Assessing Gene action for Yield and its Contributing Traits in Indian Mustard (*Brassica juncea* L.) under Timely and Late Sown Conditions

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ABSTRACT

The present investigation 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. Sixty six 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 F_1's + 12 parents + 2 standard variety Kranti and Varuna) were used for investigation for thirteen traits. 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 siliquae on main raceme in E_2, and seed yield in E_1, 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 (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 except seeds per siliquae in both E_1 and E_2 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 seeds per siliquae in both E_1 and E_2 conditions; and the proportion of h^2/H_2 suggested that at least 3 major gene group were involved in the inheritance of almost all characters. The characters under both (E_1&E_2) conditions except biological yield (g) in E_1 and E_2 conditions respectively, 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.

KEYWORD

Indian mustard, Gene action, additive and dominant gene action

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). Specific combining ability and general combining ability can provide information about the type of gene action controlling a trait. Variance for general combining ability (GCA) is the additive portion while specific combining ability (SCA) is the non-additive portion of total variance (Malik *et al.* 2004). 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.

It is highly desirable to increase the productivity and stability through development of efficient plant types, which have the genes for higher seed yield and oil content. For this there is requirement of quantitative characterization of variability present in the crop by understanding the nature of gene action involved in the inheritance of yield and its component traits.

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.

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 annual rainfall is about 1270 mm. 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

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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.,* number of siliquae on main raceme, seeds per siliqua, 1000-seed weight (g), biological yield (g), seed yield per plant (g), harvest index (%) and oil content (%). Workout gene actions for seed yield and its contributing traits using Numerical approach (Griffing, 1956 b).

RESULTS AND DISCUSSION
The components of variation showed the both additive and dominance gene action played an important role in the inheritance of number of siliquae on main raceme in E_1 condition. Seeds/ siliquae, showed dominance genetic variance in both the conditions (E_1& E_2), 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.* (1996) for oil content, Singh *et al.* (2002) for seed yield, and number of siliquae on main raceme.

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 seeds/ siliquae 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 $(\hat{h}^2/\hat{H}_2)$ 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 biological yield (g) in E_2 condition, 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 (Gilbert, 1958). 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.

CONCLUSION
The ANOVA for design of experiment of diallel crosses revealed significant differences for mean squares due to

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)
No of siliquae on main receme		5.12	2.63	65.69**	59.73**	6.6	3.32
Seeds per siliquae		2.26	0.9	1.44	3.14**	1.19	1.27
1000 Seed weight (g)		0.004	0.0002	1.60**	0.72**	0.02	0.0009
Biological yield (g)		0.7	26.77	740.14**	82.98**	20.98	9.57
Seed yield per plant (g)		0.21	0.2	44.19**	4.98**	0.23	0.33
Harvest index (%)		0.34	1.35	5.16**	4.29**	0.4	0.59
Oil content (%)		0.0002	0.007	2.09**	1.49**	0.006	0.002

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	no of siliquae on main receme		seeds per siliquae		1000 seed weight (g)	
Environment Source	**E₁ (TS)**	**E₂ (LS)**	**E₁ (TS)**	**E₂ (LS)**	**E₁ (TS)**	**E₂ (LS)**
$\hat{D}$	14.12**±5.34	13.10**±3.91	-0.07+0.12	-0.04±0.17	0.51±0.07	0.19±0.03
$\hat{F}$	11.43**±12.11	9.35**±8.86	-0.30+0.27	-0.21±0.40	0.21±0.16	0.06±0.08
$\hat{H}_1$	59.98**±10.69	51.90**±7.82	0.72+0.24	2.37±0.35	1.15±0.14	0.62±0.07
$\hat{H}_2$	55.54**±8.89	47.52**±6.50	0.84+0.20	2.52±0.29	0.91±0.12	0.56±0.06
$\hat{h}^2$	242.17**±5.94	171.06**±4.35	1.27+0.13	9.95±0.19	3.05±0.08	1.51±0.04
$\hat{E}$	2.23**±1.48	1.11**±1.08	0.40+0.03	0.42±0.04	0.00±0.02	0.00±0.01
$H_1/D^{0.5}$	2.06	1.99	3.02	7.59	1.49	1.81
$H_2/4H_1$	0.23	0.22	0.29	0.26	0.19	0.22
KD / KR	1.48	1.437	0.22	0.49	1.31	1.20
h^2/H_2	4.36	3.59	1.52	3.94	3.34	2.65
t²	0.518	1.11	0.58	4.99	0.06	5.90
a (intercept)	-6.86	-3.77	-0.09	-0.24	-0.09	-0.14
B (slope)	0.66±0.17	0.55±0.17	0.36+0.22	0.36±0.14	0.80±0.16	1.16±0.39
r	0.771	0.704	0.452	0.614	0.837	0.683
b-o/SE(b)	-3.823	-3.136	-1.602	-2.457	-4.84	-2.960
(1-b/sb)	1.910	2.499	2.785	4.365	1.208	-0.420

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

Characters	biological yield (g)		seed yield per plant (g)		harvest index		oil content (%)	
Environment Source	**E₁ (TS)**	**E₂ (LS)**	**E₁ (TS)**	**E₂ (LS)**	**E₁ (TS)**	**E₂ (LS)**	**E₁ (TS)**	**E₂ (LS)**
$\hat{D}$	113.64±36.00	15.09±7.26	6.13±1.59	0.61±0.24	0.54±0.46	0.25±0.19	0.39±0.11	0.10±0.10
$\hat{F}$	90.80±81.59	12.08±16.47	4.27±3.61	0.91±0.55	0.29±1.05	0.16±0.43	0.11±0.25	0.04±0.23
$\hat{H}_1$	632.51±72.02	90.50±14.54	36.00±3.18	5.21±0.49	4.87±0.93	3.61±0.38	1.72±0.22	1.50±0.20
$\hat{H}_2$	519.75±59.90	77.11±12.09	30.51±2.65	4.29±0.40	4.45±0.77	3.41±0.31	1.44±0.18	1.37±0.17
$\hat{h}^2$	1904.62±40.05	48.19±8.08	144.38±1.77	12.63±0.27	12.66±0.51	15.68±0.21	4.06±0.12	4.01±0.11
$\hat{E}$	7.04±9.98	3.26±2.01	0.07±0.44	0.11±0.06	0.13±0.12	0.20±0.05	0.00±0.03	0.00±0.02
$H_1/D^{0.5}$	2.35	2.44	2.42	2.92	2.98	3.78	2.07	3.88
$H_2/4H_1$	0.20	0.21	0.21	0.20	0.22	0.23	0.21	0.22
KD / KR	1.40	1.39	1.33	1.68	1.20	1.18	1.15	1.11
h^2/H_2	3.66	0.62	4.73	2.94	2.84	4.59	2.81	2.92
t²	0.19	5.46	4.55	0.26	4.54	3.97	4.10	7.46
a(intercept)	-63.63	1.57	-3.21	-0.18	-0.11	-0.33	-0.06	0.01
B (slope)	0.58±0.21	0.12±0.15	0.54±0.12	0.21±0.26	0.23±0.16	0.42±0.14	0.46±0.14	0.06±0.14
r	0.652	0.249	0.809	0.250	0.425	0.670	0.711	0.137
b-o/SE(b)	-2.710	-0.810	-4.348	-0.817	-1.480	-2.850	-3.199	-0.437
(1-b/sb)	1.910	5.540	3.572	3.009	4.740	3.840	3.759	6.497

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

treatments for almost the characters in both E_1 & E_2 conditions except seeds/ siliquae under timely (E_1) 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 harvest index in both the (E1 & E2) conditions; number of siliquae on 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 except

seeds per siliquae in both E_1 and E_2 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 seeds per siliquae in both E_1 and 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 biological yield (g) in E_2 condition, where at least one major gene groups were present.

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