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Effectiveness of Selection from Biparental Mating in *Brassica juncea* (L.) Czern & Coss

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ABSTRACT

Biparental mating was attempted in F_2 generation of three crosses of Brassica Juncea (L.) Czern & Coss., according to North Carolina Design II, including a white rust resistant common parent, i.e. Poorbijaya. Most of the characters exhibited higher magnitude of additive genetic variance in Poorbijaya x NRCDR-2 and Poorbijaya x DRMRIJ-31 crosses, where as in Poorbijaya x Varuna cross, higher magnitude of dominance variance was observed for five characters. Selection was exercised among the biparental progenies for more branching, high oil content, high seed yield/ plant and least white rust resistant (WR) infection. The 18 best recombinants were selected from the total 2160 sampled plants and evaluated in replicated trials along with 4 basic parents, which also included the national check, Varuna to compare the yielding performance. There were 17 selections which indicated higher oil content than the check Varuna and 13 selections significantly out yielded the check. The best yielder 2 selections were also showed less WR infection as compared to even resistant parent.

Key words: *Brassica Juncea, Biparental Mating, Selection, Components of Genetic Variance*

INTRODUCTION

Indian mustard [*Brassica juncea* (L.) Czern & Coss.] occupy about 80 per cent of area under Indian subcontinent, but the national yield level is low as compared to other developed countries. The low yield of mustard could be attributed to past history of natural selection under moisture stress conditions that probably exhausted variation for the sake of adaptation as also observed by Stebbins[11]. Narrow genetic base is one of the reasons for its low yield and wider susceptibility to a number of diseases like white rust, alteraria and powdery mildew.

In the presence of linkages, an enormously large recombinational potential that is expected on an independent assortment of genes, may not be realised[4]. This narrow down the range of variation, hence the rare recombinants may not be available for selection in F_2 generation. On the contrary, under the regime of inbreeding, linkage blocks would be more intensified. Due to correlated response in F_2 generation, unfavourable genetic associations are likely to limit advance under selection. Studies in *Brassica Juncea* (L.) have shown that the visual selection of single plants basis for seed yield and oil content is effective in F_2 generation[3].

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The present investigation was therefore, aimed to know the consequence of Biparental mating and effectiveness of selection from inter mated progenies with change in level of association among yield and its component characters.

MATERIALS AND METHODS

The F_2 generation of three crosses, i.e. Poorbijaya x Varuna, Poorbijaya x NRCDR-2 and Poorbijaya x DRMRIJ-31, including a white rust resistance common parent, Poorbijaya, were used to generate biparental progenies (BIPs) according to North Carolina Design II [5]. Eight F_2 plants were assigned to a set at random, four being male parents and another four as female parents. All the sixteen possible intercrosses were made among these plants. Three such sets were produced to obtain 48 biparental crosses in each of the above F_2's, totalling 144 crosses and were evaluated in a randomised complete block deign with three replications. The sets and the progenies within the sets were randomised separately. Each plot comprised two rows of 4.0 meters length, with the spacing of 30 cm between rows and 10 cm between plants. Data were recorded on the five random plants per plot in respect of ten characters. The oil content was estimated with the help of Nuclear Magnetic Resonance Spectrometer (NMR). The data for white rust (WR) infection on leaves were recorded in percentage on sampled plants after two weeks of flowering. The severity of disease was recorded by using the scale as per Anonymous[2]. The per cent infection index was calculated by the formula given by Singh[10] which was subjected to angular transformation as developed by Fisher and Yates[6]. The components of genetic variance were estimated according to Comstock and Robinson[5].

Selection was then exercised among the 2160 total biparental plants for more branching, higher yield/plant, higher oil content and least WR infection index. The best selected 18 superior plants, designed as BIPs (S-1 to S-18), were evaluated in randomised complete block design with three replications, along with 4 basic parents, which also included national check, Varuna. The plot size was of four rows of 4.0 meters length with the spacing of 30 cm between rows and 10 cm between plants. Data was recorded on five randomly selected plants per plot for oil content, WR infection index and plot yield was converted to yield/hectare. Mean over replications were taken to compare the plant progenies with national check and better basic parent in corresponding F_2 cross using critical difference (CD) values.

RESULTS AND DISCUSSIONS

The components of genetic variance presented in table 1 have demonstrated that the progenies of Poorbijaya x Varuna showed more additive variance for days to anthesis, plant height, number of secondary branches, number on siliquae on main axis and length of siliqua and in Poorbijaya x NRCDR-2, additive variance was of higher magnitude for number of primary and secondary branches, number of siliquae on main axis, length of siliqua, seed yield per plant, oil content and WR infection index, however, in Poorbijaya x DRMRIJ-31, additive genetic variance appeared to be predominant for all the character except oil content. Variance components of the current investigation was negative in some cases which appeared to have resulted due to sampling error[8] and may be equated to zero.

The magnitude of additive component (σ^2_A) was higher than dominance components (σ^2_D) in Poorbijaya x NRCDR-2 and Poorbijaya x DRMRIJ-31. Whereas, in case of Poorbijaya x Varuna, higher magnitude of dominance variance (σ^2_D) was observed for five characters. However, additive genetic variance was of higher magnitude for number of secondary branches, siliquae on main axis and length of siliqua, in all the three crosses may offer opportunity for selection. Pattern of variation for further selection for yield potential, oil content and WR infection index in given in table 2.

The oil content in the parental population varied between 40.32 to 42.43 per cent. However, among the selected plant progenies, BIPs (S-10) from the cross

Poorbijaya x NRCDR-2 showed highest oil content of 44.23 per cent followed by BIPs (S-7). All the plant progenies showing significantly less infection for white rust as compared to the susceptible parents. BIPs (S-2), (S-6), (S-9) and (S-16) were superior to the resistant parent. Selection BIPs (S-1), (S-2), (S-4), (S-6), (S-8), (S-11), (S-17) and (S-18) were significantly higher yielder than the best parent. However, when national check was considered, 13 selection were found significantly superior.

The best high yielder selections, BIP (S-2) and (S-6) also showed less WR infection even as compared to the resistant parent. This has amply demonstrated that there is a shift in yield level in desired direction due to biparental mating and selection have created a new pattern of association which was not available in mustard crop. The above finding could be attributed due to the breakdown of unfavourable linkages and exposure of rare recombinants in the population, which remain restricted due to the linkage disequilibrium[9]. Higher means and wider ranges in the BIPs were also reported earlier by Shanti Patil *et al.*[7]. Singh and Murty[9] were also able to isolate three new recombinants out yielding the best control by between 14 and 39 per cent in *Brassica campestris.*

Table 1: Components of genetic variance, degree of dominance and heritability (narrow sense) for ten characters in biparental progenies of three crosses

Cross	Estimates/ components	Days to anthesis	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of siliquae on main axis	Length of siliqua (cm)	1000-seed weight (g)	Seed yield/ plant (g)	Oil content (%)	WR infection index (%)
Poorbijaya x Varuna	σ^2_A	10.53 **	80.24 **	1.77 *	10.74**	21.17 **	0.25 **	0.05	-9.66	0.04	11.17 *
	σ^2_D	4.30 *	30.28 *	2.51 **	3.28	2.28	0.11 **	0.25 **	83.47 **	5.86 **	13.73 **
	a	0.97	0.94	1.83	0.66	0.50	1.02	3.22	-	17.83	1.70
	h^2_{ns} (%)	92.45	43.32	31.29	25.84	23.95	77.12	13.47	-5.15	0.42	8.86
Poorbijaya x NRCDR-2	σ^2_A	9.10 **	54.84 *	1.77 **	8.49**	19.99 *	0.14 **	0.13 *	37.16 **	4.03 **	20.93 **
	σ^2_D	13.46 **	61.12 **	1.02 *	3.22	11.62	0.06 *	0.17 **	-20.02	3.92 **	15.72 **
	a	1.86	1.62	1.16	0.94	1.17	1.05	1.76	-	1.51	1.33
	h^2_{ns} (%)	68.96	27.96	42.80	24.72	19.05	57.03	23.46	26.11	39.45	15.25
Poorbijaya x DRMRIJ-31	σ^2_A	12.88 **	65.86 **	0.97 **	4.97**	19.15 *	0.09 **	0.18 **	20.88 *	1.98	7.41 **
	σ^2_D	4.76 **	17.84	0.32	-0.25	11.88	0.05 *	-0.05	3.69	4.99 **	1.64
	a	0.93	0.80	0.89	-	1.20	1.21	-	0.64	2.43	0.72
	h^2_{ns} (%)	69.85	34.83	28.93	20.15	17.97	42.08	51.36	15.65	22.06	20.62

*, **; Significant at 5% and 1% level, respectively

Table 2: Comparision of BIPs (selections) plant progenies with National check (Varuna) and better basic parent for three characters

Crosses	BIPs (selections)/ basic parents	Oil content (%)	WR infection index (%)	Yield/ hectare (kg)
Poorbijaya x Varuna	S-1	43.31** (**)	3.34**	1915.7** (**)
	S-2	43.23** (**)	1.80**	2214.3** (**)
	S-3	42.96*(*)	14.24**	1675.4*
	S-4	43.14** (**)	15.62**	1821.0** (*)
	S-5	42.56** (*)	7.16**	1658.4*
Poorbijaya x NRCDR-2	S-6	42.84*	1.59**	1984.9** (*)
	S-7	44.12** (*)	9.12**	1507.8
	S-8	43.02*	5.42**	1886.6** (*)
	S-9	43.33**	1.42**	1529.6
	S-10	44.23** (*)	5.17**	1459.7*
	S-11	43.55**	10.85**	1872.8** (*)
	S-12	42.88*	3.33**	1682.6*
	S-13	42.31	9.87**	1580.6
	S-14	43.14**	6.12**	1529.6
	S-15	41.52	7.23**	1692.8*
Poorbijaya x DRMRIJ-31	S-16	38.50	1.79**	1682.3
	S-17	42.84* (*)	2.01**	2112.3** (**)
	S-18	43.35* (**)	5.56**	1926.6*(*)
	Poorbijaya	40.32	1.97**	1260.1
	Varuna	40.89	23.70**	1282.0
	NRCDR-2	42.43	20.25**	1456.8
	DRMRIJ-31	40.97	13.11**	1506.5
	CD at 5%	1.61	2.71**	415.1
	CD at 1%	2.16	3.63**	556.8

*, **; Significant at 5% and 1% level, respectively

Significance marked in the parenthesis is comparison with better basic parent.

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