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Genetic variability and heritability estimates of morphological traits in F_2 populations of rapeseed (*Brassica carinata* L.)

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Abstract

This study aimed to estimate genetic variability, heritability, and genetic advance for morphological characters in *Brassica carinata* L. A total of 22 genotypes comprised of six parental lines and their 16 bulk F_2 populations were evaluated in a randomized complete block design with three replications at The University of Agriculture Peshawar during 2013-14. Data were recorded on days to 50% flowering, primary branches plant^{-1}, main raceme length, pods on main raceme, pod length, number of seeds pod^{-1}, 100-seed weight, and seed yield plant^{-1}. Significant genetic differences were observed for all the traits studied. Among parental lines, C-93 performed better for primary branches plant^{-1} (11 branches), main raceme length (59.57 cm), pods on main raceme^{-1} (33 pods), and seeds pod^{-1} (15 seeds), C-95 for pod length (4.04 cm) and seed yield plant^{-1} (12.26 g). Among F_2 populations, C-97 x C-88 performed better for main raceme length (73.20 cm), pods on main raceme (41 pods), C-88 x C-93 for pod length (4.95 cm), seeds pod^{-1} (18 seeds), and seed yield plant^{-1} (14.71 g). Moderate ($30 < h^2 \leq 60$) to high ($h^2 > 60$) broad-sense heritability was observed for all morphological traits with maximum genetic advance, hence indicated that selection could be effective in the early generation for the improvements of these studied traits. Generally, cross combinations C-88 x C-93, C-97 x C-95, C-90 x C-93, and C-97 x C-88 performed better than their parental lines for morphological (primary branches plant^{-1}, seeds pod^{-1}, and seed yield plant^{-1}) traits and could be exploited for varietal development in future brassica breeding programs.

Keywords: Genetic variability, genetic advance, heritability, pod length, seeds pod^{-1}

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1. INTRODUCTION

Brassica carinata L. (BBCC, 2n = 34), also known as Ethiopian mustard[1], is native to Ethiopian highlands, belongs to the family Cruciferae[2]. The family Cruciferae has about 338 genera and 3709 species[3]. The only Brassica has about 159 species[4]. It can be cultivated in low rainfed areas of the world. It keeps sufficient yield levels with resistance to different biotic and abiotic stresses[5].

Pakistan produces 186.0 (1000 tones) of rapeseed from an area of 213.0 (1000 hac). In 2011-12, the total edible oil consumption was estimated to be 2.103 million tons. The local produce contributed only 0.636 million tons (30%) while the remaining 1.467 million tons (70%) were imported [6]. The production in Pakistan is insufficient to meet people's local consumption requirements; therefore, a considerable amount of hard-earned foreign exchange is spent every year on its import. It is necessary to take serious measures to improve the yield potential of oilseed crops such as bringing more oilseed crops, developing high yielding and resistant varieties of rapeseed crops, and adopting oilseed crops, developing high yielding and resistant varieties of rapeseed, and adopting new technologies [7].

The yield is a complex character that depends on many morphological traits, which are mostly inherited quantitatively. Importance of genotypic and phenotypic variability, heritability has proved by many researchers [8]. Genetic variability is a measure of the tendency of genotypes in a population to differ from one another. The variability of a character describes a character's tendency to vary in response to environmental and genetic influences. Such breeding exercises need the evaluation of genetic variability, heritability, and genetic advance [9]. The availability of genetic variability for yield and yield-associated characters is more important for identifying and selecting desirable segregating populations. The genetic variability provides the basis for a successful breeding program, and a specific character can be partitioned into heritable and non-heritable parts. Heritability plays a vital role in the breeding program of a crop. It is used to provide the necessary information on the transfer of character(s) from parents to their offsprings. Higher heritability estimates make the selection procedures very simple[10] because their information facilitates evaluating genetic and environmental effects in selecting desirable traits[11]. Estimation of heritability is also used to envisage genetic advance under selection. Genetic advance is the improvement of the genotypic mean values of selected plants over the base population. It is the measure of genetic improvement under selection. The achievement of genetic improvement under selection depends on genetic variability, heritability, and selection intensity[12]. Traits with maximum heritability and genetic advance are thought to be under the control of additive gene action, highlighting the benefits of selection based on phenotypic performance[13]. The present study's goals were to determine genetic variability in F_2 populations compared with their parental lines for morphological traits of B. carinata, estimate heritability and genetic advance for morphological characters, and identify best segregants for future brassica breeding programs.

2. MATERIALS AND METHODS

A field study was conducted at The University of Agriculture Peshawar during the crop season of 2013-14. Experimental material comprised 22 genotypes that included six parental lines and their 16 F_2 bulk populations (Table 1). The original crosses were made in 2011-12, and F_1 hybrids were studied in 2012-13. The experimental material was provided by the Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar. The experimental material was sown in a randomized complete block design (RCBD) with three replications. Ten plants from each parental line and each F_2 population per repetition were randomly selected to record data. Data were recorded on morphological traits.

Table 1. List of parental lines and their F_2 populations of *Brassica carinata* L.

S. No	Parental lines	S. No	F_2 bulk populations
1	C-88	8	C-90 x C-93
2	C-89	9	C-93 x C-90
3	C-90	10	C-93 x C-95
4	C-93	11	C-93 x C-97
5	C-95	12	C-95 x C-89
6	C-97	13	C-95 x C-93
S. No	**F_2 bulk populations**	14	C-95 x C-97
1	C-88 x C-89	15	C-97 x C-88
2	C-88 x C-90	16	C-97 x C-95
3	C-88 x C-93		
4	C-88 x C-95		
5	C-88 x C-97		
6	C-89 x C-88		
7	C-89 x C-93		

2.1. Statistical data analysis

2.1.1. Analysis of variance: The data were managed to scrutinize the variance technique proposed for randomized complete block design, as suggested[15]. Significant differences among all genotypes were further compared through the least significant difference (LSD) test using 5% probability levels. For analysis of the variance model, we followed the procedure of [16].

2.1.2. Heritability estimates: Heritability assessments can be used to guess genetic advance under selection so that the plant breeder can predict progress from different types. The broad-sense heritability was calculated by the following formulae suggested[17]:

$$\text{Heritability} = h^2_{BS} = \frac{\sigma^2_g}{\sigma^2_p}$$

Where, h^2_{BS} = Broad-sense heritability, σ^2_g = genetic variance, σ^2_p = phenotypic variance

Heritability values were categorized as low, moderate, and high, according to[18]:

Low = h2 ≤ 30, Moderate = 30 < h2 ≤ 60, High = h2 > 60

2.1.3. Genetic advance (GA): Genetic advance was computed by the following formula suggested by[19]:

$$GA = k.\sigma_p.h^2$$

Where, k = 1.76 for 10 % selection intensity, h^2 = Heritability coefficient, σ_p = Phenotypic standard deviation.

3. RESULTS AND DISCUSSIONS

3.1. Days to 50% flowering: In wild and cultivated plant species, flowering time is an important trait for studying a crop's life history that harmonizes the life cycle with local environmental conditions. Brassica genotypes exhibited significant differences for days to 50% flowering, representing sufficient variability. Differences among parental lines, their F_2 populations, and contrast between parental lines and their F_2 populations were also significant (Table 2). Significant differences among *B. carinata* were observed by [20] for days to 50% flowering. Similarly, among Ethiopian mustard accessions for days to 50% flowering [21], also reported significant differences. Parental line C-95 was early flowering (120 days), and C-89 was late flowering (132 days) (Fig-1). Two F_2 populations C-88 x C-89 and C-88 x C-90, were early flowering (120 days) and C-95 x C-97 was late flowering (137 days) (Fig-1). The mean performance showed that the

parental lines comparatively flowered earlier than their F_2 populations. Heritability and genetic advance help the plant breeder to predict the expected genetic gain under selection, so that advancement from diverse types can be anticipated. Genetic variance (19.71) was double that of environmental variance (9.55) that resulted in high heritability (67.37%) and a genetic advance of 6 days at 10% selection intensity for 50% flowering (Table 3). High heritability showed that the character was genetically controlled. Our results are in agreement with [22], who reported high heritability for days to 50% flowering in *Brassica napus* genotypes.

***3.2. Primary branches plant^{-1}*:** Number of Primary branches plant^{-1} is the yield contributing trait because it is directly associated with the number of pods plant^{-1}, which is the crucial factor that leads to an increase in final seed yield. Analysis of variance manifested significant differences among genotypes for primary branches plant^{-1}. Variability among parental lines, their F_2 hybrids, and contrast between parental lines and their F_2 hybrids were also substantial (Table 2). Our results are in line with [23], who also observed significant differences among Ethiopian mustard genotypes for primary branches plant^{-1}. Among parental lines, C-88 and C-97 produced the minimum (7) primary branches plant^{-1}, while the maximum (11) primary branches plant^{-1} were produced by C-93 (Fig-2). Among F_2 populations, primary branches plant^{-1} was minimum for C-89 x C-93 (7), while the maximum for C-97 x C-95 (14) (Fig-2). Comparatively, the plants from F_2 populations produced more primary branches plant^{-1} as compared to their parental lines. For primary branches plant^{-1}, genetic and environmental variances were 2.65 and 1.70, respectively, resulting in high heritability (60.90%) and genetic advance of 2 at 10% selection intensity (Table 3). It showed that the trait was less environmentally controlled, and selection in early generations can be possible. Our findings are in line with [24], who also reported high heritability for primary branches plant^{-1} in *Brassica carinata* lines.

***3.3. Main raceme length (cm)*:** Like other yield contributing traits, the main raceme length plays a significant role toward numbers of pods plant^{-1}, which enhanced the final seed yield of the crop. Analysis of variance manifested significant differences among genotypes for the main raceme length. Differences among parental lines, their F_2 progenies, and interaction between parental lines and their F_2 progenies were also significant (Table 2). Considerable variations for main raceme length among *Brassica carinata* lines have also been reported by [24]. Likewise, [25] manifested statistically acceptable differences among Ethiopian mustard lines for the main raceme length. Among *Brassica carinata* genotypes, the shortest (48.47 cm) main raceme length was recorded for parental line C-88 and the largest (59.57 cm) for C-93. Among F_2 populations, shortest main raceme was recorded for C-97 x C-95 (47.57 cm) and longest for C-97 x C-88 (73.20 cm) (Fig-1). Means of parental lines and their F_2 populations revealed that the F_2 population's plants had comparatively longer main raceme than their parental lines. Genetic variance (30.45) was more than environmental variance (19.32), which resulted in high heritability (61.18%) and genetic advance of 7.60 cm at 10% selection intensity for main raceme length (Table 3). It indicated that the character was genetically controlled and the predominant role of additive gene action; hence, early selection for this trait can be effective. Earlier researchers [26] reported high heritability for main raceme length in intra-specific F_2 populations while moderate was recorded for inter-specific F_2 populations for main raceme length in Brassica species.

3.4. Pods on main raceme: In Brassica species, pods on the main raceme are the significant yield influential factor because it contributes extensively toward final seed yield of a crop. Analysis of variance revealed significant differences among genotypes for pods on the main raceme. Differences among parental lines, their F_2 populations, and interaction between parental lines and their F_2 populations were also significant (Table 2). Our results for significant variations for pods on the main raceme are also supported by [27]. Pods on the main raceme were less (22) for parental line C-97, while more (33) for C-93 (Fig-1). Pods on the main raceme were the minimum (27) for F_2 population C-95 x C-93 (27) and the maximum (41) for two cross combinations C-90 x C-93 and C-97 x C-88 (Fig-1). Means of parental lines and F_2 populations were 27 and 41, respectively, so plants from F_2 populations produced more pods on the main raceme than their parental lines. Genetic and environmental variances were 21.01 and 19.75, respectively, resulting in moderate heritability (51.55%) and genetic advance of 6 at 10% selection

intensity for pods on the main raceme (Table 3). It shows that the environmental conditions had a partial effect on gene expression, and this character selection should be practiced with care. Moderate heritability was reported by [26], while [25] recorded high heritability in Ethiopian mustard lines for pods on the main raceme.

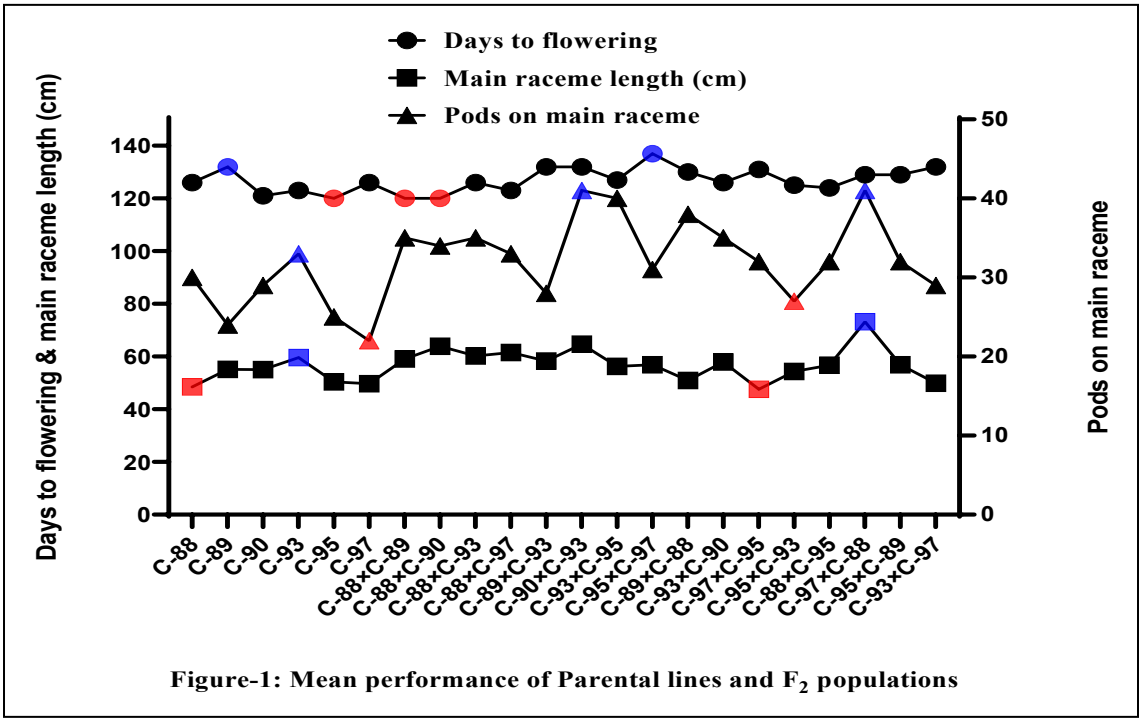

Figure-1: Mean performance of Parental lines and F_2 populations

***3.5. Pod length (cm)*:** The longest pods play a vital role in determining the seed's final seed yield and diameter, respectively. Scrutiny of variance manifested significant differences among genotypes for pod length. Differences among parental lines, their F_2 populations, and the comparison between parental lines and their F_2 populations were also substantial for pod length (Table 2). Our results are also in line with [27], who reported significant variation among accessions of *Brassica carinata* for pod length. Among parental lines, the longest pods (4.04 cm) were produced by C-95, while the shortest pods (3.32 cm) were recorded for C-88. Among F_2 populations, the shortest pods (2.99 cm) were recorded for cross combination C-97 x C-95 and the longest pods (4.95 cm) for cross combination C-88 x C-93 (Fig-3). Genetic variance (0.17) was more than environmental variance (0.05) that resulted in high heritability (78.08%) and a genetic advance of 0.64 cm at 10% selection intensity for pod length. It suggested that the character was genetically controlled, and selection in early generations can be more effective for this trait.

***3.6. Seeds pod^{-1}*:** Seeds pod^{-1} is the important trait that contributes noticeably towards the final seed yield. Statistical analysis showed significant differences among genotypes for seeds pod^{-1}. Differences among parental lines, their F_2 populations, and contrast between parental lines and their F_2 populations were also significant (Table 2). Our results are in agreement with [23], who got considerable variations among Ethiopian mustard genotypes for seeds pod^{-1}. Seeds pod^{-1} was the minimum (11) for two parental lines C-88 and C-97 and the maximum (15) for C-93. Seeds pod^{-1} were minimum (12) for three cross combinations C-95 x C-97, C-95 x C-89 and C-93 x C-97, while the maximum (18) for one F_2 population C-88 x C-93 (Fig-3). The mean performance showed that plants from parental lines and their F_2 populations had almost the same number of seeds in their respective pods. Genetic variance (1.85) was more than the environmental variance (1.03), thus concluded high heritability (64.09%) and genetic advance of 2 at 10% selection intensity for seeds pod^{-1} (Table 3). This indicated that the trait was less influenced by the environment, showing the predominant role of additive gene action.

***3.7. 100-seed weight (g)*:** The seed weight indicates the degree of seed advancement and plays a vital role in determining a genotype's yield potential. Statistical scrutiny for 100-seed weight revealed significant differences among genotypes. Parental lines and interaction between parental lines and their F_2 progeny

were significant, while F_2 populations showed non-significant differences for the 100-seed weight (Table 2). In parental lines, mean values for 100-seed weight ranged from 0.41 (C-89) to 0.48 g (C-97). In F_2 populations, mean for 100-seed weight ranged from 0.37 (C-88 x C-89) to 0.45 g (C-88 x C-97) (Fig-3). A comparison between parental lines and their F_2 populations revealed that plants had approximately the same seed weight. For 100-seed weight, genetic and environmental variances were 0.001 and 0.0003, resulting in moderate heritability (33.44%) and genetic advance of 0.02 g at 10% selection intensity (Table 3). Heritability of 33.44% revealed that the influence of environmental conditions on gene expression and selection for this character should be delayed to later generations for improvement. Our results contrast with [24], who reported high heritability for 100-seed weight in *Brassica carinata* lines.

***3.8. Seed yield plant^{-1} (g)*:** Seed yield plant^{-1} is the cumulative outcome of different traits like seeds pod^{-1}, pods plant$^{-1,}$ and 100-seed weight. Scrutiny of data for seed yield plant^{-1} revealed significant differences among genotypes. Differences among parental lines, their F_2 progenies, and interaction between parental lines and their F_2 progenies were also significant (Table 2). In parental lines, the lowest seed yield plant^{-1} (3.93 g) was produced by C-97 and the maximum (12.26 g) by C-95. In F_2 populations, the lowest (5.25 g) seed yield plant^{-1} was given by cross combination C-93 x C-97 and the maximum (14.71 g) by cross combination C-88 × C-93 (Fig-2). Our mean comparison results between parental lines and their F_2 populations revealed that plants from F_2 populations gave more seed yield than their parental lines. For seed yield plant^{-1}, the genetic variance (7.52) was greater than the environmental variance (1.78). It resulted in high heritability (80.86%) and genetic advance of 4.34 g at 10% selection intensity (Table 3). It revealed that seed yield plant^{-1} was less interrupted by environmental conditions. Our results for seed yield plant^{-1} are also supported by [21], who reported high heritability in Ethiopian mustard accessions.

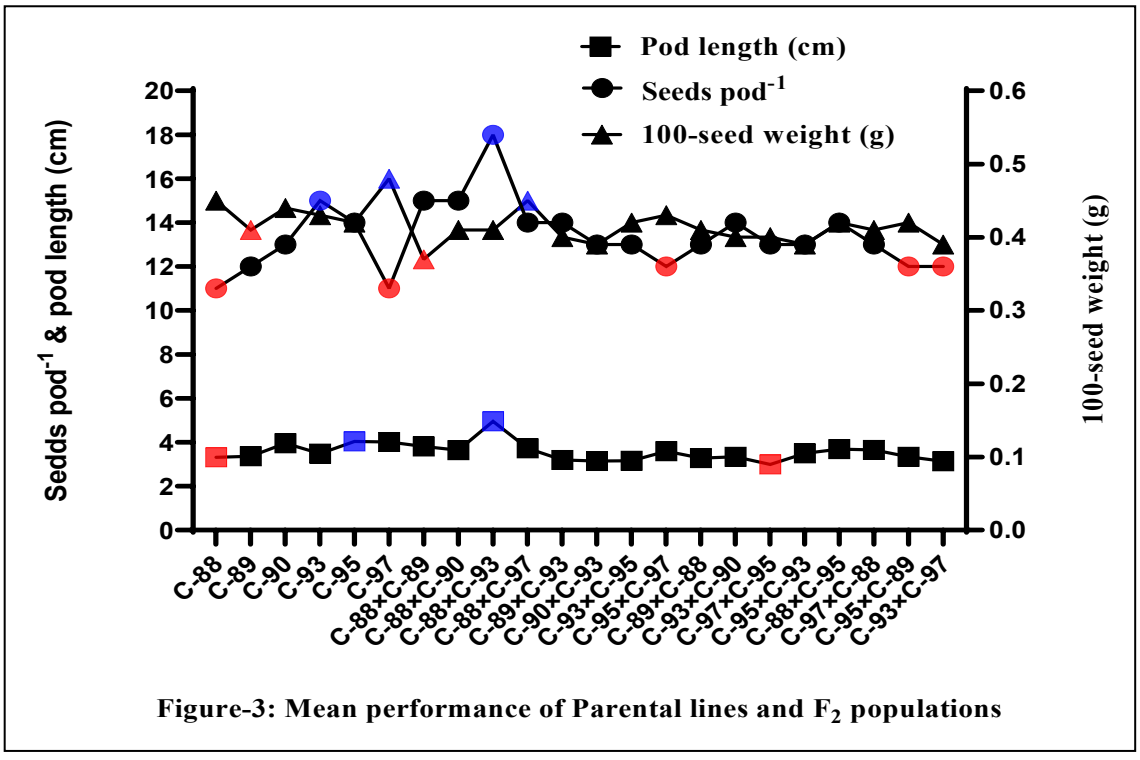

Figure-3: Mean performance of Parental lines and F_2 populations

Table 2. Mean squares for different morphological traits

SOV	Replication (df = 02)	Genotypes (df = 21)	Parents (df = 05)	F_2 populations (df = 15)	Parents vs. F_2s (df = 01)	Error (df = 42)	CV (%)
Days to 50% flowering	15.80	68.67**	63.83**	66.62**	123.62**	9.55	2.44
Primary branches plant^{-1}	0.57	9.66**	7.66**	10.30**	10.02*	1.70	13.91
Main raceme length	48.49	110.66**	54.06*	115.31**	323.83**	19.32	7.76
Pods on main raceme	46.5	82.77**	55.41*	56.75**	609.80**	19.75	13.9
Pod length	0.06	0.55**	0.35**	0.63**	0.43**	1.99	6.12
Seeds pod^{-1}	0.52	6.57**	7.35**	6.17**	8.66**	1.03	7.68
100-seed weight	0.005	0.002**	0.002*	0.001	0.011**	0.001	6.36
Seed yield plant^{-1}	0.76	24.33**	30.91**	21.12**	39.49**	1.78	13.8

, ** = significant at 1% and 5% level of probability

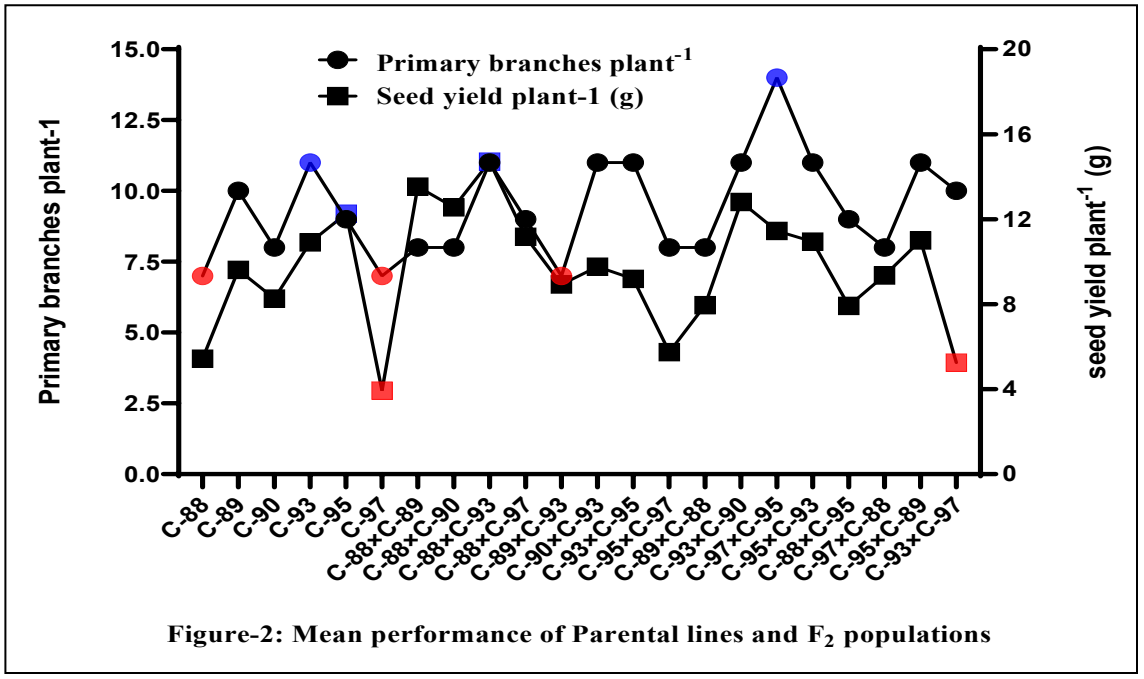

Figure-2: Mean performance of Parental lines and F_2 populations

Table 3. Environmental variance (V_e), Genotypic variance (V_g), Phenotypic variance (V_p), heritability (h^2), and genetic advance (G.A) for morphological and biochemical traits.

Traits	Ve	Vg	Vp	h^2_{BS} (%)	G.A
Days to 50% flowering	9.55	19.71	29.25	67.37	6.41
Primary branches plant^{-1}	1.70	2.65	4.35	60.90	2.24
Main raceme length	19.32	30.45	49.77	61.18	7.60
Pods on main raceme	19.75	21.01	40.75	51.55	5.79
Pod length	0.05	0.17	0.22	78.08	0.64
Seeds pod^{-1}	1.03	1.85	2.88	64.09	1.91
100-seed weight (g)	0.0003	0.001	0.00	33.44	0.02
Seed yield plant^{-1} (g)	1.78	7.52	9.29	80.86	4.34

4. CONCLUSIONS

All the studied characters were significantly different among Brassica genotypes. Maximum seeds pod^{-1} and seed yield plant^{-1} were given by cross combination C-88 x C-93. Higher heritability coupled with maximum genetic advance was estimated for days to flowering, main raceme length, primary branches plant^{-1}, pod length, seeds pod^{-1}, and seed yield plant^{-1}. F_2 population C-88 x C-93 gave maximum pod length, seeds pod$^{-1,}$ and seed yield plant^{-1}. Cross combinations C-88 x C-93, C-97 x C-95, C-90 x C-93, and C-97 x C-88 performed better for most of the traits so that these segregants could be exploited for varietal development in future brassica breeding programs.

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CONFLICT OF INTEREST

The authors declare no conflict of interest.

REFERENCES

1. Broadening the genetic base of Abyssinian mustard (Brassica carinata A. Braun) through introgression of genes from related allotetraploid species. Spanish Journal of Agricultural Research. 2014;12(3):742–752. doi:10.5424/sjar/2014123-5365
2. Williams PH. Rapid-Cycling Brassicas (RCB's) in Hands-on Teaching of Plant Biology. In: Tested Studies for Laboratory Teaching. Proceedings of the Tenth Workshop/Conference of the Association for Biology Laboratory Education (ABLE). 1989. p. 1–30.
3. Warwick SI, Francis A, Al-Shehbaz IA. Brassicaceae: Species checklist and database on CD-ROM. Plant Systematics and Evolution. 2006;259(2–4):249–258. doi:10.1007/s00606-006-0422-0
4. Zhou WJ, Zhang GQ, Tuvesson S, Dayteg C, Gertsson B. Genetic survey of Chinese and Swedish oilseed rape (*Brassica napus* L.) by simple sequence repeats (SSRs). Genetic Resources and Crop Evolution. 2006;53(3):443–447. doi:10.1007/s10722-004-7862-6
5. Getinet A, Rakow G, Downey RK. Agronomic performance and seed quality of Ethiopian mustard in Saskatchewanl. 2003.
6. Anonymous. No Title. Economic Survey of Pakistan. 2011-12. Ministry of Finance, Government of Pakistan. 2012:23.
7. Shah AH, Gilani MM, Khan FA. Comprehensive selection of yield and yield influencing characters in Brassica species. Int. J. Agri. Biol. 2000;2(3):245–247.
8. Ali N, Javidfar F, Attary AA. Genetic variability, correlation, and path analysis of yield and its components in winter rapeseed (Brassica napus L.). Pak. J. Bot. 2002;34(2):145–150.

9. Chaudhary SPS, Sharma SN, Singh AK. Line x tester analysis in Indian mustard [Brassica juncea (l.) czern & coss.]. The Indian Journal of Genetics & Plant Breeding (India). 1997.
10. Khan FA, Ali S, Shakeel A, Saeed A, Abbas G. Genetic variability and genetic advance analysis for some morphological traits in *Brassica napus* L. J. Agric. Res. 2006;44(2):83–88.
11. Tariq Mahmood, Muhammad Ali SI and MA. Genetic Variability and Heritability Estimates in Summer Mustard (*Brassica juncea* L.). Asian Journal of Plant Sciences. 2003;2(1):77–79. doi:10.3923/ajps.2003.77.79
12. Allard RW. Principles of plant breeding. John Wiley & Sons; 1999.
13. Aytaç Z, Kinaci G. Genetic variability and association studies of some quantitative characters in winter rapeseed (*Brassica napus* L.). African Journal of Biotechnology. 2009;8(15):3547–3554. doi:10.5897/AJB2009.000-9350.
14. Nausheen, Farhatullah, Khalil IH, Amanullah. Heterosis and heterobeltiotic studies of F_1 hybrids in *Brassica carinata* L. Pakistan Journal of Botany. 2015;47(5):1831–1837.
15. Steel RGD, Torrie JH. Principles and procedures of statistics. McGraw-Hill Book Company, Inc., New York, Toronto, London; 1960.
16. Gomez AA, Wiley J. Statistical Procedures for Agricultural Research. 6.
17. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. Kalyani.; 1977.
18. Robinson HF, Comstock RE, Harvey PH. Genotypic and Phenotypic Correlations in Corn and Their Implications in Selection 1. Agronomy Journal. 1951;43(6):282–287.
19. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. Indian Council of Agricultural Research, New Delhi.; 1954.
20. Walle T, Wakjira A, Mulualem T. Analysis of Genetic Parameters on Ethiopian Mustard (*Brassica Carinata* A. Braun) Genotypes in North-western Ethiopia. Plant Breeding and Seed Science. 2015;69(1):25–34. doi:10.1515/plass-2015-0003
21. Yohannes MTW, Belete YS. Genetic variability of Ethiopian mustard (*Brassica carinata* A. Brun) accessions based on some morphological characters. International Journal of Plant Breeding and Genetics. 2013;7(3):169–175.
22. Nasim A, Farhatullah, Iqbal S, Shah S, Azam SM. Genetic variability and correlation studies for morpho-physiological traits in *Brassica napus* L. Pakistan Journal of Botany. 2013;45(4):1229–1234.
23. Sheikh FA, Banga S, Banga SS, Najeeb S. Development of Ethiopian mustard (Brassica carinata) with broad genetic base through interspecific hybridization with elite lines of *Brassica napus* and *Brassica juncea*. Journal of Agricultural Biotechnology and Sustainable Development. 2011;3:77–84.
24. Ali Y, Nasim A, General D, Pakhtunkhwa K, Azam SM, Agriculture F. Heritability and Correlation Analysis for Morphological and biochemical traits in *Brassica carinata* L. Sarhad Journal of Agriculture. 2013;29(3):359–370.
25. Muthoni J. Characterization of Ethiopian mustard (*Brassica carinata* A. Braun) lines for vegetative agro morphological traits at Arusha, Tanzania. Journal of Horticulture and Forestry. 2010.
26. Khan FU, Farhatullah R, Mohammad F. Heritability Estimates in Intra and Inter-Specific F2 Populations of Brassica. Journal of Biology, Agriculture and Healthcare. 2014;4(20):102–107.
27. Zada M, Zakir N, Ashiq Rabbani M, Shinwari ZK. Assessment of genetic variation in Ethiopian mustard (*Brassica carinata* A. Braun) germplasm using multivariate techniques. Pakistan Journal of Botany. 2013.