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Original Research Article

Triple Test Cross Analysis for Seed Yield, Oil Content and Its Component for Indian mustard (*Brassica juncea* L. Czern and Coss.)

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A B S T R A C T

The genetic basis for yield and yield contributing characters were investigated using triple test cross analysis in Indian mustard. The variation due to additive×additive type epistasis (i) was non-significant for all the characters except days to 50% flowering and days to maturity. The variation due to additive×dominance + dominance×dominance type epistasis (j+l) were non-significant for all the characters whereas, total epistasis were found significant for all the characters. Expression of epistasis was dependent on particular cultivars. Various lines contributed significant and positive epistatic deviations to the total epistasis. Additive (*D*) and dominance (*H*) genetic components controlled the manifestation of all the characters. However, The average degree of dominance $(H/D)^{1/2}$ ranged from 0.40 for primary branches per plant to 2.45 harvest index. Due to influence of epistatic effects for majority of the traits, recurrent selection may be recommended to develop high yielding Indian mustard varieties.

Keywords

Indian mustard (*Brassica juncea* L. Czern and Coss.)

Introduction

Rapeseed and mustard crops belong to genus *Brassica* and family Cruciferae having chromosome no. 2n=4X=36 in Indian mustard. This has become one of the most important sources of vegetable oil with the passage of time. Vegetable oils are one of the high value agricultural commodities. With the increase in world population, demand for high quality oilseeds continues to increase. Rapeseed and mustard are annually grown on about 28.46 million hectares in the world and provide 48.28 million tons of oilseed production. Rapeseed-mustard is the third important oilseed crop in the world after soybean (*Glycine max*) and palm (*Elaeis guineensis* Jacq.) oil. One of the main constraints is lack of reliable genetic information about the inheritance of yield and yield components on which breeding methodology is framed out. Different biometrical techniques viz., biparental cross (Comstock & Robinson, 1948, 1952), diallele and partial diallele cross (Hayman, 1954) and line x tester cross (Kempthorne, 1957) have been developed which provide information about additive and dominance genetic variances and fail to produce information about epistasis variance because their procedures are based on certain genetical assumptions including absence of non-alleleic interactions (Mather & Vines, 1952; Ospal, 1956; Sing & Sing, 1976). Some other biometrical tools *viz.*, generation mean analysis (Hayman, 1958; Jinks & Jones 1958), triallele and quadriallele analysis (Rawlings & Cokerham, 1962 a & b) and triple test cross (Kerasy & Jinks, 1968) provide information about all three components of genetic variance *i.e.*, additive, dominance and epistatic variances. The choice of most efficient breeding procedure depends on knowledge of the gene action controlling the economic characters. Most genetic models used to estimate the components of continuous variation assume absence of non-allelic interactions whereas, the facts is often contrary.

Triple test cross (TTC) design developed by Kearsey & Jinks (1968) is an extension of North Carolina Design III of Comstock & Robinson (1952) that is applicable to any population irrespective of its mating system and its gene and genotype frequencies (Kearsey & Jinks (1968). In the absence of epistasis TTC also provides unbiased estimates of additive (*D*) and dominance (*H*) components of genetic variation, degree of dominance $[(H/D)^{1/2}]$ as well as the direction of dominance (*rs.d*) with high degree of precision (Kerasy & Jinks, 1968). Ketata *et al.,* (1976) suggested a similar model of TTC where testers L1, L2 and L3 (L3=L1 x L2) were crossed to a number of varieties instead of F_2 individuals as proposed by Kerasy & Jinks (1968). The present study aims to detect epistasis along with estimation of additive and dominance components for different physio-morphological traits; genetically least exploited traits in Indian mustard. The information obtained through present study would help in understanding the genetic basis of the traits studied and making breeding strategy for the development of high yielding cultivar (s) or valuable germplasm in Indian mustard.

Materials and Methods

To study the relative magnitude of epistasis in comparison to additive and dominance components in Indian mustard *(Brassica juncea* L. Czern & Coss.*)*, the experimental materials were generated following triple test cross (TTC) design. The three testers, L_1 (NQR8807-13), L_2 (Divya-33) and their F_1 (NQR8807-13 x Divya-33) were crossed with eleven promising strains *i.e.*, Maya, JC 1359-23-558, Pusa Mustard 21, JC 3762, RGN 73, RH (OE) 0903, NDYR 8, LES 42, LES 43 LES 44 and LES 45 selected on the basis of their diverse genetic origin. Testers were used as male parents whereas, lines were used as female parents in TTC experiment. The resulting 22 single and 11 three-way crosses along with eleven lines and three testers were grown in randomized block design with three replications.

These strains/varieties were selected from the collection of genetic stock available in the oilseed section and investigation was conducted at Genetics and Plant Breeding Research Farm of Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.) during the *rabi* season 2012-13. Within each replication, each line was represented by row of 30 plants at a distance of 15 cm maintained by thinning. Each row was spaced 45 cm apart. Observations recorded on days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, length of main raceme, siliquae on main raceme, seeds per siliqua, seed yield per plant, 1000-seed weight, harvest index and oil content.

Results and Discussion

Highly significant differences in treatment, hybrids and parents were noted for all the traits whereas in lines showing highly significant for all the character except seeds/siliqua and in testers highly significant for all the characters except in siliquae on main raceme, seeds/siliqua and 1000 seed weight indicating presence of considerable variability among the genotypes (Table 1). The significant mean squares of P_1+P_2 Vs. F_1 were observed for all the characters except secondary braches/plant, siliquae on main raceme, seeds/siliqua, 1000 seed weight and oil content while in case of P_1 vs. P_2 significant mean squares were observed for all the traits excepting days to 50% flowering, days to maturity, siliquae on main raceme, seeds/siliqua and 1000 seed weight. These characters showed existence of worth of variations between testers (L_1 and L_2). High differences between L_1 and L_2 resulted into expression of high mean performance of their F_1 (L_3) as revealed by significant mean squares due to P_1 + P_2 vs. F_1. Since two testers represented highly significant differences for each character, therefore they would provide precise estimates of additive and dominance variance as reported by Kearsey & Jinks (1968). Except secondary branches/plant, seeds/siliqua and seed yield/plant, lines vs. testers were highly significant for all traits. In case of hybrids *vs* parents all the character showed highly significant mean square while for plant height, secondary branches/plant, seeds/siliqua and seed yield/plant.

Detection of epistasis

The analysis of variance for test of epistasis revealed that epistasis or non-allelic interaction were absent for most of the character in the present study except days to 50% flowering and days to maturity (Table 2). Significance of epistatic gene action in expression of yield and several yield components has also been reported earlier in rapeseed-mustard (Hirve & Tiwari, 1990; Ram Bhajan *et al.,* 1994). The (j+l) type epistasis, covering additive × dominance + dominance × dominance non-allelic interactions were non-significant while total epistasis were significant for all the characters. Results were in conformity to findings of many researchers: In barley, Prakash *et al.,* (2004) observed significant epistatic effects for flag leaf area. Epistatic effects were found for days to flowering by Kulshreshtha *et al.,* 1993; Saleem *et al.,* 2005b in rice. Non-allelic interactions were also documented for harvest index (Verma *et al.,* 1994) and yield/plant (Saleem *et al.,* 2005a) in rice. The interaction between (i) type epistasis × block and (j+ l) type epistasis × block were non-significant for all the characters. This indicated homogeneity of interaction variances for all characters studied. Therefore, the interactions were tested against pooled error (total epistasis × block). The interaction variance is again non-significant for all these characters.

Analysis of variances for sums and differences in triple test cross progenies for different characters are presented in (Table 3). The variation due to sums (L_1+ L_2) and differences (L_1–L_2) were found to be significant for all the characters. The mean squares due to sums and differences were used to estimate additive (D) and dominance (H) variances, respectively.

Additive and dominance component

Triple test cross analysis provides not only precise test of epistasis but also gives unambiguous estimates of additive (D) and dominance (H) components of genetic variation and average degree and direction of dominance.

Table.1 Analysis of variance (ANOVA) for 13 character in Indian mustard

Source of Variation	Degree of freedom	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Length of main raceme (cm)	Siliquae on main raceme	Seeds/ siliqua	1000 Seed weight (g)	Biological yield/plant	Seed yield/Plant (g)	Harvest index (%)	Oil content (%)
Replications	2	1.90*	1.58	3.45	0.05	1.26	2.02	4.01	0.37	0.02	3.40	0.40	0.31	0.07
Treatments	46	8.35**	81.74**	527.68**	1.76**	15.41**	136.09**	71.22**	3.40**	0.77**	785.54**	39.35**	53.96**	2.90**
Hybrids	32	8.25**	49.09**	562.53**	1.78**	17.39**	157.62**	87.71**	3.59**	0.73**	718.41**	29.86**	59.03**	2.63**
Parents	13	8.90**	152.24**	481.30**	1.41**	11.68**	86.06**	35.39**	3.17**	0.87**	725.03**	58.71**	45.19**	3.75**
Lines	10	10.2**	156.62**	381.82**	1.38**	13.56**	93.63**	42.30**	3.45	1.13**	206.02**	30.99**	36.28**	3.98**
Testers	2	4.11**	4.11*	508.83**	1.77**	8.06**	23.73**	0.09	2.86	0.02	829.00**	181.24**	70.55**	2.25**
P1+P2 Vs. F1	1	6.72**	6.72**	214.94**	2.42**	1.39	44.81**	0.02	3.55	0.02	1058.00**	207.717**	63.48**	0.02
P1 vs. P2	1	1.5	1.50	802.73**	1.13*	14.73**	2.67	0.17	2.16	0.02	600.00**	154.77**	77.63**	4.48**
Lines vs. testers	1	5.58**	404.76**	1420.99**	0.92*	0.05	135.02**	36.75*	0.93	0.02	5707.18**	90.80**	83.59**	4.30**
Hybrids vs. Parents	1	4.31**	210.49**	15.35	5.76**	0.59	97.63**	9.66	0.25	0.68**	3720.18**	91.41**	5.80**	0.65**
Error	96	0.48	0.95	11.94	0.17	1.09	3.36	4.19	1.02	0.03	5.42	0.37	59.51	0.04

*, ** significant at 5% and 1% level, respectively.

Table.2 ANOVA for the test of epistasis of triple test cross for thirteen characters in Indian mustard

Source of Variation	Degree of freedom	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Length of main raceme (cm)	Siliquae on main raceme	Seeds/ siliqua	1000 Seed weight (g)	Biological yield/Plant	Seed yield/Plant (g)	Harvest index (%)	Oil content (%)
i type epistasis	1	116.48**	393.82*	480.12	31.06	77.83	756.48	14.48	5.13	0.07	1.78	253.93	218.66	1.18
j + l type epistasis	10	64.15	1.97	1241.58	1.72	32.07	164.66	176.01	5.46	0.75	887.59	6.83	39.22	1.73
Total epistasis	11	68.90**	412.55**	12895.95**	48.31**	398.58**	2403.11**	1774.63**	59.75**	7.56**	8877.69**	322.19**	600.87**	18.45**
i type epistasis × block	2	29.12	98.45	120.03	7.76	19.46	189.12	3.62	1.28	0.02	0.45	63.48	54.66	0.29
j + l type epistasis × block	20	11.27	58.71	1796.56	7.75	57.24	342.99	271.12	14.13	1.28	1209.93	45.84	83.64	2.58
Total epistasis × block	22	12.89	62.32	1644.15	7.75	53.80	329.00	246.79	12.9	1.16	1099.97	47.44	81.00	2.37

*, ** significant at 5% and 1% level, respectively.

Table.3 ANOVA for sums and differences in triple test cross for thirteen characters in Indian mustard

Source of Variation	**Degree of freedom**	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**Primary branches/ plant**	**Secondary branches/ plant**	**Length of main raceme (cm)**	**Siliquae on main raceme**	**Seeds/ siliqua**	**1000 Seed weight (g)**	**Biological yield/plant (g)**	**Seed yield/plant (g)**	**Harvest index (%)**	**Oil content (%)**
Sums (L_1+L_2)														
Replication	2	6.30	2.94	8.24	0.077	6.54	7.28	26.04	4.27	0.01	6.53	0.41	1.40	0.18
Lines (Sums)	10	22.67**	62.80**	1230.66**	3.18**	29.94**	326.18**	183.14**	6.64*	1.43**	1065.01**	76.26**	40.88**	5.88**
Error	20	0.74	2.00	33.70	0.45	2.75	7.13	9.84	2.22	0.05	15.97	0.53	0.78	0.12
Differences (L_1-L_2)														
Replication	2	0.12	0.58	39.21	0.05	6.89	0.45	1.71	0.20	0.03	28.89	0.25	1.02	0.00
Lines (Differences)	10	8.14**	108.56**	764.95**	0.64**	22.09**	279.38**	91.74**	7.02*	1.34**	2812.09**	65.3**	240.81**	5.63**
Error	20	0.82	2.71	14.94	0.20	1.85	7.28	5.00	2.37	0.08	9.29	0.76	0.86	0.00

Table.4 Estimates of additive (D), dominance (H) variance components and degree of dominance

Components	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**Primary branches/ plant**	**Secondary branches/ plant**	**Length of main raceme (cm)**	**Siliquae on main raceme**	**Seeds/ siliqua**	**1000 Seed weight (g)**	**Biological yield/Plant (g)**	**Seed yield/plant (g)**	**Harvest index (%)**	**Oil content (%)**
D	29.25**	81.07**	2782.62**	3.63**	36.26**	425.41**	231.07**	5.88*	1.84**	1398.73**	100.97**	53.46**	7.68**
H	9.76**	141.14**	1000.00**	0.59**	26.98**	362.81**	115.65**	6.19*	1.68**	3737.06**	86.04**	319.93**	7.51**
$(H/D)^{1/2}$	0.58	1.32	0.60	0.40	0.86	0.92	0.71	1.03	0.96	1.63	0.92	2.45	0.99
r	-0.132	0.320	0.179	0.036	0.512	0.209	-0.171	-0.380	-0.111	-0.935**	-0.104	-0.67**	0.224

*, ** significant at 5% and 1% level, respectively

The additive and dominance components of genetic variances and degree of dominance are given in Table 4. The estimates of additive (D) genetic variances and dominance (H) variances were highly significant for all the characters except seeds/siliqua. The average degree of dominance $(H/D)^{1/2}$ ranged from 0.40 for primary branches/plant to 2.45 for harvest index. Over dominance were observed for days to maturity, seeds/siliqua, biological yield/plant and harvest index whereas, partial dominance were recorded for days to 50% flowering, plant height, primary branches/ plant, secondary branches/plant, length of main raceme, siliquae on main raceme, seed yield/plant, 1000-seed weight and oil content.

Negative and non-significant correlation (r) were noticed for days to 50% flowering, siliquae on main raceme, seeds/siliqua, 1000 seeds weight and seed yield/plant while, negative and significant for biological yield and harvest index. Positive and non-significant of correlation were recorded for days to maturity, plant height, primary branches/plant, secondary branches/plant, length of main raceme and oil content (Table 4). This design has successfully been applied by several workers in *Brassica* crops, employing in one or another form, taking F_2 population (Singh, 1986) or homozygous parents and their hybrids (Singh, 1989; Sriram, 1990; Ram Bhajan *et al.*, 1994). The importance of additive as well as dominance gene effects in inheritance of seed yield has been reported by Yadav *et al.*, 1983 and Jindal, 1980 noted significance of additive and non-additive variance for length of main raceme. Malviya *et al.*, 2009 also found epistasis for days to maturity and siliquae on main raceme. The predominance of dominance genetic variance was recorded for days to maturity, seeds/siliqua, biological yield/plant and harvest index. Krishna Nand (2000) also recorded predominance of dominance genetic variance for number. of seeds/siliqua.

The average degree of dominance suggested over dominance for days to maturity, seeds/ siliqua, biological yield/plant and harvest index while remaining characters were under control of partial dominance. Krishna Nand (2000) also reported over dominance for days to 50 % flowering while partial dominance for plant height, number of secondary branches/plant, length of main raceme, number of seeds/siliqua, 1000-seed weight, seed yield/plant and oil content.

The additive × additive epistatic component was significant only for days to 50% flowering and days to maturity and this epistatic component may act in fixable manner if handled carefully with such intention. The present study revealed that epistasis is an integral part of genetic system in Indian mustard for all the characters, therefore recurrent selection may be recommended for cultivar development from present triple test cross population.

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