GENETIC ARCHITECTURE FOR YIELD AND ITS COMPONENT TRAITS IN INDIAN MUSTARD (*BRASSICA JUNCEA.* (L) CZERN & COSS)

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The present study was initiated to isolate the desirable parents exhibiting stable performance in F_1 and F_2 generation and also to have the estimation of nature and magnitude of genetic components involved in the inheritance of yield and its component traits in Indian mustard.

MATERIAL & METHODS

In the present study nine parents namely ; RH-30, Prakash, yellow rai K-1, RH-785, RC-1425, RH-780, RC-423 and RC-781 selected at random were hybridized in half diallelic fashion. The F_1 and F_2 generation of all the crosses along with their parents were grown in a randomized block design consisting of three replications. The F_1's and parents comprised of a single row each of 6 meter length and 45 cm apart, while F_2's had five rows plot of 6 meter length and 45 cm apart in all the replications. A spacing of 15 cm form plant to plant was also maintained for each genotype among all the replications. The data were recorded on five randomly selected plants from F_1's and parents and 20 plants from F_2's in each replications on the following quantitative traits ; seed yield, plant height, length of main raceme, primary branches, secondary branches, siliqua length, seeds per siliqua, siliquae on main raceme and 1000-seed weight. The data recorded for above traits were subjected to diallel analysis as per method suggested by Griffing (1956) method 2 and Model 1 for F_1's and F_2's ; Hayman (1954) for F_1's and Jinks (1956) for F_2's.

RESULTS AND DISCUSSION

The mean squares due to genotypes were significant for all the traits in F_1 and F_2 generation. The mean squares due to general and specific combining ability were also significant for all the traits in both generations (Table - 1). In order to have the clear picture with respect to additive and non-additive genetic components, the unbiased estimates due to general (6_g^2) and specific (6_s^2) combining ability were calculated which were further utilized to have the estimation of ratio $6_s^2/6_g^2$. This ratio indicated the presence of both additive and non-additive genetic components with the latter being more important for all the traits in F_1 and F_2 generation except for length of main raceme in F_1 generation and 1000-seed weight in both the generations. The differences in the estimation of these components in F_1 and F_2 generation for above traits may be due to the change in the distribution of genes in F_2 population or may be due to coupling phase of linkage (Robinson et al. 1960). The presence of non-additive genetic components have been reported by Chauhan and Singh (1979) and Yadav et al. (1981) for seed yield and Yadava et al. (1981) for secondary branches, siliqua length, seeds per siliqua, primary branches and 1000-seed weight.

The additive (D) and dominance component (H_1) was observed to be significant for all the traits in F_1 and F_2 generation (table-2). However, the magnitude of H_1 was higher as compared to D for all the traits in both the generations except for plant height, siliqua length and 1000-seed weight in F_1 and F_2 generation. These results were further confirmed when the ratio (H_1/D) 1/2, which measures the degree of dominance showed the presence of over-dominance for all the traits except for the above traits. Further, the ratio, $H_2/4H_1$ indicated the asymmetrical distribution among parents for all the traits in both the generations except for siliquae on main raceme in F_1 generation. The estimates with respect to the proportion of dominant and recessive genes in parents measured by $(4\ DH_1)1/2 + F\ /\ (4\ DH_1)1/2\text{-}F$ showed that for every one recessive gene affecting different traits there were about one to three dominant genes. The ratio h^2/H_2 measuring number of alleles or allele groups exhibiting dominance, was observed to be low for most of the traits. The low value recorded for this ratio might have been underestimated because of complementary interaction (Mather and Jones, 1971) and, therefore, no valid interpretation about gene groups exhibiting dominance could be made. The heritability (n.s.) was recorded to be of high order with respect to plant height, length of main raceme and siliqua length in both the generations.

The estimates of general combining ability effects presented in table-3 indicated that a parent 'Prakash' exhibited significant positive gca affects for seed yield, plant height, primary branches and siliqua length in F_1 and F_2 generation. A parent RC-781 attained significant positive gca effects for seed yield, plant height, primary branches and siliqua length in F_1 and F_2 generation. A parent RC-781 attained significant positive gca effects for plant height, primary branches and secondary branches in both the generations. Finally, the parent yellow rai K-1 was good general combiner for secondary branches ; RH-785 and RH-780 for tallness and seeds per siliqua ; RC-1425 for length of main raceme and RC-423 for tallness and primary branches. The order of suitability of good combiners based on per se performance and gca effects were different. But the order was same when the parents were selected on the basis of gca effects and array means confirming thereby the results of Yadav et al. (1981). The results obtained from both Griffing and Hayman's analysis indicated the preponderance of non-additive genetic component for most of the characters in F_1 and F_2 generation though the presence of appreciable amount of additive genetic component can not be ruled out. In order to utilize both additive and non-additive genetic variances, it would be worth while to make selection in further generations.

The dominance variance can be utilized by developing hybrid varieties, provided some cytoplasmic-genetic male sterile line with specific restorer is available.

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Table-1 : Analysis of Variance for Combining Ability in F_1 and F_2 (in parenthesis) generation.

Source	d.f.	Seed yield	Plant height	Length of main raceme	Primary branches	Secondary branches	Siliqua length	Seeds per siliqua	Siliquae on main raceme	1000-seed weight
GCA	8	750.00* (3631.17)*	212.20* (214.31)*	288.64* (147.77)*	2.57* (1.39)*	19.23* (21.80)*	0.46* (5.54)*	2.86* (55.39)*	166.35* (1.44)*	1.63* (3.63)
SCA	36	533.94* (2153.94)*	123.65* (125.13)*	32.07* (32.73)*	0.52* (0.40)*	14.11* (4.75)*	0.06* (1.63)*	1.65* (12.85)*	144.17* (.41)*	0.14* (0.14)*
Error	88	232.14 (207.63)	2o.70 (16.49)	8.56 (2.43)	0.18 (0.02)	1.64 (0.33)	0.03 (0.81)	0.30 (6.80)	98.30 (0.12)	0.01 (0.004)
$6^2s/6^2g$		10.73 (6.20)	5.92 (6.03)	0.92 (2.29)	1.54 (3.16)	7.84 (2.26)	0.75 (2.41)	5.86 (1.37)	7.34 (2.41)	0.87 (0.39)

Table 2 : Estimates of Components of Variation in F_1 and F_2 (in parenthesis) generation.

D	129.10* (172.7)*	451.00* (1130.00)*	120.20* (83.83)*	1.69* (0.33)*	8.88* (13.91)*	0.36* (8.69)*	2.35* (46.00)*	82.26* (1.61)*	1.44* (0.91)*
H_1	1616.00* (7882.00)*	518.00* (496.40)*	122.20* (142.10)*	1.74* (1.83)*	50.20* (18.67)	0.19* (5.51)*	7.00* (59.68)*	346.90* (1.84)*	0.89* (0.60)*
(H_1/D) 1/2	3.54 (6.76)	0.60 (0.66)	1.02 (1.30)	1.01 (2.82)	2.38 (1.16)	0.72 (0.80)	1.72 (1.14)	2.05 (1.17)	0.79 (0.81)
$H_2/4H_1$	0.20 (0.20)	0.16 (0.21)	0.21 (0.20)	0.21 (0.18)	0.22 (0.22)	0.12 (0.18)	0.18 (0.18)	0.25 (0.15)	0.14 (0.20)
$(4DH_1)$ 1/2 + F	1.40	1.80	1.44	0.55	1.45	4.30	2.38	0.38	3.97
$(4DH_1)$ 1/2 − F	(0.81)	(2.00)	(1.79)	(1.12)	(1.82)	(2.19)	(2.50)	(3.70)	(0.58)
h^2/H_2	1.23 (2.14)	1.05 (0.41)	0.10 (0.15)	0.55 (0.13)	1.27 (0.60)	0.85 (0.11)	0.33 (−0.003)	0.03 (0.12)	0.06 (0.85)
Heritability	5.12 (2.05)	93.26 (94.81)	53.54 (48.20)	32.75 (11.12)	15.36 (56.78)	105.11 (70.80)	32.50 (71.83)	10.27 (82.89)	140.17 (47.45)

* *Denotes significance at $P = 0.05$*

Table-3 : Estimates of general combining ability effects in F_1 and F_2 (in parentesis) generation.

	Seed yield	Plant height	Length of main raceme	Primary branches	Secondary branches	Siliqua length	Seeds per siliqua	Siliquae on main raceme	1000-seed weight
RH-30	9.80*	−1.38	6.49*	−0.87*	−1.58*	0.14	−0.42*	4.02	0.89*
	(−2.78)	(−7.24)*	(−0.14)	(−0.31)*	(−1.51)*	(0.44)	(−2.58)*	(−0.35)*	(1.47)
Prakash	8.72*	9.11	−1.76*	0.25*	0.01	0.14*	−0.06	1.11	0.10*
	(44.04)*	(14.38)*	(4.48)*	(0.12)*	(2.65)*	(0.92)*	(2.08)*	(0.32)*	(−0.15)
Yellow rai K-1	−16.82*	−35.45*	−1.84*	−0.65*	0.93*	−0.21	−0.72*	−4.75	−0.49*
	(−11.41)	(−24.84)*	(−6.33)*	(−0.18)*	(0.60)*	(−0.91)*	(−2.80)*	(0.30)*	(0.17)
RH-785	−3.52	6.36*	−1.02	−0.06	0.25	−0.19	0.78*	0.47	0.17*
	(8.74)*	(5.03)*	(2.46)*	−0.25*	(−0.71)*	(2.02)*	(1.71)*	(0.74)*	(−0.81)
RC-1426	4.87	19.37*	4.14*	−0.65*	−2.03*	−0.21	−0.44*	8.09	−0.14*
	(−10.66)*	(−18.10)*	(−3.55)*	(−0.16)*	(−1.11)*	(−2.15)*	(−0.73)*	(−0.05)	(−0.28)
RC-1425	5.33	0.59	5.68	−0.38*	−0.05	0.34	0.40*	−1.54	−0.19*
	(−7.47)*	(2.76)	(3.36)*	(−0.28)*	(0.59)*	(0.02)	(0.70)	(−0.38)*	(−0.28)
RH-780	−4.03	14.47*	−2.13*	0.02	−0.29	−0.04	0.52*	−0.14	(−0.22)*
	(2.01)	(9.10)*	(1.38)	0.16*	(−1.28)*	−0.27	(3.24)*	(0.14)	(−0.25)
RC-423	−2.58	8.42*	0.73	0.49*	0.24	−0.03	−0.29*	2.17	−0.01
	(−5.81)	3.87*	(1.83)*	(0.11)*	(−0.59)*	(0.16)	(−2.49)*	(−0.11)	(−0.41)
RC-781	−1.79	12.27*	−10.28 *	1.85*	2.52	−0.19	0.22	−2.87	−0.13*
	(−16.72)*	15.04*	(−3.49)*	(0.81)*	(1.42)*	(−0.77)	(0.88)*	(−0.01)	(−0.23)
S.E. (gi)	4.31	1.28	0.83	0.12	0.36	0.05	0.15	2.8	0.03
S.E. (gi)	(4.28)	(1.14)	(0.44)	(0.04)	(0.16)	(0.25)	(0.35)	(0.12)	(0.017)