Components of Genetic Variation for Yield Traits in Crosses of Indian Mustard [*Brassica juncea* (L.) Czern. & Coss.]

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A field experiment comprising of 4 F_1s, derived from crossing of contrasting parents for the characters *viz.*, plant height, primary branches/plant, siliqua/plant seeds siliquae, test weight and seed yield/plant and their 4F_2s, 4B_1s and 4B_2s was carried to study the genetic variability and inheritance of the yield attributing traits during *rabi* season in a non-replicated, compact family block design. A high coefficient of variation was observed in the F_2 of all the crosses, especially for yield/plant and number of siliqua/plant. Higher narrow sense heritability estimates were recorded for seed yield/plant followed by plant height and siliqua/plant in all the four crosses while number of primary branches/plant and seeds/siliquae showed low heritability. Genetic advance as percentage of mean was high for seed yield/plant and siliqua/ plant in most of the crosses. Selection for high number of siliqua/plant is expected to be the crucial selection criteria for yield improvement. Component of additive genetic variation for traits *viz.,* plant height, primary branches/plant, siliqua/plant and seed yield/plant in cross QM-2 x Pusa Barani was highest in magnitude compared to other three crosses for these traits. Importance of additive gene action was revealed in the inheritance of most of the characters under study.

Key Words: Coefficient of variation, Genetic advance, Heritability, Mustard, Variability

Introduction

Indian mustard [*Brassica juncea* (L.) Czern. & Coss.] is one of the most important oilseed crops of the country and it covers about more than six million ha during *rabi* season accounting about 13% of world's oilseed area and 7% of production (Singh and Dixit, 2008). Presently, average yield of oilseed is just around one ton/ha which need be increased to at least 1.3 and 1.6 ton by 2010 and 2015, respectively, if the country has to achieve self-sufficiency in edible oil (Hedge, 2006). With limited scope to bring additional area under oilseeds cultivation bulk of future increases in oilseed production have to come primarily from a combination of high yielding plant types and standard crop management practices. Therefore, there is a need of concentrated effort to develop high yielding varieties of this crop for increasing it's productivity and production. It is well known that useful biometrical information and the extent of the existing variability of the various economic or agronomic traits in the existing working germplasm are usually required in evolving superior, stable and widely adaptable varieties in field crops. Thus, information on the nature and magnitude of genetic variability operative in the inheritance of various yield component traits and yield itself would always be helpful to the plant breeders in selecting the parental genotypes to be utilized in breeding programme.

Materials and Methods

A field experiment was carried out during *rabi* season, 2005-06 at the Agriculture Research Farm of the Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. This research farm is situated at $25^0 2'$ N latitude and $83^0 03'$ E longitude at an altitude of 128.93 meters above the sea level. The material used in the present investigation comprised of four crosses (F_1s) involving six parental lines, their four F_2s and eight back crosses of Indian mustard. All the crosses and parental genotypes were evaluated in non-replicated, compact family blocks during *rabi* season 2006-2007. Three rows of parental and F_1 lines, 10 rows of F_2 and 6 rows of each back cross generation were raised for recording data. The spacing between row to row and plant to plant were 30 cm and 45 cm, respectively. Boarder plants were excluded for recording data. All the recommended package of practices for growing good crop were followed. The parental lines utilized were Agrani, NUDH-YJ-1, QM-2, Pusa Barani, Pusa Bahar, and LES-39. Four crosses were made from these parents *viz.*, cross 1 = Agrani×NUDH-YJ-1, cross 2= QM-2× Pusa Barani, cross 3 = NUDH-YJ-1×Pusa Barani

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Results and Discussion

The extent of variability in the present set of genotypes with respect to yield and yield components was estimated in terms of range, mean and coefficient of variation (CV). The range of variation for the all the traits *viz.*, plant height, primary branches/plant, siliqua/plant, seeds/siliquae, 1000-seed weight and seed yield/plant was higher in F_2 than both the back crosses (B_1 and B_2) in all the four crosses. Similarly CV for all the traits was higher in the F_2 of all the four crosses as compared to their respective parents, F_1s and back crosses, except seeds per siliquae (B_2). High estimates of coefficient of variation (> 30%) were recorded in the F_2 of all the crosses, for traits namely number of primary branches/plant, number of siliqua/plant and seed yield/plant (Table 1). Ali *et al.* (2002) and Singh (2004) working with mustard have also reported high CV for yield and yield components. Presence of considerable amount of variability suggest a good scope of practicing selection for these traits. In oilseed *Brassica***,** there is a compensatory relationship between number of seeds/ siliquae and test weight. Hence, an optimum number of seeds/siliquae coupled with high test weight would be a desirable criterion for improving yield in mustard. Yield as such is a complex trait being an integrated function of action and interaction of a number of yield components which themselves are often very complex quantitative attributes. In order to resolve the nature of inheritance of yield and yield component traits the components of genetic variation *viz.*, additive genetic variation, dominance genetic variation, degree of dominance, heritability estimates in narrow sense, and genetic advance as percentage of mean were estimated for all the characters under study in F_2 of four crosses (Table 2). In cross I and cross II, all the traits under study exhibited preponderance of additive genetic variance as compared to dominance genetic variance. The estimates of average degree of dominance revealed partial dominance in the inheritance of all the traits. In cross III (NUDH-YJ-1 x Pusa Barani), except for seeds/siliquae, all the traits exhibited higher magnitude of additive genetic variance than dominance genetic variance. The degree of dominance revealed complete dominance for seeds/siliquae and partial dominance for rest of the traits. Earlier workers have reported additive gene action (Sheikh and Singh, 2004), dominant gene action (Rai *et al.*, 2005) as well as both (Rishipal and Kumar, 1993) for seeds/siliquae. In cross IV (LES-39 x Pusa Bahar), primary branches/plant and siliqua per plant exhibited importance of dominance genetic variance over additive genetic variance while rest of the traits exhibited preponderance of additive genetic variance. The degree of dominance revealed over dominance for primary branches/plant and siliqua/plant. Rest of the characters exhibited partial dominance. Earlier workers in mustard have reported preponderance of dominance gene effect (Prakash *et al.*, 1998) for primary branches/plant.

Overall, in all the four crosses, degree of dominance revealed partial dominance for plant height, test weight and seed yield/plant (Table 2). Earlier workers in mustard have reported both partial dominance (Prakash *et al.*, 1998; Rai *et al.*, 2005) as well as additive gene action (Verma and Kushwaha, 1999; Sheikh and Singh, 2004) in the inheritance of plant height. Rishipal and Kumar (1993) have reported importance of both additive and dominance effect for test weight whereas, Singh *et al.* (2002) have reported importance of over dominance for it**.** Contrary to present finding, seed yield/plant has been reported to be governed mainly by dominance gene effect (Singh, 2004). Where as Rai *et al.* (2005) have reported partial dominance for seed yield/plant as is revealed in the present set of material. Comparison of the estimates of additive and dominant genetic variance in different crosses, it is revealed that the highest magnitude of additive genetic variance was observed in cross II for plant height followed by primary branches per plant, siliqua/plant and seed yield/plant. Seeds/siliquae and test weight showed nearly equal amount of additive genetic variance in all the crosses. Thus, we may follow single plant selection in F_2 progeny of cross II for improving component traits like plant height, primary branches/plant and siliqua/plant. This may be fruitful in isolating a superior line having increased yield. In cross IV which included parents namely LES-39 and Pusa Bahar, the siliqua/plant showed higher magnitude of dominant genetic variance as well as over dominance for the trait as compared to other crosses. So, we may go for hybrid breeding for this trait. Narrow sense heritability which is heritable portion of variance for

Table 1. Range and coefficient of variation (CV) of four crosses for yield contributing traits in Indian mustard.

Traits/ Crosses			Generations					
			P_1	P_2	F_1	B_1	B_2	F_2
Trait 1	C_1	Range	136-151	167-188	168-186	125-208	132-198	102-213
		CV	6.40	5.20	5.09	10.30	10.50	13.70
	C_2	Range	151-172	142-162	147-170	125-220	134-194	97-205
		CV	4.35	4.22	4.58	12.83	8.52	15.32
	C_3	Range	157-188	142-167	168-183	131-223	145-205	116-200
		CV	5.20	4.56	2.75	8.32	9.57	12.98
	C_4	Range	159-186	138-156	164-174	147-215	113-207	106-196
		CV	4.93	3.96	1.87	8.11	10.28	12.68
Trait 2	C_1	Range	4-6	4-6	5-7	3-9	3-8	1-8
		CV	17.87	16.76	10.93	21.87	22.31	30.32
	C_2	Range	5-6	5-7	4-6	4-9	3-10	3-10
		CV	9.50	12.49	13.04	26.07	27.72	32.27
	C_3	Range	4-7	5-7	6-8	2-10	4-10	2-10
		CV	16.76	12.49	9.58	25.10	21.08	34.44
	C_4	Range	4-7	4-6	5-7	4-9	3-9	2-9
		CV	13.58	12.96	12.63	23.34	24.44	30.62
Trait 3	C_1	Range	167-215	238-304	270-304	168-377	184-399	102-357
		CV	13.38	13.03	4.11	20.03	23.66	34.63
	C_2	Range	189-256	193-250	202-256	174-436	181-376	89-524
		CV	9.55	9.22	7.40	26.60	23.18	36.42
	C_3	Range	208-324	193-250	313-380	148-347	144-369	93-369
		CV	13.03	9.22	5.80	21.25	24.92	38.42
	C_4	Range	181-275	168-211	205-265	111-369	117-433	82-465
		CV	9.35	7.37	6.21	28.11	27.96	33.79
Trait 4	C_1	Range	11.67-14.67	12.67-15.67	10-12.67	9.33-14.33	9.67-15.33	9.33-16.33
		CV	6.34	5.53	6.84	9.84	11.14	12.08
	C_2	Range	9.33-14.33	9-12.33	10.33-14.67	9.33-14.33	9-13.67	6.33-17.0
		CV	13.75	8.52	9.94	13.18	14.38	13.36
	C_3	Range	12.67-15.67	9.33-12.33	11-13.67	8-15	5.33-16.33	8.33-15.67
		CV	5.53	10.31	6.80	14.57	16.43	15.73
	C_4	Range	15.33-17.67	10.67-12.67	13-14.67	10-17.67	9.33-16.67	7.58-17.0
		CV	4.33	5.26	4.64	10.28	12.83	12.25
Trait 5	C_1	Range	2.44-3.22	2.73-3.84	2.52-3.83	2.9-4.37	2.40-4.17	2.56-5.0
		CV	6.94	10.83	7.60	15.04	16.44	23.95
	C_2	Range	7.98-10.95	9.59-13.78	9.76-13.92	9.44-21.57	9.33-16.99	5.15-26.15
		CV	11.57	11.12	11.38	28.23	27.43	40.00
	C_3	Range	2.73-2.84	2.97-3.86	3.24-3.81	3.27-4.69	2.82-4.62	3.04-5.57
		CV	10.83	11.11	5.83	17.82	20.21	20.21
	C_4	Range	2.37-2.96	5.02-5.78	3.31-4.23	3.08-5.2	3.2-5.69	2.6-4.48
		CV	4.88	11.05	7.76	25.42	23.68	35.62
Trait 6	C_1	Range	2.73-2.84	2.97-3.86	3.24-3.81	3.27-4.69	2.82-4.62	3.04-5.57
		CV	10.03	8.42	7.40	11.69	14.24	15.00
	C_2	Range	2.44-3.16	2.95-3.86	2.76-3.91	2.96-3.87	2.91-3.94	2.32-5.4
		CV	8.22	8.47	9.94	15.65	17.25	18.38
	C_3	Range	9.3-13.61	9.63-13.78	13.17-16.58	8.63-21.5	8.62-26.32	5.44-17.63
		CV	8.42	7.87	11.15	15.53	14.44	15.76
	C_4	Range	9.73-11.21	9.12-12.95	9.59-12.63	8-24.66	7.63-26.89	5.53-25.5
		CV	4.88	11.05	7.76	25.42	23.68	35.63

Trait 1 = plant height, trait 2 = number of primary branches/plant, trait 3 = number of siliqua/plant, trait 4 = number of seeds/siliquae, trait 5 = test weight and trait 6 = seed yield/plant.

which selection can successfully be practiced was studied in four crosses. Estimate of narrow sense heritability was highest for seed yield/plant followed by plant height and test weight among all the four crosses under study. Singh *et al*. (2002); Mahala *et al*. (2003) and Rai *et al*. (2005) reported moderate to high estimates of heritability for yield/plant. High narrow sense heritability for seed yield/plant offers good opportunity for exploiting fixable variability for the improvement in seed yield in mustard. Primary branches/plant and seeds/siliquae, recorded lowest

Table 2. Estimates of degree of dominance, heritability and genetic advance in F_2s of Indian mustard

Estimates	Crosses	Plant Height	Primary branches/Plant	Siliqua/Plant	Seeds/Siliquae	Test weight	Seed yield/Plant
	Range	11.67-14.67	12.67-15.67	10-12.67	9.33-14.33	9.67-15.33	9.33-16.33
s^2A	C_1	305.15	0.79	2570.21	1.36	0.22	5.71
	C_2	347.73	1.46	4830.03	1.13	0.27	19.67
	C_3	298.40	1.16	3887.79	1.28	0.27	8.21
	C_4	286.18	0.65	1940.69	1.32	0.22	14.33
σ^2D	C_1	64.65	0.49	1279.61	0.33	0.03	0.02
	C_2	105.03	1.32	1408.47	0.36	0.10	0.84
	C_3	46.60	0.95	1519.37	1.40	0.09	1.05
	C_4	68.86	0.92	2279.43	1.09	0.06	1.47
$(\sigma^2D/ \sigma^2A)^{1/2}$	C_1	0.46	0.79	0.71	0.49	0.37	0.06
	C_2	0.55	0.95	0.54	0.56	0.37	0.21
	C_3	0.40	0.91	0.62	1.05	0.58	0.36
	C_4	0.49	1.19	1.08	0.91	0.52	0.32
H^2(ns)	C_1	67.27	39.90	56.64	58.64	58.57	66.67
	C_2	69.39	45.38	73.01	36.45	60.00	89.21
	C_3	75.47	44.27	65.00	36.36	62.79	78.19
	C_4	73.00	31.25	44.34	46.48	66.67	86.43
GS	C_1	29.32	1.16	78.60	1.83	0.79	4.58
	C_2	32.00	1.68	122.33	1.32	0.83	8.63
	C_3	30.91	1.48	103.82	1.41	0.85	5.22
	C_4	29.75	0.93	60.43	1.61	0.79	7.25
GSm	C_1	18.98	24.89	40.41	14.55	20.63	42.76
	C_2	21.90	30.43	54.77	10.02	22.74	73.51
	C_3	20.17	31.49	51.44	11.82	20.43	47.20
	C_4	19.07	19.75	30.86	11.70	22.83	63.43

Abbreviations: σ^2A= Additive variance, σ^2D = Dominance variance, $(\sigma^2D/ \sigma^2A)^{1/2}$ = Degree of dominance, Hns = Heritability in narrow sense, GS = Genetic Advance, GSm = GS as percentage of Mean, CV = Coefficient of variation, C_1= Cross 1 (Pusa Agrani × NUDH-YJ-1), C_2= Cross 2 (QM-2 × Pusa Barani) C_3 = Cross 3 (NUDH-YJ-1 × Pusa Barani) C_4= Cross 4 (LES-39 × Pusa Bahar).

estimates of narrow sense heritability in all the four crosses. This suggested poor scope of improving yield in mustard through selection for component traits namely primary branches/plant and seed/siliquae. Beside the heritability, genetic advance accomplishes meaningful genetic progress in crop improvement programme, therefore, selection of a character should be based on high heritability coupled with high genetic advance. High genetic advance as per cent of mean coupled with high heritability was observed for seed yield/plant and siliqua/plant in most of the crosses. Test weight which recorded high narrow sense heritability had poor genetic advance as percent of mean. This suggested that effective improvement in yield can be achieved by practicing selection for siliqua/plant rather than test weight. In cross III (NUDH-YJ-1 x Pusa Barani), highest genetic advance was observed for siliqua/plant followed by plant height (Table 2). Low Genetic advance was recorded for test weight, seeds/siliquae and primary branches/plant. The present findings regarding heritability and genetic advance are in accordance with those of Mahala *et al.* (2003) and Singh *et al.* (2003).

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