Study on Gene Action for Yield and its Contributing Traits in Indian Mustard (*Brassica juncea* L.) under Timely Sown and Late Sown Condition

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Abstract—*The present investigation entitled "Genetic analysis of seed yield and its contributing characters using diallel cross analysis in Indian mustard (Brassica juncea L. (Czern and Coss)'' was conducted at Research Farm of Department of Genetics & Plant Breeding, Narendra Deva University of Agriculture and Technology, Narendra Nagar, Faizabad (U.P.) during rabi, 2015-16. The material for present investigation comprised of 66 F'₁s developed by crossing 12 diverse lines viz., NDYR 08, NDRE-08-04, NDRE-04, Narendra Rai, DRMR1127, EC399301, PAB-09-07, MCP 807, RAURD-09-02, NPJ 121, PAB-09-05 and DRMR-IJ-11275 in half diallel fashion design. A total of 80 treatments (66 F₁'s + 12 parents + 2 standard variety Kranti and Varuna) were used for investigation for seven traits. The ANOVA for diallel crosses revealed significant differences for mean square due to treatments for almost all the characters in both E₁ & E₂ conditions.*

Diallel cross analysis revealed the role of both additive and non-additive gene action for most of the characters in both conditions (E₁ and E₂), except for number of primary branches per plant in both the (E1 & E2) condition; plant height, length of main raceme in E₂, and seed yield in E₁, where dominance gene action played an important role. Average degree of dominance revealed the presence of over-dominance for all the characters in both the conditions (E₁ and E₂). The distribution of genes in the parents with positive and negative effects was asymmetrical for all the characters in both E₁ and E₂ conditions. The ratio of dominant and recessive alleles (KD/KR) indicated that dominant alleles were more frequent than the recessive ones for all the characters except for days to 50% flowering and secondary branches per plant in E₂ condition; primary branches per plant in both E₁ and E₂ conditions; and days to maturity in E₂ conditions where recessive genes were more frequent The proportion of h²/H₂ suggested that at least 3 major gene group were involved in the inheritance of almost all characters. The characters under both (E₁&E₂) conditions except plant height (cm) in E₁ and E₂ condition, where at least one major gene group was present. Positive values of correlation coefficient (r) between parental order of dominance (wr+vr) and parental measurement (Yr) for all the characters suggested the role of recessive genes were present.

Keywords: *Gene action, Indian mustard, additive and dominant gene action.*

1. INTRODUCTION:

Brassica occupies a prominent place in world's agrarian economy as vegetables, oilseed, feed, fodder, green manure and condiment. Brassica (rapeseed-mustard) is the second most important edible oilseed crop in India after groundnut and accounts for nearly 30% of the total oilseeds produced in the country. When compared to other edible oils, the rapeseed mustard oil has the lowest amount of harmful saturated fatty acids. It also contains adequate amount of the two essential fatty acids, linoleic and linolenic, which are not present in many of the other edible oils. Oilseed production assumes great importance in India because of gap in demand and supply of edible oils, which forced our country to import vegetable oils of millions of rupees, causing a heavy drain of the foreign exchange in past years (Khulbe *et al.,* 1998).

The understanding of the relative contribution of the genetic components *i.e,* additive, dominance, epistasis and linkage that control the variation is of great importance for any improvement in a trait under a breeding programme. Information regarding additive genetic variance, dominance variance, environmental component of variation, proportion of positive and negative genes, distribution of genes among the parents, maternal and reciprocal effects, ratio of dominant and recessive genes and average degree of dominance can be obtained through the diallel analysis (Hayman's approach). Information regarding relative importance of average effect of genes, dominance deviation and effect due to epistasis, in determining genotypic values of individuals and consequently, mean genotypic values of families and generations can be derived through generation mean analysis.

The fundamental objectives of plant breeders is to evolve the variety which combine productivity with quality under favorable and stress conditions. However, this superiority of the improved type caused by certain specific gene combinations can be marshaled in a specific plant of variety and it depends on the system through which the genes in the material available are mobilized.

2. MATERIALS AND METHODS:

The experiment was conducted during crop season *rabi*, 2015-16 at Research Farm of Department of Genetics & Plant Breeding, Narendra Deva University of Agriculture and Technology, Narendra Nagar, Faizabad (U.P.). This area falls in sub-tropical climatic zone. The soil type is sandy loam. The climate of district Faizabad is semi-arid with hot summer and cold winter. The experimental material consisting 80 treatments (66 F_1's + 12 parents + 2 standard variety Kranti and Varuna) were sown in Randomized Block Design with three replications in two dates of sowing *i,e.* on October 12 timely sown (TS) and November 2 late sown (LS), 2015. The entries were sown in a single row plot of 3 m with inter and intra-row spacing of 45 cm and 15 cm, respectively. The material for present investigation comprised of 66 F'$_1$s developed by crossing 12 diverse lines *viz.*, NDYR 08, NDRE-08-04, NDRE-04, Narendra Rai, DRMR1127, EC399301, PAB-09-07, MCP 807, RAURD-09-02, NPJ 121, PAB-09-05 and DRMR-IJ-11275 in half diallel fashion design. A total of 80 treatments (66 F_1's + 12 parents + 2 standard variety Kranti and Varuna) were used for investigation for seven traits *viz:* days to 50 % flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, length of main raceme (cm) and seed yield per plant (g). Workout gene actions for seed yield and its contributing traits using Numerical approach (Griffing, 1956 b).

3. RESULTS

The components of variation showed the both additive and dominance gene action played an important role in the inheritance of days to maturity, Length of main receme (cm) in both the conditions (E_1 & E_2) and plant height, and length of main raceme in E_1 condition. Days to 50% flowering, Plant height (cm) and Primary branches/ plant showed dominance genetic variance in both the conditions (E_1 & E_2). While, the Secondary branches / plant showed additive gene action in E_1 condition, where dominance gene action played an important role in the inheritance. Similar finding were reported by Kumar *et al.* (1994), Lal *et al.* (2011), and Singh & Singh (2012).

The inconsistency in the estimates of analytical method may be explained on the ground that the estimates obtained through the formulae of the mean of the degree of dominance may not be appropriate for explaining the degree of dominance in real sense, Since, particular combination of either positive or negative alleles may have complementary type of gene action or simply correlated gene distribution may seriously inflate the mean degree of dominance and convert to partial dominance into a apparent over dominance (Hayman,1954). These are in confirmation to the earlier findings of Singh *et al.* (2002) for seed yield, number of secondary branches per plant.

The ratio $(\hat{H}_2/4\hat{H}_1)^{1/2}$ which estimates frequency of alleles with positive and negative effects in parents showed an asymmetrical distribution of alleles with positive and negative effects since this value was less than 0.25. This suggested that the distribution of loci among these parents was not balanced in the characters under study.

The ratio of dominant and recessive alleles (KD/KR) indicated the dominant alleles for all the characters except Primary branches/ plant in both conditions, where recessive genes were frequent. The ratio determines the extent of genetic gain that can be made in a particular direction. If the alleles present in the population are pre dominantly of recessive nature, the extent of genetic advance will be limited. The ratio of $\left(\hat{h}^2/\hat{H}_2\right)$ which estimates the number of genes groups suggested that at least 3 major gene group was involved in the inheritance of almost the characters under both (E_1 & E_2) conditions except plant height (cm) in E_1 and E_2 conditions respectively, where at least one major gene groups were present.

This may be due to the cancelling effects of dominant gene with positive and negative effects, which nullify the effects of each other. It is not much reliable as it under estimates the number of genes and provides no information about group of genes exhibiting little or no dominance. The complementary gene interaction also depresses this ratio, hence the value may differ from actual numbers.

The correlation coefficient (r) between parental order of dominance (wr+vr) and parental measurement (Yr) for all the characters suggested the role of recessive genes was present. This indicated that higher expression of these traits was controlled by dominant genes. The positive value of correlation was observed for rest of the traits. The negative correlation suggest preponderance of dominant genes while positive value suggested preponderance of recessive genes in the expression of traits.

4. DISCUSSION

The ANOVA for design of experiment of diallel crosses revealed significant differences for mean squares due to treatments for almost the characters in both E_1 & E_2 conditions. Diallel cross analysis revealed the role of both additive and non-additive gene action for most of the characters in both conditions (E_1 and E_2), except for number of primary branches per plant in both the (E1 & E2) conditions; plant height, length of main raceme in E_2, and seed yield in E_1, where dominance gene action played important role. Average degree of dominance revealed the presence of over-dominance for all the characters in both the conditions (E_1 and E_2). The distribution of genes in the parents with positive and negative effects was asymmetrical for all the characters in both E_1 and E_2 conditions. The ratio of dominant and recessive alleles (KD/KR) indicated that dominant alleles were more frequent

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than the recessive ones for all the characters except for days to 50% flowering and secondary branches per plant in E_2 condition; primary branches per plant in both E_1 and E_2 conditions; and days to maturity in E_2 conditions where recessive genes were more frequent.

The proportion of h^2/H_2 suggested that at least 3 major gene group was involved in the inheritance of almost all the characters under both (E_1 & E_2) conditions except plant height (cm) in E_1 and E_2 condition, where at least one major gene groups were present.

Table 1: ANOVA for a set of 12 x 12 diallel crosses in Indian mustard under timely sown (TS) and late sown (LS) condition involving parents and F_1s

Characters	d.f.	Source of variation					
		Replication		Treatments		Error	
		2		79		158	
		E_1 (TS)	E_2 (LS)	E_1 (TS)	E_2 (LS)	E_1 (TS)	E_2 (LS)
Days to 50% flowering		1.078	0.16	88.74**	61.32**	0.53	0.56
Days to maturity		0.09	1.12	149.71**	99.10**	0.46	0.62
plant height (cm)		50.67	4.32	395.05**	102.34**	17.76	7.22
Primary branches/ plant		2.45	1.78	1.95**	1.15*	1.05	0.66
secondary branches per plant		1.95	1.7	60.53**	2.47**	3.96	1.1
Length of main receme (cm)		1.99	0.8	84.72**	76.38**	8.33	3.97
Seed yield per plant (g)		0.21	0.20	44.19**	4.98**	0.23	0.33

Note-, ** significant at 5% & 1% probability levels, respectively.*

Table 2: Estimates of parameters $\hat{D}, \hat{F}, \hat{H}_1, \hat{H}_2, \hat{h}^2, \hat{E}$ and other related statistics for 7 quantitative characters in 12 x 12 diallel crosses of Indian mustard under timely sown (TS) and late sown (LS) condition

Characters / Environments / Source	days to 50 % flowering		days to maturity		plant height	
	E_1 (TS)	E_2 (LS)	E_1 (TS)	E_2 (LS)	E_1 (TS)	E_2 (LS)
$\hat{D}$	31.62**±3.02	14.03**±1.98	16.51**±12.47	21.95**±4.03	174.59±45.20	70.44±6.52
$\hat{F}$	17.57**±6.86	-0.96±4.50	-14.46±28.27	38.55**±9.14	181.61±102.45	80.25±14.78
$\hat{H}_1$	63.88**±6.05	38.42**±3.97	119.44**±24.96	93.53**±8.07	457.43±90.43	101.09±13.05
$\hat{H}_2$	57.07**±5.03	36.53**±3.30	88.47**±20.76	72.76**±6.71	386.04±75.22	77.02±10.85
$\hat{h}^2$	245.10**±3.36	150.57**±2.20	140.63**±13.88	423.99**±4.49	305.84±50.29	160.13±7.26
$\hat{E}$	0.17**±0.83	0.17**±0.55	0.15**±3.46	0.21**±1.11	6.14±12.53	2.38±1.80
$(H_1/D)^{0.5}$	1.42	1.65	2.69	2.06	1.61	1.19
$(H_2/4H_1)$	0.22	0.23	0.18	0.19	0.21	0.19
(KD/KR)	1.48	0.59	0.72	2.48	1.94	2.81
(h^2/H_2)	4.29	4.12	1.59	5.82	0.79	2.07
t^2	0.94	0.06	3.52	6.18	1.59	2.25
a (intercept)	-4.54	-4.31	-1.11	-9.58	13.25	0.12
B (slope)	0.81±0.11	0.86±0.13	0.34±0.16	0.56±0.11	0.25±0.20	0.63±0.13
R	0.920	0.893	0.555	0.848	0.362	0.824
b-o/SE(b)	-7.438	-6.260	-2.110	-5.066	-1.227	-4.599
(1-b/sb)	1.677	1.008	4.007	3.890	3.653	2.681

Note-, ** significant at 5% & 1% probability levels, respectively.*

Characters	primary branches per plant		secondary branches per plant		length of main raceme		seed yield per plant (g)	
Environments Source	E_1 (TS)	E_2 (LS)	E_1 (TS)	E_2 (LS)	E_1 (TS)	E_2 (LS)	E_1 (TS)	E_2 (LS)
$\hat{D}$	0.01**±0.17	-0.13±0.06	0.63**±2.72	-0.07±0.13	24.40**±5.10	26.95**±3.98	6.13±1.59	0.61±0.24
$\hat{F}$	-0.16±0.40	-0.19±0.14	1.16**±6.18	-0.30±0.30	15.94**±11.56	18.97**±9.02	4.27±3.61	0.91±0.55
$\hat{H}_1$	1.26**±0.35	0.59**±0.13	65.19±5.46	1.73**±0.26	71.93**±10.21	64.64**±7.96	36.00±3.18	5.21±0.49
$\hat{H}_2$	1.31**±0.29	0.64**±0.10	61.60**±4.54	1.83**±0.22	65.39**±8.49	59.47**±6.62	30.51±2.65	4.29±0.40
$\hat{h}^2$	5.35**±0.19	3.69**±0.07	209.70**±3.03	7.78**±0.14	186.70**±5.67	144.57**±4.43	144.38±1.77	12.63±0.27
$\hat{E}$	0.35**±0.04	0.22**±0.01	1.34**±0.75	0.36**±0.03	2.77**±1.41	1.29**±1.10	0.07±0.44	0.11±0.06
$\left(H_1/D\right)^{0.5}$	9.08	2.07	10.10	4.72	1.71	1.54	2.42	2.92
$\left(H_2/4H_1\right)$	0.25	0.27	0.23	0.26	0.22	0.23	0.21	0.20
$\left(KD/KR\right)$	0.25	0.49	1.19	0.41	1.47	1.58	1.33	1.68
$\left(h^2/H_2\right)$	4.08	5.72	3.40	4.25	2.85	2.43	4.73	2.94
t^2	9.68	1.57	17.20	0.81	4.03	0.52	4.55	0.26
a (intercept)	-0.05	-0.07	0.11	-0.12	-4.72	-5.11	-3.21	-0.18
B (slope)	0.24±0.12	0.24±0.20	0.00±0.10	0.27±0.22	0.61±0.12	0.74±0.15	0.54±0.12	0.21±0.26
R	0.519	0.346	0.004	0.362	0.848	0.838	0.809	0.250
b-o/SE(b)	-1.920	-1.166	-0.013	-1.229	-5.070	-4.856	-4.348	-0.817
(1-b/sb)	6.026	3.684	9.351	3.185	3.243	1.707	3.572	3.009

Note-, ** significant at 5% & 1% probability levels, respectively.

REFERENCES

[1] Griffing, B. (1956b). A generalized treatment of the use of diallel crosses in quantitative inheritance. *Heredity*, **10**: 31-50.

[2] Khulbe, R. K. Pant, D. P. and Rawat, R. S. (1998). Combining ability analysis for yield and its components in Indian mustard. *Journal of Oilseeds Research*; 15(2):219-226. 4.

[3] Lal Mohan; Singh, D.P. and Bagadi, D.L. (2011). Combining ability analysis for seed yield and its components in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Agricultural Science Digest,* **31**(1): 35-37.

[4] Malik, S. I., H. N. Malik, N.M. Minhas and M. Munir (2004). General and specific combining ability studies in maize. *Int. J. Bio.,* 6: 856–9.

[5] Singh, D. K., Kumar, K. and Singh, P. (2012). Heterosis and heritability analysis for different crosses in Brassica juncea with inheritance of white rust resistance. *Journal of Oilseed Brassica*, 3(1):18-26.

[6] Kumar,P.; Gupta, S.K.; Dhawan, K.; Kamboj, M.C. and Mehta, S.L. (1994). Genetic architecture of oil content in Indian mustard. *Crop Res.,* **7**(1): 68-71.

[7] Hayman, B.I., (1954b). The analysis of variance of diallel tables. *Biometrics*, **10**: 235–44.