

ORIGINAL ARTICLE

Combining ability analysis of F₁ and F₂ diallel in Indian mustard (*Brassica juncea* L. Czern & Coss) under normal (E₁) and moisture stress (E₂) environments

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ABSTRACT

Combining ability analysis of 10 x 10 half diallel set of crosses in Indian mustard for ten quantitative traits revealed that preponderance of non-additive gene effects for all the characters in both the generations under both the environments (E₁ & E₂). The high magnitude of *gca* and *sca* effects indicated the presence of both additive and non-additive gene interactions for the inheritance of different traits. The parent RN-393 and Vardan in F₁ generation and parent GM-3 and RGN-229 in F₂ generations were good general combiners for seed yield per plant under both the environments. Among the cross combinations, cross PBR-357 x Kranti, CS-52 x GM-3 and Bio-902 x RGN-229 good specific cross combinations for seed yield in both the generations under both the environments.

Key words: - *Brassica juncea*, *GCA*, *SCA* and Indian mustard

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INTRODUCTION

Indian mustard is an important *rabi* oil seed crop in India and occupies a premier position among the oilseed crops. It is popularly known as rai, raya or laha in India. Indian mustard belongs to family Brassicaceae (Crucifereae) and genus Brassica. Indian mustard or brown mustard [*Brassica juncea* (L.) Czern&Coss] is a natural amphidiploid having 36 chromosomes (2n). It is largely self-pollinated but certain amount of cross pollination (2-15%) may take place due to honeybees [16-19]. Mustard was originated in China and from there; it was introduced to India (Vaughan, 1977). Rapeseed and Mustard are the major *Rabi* oilseed crops of India. Oil content in mustard seed varies from 37 to 49 per cent. The oil obtained is the main cooking medium in Northern India and cannot be easily replaced by any other edible oil. Moisture stress is major limiting factor in productivity of rapeseed-mustard. Majority of the cultivation is still dependent on rainfall and conserved moisture. Brassica species are mostly grown on light texture soil using conserved moisture from monsoon rains. Crop inevitably suffers from drought stress during the reproductive period of growth after depletion of stored water [7]. Hence development of drought tolerant/ resistant varieties of Indian mustard is essential to increase the production. Population of India is increasing rapidly and consequently edible oil demand is also going up day-by-day. Hence, it has become necessary to enhance the present production by developing superior varieties of Indian mustard. Development of superior varieties could be done by reshuffling the genes through hybridization from suitable parents. Moreover, it is also necessary to know about the nature and magnitude of gene action responsible for controlling the inheritance of various yield attributes along with combining ability of the parents and their cross combinations in order to exploit them in further crop improvement programme.

MATERIALS AND METHODS

Ten parents *viz*; CS-52, GM-3, PBR-357, Vardan, RH-30, Bio-902, Kranti, NRCDR-2, RGN-229 and RN-393 were crossed in diallel fashion (excluding reciprocal) to produce 45 F_1 's during *rabi* 2014-15. The resultant F_1 seed of each cross were raised at regional station (IARI), Wellington, Nilgiris (Tamil Nadu) to obtain F_2 's in off season nursery in summer 2015. The parents and their 45 F_1 's and 45 F_2 's were grown in randomized block design with three replications under two environments namely, normal (E_1) and moisture stress (E_2) at Agronomy farm S.K.N. College of Agriculture, Jobner, Jaipur. In both the environments pre-sowing irrigation was given to facilitate germination of seeds. In normal environment (E_1) and moisture stress environment (E_2), one irrigation was given at 45 days after sowing i.e. at about initiation of flowering. Moisture stress environment was created by stopping further irrigation in E_2 i.e. no irrigation was given after 45 days in E_2 . In normal environment (E_1), the second and last irrigation was given at 70 days after sowing. Observations were recorded on days to flowering, days to maturity, plant height (cm), primary branches per plant, length of main raceme (cm), number of siliqua on main raceme, number of seeds per siliqua, 1000-seed weight (g), seed yield per plant (g) and oil content (%). Mean value of sample for various traits were subjected to combining ability analysis method II model I of Griffing [3].

RESULTS AND DISCUSSION

The pooled analysis of variance for combining ability revealed the significance of mean square due to *gca* and *sca* for all the characters in both the generation except *SCA* for oil content in F_1 generation. Mean square due to *GCA* x Environment were significant for all the characters under both the environment except number of seed per siliqua, seed yield per plant and oil content in both the generation and number of siliqua on main raceme and 1000-seed weight in F_1 generations. Similarly, *SCA* x Environment were significant for all the characters except number of seeds per siliqua and oil content in both the generation and seed yield per plant in F_1 generation (Table 1 & 2). Similar results were also reported by Sheikh & Singh [12], Vaghela *et al.* [16] and Saini & Patel [11].

The individual analysis of variance for combining ability (Table 3 and 4) revealed that mean squares due to *GCA* were significant for all the characters in both the generations under both the environments except for number of siliqua on main raceme and oil content in E_1 , days to 50 % flowering and number of seeds per siliqua in E_2 in F_1 generation and days to 50 % flowering in E_2 in F_2 generation. Similarly, mean square due to *SCA* were also significant for all the characters in both the generations under both the environments except for oil content under both the environments and number of primary branches per plant in E_2 in F_1 generations. The significant differences of *GCA* and *SCA* indicated that both additive and non-additive gene effects played an important role in the genetic control of the traits under study. Similar finding were obtained by Gupta *et al.* [4], Azzinia *et al.* [1], Vaghela *et al.* [16] and Kumar *et al.* [6].

The *GCA/SCA* variance was found less than unity which indicated preponderance of non-additive gene action observed in both the generations under both the environments. Similar finding were obtained by Chauhan *et al.* [2], Oghan *et al.* [9], Lal *et al.* [8] and Patel *et al.* [10]. The presence of predominantly large amount of non-additive gene action would be required for the maintained of heterozygosity in the population. Breeding method such as biparental mating followed by reciprocal recurrent selection may increase frequency of genetic recombination and fasten the rate of genetic improvement [5].

The estimates *gca* of the parents revealed that no single parent was a good general combiner for all the traits under study. However, it is evident from results that high *gca* effects for seed yield per plant in the parent namely RN-393 and Vardan in F_1 generation and parent GM-3 and RGN-229 in F_2 were found to be good general combiners for seed yield under both the environments. The *gca* is due to the additive and additive x additive gene effects which are fixable components of genetic variation [3]. Therefore, it would be worthwhile to use above parent lines in hybridization programme. The results of *sca* effects of hybrids revealed that none of the hybrid were consistently superior for all the characters. The estimates of *sca* effects revealed that three cross combinations namely, PBR-357 x Kranti, CS-52 x GM-3 and Bio-902 x RGN-229 exhibited positively significant *sca* effects for seed yield per plant under both the generations and environments (Table 5). Cross combination NRCDR-2 x RN-393 in E_1F_1 , PBR-357 x Kranti in E_2F_1 , Vardan x RH-30 in E_1F_2 and GM-3 x RN-393 in E_2F_2 showed highly significant desirable negative *sca* effects for days to 50 % flowering. Kranti x NRCDR-2 in E_1F_1 , GM-3 x RH-30 in E_2F_1 , CS-52 x Bio-902 in E_2F_1 and RGN-229 x RN-393 in E_2F_2 negatively *sca* effects for days to maturity; RGN-229 x RN-393 in E_1F_1 , PBR-357 x Kranti in E_2F_1 , NRCDR-2 x RN-393 in E_1F_2 and RGN-229 x RN-393 in E_2F_2 negative *sca* effects for plant height; PBR-357 x Kranti in E_1F_1 , CS-52 x Bio-902 in E_2F_1 and E_1F_2 and GM-3 x Vardan in E_2F_2 positively significant *sca* effects for number of primary branches per plant; RH-30 x NRCDR-2 in E_1F_1 , CS-52 x PBR-357 in E_2F_1 , CS-52 x Bio-902 in E_1F_2 and CS-52 x RGN-229 in E_2F_2 positively

significant sca effects for length of main raceme; RH-30 x NRCDR-2 in E_1F_1 , PBR-357 x RGN-229 in E_2F_1 , CS-52 x NRCDR-2 in E_1F_2 and CS-52 x RGN-229 in E_2F_2 significant sca effect for siliqua on main raceme; RH-30 x Bio-902 in E_1F_1 , GM-3 x RGN-229 in E_2F_1 , CS-52 x RH-30 in E_1F_2 and CS-52 x PBR-357 in E_2F_2 positively significant sca effects for number of seeds per siliqua; GM-3 x Vardan in E_1F_1 , GM-3 x PBR-357 in E_2F_1 , CS-52 x RGN-229 in E_1F_2 and Kranti x NRCDR-2 in E_2F_2 positively significant sca effects for 1000-seed weight; PBR-357 x Kranti in E_1F_1 , Bio-902 x NRCDR-2 in E_2F_1 , CS-52 x GM-3 in E_1F_2 and E_2F_2 positively significant sca effects for seed yield per plant and cross GM-3 x Vardan in E_1F_1 , PBR-357 x Vardan in E_2F_1 , Cs-52 x Vardan in E_1F_1 and PBR-357 x Kranti in E_2F_2 was good specific combiner for oil content (Table 6). It was observed for most of the characters that there was close association between mean performance and gca effects of the parents. However, combinations having high mean value did not exhibit high sca effects for all the characters suggested that only good general combiner on the basis of mean performance may be reliable but not good specific combiners. Parent involved these crosses were H x H, H x L, L x H and L x L combiners. The cross combinations involving either both or one parent with high gca effects indicated additive gene action in controlling the expression of these trait. These cross combination would be give rise to transgressive segregates in later generation. While cross combinations involving L x L combiners reflected non-additive gene action, which is non-fixable in nature and could be exploited only through heterosis breeding for further improvement of the respective traits. Similar finding were reported by earlier Srivastava *et al.* [15], Singh *et al.* [13] and Singh *et al.* [14].

Table 1 Pooled ANOVA showing mean sum of squares for combining ability in F_1 diallel (Parents + F_1) for various characters in normal (E_1) and moisture stress (E_2) environments

Source of variation →	GCA	SCA	Environment	GCA X Env.	SCA X Env	Error
Characters	(df = 9)	(df = 45)	(df = 1)	(df = 9)	(df = 45)	(df = 16)
Days to 50% flowering	5.70**	1.68**	5338.07**	6.870**	1.96**	0.95
Days to maturity	8.60**	7.35**	4925.46**	12.45**	9.35**	0.91
Plant height (cm)	110.42**	69.76**	3755.710**	76.23**	26.13**	10.69
Number of primary branches per plant	0.06**	0.15**	23.109**	0.09**	0.07**	0.02
Length of main raceme (cm)	33.03**	59.75**	15617.82**	15.49**	26.30**	6.05
Number of siliqua on main raceme	11.70*	37.96**	2414.36**	6.59	11.51**	5.03
Number of seeds per siliqua	0.883*	1.29**	36.99**	0.31	0.2	0.38
1000 seed weight (g)	0.38**	0.12**	31.63**	0.05	0.09**	0.04
Seed yield per plant (g)	7.58**	4.44**	212.09**	0.22	0.45	0.46
Oil content (%)	0.92**	0.379	66.83**	0.406	0.23	0.26

* and ** represents significant at 5% and 1% level of significance respectively

Table 2 Pooled ANOVA showing mean sum of squares for combining ability in F_2 diallel (Parents + F_2) for various characters in normal (E_1) and moisture stress (E_2) environments

Source of variation →	GCA	SCA	Environment	GCA X Env.	SCA X Env	Error
Characters	(df = 9)	(df = 45)	(df = 1)	(df = 9)	(df = 45)	(df = 216)
Days to 50% flowering	2.588**	2.129**	4055.297**	2.369**	2.495**	0.926
Days to maturity	9.301**	10.347**	6867.638**	12.099**	11.296**	0.80
Plant height (cm)	40.784**	56.539**	22417.870**	52.663**	63.983**	10.368
Number of primary branches per plant	0.120**	0.151**	20.812**	0.096**	0.063**	0.019
Length of main raceme (cm)	63.057**	31.397**	11091.320**	43.224**	16.663**	6.442
Number of siliqua on main raceme	20.445**	16.396**	4388.746**	14.333**	10.406**	4.731
Number of seeds per siliqua	2.591**	1.759**	31.074**	0.098	0.127	0.382
1000 seed weight (g)	0.46**	0.19**	9.13**	0.11**	0.07**	0.03
Seed yield per plant (g)	5.23**	5.70**	90.88**	0.39	0.69**	0.36
Oil content (%)	0.861**	0.848**	53.597**	0.327	0.199	0.268

* and ** represents significant at 5% and 1% level of significance respectively

Table 3 ANOVA showing mean sum of squares and variances for combining ability in F₁ diallel (Parents + F₁) for various characters in normal (E₁) and moisture stress (E₂) environments

Characters	Env.	Source of variation			Variance		
		GCA (df = 9)	SCA (df = 45)	Error (df = 108)	GCA Variance	SCA Variance	GCA / SCA ratio
Days to 50% flowering	E ₁	11.279**	2.009**	0.89	0.772	1.118	0.690
	E ₂	1.296	1.636*	1.019	0.028	0.616	0.045
Days to maturity	E ₁	6.382**	6.708**	0.98	0.027	5.728	0.004
	E ₂	14.671**	9.997**	0.846	0.389	9.151	0.042
Plant height (cm)	E ₁	119.183**	53.943**	10.319	5.436	43.623	0.124
	E ₂	67.467**	41.955**	11.067	2.126	30.888	0.068
Number of primary branches per plant	E ₁	0.06**	0.123**	0.018	0.005	0.104	0.040
	E ₂	0.098**	0.101	0.021	0.0002	0.079	0.003
Length of main raceme (cm)	E ₁	34.866**	57.418**	5.882	1.879	51.536	0.036
	E ₂	13.658*	28.640**	6.222	1.248	22.418	0.055
Number of siliqua on main raceme	E ₁	3.944	26.996**	5.684	1.921	21.312	0.090
	E ₂	14.354*	22.484**	4.381	0.677	18.103	0.037
Number of seeds per siliqua	E ₁	0.847*	0.802**	0.407	0.003	0.395	0.009
	E ₂	0.352	0.695*	0.358	0.028	0.337	0.084
1000 seed weight (g)	E ₁	0.15**	0.05*	0.03	0.01	0.02	0.43
	E ₂	0.28**	0.16**	0.05	0.01	0.10	0.18
Seed yield per plant (g)	E ₁	3.98**	2.94**	0.48	0.29	2.46	0.11
	E ₂	3.81**	1.95**	0.43	0.28	1.51	0.18
Oil content (%)	E ₁	0.349	0.226	0.243	0.01	0.016	0.604
	E ₂	0.979*	0.385	0.287	0.049	0.097	0.507

* and ** represents significant at 5% and 1% level of significance respectively

Table 4 ANOVA showing mean sum of squares and variances for combining ability in F₂ diallel (Parents + F₂) for various characters in normal (E₁) and moisture stress (E₂) environments

Characters	Env.	Source of variation			Variance		
		GCA (df = 9)	SCA (df = 45)	Error (df = 108)	GCA Variance	SCA Variance	GCA / SCA Variance ratio
Days to 50% flowering	E ₁	3.047**	2.449**	0.769	0.049	1.680	0.029
	E ₂	1.909	2.174*	1.083	0.022	1.090	0.020
Days to maturity	E ₁	16.725**	10.573**	0.943	0.512	9.629	0.053
	E ₂	4.673**	11.069**	0.656	0.533	10.413	0.051
Plant height (cm)	E ₁	46.818**	94.54**	10.199	3.977	84.349	0.047
	E ₂	46.629**	25.973**	10.537	1.721	15.436	0.111
Number of primary branches per plant	E ₁	0.069**	0.078**	0.019	0.000	0.058	0.011
	E ₂	0.145**	0.135**	0.018	0.000	0.116	0.007
Length of main raceme (cm)	E ₁	49.342**	26.868**	5.990	1.872	20.877	0.089
	E ₂	56.938**	21.191**	6.892	2.978	14.299	0.208
Number of siliqua on main raceme	E ₁	16.394*	19.463**	5.645	0.255	13.817	0.018
	E ₂	18.383**	7.338*	3.816	0.920	3.521	0.261
Number of seeds per siliqua	E ₁	1.711**	0.903**	0.405	0.067	0.498	0.135
	E ₂	0.977*	0.982**	0.358	0.000	0.624	0.000
1000 seed weight (g)	E ₁	0.12**	0.05**	0.02	0.00	0.03	0.25
	E ₂	0.44**	0.21**	0.05	0.03	0.16	0.19
Seed yield per plant (g)	E ₁	1.96**	3.67**	0.41	0.12	3.26	0.04
	E ₂	3.66**	2.72**	0.31	0.27	2.41	0.11
Oil content (%)	E ₁	0.571*	0.475**	0.244	0.007	0.230	0.034
	E ₂	0.616*	0.571**	0.291	0.003	0.280	0.013

* and ** represents significant at 5% and 1% level of significance respectively

Table:-5 Top ranking crosses for seed yield per plant in Indian mustard

Crosses	Per se performance	SCA effects	GCA effects			
			E ₁		E ₂	
			F ₁	F ₂	F ₁	F ₂
PBR-357 x Kranti	15.31	3.80**	RN-393	GM-3	RN-393	CS-52
CS-52 x GM-3	12.42	2.84**	Vardan	RGN-229	Vardan	RGN-229
Bio-902 x RGN-229	12.09	2.16**	-	-	-	GM-3

Table:-6 Estimates of SCA effects of top cross combinations in F₁ generations for different characters in Indian mustard

Characters	Cross Combinations		SCA effects	
	F ₁		F ₁	
	E ₁	E ₂	E ₁	E ₂
Days to 50 % flowering	NRCDR-2 x RN-393	PBR-357 x Kranti	-2.50**	-2.70**
	CS-52 x RN-393	Vardan x Kranti	-2.30*	-2.28*
	PBR-357 x Vardan	NRCDR-2 x RGN-229	-2.22*	-1.89*
Days to maturity	Kranti x NRCDR-2	GM-3 x RH-30	-4.50**	-4.88**
	Vardan x Kranti	Vardan x NRCDR-2	-4.25**	-3.88**
	RGN-229 x RN-393	RH-30 x RN-393	-4.02**	-3.80**
Plant height	RGN-229 x RN-393	PBR-357 x Kranti	-14.80**	-9.14
	GM-3 x RGN-229	CS-52 x RGN-229	-9.31**	-8.93**
	CS-52 x GM-3	GM-3 x Bio-902	-9.22**	-6.63*
Number of primary branches	PBR-357 x RGN-229	CS-52 x Bio-902	0.94**	0.61**
	CS-52 x Bio-902	Bio-902 x RGN-229	0.70**	0.55**
	NRCDR-2 x RGN-229	GM-3 x RGN-229	0.47**	0.48**
Length of main raceme	RH-30 x NRCDR-2	CS-52 x PBR-357	18.26**	8.88**
	CS-52 x RN-393	NRCDR-2 x RN-393	16.00**	8.70**
	PBR-357 x Vardan	PBR-357 x RGN-229	13.81**	6.65**
Number of siliqua on main raceme	RH-30 x NRCDR-2	PBR-357 x RGN-229	12.41**	7.72**
	GM-3 x RN-393	NRCDR-2 x RN-393	9.92**	6.42**
	CS-52 x RN-393	CS-52 x PBR-357	8.53**	6.25**
Number of seeds per siliqua	RH-30 x Bio-902	GM-3 x RGN-229	2.08**	1.42*
	RGN-229 x RN-393	RH-30 x Bio-902	1.79**	1.32*
	Kranti x RN-393	RH-30 x NRCDR-2	1.46*	1.15*
1000-seed weight	GM-3 x Vardan	GM-3 x PBR-357	0.43**	0.68**
	Vardan x NRCDR-2	Kranti x NRCDR-2	0.39**	0.61**
	Vardan x Kranti	GM-3 x NRCDR-2	0.35*	0.59**
Seed yield per plant	PBR-357 x Kranti	Bio-902 x NRCDR-2	3.80**	2.37**
	Vardan x RH-30	Vardan x RH-30	3.43**	2.26**
	Bio-902 x NRCDR-2	Vardan x Bio-902	3.07**	2.03**
Oil content	GM-3 x Vardan	PBR-357 x Vardan	0.97*	1.18*
	-	PBR-357 x Kranti	-	1.13*
	-	RH-30 x RGN-229	-	1.13*

contd...

Table:-6 Estimates of SCA effects of top cross combinations in F₂ generations for different characters in Indian mustard

Characters	Cross Combinations		SCA effects	
	F ₂		F ₂	
	E ₁	E ₂	E ₁	E ₂
Days to 50 % flowering	Vardan x RH-30	GM-3 x RN-393	-2.67*	-2.80*
	PBR-357 x Kranti	CS-52 x Bio-902	-2.59*	-2.24*
	GM-3 x PBR-357	PBR-357 x RGN-229	-2.01*	-2.13*
Days to maturity	CS-52 x Bio-902	RGN-229 x RN-393	-5.66**	-6.19**
	Vardan x NRCDR-2	GM-3 x Kranti	-5.57**	-5.24**
	Bio-902 x Kranti	Kranti x NRCDR-2	-4.35**	-4.94**
Plant height	NRCDR-2 x RN-393	RGN-229 x RN-393	-16.07**	-8.17*
	GM-3 x NRCDR-2	Bio-902 x NRCDR-2	-14.99**	-7.90*
	CS-52 x PBR-357	Vardan x Kranti	-11.21**	-6.40*
Number of primary branches	CS-52 x Bio-902	GM-3 x Vardan	0.57**	1.10**
	GM-3 x RGN-229	Kranti x RN-393	0.48**	0.65**
	Bio-902 x NRCDR-2	RH-30 x Bio-902	0.46**	0.62**
Length of main raceme	CS-52 x Bio-902	CS-52 x RGN-229	12.10**	13.11**
	CS-52 x NRCDR-2	CS-52 x RN-393	8.15**	7.29*
	Vardan x RH-30	RH-30 x RN-393	7.19*	5.84*
Number of siliqua on main raceme	CS-52 x NRCDR-2	CS-52 x RGN-229	9.35**	6.20*
	Vardan x RH-30	GM-3 x RGN-229	7.86**	5.48*

	Bio-902 x NRCD-2	RH-30 x RN-393	7.40*	4.05*
Number of seeds per siliqua	CS-52 x RH-30	CS-52 x PBR-357	1.81*	2.21**
	PBR-357 x Kranti	PBR-357 x RH-30	1.75*	1.66*
	RH-30 x NRCD-2	GM-3 x Bio-902	1.54*	1.55*
1000-seed weight	CS-52 x RGN-229	Kranti x NRCD-2	0.52**	0.80**
	GM-3 x Vardan	CS-52 x RGN-229	0.52**	0.60**
	NRCD-2 x RGN-229	GM-3 x Vardan	0.36**	0.56**
Seed yield per plant	CS-52 x GM-3	CS-52 x GM-3	2.27**	2.84**
	Bio-902 x RGN-229	GM-3 x Bio-902	2.16**	2.21**
	PBR-357 x Kranti	PBR-357 x Vardan	1.57**	2.19**
Oil content	CS-52 x Vardan	PBR-357 x Kranti	1.43*	1.31*
	RH-30 x RN-393	-	0.93*	-
	-	-	-	-

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