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Genetic components analysis for seed yield and its contributed traits in Indian mustard (*Brassica juncea* L. Czern & Coss)

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Abstract

Analysis of variance revealed that the genotypes were genetically-differ to each for all the characters. Genetic components analysis exhibited that both additive and dominance components were highly significant for almost all the traits indicating the role of both additive as well as non-additive gene action in controlling the expression of concerned traits. In general dominance component values were higher than that of additive component for all the traits. The estimates of average degree of dominance indicated presence of over-dominance for all the traits.

Keywords: *Brassica*, genetic components, Indian mustard and seed yield

1. Introduction

The oil obtained from different forms of rapeseed mustard show slight variation in percentage of oil. The oil content varied from 37 to 49 per cent. Mustard oil contains about 70% mono-unsaturated fatty acid (MUFA) of which 42% is erucic acid and 12% oleic acid. The seed and oil are used as condiments in the preparation of pickle and for flavour carrying out vegetables. The oil is utilized for human consumption throughout northern India in cooking and frying purposes. The oil cake is used as a cattle feed and manure. Green stems and leaves are a good source of green fodder for cattle.

2. Materials & Methods

The present investigation was carried out at Oil Seed Research Farm, Kalyanpur of Chandra Shekhar Azad University of Agriculture & Technology, Kanpur, during rabi season 2013-15. The experiment was conducted in Randomized Block Design (RBD) with three replications. 7 parents/strains (Varuna, RK-9101, Pusa jagannath, RH-9801, Pusa bahar, Rohini & Kanti) were crossed in diallel mating design (excluding reciprocal crosses). 28 genotypes (21 F₁ + 7 parents) were evaluated for 13 characters viz. Days to flowering, Number of primary branches, Number of secondary branches, Days to maturity, Plant height, Number of siliquae per plant, Length of main raceme, Number of seeds per silique, Biological yield per plant (g), Harvest index (%), 1000-Seed weight (g), Oil content (%) and seed yield per plant (g). The parents and F₁s were growing in single row of five meter length spaced 45 cm apart. The distance of 15 cm between the plants in a row maintained by thinning. All the recommended agronomic practices were followed for raising the good crop. The components of variance in diallel cross were computed by the use of formula suggested by Hayman (1954a)^[9]. Oil content was estimated with the help of NMR.

3. Results & Discussion

The results of analysis of variance are presented in table-1. The analysis of variance was carried out for thirteen characters for testing the significance of differences amongst the genotypes. Highly significant differences were recorded among the treatments for all the characters. Analysis of variance further indicated highly significant differences among the parents except number of secondary branches per plant and biological yield. Highly significant differences were also found among F₁s for all the characters except days to flowering, number of primary branches, number of seeds per siliquae, biological yield, parent vs. F₁s revealed highly significant differences for all the characters except biological yield. Similar findings were also observed by Kumar *et al.* (2000)^[13], Dond *et al.* (2012)^[4], Ghosh *et al.* (2002)^[6], Goswami *et al.* (2005)^[7], Monalisa *et al.* (2005)^[16], Nair *et al.* (2005)^[17], Lohia *et al.* (2008)^[15], Singh *et al.* (2008b)^[22], Nigam *et al.* (2009)^[18], Gupta *et al.* (2010)^[8], Frasad *et al.* (2012), Arifullah *et al.* (2012)^[1], and Dholu *et al.* (2014)^[3].

The results of analysis of components of genetic variance are presented in table-2, 3 and 4. Analysis of components was carried out for all the thirteen characters in F_1 generation. Regression coefficient 'b_i' deviated from less than unity for all the characters except days to maturity. Such significant deviation of regression coefficient from unity indicates non-allelic gene interaction (*epistasis*), while the regression coefficient did not deviate significantly from unity for plant height and number of siliquae per plant, indicating the involvement of additive gene action. The estimates of all genetic components viz., \hat{D} , \hat{H}_1 , \hat{H}_2 , \hat{F} , \hat{h}^2 and \hat{E} along with their standard errors were calculated. The estimates of additive components (\hat{D}) were highly significant for Day to flowering, number of primary branches, number of secondary branches, days to maturity, plant height, length of main raceme, number of siliquae per plant and number of seeds per siliqua, biological yield, harvest index, 1000 seed weight, oil content and seed yield per plant. The estimated dominance components (\hat{H}_1 and \hat{H}_2) was highly significant for all character except harvest index. The estimates of \hat{H}_1 were higher than that of the estimates of \hat{h}_i for all characters. It indicates unequal distribution of positive and negative alleles. The dominant components exhibited the prevalence of non-additive gene action for controlling these attributes. All the estimates of \hat{F} (mean of Fr value, where Fr is the proportion of negative effects of Genes in r^{th} parents) was positive and significant for all the characters except number of secondary branches and harvest index. Indicating the excess of dominant, positive Genes for controlling the characters. Similar findings were also observed by Kumar *et al.* (2000) [13], Ghosh *et al.* (2002) [6], Goswami *et al.* (2005) [7], Monalisa *et al.* (2005) [16], Nair *et al.* (2005) [17], Lohia *et al.* (2008) [15], Singh *et al.* (2008b) [22], Nigam *et al.* (2009) [18], Gupta *et al.* (2010) [8], Dond *et al.* (2012) [4], Frasad *et al.* (2012), Arifullah *et al.* (2012) [1], Dholu *et al.* (2014) [3].

The estimates of \hat{h}^2 were positive and highly significant for all the characters except harvest index, Exhibiting that mean direction of dominance was positive. The values of \hat{E} Component were highly significant for all the characters except 1000 seed weight. The \hat{E} Values of this traits did not show significance, indicating that these characters were less stable than other characters having environmental inferences

and vice-versa. Kumar *et al.* (2000) [13], Ghosh *et al.* (2002), Goswami *et al.* (2005), Monalisa *et al.* (2005) [16], Nair *et al.* (2005) [17], Lohia *et al.* (2008) [15], Singh *et al.* (2008b) [22], Nigam *et al.* (2009) [18], Gupta *et al.* (2010) [8], Dond *et al.* (2012), Frasad *et al.* (2012), Arifullah *et al.* (2012) [1], Dholu *et al.* (2014) [3].

The estimates of mean degree of dominance (\hat{H}_1/\hat{D})^{0.5} were more than unity for days to flowering, number of seeds per siliqua, biological yield, 1000-seeds weight and oil content indicating over dominance in this traits. The proportion of genes with positive and negative effects ($\hat{H}/4\hat{H}_1$) were near or equal to theoretical value (0.25) for all the four characters namely, days to flowering, number of seed per plant, number of siliquae per plant, and biological yield indicating that positive and negative genes were symmetrically distributed among the parents for these attributes. The ratio of dominant and recessive alleles, i.e., $(4\hat{D}\hat{H}_1)^{0.5} + \hat{F}/(4\hat{D}\hat{H}_1)^{0.5} - \hat{F}$ or KD/KR were more than one for days to flowering, plant height, number of primary branches, length of main raceme, number of siliquae per plant, number of seeds per siliqua, 1000-seed weight, oil content and seed yield per plant. While rest of the traits had values less than one which revealed that dominant genes were more frequent than recessive genes in the above

characters. The ratio \hat{h}^2/\hat{H}_2 which measures the group of genes showing dominance was less than unity for all the characters. except days to flowering, number of primary branches per plant, number of secondary per plant, days to maturity, plant height, number of siliquae per plant, number of seeds per siliqua, biological yield, 1000-seed weight and seed yield per plant. In which more than one gene groups were responsible for the expression of these traits. The coefficient of correlation (r) between parental order of dominance and parental measurements were found positive for all the traits. Similar findings were also observed by Kakroo *et al.* (2000), Katiyar *et al.* (2000), Kant *et al.* (2001), Ghosh *et al.* (2002) [6], Parmar *et al.* (2004), Goswami *et al.* (2005) [7], Monalisa *et al.* (2005) [16], Prajapati *et al.* (2009), Singh *et al.* (2009b), Gupta *et al.* (2010) [8], Chauhan *et al.* (2011), Dond *et al.* (2012) [4], Frasad *et al.* (2012), Lal *et al.* (2013), Dholu *et al.* (2014) [3].

Table 1: ANOVA of parents + F_1 's for 13 characters in a 7 x 7 parental diallel cross of Indian mustard: mean sum of squares.

Source of variation	d.f.	Days to flowering	No. of primary branches/plant	No. of secondary branches/plant	Days to maturity	Plant height (cm)	Length of main raceme (cm)	No. of siliquae per plant	No. of Seeds per siliqua
Replicates	2.00	1.58	3.05*	17.19**	3.96	100.14	55.87***	174.73***	0.15
Treatments	27.00	3.86***	3.32***	5.93**	112.38***	354.26***	467.84***	152.46***	4.84***
Parents	6.00	4.33**	7.86***	5.21*	111.19***	754.74***	720.60***	312.41***	7.87***
Hybrids	20.00	2.01	0.95	4.45*	104.32***	215.18***	410.88***	102.92***	2.19
Parent Vs.Hybrids	1.00	38.11***	23.53***	39.68***	280.78***	733.05**	90.48***	183.43***	39.68***
Error	54.00	1.19	0.91	2.26	1.84	64.61	3.61	12.80	1.48
Total	83.00	2.07	1.75	3.82	37.85	159.69	155.88	62.13	2.54
Replicates	2.00	18.37***	30.57**	0.00	0.28*	2.43	Replicates	2.00	18.37***
Treatments	27.00	3.85*	22.85***	0.21***	3.59***	10.88***	Treatments	27.00	3.85*
Parents	6.00	2.54	38.77***	0.17***	4.95***	25.37***	Parents	6.00	2.54
Hybrids	20.00	2.25	19.07***	0.16***	2.81***	4.94*	Hybrids	20.00	2.25
Parent Vs.Hybrids	1.00	43.75***	2.83	1.55***	10.95***	42.74***	Parent Vs.Hybrids	1.00	43.75***
Error	54.00	2.15	4.43	0.00	0.09	2.21	Error	54.00	2.15
Total	83.00	3.09	11.05	0.07	1.23	5.04	Total	83.00	3.09

*Significant at p = 0.05; **Significant at p = 0.01

Table 2: Estimates of b_i , SE_{b_i} ($b-0$)/ SE_{b_i} , and t^2 for 13 characters of F_1 's in a 7 x 7 parental diallel cross of Indian mustard

Character	b_i	SE_{b_i}	$(b-0)/SE_{b_i}$	$(1-b)/SE_{b_i}$	t^2
Days to flowering	0.491	0.234	2.097	2.178**	1.079**
No. of primary branches/plant	0.700	0.135	5.172	2.217**	2.391**
No. of secondary branches/plant	0.660	0.222	2.968	1.527**	0.506**
Days to maturity	1.032	0.108	9.603	-0.301	0.330**
Plant height (cm)	0.904	0.173	5.213	0.556**	0.009*
Length of main raceme (cm)	0.654	0.097	6.752	3.578**	7.379**
No. of siliquae/ plant	0.916	0.202	4.538	0.416**	0.011
No. Seeds/siliqua	0.583	0.132	4.409	3.152**	4.685**
Biological yield/plant (g)	0.329	0.320	1.029	2.098**	0.354**
Harvest index (%)	0.091	0.056	1.625	16.23**	2.437**
1000-seed weight (g)	0.641	0.063	10.175**	5.698	20.524**
Oil content (%)	0.425	0.303	1.403	1.901**	0.357**
Seed yield/plant (g)	0.441	0.252	1.748	2.215**	0.932*

*Significant at $p = 0.05$, **Significant at $p = 0.01$ **Table 3:** Estimates of variance components for 13 characters in a 7x 7 parental diallel cross of F_1 's in Indian mustard.

Characters	\hat{D}	\hat{H}_1	\hat{H}_2	\hat{F}	\hat{h}^2	\hat{E}	$(\hat{H}_1/\hat{D})^{0.5}$	$\hat{H}_2/4\hat{H}_1$	KD/KR	\hat{h}^2/\hat{H}_2	r
Days to flowering	1.04**	1.76**	1.79**	0.04**	6.91**	0.40**	1.30	0.255	1.031	3.864	0.9476
SE	0.24	0.57	0.50	0.57	0.34	0.08					
No. of primary branches/plant	2.29**	1.49**	1.13**	1.86**	4.23**	0.33**	0.81	0.190	3.026	3.738	0.9805
SE	0.22	0.53	0.47	0.53	0.32	0.08					
No. of secondary branches/plant	0.80**	0.56**	1.02**	-1.99	6.95**	0.93**	0.83	0.455	-0.196	6.834	0.9813
SE	0.15	0.35	0.31	0.35	0.21	0.05					
Days to maturity	36.42**	28.14**	18.84**	-25.95	52.07**	0.64**	0.88	0.167	0.423	35.836	0.9729
SE	1.77	4.26	3.76	4.25	2.52	0.64					
Plant height (cm)	229.62**	93.46**	70.37**	94.33**	126.02**	21.96**	0.64	0.188	1.950	1.791	0.9598
SE	16.34	39.34	34.66	39.20	23.28	5.78					
Length of main raceme (cm)	238.38**	164.21**	143.01**	2.28**	15.99**	1.83**	0.83	0.218	1.012	0.112	0.9724
SE	21.13	50.88	44.83	50.70	30.11	7.47					
No. of siliquae/plant	97.94**	3.72**	5.45**	8.48**	31.19**	6.19**	0.20	0.366	1.571	5.724	0.9935
SE	3.02	7.27	6.40	7.24	4.30	1.07					
No. of seeds/siliquae	2.14**	3.00**	2.86**	1.48**	7.17**	0.48**	1.18	0.238	1.819	2.507	0.99
SE	0.41	0.98	0.86	0.97	0.57	0.14					
Biological yield/plant (g)	-0.06	1.33**	1.61**	-0.83	7.72**	0.91**	4.632	0.303	-0.182	4.782	0.8593
SE	0.34	0.81	0.72	0.81	0.48	0.12					
Harvest index (%)	11.13**	-3.95	-2.92	-4.91	-0.35	1.79**	0.596	0.185	0.460	0.119	0.9971
SE	0.09	0.22	0.19	0.21	0.13	0.03					
1000-seed weight (g)	0.06**	0.28**	0.18**	0.10**	0.29**	0.00	2.224	0.157	2.393	1.639	0.3489
SE	0.01	0.02	0.02	0.02	0.01	0.00					
Oil content (%)	1.62**	2.58**	2.31**	0.63**	2.03**	0.03**	1.263	0.223	1.366	0.879	0.9458
SE	0.28	0.68	0.60	0.68	0.40	0.10					
Seed yield / plant (g)	7.72**	3.12**	2.54**	4.20**	7.61**	0.74**	0.636	0.203	2.492	3.000	0.9819
SE	0.73	1.75	1.54	1.74	1.03	0.26					

*Significant at $P = 0.05$, **Significant at $P = 0.01$ **Table 4:** Grand mean, heritability and genetic gain in 13 characters in F_1 's diallel generation of Indian mustard

Character	Estimate of genetic components					
	Component analysis			combining ability analysis		
	\hat{D}	\hat{H}_1	$(\hat{H}_1/\hat{D})^{0.5}$	$\hat{\sigma}_g^2$	$\hat{\sigma}_s^2$	GPR
Days to flowering	1.04**	1.76*	1.30	0.24	0.54	0.44
No. of primary branches/ plant	2.29**	1.49**	0.81	0.26	0.37	0.70
No. of secondary branches/plant	0.80**	0.56**	0.83	0.51	0.26	1.97
Days to maturity	36.42**	28.14**	0.88	15.54	7.41	2.10
Plant height (cm)	229.62**	93.46**	0.64	41.92	16.33	2.57
Length of main raceme (cm)	238.38**	164.20**	0.83	62.37	38.58	1.61
No. of siliquae/plant	97.94**	3.72**	0.19	22.59	1.74	12.98

No. of seeds /siliqua	2.15**	3.00**	1.18	0.26	0.79	0.33
Biological yield/plant (g)	-0.06	1.33**	4.63	0.10	0.48	0.20
Harvest index (%)	11.13**	-3.95	0.60	3.56	-1.27	-0.81
1000-seed weight (g)	0.06**	0.28**	2.22	0.01	0.07	0.15
Oil content (%)	1.62**	2.58**	1.26	0.32	0.67	0.48
Seed yield / plant (g)	7.72**	3.12**	0.64	1.19	0.68	1.73

$$\hat{\sigma}_g^2 = 1/2 \sigma_A^2 + 1/4 \sigma_{AA}^2 + \dots$$

$$\sigma_A^2 = 2 \sigma_g^2 \text{ (in the absence of epistasis)}$$

OD = Over dominance
PD = Partial dominance

$$\hat{\sigma}_s^2 = \sigma_D^2 + \sigma_{AA}^2 + \sigma_{AD}^2 + \sigma_{DD}^2$$

$$\sigma_D^2 = \sigma_s^2 \text{ (in the presence of epistasis)}$$

CD = Complete dominance
**Significant at p = 0.01

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