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GENETIC STUDIES OF F_2 POPULATIONS IN MUSTARD *(Brassica species)*

Snehal V. Pawar[1], S. R. Kamdi[2], P. S. Kalpande[3], Sakshi V. Ingle[4], J. S. Renjini[5] and Anjali D. Sable[6]

ABSTRACT

The present investigation was undertaken using F_2 generations derived from three interspecific crosses *viz.*, Kranti x PC-6, ACN-9 x PC-6, TAM 108-1 x PC-6 of mustard. The material was evaluated in Randomized Block Design in three replications at All India Coordinated Research Project on Linseed and Mustard, College of Agriculture, Nagpur, during *rabi* 2022-2023. Observations were recorded on nine quantitative characters. Genotypic coefficient of variation was moderate to high for all characters except for days to first flower and days to maturity. The broad sense heritability was high for all characters under study except for days to first flower and siliquae density on main branch where moderate heritability was recorded. The expected genetic advance among all F_2 population indicated significant progress under selection for plant height, number of branches plant^{-1}, number of siliquae plant^{-1}, siliquae density on main branch, 1000 seed weight and seed yield plant^{-1}. Superior 30 individual plants were identified on the basis of GCV, heritability and genetic advance for economics traits *viz.*, seed yield plant^{-1}, number of siliquae plant^{-1} and number of branches plant^{-1} at 5% selection intensity, which were suggested to be carried forward by plant to row method for exploiting improvement in the selected material.

(Key words: Mustard, genetic study, F_2 population, GCV, PCV, heritability, genetic advance, interspecific crosses)

INTRODUCTION

The genus *Brassica* is an important member of the Cruciferae family. It comprises of several economically important species which yield edible roots, stems, leaves, buds, flowers and seed as condiment. Mustard plays an important role in the oil seed economy of the country. It has 38 to 42% oil and 24% protein. Mustard is rich in minerals like Calcium, Manganese, Copper, Iron, Selenium, Zinc, Vitamin (A, B and C) and Proteins. Rapeseed mustard (*Brassica* Spp.) is the second most important oil seed crop of the country after groundnut which contributes about 25-30% of total oil seeds production. In India, however production of edible oil is in shortage due to tremendous demand. Vigorous efforts are needed to increase the yield level and to achieve the self-sufficiency. Yield is product of multiple interaction of contributing characters. Creation of variability in yield contributing characters is necessary.

Presence of variability is the prerequisite for crop improvement and segregating generation obtained by hybridization between distant parents is one of the popular sources of increasing variability and its assessment is one of important programmes. The evaluation of genetic parameters, such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h^2) and genetic advance (GA%) is important as a preliminary step to facilitate effective selection of genotype (Chaudhary *et al*., 2023). There are varying reports about the reliability of early generation selection. Therefore, present study was planned to genetic studies of F_2 population in mustard.

MATERIALS AND METHODS

The present investigation was undertaken using F_2 generations derived from three interspecific crosses *viz*., Kranti x PC-6, ACN-9 x PC-6, TAM 108-1 x PC-6 of mustard. During *rabi* 2022-23 selfed seeds of F_1 along with P_1 and P_2 were planted in Randomised Block Design in three replications at AICRP on Linseed and Mustard, College of Agriculture, Nagpur. All the recommended cultural practices were followed to raise a good crop. The data recorded on 50 plants of F_2 and 5 plants of parents on 9 quantitative characters *viz*., days to maturity, plant height (cm), number of branches plant^{-1}, siliqua length, number of siliquae plant^{-1}, siliquae density, 1000 seed weight (g) and seed yield plant^{-1} (g) at maturity except for days to first flower. Data were subjected to statistical analysis as per the procedure for Analysis of variance by Panse and Sukhatme (1954), GCV and PCV by Burton and Devane (1953), heritability by Hanson *et al*. (1956) and genetic advance by Robinson *et al.* (1949).

RESULTS AND DISCUSSION

In the present study, analysis of variance for yield and its components showed significant difference among

1,3,4,5 & 6. P. G. Students, Agril. Botany Section, College of Agriculture, Nagpur, India
2. Mustard Breeder, AICRP on Linseed and Mustard, College of Agriculture, Nagpur, India

the genotypes and generations which indicated the presence of substantial variability in the material under studied indicated that all the characteristics were highly significant at 0.05 and 0.01 probability level (Table 1). This revels that the genetic parameters can be estimated for all the characters. These results were in conformity with Bohare *et al*. (2015). They also reported significant difference among genotypes for characters *viz*., days to first flower, days to maturity, plant height (cm), number of branches plant^{-1}, siliqua length, number of siliquae plant^{-1}, siliquae density on main branch, 1000 seed weight (g) and seed yield plant^{-1} (g).

Data regarding variability, heritability and genetic advance estimated for nine quantitative traits of three F_2 crosses are presented in Table 2. Days to first flower showed low variability as low values were reported for genotypic coefficient of variation and phenotypic coefficient of variation. Low difference between genotypic coefficient of variation and phenotypic coefficient of variation indicates that this character is least influenced by the environment. Sapkal *et al*. (2023) also observed low variability for days to flower in their studies in mustard. All three crosses showed moderate to high heritability accompanied with low genetic advance indicating that this character governed by the non-additive gene action and resemblance due to influence of environment. Pawar *et al*. (2019) also reported similar results and concluded ineffectiveness of selection for days to first flower in F_2 generation in soybean.

The genetic parameters calculated for days to maturity revealed that genotypic coefficient of variation and phenotypic coefficient of variation were low for all the crosses. Results reported are in accordance with Kumar *et al*. (2019), who also reported low GCV and PCV for days to maturity in mustard. F_2 variances calculated varied from low to moderate among the crosses. The estimates of heritability were found high coupled with low to moderate genetic advance as per cent of mean in all crosses in mustard (Gowthami *et al*., 2015). This indicated significant role of non-additive gene action and significant role of environment influencing this character hence selection is not effective for early maturing plant in F_2 generation.

F_2 population of all the crosses showed maximum variation and had high F_2 variance for plant height. Moderate GCV and PCV values were present for this trait but low difference between the GCV and PCV indicates least influence of environment on plant height. Kumar *et al*. (2019) also observed low difference between the GCV and PCV for plant height in mustard. The high heritability coupled with high genetic advance as per cent mean was observed for plant height in all crosses indicating the predominance additive gene action for the trait. High heritability coupled with high genetic advance as per cent mean was also observed by Bohare *et al*. (2015) and Sapkal *et al*. (2023) in mustard. The genetic parameters calculated for number of branches plant^{-1} revealed that all the crosses exhibited high genetic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance as per cent of mean. This indicates that there is a lesser influence of environment and exhibits additive gene action in the expression of this character which is amenable for selection. Shekhawat *et al*. (2014) also found lesser influence of environment in the expression for number branches plant^{-1} in mustard.

Siliqua length showed moderate to high genetic coefficient of variation, phenotypic coefficient of variation, high heritability, medium to high genetic advance as per cent of mean for all the crosses. The moderate to high GCV and PCV, high heritability coupled with medium to high genetic advance as per cent mean was observed for siliqua length in all crosses indicating the predominance additive gene action for the trait. Highest PCV and GCV indicated the existence of substantial variability for number of siliquae plant^{-1}. It also indicated greater scope for selection to improve upon this character. Low differences between PCV and GCV for this trait indicated the lower influence of environment and reflect on reliability of selection based on phenotypic performance. Sapkal *et al.* (2023) and Chaurasiya *et al*. (2019) also found low differences between PCV and GCV for number of siliquae plant^{-1} in mustard. High heritability coupled with high genetic advance as per cent mean was observed for number of siliquae plant^{-1}. Naturally, selection based on phenotypic observations for this character would be effective. Similar findings of high heritability and genetic advance for number of siliquae plant^{-1} had reported by several researchers *viz.*, Bohare *et al*. (2015) and Gowthami *et al*. (2015) in mustard.

Moderate to high values of GCV and high PCV indicates that there is substantial variation is present but it also suggests that there is scope to enrich variation for siliquae density on main branch. Difference between GCV and PCV showed influence of environment on this character. Medium to high heritability coupled with high genetic advance as per cent of mean recorded in all crosses. High heritability coupled with high genetic advance as per cent of mean indicates that least influence of environment on the expression of character and prevalence of additive gene action in their inheritance, since amenable for the simple selection by visual means. Prevalence of additive gene action in inheritance of siliquae density on main branch also reported by Sapkal *et al.*(2023) in mustard. The study of genetic parameters for the trait 1000 seed weight indicated moderate to high values of GCV and PCV that means there is substantial variation is present but it also suggests that there is scope to enrich variation for this character. Minimum difference between GCV and PCV showed least influence of environment on this character. Present results are in accordance with Shekhawat *et al*. (2014), who also observed minimum difference between GCV and PCV which showed least influence of environment on 1000 seed weight in mustard. High heritability along with high genetic advance as per cent of mean were also observed in this study. Similar results were reported by Chaurasiya *et al*. (2019), who found high heritability along with high genetic advance as per cent of mean for 1000 seed weight in mustard.

Table 1. Analysis of variance for various characters in mustard

Sources of variation	d. f.	Days to first flower	Days to maturity	Plant height (cm)	No. of branches plant^{-1}	Siliqua length (cm)	No. of siliquae plant^{-1}	Siliquae density on main branch (%)	1000 seed weight(g)	Seed yield plant^{-1} (g)
Replication	2	3.42	23.53	21.62	0.17	0.44	1108.60	0.01	0.37	3.88
Genotype	6	64.06**	43.78**	887.46**	2.52**	1.10**	2984.93**	0.01**	2.04**	9.44**
Error	12	2.79	8.38	27.73	0.35	0.13	499.49	0.01	0.23	1.06

*Significantat 5% level ** Significant at 1% level

Table 2. Estimation of genetic parameters of each F_2 population of mustard

Cross	Parameters	Days to first flower	Days to maturity	Plant height (cm)	No. of branches plant^{-1}	Siliqua length (cm)	No.of siliquae plant^{-1}	Siliquae density on main branch (%)	1000 seed weight (g)	Seed yield plant^{-1} (g)
Kranti x	Mean	45.67	112.89	174.46	4.20	3.77	117.02	0.49	3.37	5.16
PC-6	Range	14.00	27.00	85.00	8.00	3.10	127.00	0.68	3.74	9.00
	VF_2	7.20	43.72	654.36	2.89	0.32	1642.16	0.01	0.65	5.23
	GCV (%)	4.84	5.59	14.42	**35.27**	11.38	**34.01**	17.33	22.49	**38.92**
	PCV (%)	5.88	5.86	14.66	40.45	14.90	34.63	24.50	23.90	44.34
	Heritability	67.87	90.97	96.75	**76.02**	58.29	**96.45**	50.04	88.60	**77.08**
	GA	3.75	12.39	50.98	2.66	0.67	80.51	0.13	1.47	3.63
	GAM	8.22	10.98	29.22	**63.34**	17.90	**68.80**	25.26	43.62	**70.40**
ACN-9 x	Mean	48.55	111.04	142.77	4.20	3.35	181.42	0.50	3.41	10.02
PC-6	Range	14.00	23.00	105.00	8.00	4.30	126.00	0.72	3.93	10.38
	VF_2	14.66	28.71	582.94	4.78	0.62	1424.38	0.02	0.87	7.36
	GCV (%)	5.41	4.61	16.50	**47.97**	20.67	**20.59**	25.35	25.47	**25.07**
	PCV (%)	7.89	4.83	16.91	51.99	23.47	20.80	30.88	27.40	27.06
	Heritability	47.07	91.10	95.22	**85.13**	77.52	**98.01**	67.40	86.38	**85.81**
	GA	3.71	10.06	47.36	3.84	1.26	76.20	0.22	1.66	4.80
	GAM	7.65	9.06	33.17	**91.17**	37.48	**42.00**	42.88	48.76	**47.84**
TAM	Mean	49.61	114.55	178.70	4.80	4.52	114.10	0.52	4.12	8.81
PC-6	Range	13.00	14.00	96.00	9.00	4.50	95.00	0.66	4.00	13.60
108-1 x	VF_2	8.87	60.72	591.02	4.06	0.45	1654.06	0.02	0.52	11.09
	GCV (%)	4.26	6.53	13.26	**38.18**	12.83	**35.49**	26.26	16.58	**34.47**
	PCV (%)	6.00	6.80	13.57	41.16	14.87	35.64	29.83	17.45	37.80
	Heritability	50.29	92.03	95.36	**86.07**	74.43	**99.16**	77.47	90.27	**83.19**
	GA	3.09	14.77	47.76	3.57	1.03	83.08	0.25	1.34	5.71
	GAM	6.22	12.90	26.66	**72.97**	22.80	**72.81**	47.61	32.45	**64.78**

Table 3. List of superior individual plant selected from three F_2 crosses

Sr. No.	Single plant selected in F_2	Number of siliquae plant^{-1}	Number of branches plant^{-1}	Seed yield plant^{-1} (g)
1	C_1-73	257	8	14.8
2	C_1-71	220	7	12.4
3	C_1-82	210	8	10.6
4	C_1-14	205	6	9.9
5	C_1-145	204	4	9.7
6	C_1-5	201	5	9.7
7	C_1-80	190	5	9.6
8	C_1-74	188	4	9.8
9	C_1-144	187	3	9.4
10	C_1-16	185	4	9.2
11	C_2-37	248	7	12.4
12	C_2-93	247	6	10.6
13	C_2-107	245	5	9.8
14	C_2-30	244	6	9.5
15	C_2-114	243	4	9.2
16	C_2-103	240	4	9.3
17	C_2-115	236	5	13.4
18	C_2-100	232	6	14.2
19	C_2-88	230	3	15.2
20	C_2-69	228	4	12.4
21	C_3-104	225	8	15.4
22	C_3-61	196	7	15.2
23	C_3-75	194	7	14.9
24	C_3-66	188	5	15.3
25	C_3-71	187	6	14.2
26	C_3-69	185	5	13.8
27	C_3-76	183	3	13.5
28	C_3-77	180	4	13.6
29	C_3-59	175	4	12.5
30	C_3-145	178	3	11.3

C_1- Kranti x PC-6

C_2- ACN-9 x PC-6

C_3- TAM 108-1 x PC-6

Highest PCV and GCV indicated the existence of substantial variability for seed yield plant^{-1}. It also indicated greater scope for selection to improve upon this character. Low differences between PCV and GCV for this trait indicated the lower influence of environment and reflect on reliability of selection based on phenotypic performance. Similar results such as highest PCV and GCV and low differences between PCV and GCV were also noted by Kumar *et al.* (2019) and Sapkal *et al.* (2023) in mustard. High heritability along with high genetic advance as per cent of mean indicated least influence of environment on seed yield plant^{-1}.

In the present study, three F_2 populations were evaluated for important genetic parameters such as genotypic coefficient of variation, heritability and expected genetic advance for nine quantitative traits. All crosses reported high genotypic coefficient of variation, heritability and genetic advance as per cent of mean for number of branches plant^{-1}, number of siliquae plant^{-1} and seed yield plant^{-1} hence would be useful for obtaining potential segregants with maximum number of branches plant^{-1}, number of siliquae plant^{-1} and seed yield plant^{-1}. So, 30 single plants were selected on the basis of these four traits at 5%

selection intensity (Table 3) which were suggested to be carried forward by plant to row method for exploiting improvement in the selected material.

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