all evaluated traits, which can be exploited in the development of lines within the breeding program. Genetic gains were significant for the number of siliques per plant and seed productivity across all populations. Most of the superior genotypes originated from the NACE-D (24.15%) and NACE-61 (22%) populations. The information obtained in this study contributes to the efficiency of the breeding program, as it will guide improvement strategies for developing rapeseed cultivars adapted to tropical conditions.

Acknowledgments:

This work was supported by the National Council for Scientific and Technological Development – CNPq [numbers 405966/2022-9]

Statement of contributions:

All authors contributed to the study conception and design. Material preparation, methodology, data collection, analysis, writing - review and editing were performed by WSC, BGL, CGG and EVR. VRN and JPPAC help in data collection and data organizing. The first draft of the manuscript was written by WSC. Funding acquisition, resources and supervision: BGL. All authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

Conflict of Interest:

The authors have no relevant financial or non-financial interests to disclose.

References

Akinyosoye ST, Agbeleye OA, Adetumbi JA, Ukachukwu PC (2021) Selection for earliness and seed yield in Mung bean accessions using REML/BLUP. Pesquisa Agropecuária Brasileira 56:e02290. https://doi.org/10.1590/S1678-3921.pab2021.v56.02290

Almeida PH, Vilela VJ, Torres IY, Uberti A, Delima RO, Reis EFD (2024) Genetic potential of maize populations derived from commercial hybrids for interpopulation breeding. Revista Caatinga 37:e11736. https://doi.org/10.1590/1983-21252024v3711736rc

Batista LG, Gaynor RC, Margarido GRA, Byrne T, Amer P, Gorjanc G, Hickey JM (2021) Longterm comparison between index selection and optimal independent culling in plant breeding programs with genomic prediction. PLoS ONE. 16:e0235554. https://doi.org/10.1371/journal.pone.0235554

Bergo CL, Miqueloni DP, Pedrozo CA, Resende MDVde (2019) Genetic parameters to production characters of palm heart in halfsibs progenies of palm peach. Ciência Rural 49:e20180638. https://doi.org/10.1590/0103-8478cr20180638

Bernardo R (2020) Breeding for quantitative traits in plants. Woodbury: Stemma Press.

Bezerra ARG, Resende MDVD, Silva FLD, Sediyama T, Cruz CD, Silva FCDS, Silva AFD (2023) Combined BLUP selection indexes with parents and F_2 populations in soybean (*Glycine max*) breeding. Crop Breeding and Applied Biotechnology 23:e45412346. https://doi.org/10.1590/1984-70332023v23n4a41

Bocianowski J, Liersch A (2021) Multi-environmental evaluation of winter oilseed rape genotypic performance using mixed models. Euphytica 217:1-9. https://doi.org/10.1007/s10681-020-02760-1

Borém A, Miranda GV, Fritsche-Neto R (2017) Plant Breeding. Editora UFV, Viçosa

Candido WdosS, Silva CMe, Costa ML, Silva BEdeA, Miranda BLde, Pinto JFN, Reis EFdos (2020) Selection indexes in simultaneous increment of yield components in topcross hybrids of green maize. Pesquisa Agropecuária Brasileira 55:e01206. https://doi.org/10.1590/ S1678-3921.pab2020.v55.01206

Carvalho MS, Ferreira MFdaS, Oliveira WBdosS, Marçal TdeS, Guilhen JHS, Mengarda LHG, Ferreira A (2020) Genetic diversity and population structure of *Euterpe edulis* by REML/BLUP analysis of fruit morphology and microsatellite markers. Crop Breeding and Applied Biotechnology 20:e31662048. http://dx.doi.org/10.1590/1984-70332020v20n4a61

Casagrande CR, Mezzomo HC, Silva CMe, Lima GW, Palheta-Souza DJ, Borém A, Nardino M (2022) Selection indexes based on genotypic values applied to Brazilian tropical wheat breeding. Agronomy Science and Biotechnology 8:1-16. https://doi.org/10.33158/ASB.r171.v8.2022

Channaoui S, Mazouz H, Labhilili M, Fechtali ME, Nabloussi A (2022) Inheritance of dwarfism and narrow lobed-leaf in two rapeseed (*Brassica napus* L.) mutant lines. Heliyon 8:e12649. https://doi.org/10.1016/j.heliyon.2022.e12649

Cruz CD (2013) GENES: a software package for analysis in experimental statistics and quantitative genetics. Acta Scientiarum. Agronomy 35:271-276. https://doi.org/10.4025/actasciagron.v35i3.21251

Falconer DS, Mackay TF (1996) Introduction to quantitative genetics. Harlow: Longman Group Ltd, London.

Ferreira Júnior JA, Gonçalves GMB, Crevelari JA, Vettorazzi JCF, Gonçalves VML, Durães NNL, Viana AP, Pereira MG (2020) Genetic progress in maize from advanced cycles of reciprocal recurrent selection through REML/BLUP. Australian Journal of Crop Science 14:1295-1301. https://doi.org/10.21475/ajcs.20.14.08.p2562

Ghafoor I, Kanwal A, Makhdoom M, Kanwal S, Ashraf MA, Ahsan A, Gulnaz S, Ajmal S, Ahmad J, Nadeem M, Rehman AU, Zulkifal M, Riaz M, Parveen N (2023) Genetic evaluation of *Brassica napus* for various yield and oil contributing attributes. Biological and Clinical Sciences Research Journal 174. https://doi.org/10.54112/bcsrj.v2023i1.174

Gomes ABS, Oliveira TRA, Cruz DP, Gravina GA, Daher RF, Araújo LC, Araújo KC (2018) Genetic gain via REML/BLUP and selection indices in snap bean. Horticultura Brasileira 36:195-198. https://doi.org/10.1590/S0102-053620180208

Govindaraj M, Vetriventhan M, Srinivasan M (2015) Importance of Genetic Diversity Assessment in Crop Plants and Its Recent Advances: An Overview of Its Analytical Perspectives. Genetics Research International 2015:14. http://dx.doi.org/10.1155/2015/431487

Hallauer AR, Carena MJ, Miranda Filho JB (2010) Quantitative genetics in maize breeding. Springer, New York

Harker KN, O'Donovan JT, Smith EG, Johnson EN, Peng G, Willenborg CJ, Gulden RH, Mohr R, Gill KS, Grenkow LA (2015) Seed size and seeding rate effects on canola emergence, development, yield and seed weight. Canadian Journal of Plant Science 95:1-8. https://doi.org/ 10.4141/CJPS-2014-222

Krüger CAMB, Silva JAG, Medeiros SLP, Gaviragh J (2011) Heritability and phenotypic correlation of characters related to grain yield and morphology of canola. Pesquisa Agropecuária Brasileira 46:1625-1632. https://doi.org/10.1590/S0100-204X2011001200007

Leite WS, Unêda-Trevisoli SH, Silva FM, Silva AJ, Mauro AODi (2018) Identification of superior genotypes and soybean traits by multivariate analysis and selection index. Revista Ciência Agronômica 49:491-500. https://doi.org/10.5935/1806-6690.20180056

Li S, Zhu Y, Varshney RK, Zhan J, Zheng X, Shi J, Wang X, Liu G, Wang H (2020) A systematic dissection of the mechanisms underlying the natural variation of silique number in rapeseed (*Brassica napus* L.) germplasm. Plant Biotechnology Journal 18:568-580. https://doi.org/ 10.1111/pbi.13224

Lustri EA, Siqueira WJ, Azevedo Filho JAde, Vianna SA, Colombo CA (2021) Estimates of genetic parameters for juvenile traits in macaw palm. Bragantia 80:e2821. https://doi.org/10.1590/1678-4499.20200463

Muhammad Ali, Raziuddin, Ibni Amin Khalil, Naqib Ullah Khan, Sana Ullah Khan, Monsif Ur Rehman, Gul Ghani Afridi and Ghulamullah (2014) Genetic analysis of yield and yield related attributes in *Brassica napus*. Pure and Applied Biology 3:175-187.

Mulamba NN, Mock JJ (1978) Improvement of yield potential of the Eto Blanco maize (*Zea mays* L.) population by breeding for plant traits. Egyptian Journal of Genetics and Cytology 7:40-51.

Nur-E-Nabi Md, Haq MdE, Ahmed M, Hossain MdM, Shefat-al-Maruf Md, Mahmud F, Parveen S, Harun-Ur-Rashid Md (2019) Genetic Variability, Correlation and Path Coefficient Analysis in Advanced Generation of *Brassica napus* L. Journal of Scientific Research & Reports 22:1-12. https://doi.org/10.9734/JSRR/2019/v22i330090

Parveen S, Rashid MH, Bhuiyan MSR (2013) Genetic variation and selection criteria for seed yield related traits in rape seed (*Brassica napus* L.). Bangladesh Journal of Plant Breeding and Genetics 26:15-22. https://doi.org/10.3329/bjpbg.v26i2.23845

Pedro C, Marçola MA, Charimba AM, Queiroz LGCde, Souza JCde (2023) Genetic potential of maize full-sib progenies subjected to a reciprocal recurrent selection. Pesquisa Agropecuária Brasileira 58:e03134. https://doi.org/10.1590/S1678-3921.pab2023.v58.03134

Piepho HP, Möhring J, Melchinger AE, Büchse A (2008) BLUP for phenotypic selection in plant breeding and variety testing. Euphytica 161:209-228. https://doi.org/10.1007/s10681-007-9449-8

Pimentel AJB, Guimarães JFR, Souza MAde, Resende MDVde, Moura LM, Rocha JRASC, Ribeiro G (2014) Estimation of genetic parameters and prediction of additive genetic value for wheat by mixed models. Pesquisa Agropecuária Brasileira 49:882-890. https://doi.org/10.1590/S0100-204X2014001100007

Rahman MM, Chowdhury MAZ, Hossain MG, Amin MN, Muktadir MA, Rashid MH (2011) Gene action for seed yield and yield contributing characters in turnip rape (*Brassica rapa* L.). Journal of Experimental Biosciences 2:67-76.

Rameeh V (2015) Genetic variability and interrelationships among quantitative traits in rapeseed (*Brassica napus* L.) advanced lines. The Journal of Agricultural Sciences 10:158-167. https://doi.org/10.4038/jas.v10i3.8069

Resende MDV de (2002) Biometric Genetics and Statistics in Plant Breeding. Embrapa, Brasília

Resende MDV de (2015) Quantitative and Population Genetics. Suprema, Visconde do Rio Branco

Resende MDV de (2007) Mathematics and Statistics in Experimental Analysis and Genetic Improvement. Colombo: EMBRAPA Florestas, Brasília

Resende MDV de (2016) Software Selegen-REML/BLUP: a useful tool for plant breeding. Crop Breeding and Applied Biotechnology 16:330-339. http://dx.doi.org/10.1590/1984-70332016v16n4a49

Resende MDV de, Alves RS (2022) Statistical significance, selection accuracy, and experimental precision in plant breeding. Crop Breeding and Applied Biotechnology 22:e42712238. http://dx.doi.org/10.1590/1984-70332022v22n3a31

Resende MDV de, Duarte JB (2007) Precision and Quality Control in Cultivar Evaluation Experiments. Pesquisa Agropecuária Tropical 37:182-194.

Rodrigues F, Pinho RGV, Albuquerque CJB, Pinho EVRV (2011) Selection Index and Estimation of Genetic and Phenotypic Parameters for Characteristics Related to Green Corn SYuction. Ciência e Agrotecnologia 35:278-286. https://doi.org/10.1590/S1413- 70542011000200007

Sabbahi R, Azzaoui K, Rhazi L, Ayerdi-Gotor A, Aussenac T, Depeint F, Taleb M, Hammouti B (2023) Factors Affecting the Quality of Canola Grains and Their Implications for Grain-Based Foods. Foods 12:2219. https://doi.org/10.3390/foods12112219

Salgotra RK, Chauhan BS (2023) Genetic Diversity, Conservation, and Utilization of Plant Genetic Resources. Genes 14:174. https://doi.org/10.3390/genes14010174

Sarwar G, Hossain MS, Rashid MU, Parveen S (2015) Assessment of Genetic Variability for Agro-Morphological Important Traits in Aman Rice (*Oryza Sativa* L.). International Journal of Applied Sciences and Biotechnology 3:73-79. https://doi.org/10.3126/ijasbt.v3i1.11896

Searle SR, Casella G, McCulloch CE (1992) Variance components. John Wiley & Sons, New York

Shafey S, El-Maaty SA, Habbasha SFE, Elarabi NI (2023) Evaluation of the growth, yield traits and the genetic diversity of some *Brassica napus* genotypes under Egyptian conditions. Beni-Suef University Journal of Basic and Applied Sciences 48:1-15. https://doi.org/10.1186/s43088-023-00388-3

SBCS (2016) Brazilian Society of Soil Science. Lime and Fertilization Manual for the States of Rio Grande do Sul and Santa Catarina / Brazilian Society of Soil Science - Southern Regional Nucleus. Soil Chemistry and Fertility Commission. - RS/SC.

USDA (2023) United States Departmento of Agriculture. Oilseeds: World Markets and Trade.