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COMBINING ABILITY AND HETEROSIS FOR YIELD AND YIELD CONTRIBUTING TRAITS IN *BRASSICA RAPA* (L.) SSP. *DICHOTOMA* (ROXB.) HANELT

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Abstract

Combining ability was studied for yield and yield contributing traits in 5 × 5 diallel cross in *Brassica rapa* (L.) ssp. *dichotoma* (Roxb.) Hanelt. Primary branches plant^{-1}, pods main raceme^{-1}, pod length, 100-seed weight and seed yield plant^{-1} were significantly different. Heritability and genetic advance estimates were moderate for primary branches plant^{-1}, pods main raceme^{-1}, 100 seed weight whereas were high for seed yield plant^{-1}. Parental line G-909 for primary branches plant^{-1}, pods main raceme^{-1} and seed yield plant^{-1}, genotype G-902 for pod length and genotype G-403 for 100-seed weight were the best general combiners. Based on combing ability and heterosis, the F_1 hybrids G-909 × G-265 (for primary branches plant^{-1}), G-265 × G- 403, G-1500 × G-909 (for pods main raceme^{-1}), G-403 × G-909 (for pod length), G-265 × G-1500 (for 100-seed weight) and G-1500 × G-902, G-909 × G-902 (for seed yield plant^{-1}) can be utilized in future breeding endeavors. Non-additive genetic control, as predominant mechanism, for all the traits necessitates the use of schemes like bi-parental mating design, diallel selective mating followed by recurrent or reciprocal recurrent selection.

Key words: Combining ability, Yield, Heterosis, Heritability, *Brassica rapa.*

Introduction

Brassica is grown world widely for a variety of uses. Some of them are important sources of edible and industrial oils, vegetables, condiments, fodder, forage (Kanwal *et al*., 2014) and for production of biodiesel due to having high levels of glucosinolate compounds (Ahmad *et. al*., 2012). Rapeseed and mustard is one of the major oilseed crops in Pakistan. Edible oil shortage is persisted in Pakistan despite some developments in the agriculture sector, due to increase in per capita consumption and high population growth rate; national edible oil requirement is going to increase in the years to come (Farhatullah *et al.,* 2004). For example in the crop season of 2011-12, rapeseed and mustard were planted over 0.201 million hectares that resulted in a production of 0.164 million tons (PBS, 2012-13). A greater share of the national edible oil requirement was met from imports. The five year average yield (2005-2009) in Khyber Pakhtunkhwa (458 kg ha^{-1}) is low compared to that of other provinces (Punjab 852; Sindh 1029 & Balochistan 551 kg ha^{-1}) (PBS, 2011-12) necessitating crop improvement. Lower edible oil production is partly due to non-availability of high yielding lines (Nassimi *et al.,* 2006a). This huge production consumption gape can be reduced by breeding improved cultivars (Azam *et al*., 2013). Identification of superior parents, promising cross combinations and logically adopted breeding methodology as pre-requisites for development of high yielding genotypes (Acharya & Swain, 2004). Diallel analysis is one of the efficient, convenient and often used biometrical tools that provide the estimates of genetic parameters regarding combining ability and information on the selection of parents from the study of F_1 generation with or without reciprocals (Aghao *et al*., 2010; Ahmad *et al.,* 2009). General combining ability (GCA) refers to average performance of an inbred in a series of cross combinations, and specific combining ability (SCA) is the deviation of inbred lines in hybrid combination from the individual average performance of the inbred lines (Sprague & Tatum, 1942). Potential of inbred lines in cross combinations is well depicted by GCA and SCA effects (Rameeh, 2011; Huang *et al.,* 2010; Ahmad *et al.,* 2009) and their reciprocals (Turi *et al.,* 2011). Gene actions, their nature and magnitude, involved in quantitative traits expression is elucidated by combining ability studies (Ahmad *et al.,* 2009). GCA and SCA variances are attributed to additive portion and non-additive genetic effects, respectively (Malik *et al.,* 2004). Exploitation of heterosis can be instrumental in increasing seed yield. Heterosis is better realized if pedigree involves inbreds of indigenous background having the adaptive advantage and exotic germplasm (Riaz *et al.,* 2001) to establish genetically distant heterotic groups (Girke *et al.,* 2012). Heterotic investigations can provide basis for exploitation of valuable hybrid combinations in future breeding schemes (Nassimi *et al.,* 2006b) and for this reason, the achievement of heterosis has become a major objective for the breeders of canola (Riaz, *et al*., 2013) and related species. In addition, cytoplasmic male sterile line, its corresponding maintainer line and restorer can be used for hybrid seed production in Brassica (Ahmad *et al*., 2012).

The present study was therefore aimed to study heritability, identify superior general combiners and hybrid combinations on basis of combining ability and heterosis, elucidate prevalent types of gene actions involved in various traits expression and enlist breeding schemes based on genetic effects involved.

Material and Methods

A 5 x 5 full diallel in *B. rapa* (L.) ssp. *dichotoma* (Roxb.) Hanelt (syn. *B. campestris* var. brown *sarson*) was planted during 2011-12 in randomized complete block (RCB) design with two replications at The University of Agriculture, Peshawar, Pakistan. All the parents entering the diallel were developed from local germplasm of Pakistan except G-265 which was an introduction (PI-367601). Each replication contained 25 sub-plots which consisted two rows with row length of four meters. Row to row and plant to plant spacing was kept 50 and 30 cm, respectively. Plant population was maintained by thinning and manual weeding was done when needed. Data was recorded on ten randomly selected plants for primary branches plant^{-1}, main raceme length, pods main raceme^{-1}, seeds pod^{-1}, pod length, pod width, 100-seed weight and seed yield plant^{-1}. The analysis of variance was conducted according to Gomez & Gomez (1984). Heritability (broad sense) was estimated by variance components method from ANOVA as described by Panse and Sukhatme (1967). Genetic advance as a percent of mean was computed following Allard (1960). Heritability estimates were classed as low (<0.30), moderate (0.30-0.60) and high (>0.60) whereas genetic advance as percent of mean categorized low (<10%), moderate (10-20%) and high (>20%) following Johnson *et al.,* (1955). Combining ability analysis was conducted as outlined by Griffing (1956) Method-I, based on Eisenhart's Model-II. Mid and high parent heterosis was computed following Fehr *et al.,* (1987) and a two tailed *t* test was used to test the significance of the heterosis from mid and high parent values, respectively.

Results and Discussion

Analysis of variance and heritability: Data perusal revealed significant differences for all the traits except main raceme length, pod width, and seeds pod^{-1}(Table 1) which confirmed existence of sufficient genetic variability for the said traits. Nasim *et al.,* (2013) reported highly significant differences for pod length, width, seed pod^{-1}, 100 seed weight whereas non-significant for primary branches plant^{-1}, pods main raceme^{-1}and main raceme length. Results for pod length, seed pod^{-1}, 100-seed weight and seed yield plant^{-1} are in conformity with Turi *et al.,* (2011). They reported significant mean squares for the said traits. Sabaghnia *et al.,* (2010) reported highly significant differences for pod length and non-significant differences for 1000-seed weight. Shen *et al.,* (2005); Rameeh (2012) reported highly significant differences for seed pod^{-1}, 1000-seed weight and seed yield. Present results were strengthened by findings of Sincik *et al.,* (2011) as they reported significant differences for pods on main raceme and seed yield plant^{-1} and non-significant differences for seeds pod^{-1} and 1000-seed weight.

Heritability and genetic advance as percent of mean estimates, computed for traits with significant differences, were moderate for primary branches plant^{-1}, pods main raceme^{-1}, 100 seed weight whereas they were unexpectedly high for seed yield plant^{-1}. However, for pod length moderate heritability with low genetic advance as percent of mean (subsequently the term genetic advance will be used) were recorded (Table 1). Singh *et al.,* (2011) reported high heritability and moderate genetic advance for 1000 seed weight, pods main raceme^{-1} and seed yield plant^{-1} however both heritability and genetic advance were moderate for primary branches plant^{-1}. Nasim *et al.,* (2013) reported high heritability coupled with high genetic advance (pod length); moderate heritability with high genetic advance (100-seed weight); moderate heritability with moderate genetic advance (pods main raceme^{-1}) and low heritability with low genetic advance (primary branches plant^{-1}). Their results are in contrast for pod length though categorical differences are there for other traits as well. Heritability and genetic advance for polygenic trait like seed yield generally remains low than oligogenics like 100 seed weight but it was reported to be higher in some previous investigations (Tahir *et al.,* 2006; Sadat *et al.,* 2010; Singh *et al.,* 2011; Tahira *et al.,* 2011; Zare & Sharafzadeh, 2012). It may be attributed to the experiment being conducted during a single year and location with only two replications but even with investigations stretching over 2 years and more replications (Tahira *et al.,* 2011; Zare & Sharafzadeh, 2012) similar results were obtained. Even then less locations and experimental noise from unknown sources are detrimental to true heritability estimates.

Table 1. Genotype mean square, error mean square, coefficient of variation (CV), heritability (broad sense) and genetic advance (G.A.) as percent of mean for yield and its contributing traits in *B. rapa* (L.) *ssp. dichotoma* (Roxb.) Hanelt.

Plant traits	Mean squares		CV (%)	Heritability (Broad sense)	G.A. (% of mean)
	Genotype	Error			
Primary branches plant^{-1}	23.79*	11.34	19.4	0.35	15.02
Main raceme length	67.99^{ns}	49.73	10.3	-	-
Pods main raceme^{-1}	199.8**	57.44	11.0	0.55	15.99
Pod length	0.104**	0.037	5.5	0.47	6.28
Pod width	0.00074^{ns}	0.00042	5.6	-	-
Seed pod^{-1}	3.699^{ns}	2.769	11.7	-	-
100-seed weight	0.0020*	0.0009	14.1	0.37	11.64
Seed yield plant^{-1}	463.8**	90.13	19.8	0.67	41.04

** Significant at p≤0.01, * Significant at p≤0.05, ns; Non-significant

Table 2. Analysis of variance for combining ability yield and its contributing traits in *B. rapa* (L.) *ssp. dichotoma* (Roxb.) Hanelt.

Plant traits	Mean squares			
	GCA (df=4)	SCA (df=10)	RCA (df=10)	Error (df=24)
Primary branches plant^{-1}	8.83ns	16.86**	8.15ns	5.67
Pods main raceme^{-1}	264.8**	88.80**	44.97ns	28.72
Pod length	0.043ns	0.070**	0.037ns	0.019
100-seed weight	0.0002ns	0.0012*	0.0010*	0.0005
Seed yield plant^{-1}	55.25ns	348.5**	185.9**	45.07

** Significant at p≤0.01, * Significant at p≤0.05, ns; Non-significant, General combining ability (GCA), Specific combining ability (SCA) and reciprocal effects (RCA)

Table 3. General combining ability effects for primary branches plant^{-1}, pods main raceme^{-1}, pod length, 100-seed weight and seed yield plant^{-1} traits in *B. rapa* (L.) *ssp. dichotoma* (Roxb.) Hanelt.

Genotypes	Primary branches plant^{-1}	Pods main raceme^{-1}	Pod length	100-seed weight	Seed yield plant^{-1}
G-265	0.48	-2.29	0.05	-0.0051	0.63
G-403	-0.78	-2.53	-0.01	0.0071	-2.67
G-902	0.74	3.01	0.08	0.0029	1.31
G-909	0.78	7.37	-0.09	-0.0020	2.87
G-1500	-1.24	-5.56	-0.03	-0.0029	-2.15
S.E(*gi*) ±	0.67	1.52	0.038	0.0060	1.90
S.E(*gi-gj*) ±	1.06	2.40	0.061	0.0095	3.00

S.E (gi): standard error of GCA of *ith* parent and S.E (gi-gj): standard error of difference of GCA of *ith* and *jth* parents

Combining ability and heterosis: Traits exhibiting significant differences were further subjected to combining ability analysis and heterosis was computed. GCA mean square was significant for pods on main raceme only, while SCA component was significant for all the traits. RCA mean squares were non-significant for all the traits except 100-seed weight and seed yield plant^{-1} (Table 2). Diallel along with other mating schemes is used to select genotypes entering the hybridization schemes. Parents having good GCA effects can be used in development of synthetic varieties and cross combinations displaying promising results can be used to harness hybrid vigor. Moreover the relative variances due to GCA, SCA, RCA and GCA/SCA indicating predominant type of genetic variance gives an insight into the breeding procedures that are likely to bring desired improvement.

Primary branches plant^{-1}: Positive combining ability effects are desirable for higher number of branches contribute to yield. Parental lines G-265, G-902 and G-909 exhibited positive GCA effects of 0.48, 0.74 and 0.78, respectively. The maximum negative GCA effect (-1.24) was recorded for genotype G-1500 followed by -0.78 (G-403) (Table 3). Eight out of 10 F_1 crosses exhibited positive SCA effects ranged 0.39 to 2.46. The maximum positive SCA effects was noted for F_1 hybrid G-403 × G-1500 (2.46) followed by G-265 × G-403 (2.44). The maximum negative SCA effect (-0.56) was noted for the F_1 hybrid G-902 × G-1500 followed by G-265 × G-1500 (-0.05) (Table 4). RCA effects for nine out of ten crosses were positive, ranged 0.20 to 3.15. The highest positive RCA effect of 3.15 was noted for cross combination G-909 × G-265 followed by G-1500 × G-902 (2.90). Negative RCA effect (-1.35) was noted for hybrid G-1500 × G-265 (Table 5). Significant SCA mean square indicated that non-additive genetic effects were involved (Table 2). Preponderance of non-additive genetic effects was also confirmed by relative magnitude of σ^2_{GCA} (-0.750), σ^2_{SCA} (6.664), σ^2_{RCA} (1.240) and $\sigma^2_{GCA}/\sigma^2_{SCA}$ (-0.113) (Table 6). Acharya & Swain (2004); Gupta *et al.,* (2011) in Indian mustard and Akbar *et al.,* (2008) in rapeseed reported highly significant GCA and SCA effects. Teklewold & Becker, (2005) reported significant GCA and non-significant SCA in Ethiopian mustard. Noshin *et al.,* (2007) reported highly significant GCA, significant SCA and non-significant reciprocal effects. Earlier findings for SCA in yellow *sarson* (Singh *et al.,* 2001) and Indian mustard (Singh *et al.,* 2010) are in agreement. Gupta *et al.,* (2006 & 2011) reported prevalence of non-additive genetic control. Aher *et al.,* (2009) reported preponderance of additive genetic effects whereas Acharya & Swain (2004) findings revealed equal importance of additive and non-additive control. Positive heterosis of either type was observed for 19 out of 20 hybrids. For mid parent heterosis 15 of the positive values were significant, however for heterobeltiosis only 8 of these 19 were significant. Mid parent heterosis ranged 8.1 (G-909 x G-1500) to 99.1 % (G-403 x G-265) whereas heterobeltiosis varied from 1.4 (G-909 x G-1500) to 70.3 % (G-403 x G-265) (Table 7). Nassimi *et al.,* (2006b); Turi *et al.,* (2006); Gupta *et al.,* (2011) reported positive significant mid and better parent heterosis which strengthen the findings of the current study. Moreover, Mahto & Haider, (2004) also reported positive significant mid parent heterosis. However, non-significant positive heterosis over mid parent (Cheema & Sadaqat, 2004) and better parent (Cheema & Sadaqat 2004; Gupta *et al.,* 2006) were also reported.

Table 4. Specific combining ability effects for primary branches plant^{-1}, pods main raceme^{-1}, pod length, 100-seed weight and seed yield plant^{-1} traits in *B. rapa* (L.) *ssp. dichotoma* (Roxb.) Hanelt.

F1 Hybrids	Primary branches plant	Pods main raceme^{-1}	Pod length	100-seed weight	Seed yield plant^{-1}
G-265 × G- 403	2.44	9.24	0.16	-0.026	8.78
G-265 × G-902	1.52	6.80	0.10	-0.029	12.00
G-265 × G-909	1.63	-5.96	0.02	-0.014	6.79
G-265 × G-1500	-0.05	-3.78	-0.12	0.031	-6.89
G-403 × G-902	1.43	-8.56	0.07	-0.007	6.65
G-403 × G-909	0.39	-3.02	0.21	0.011	-2.31
G-403 × G-1500	2.46	-6.94	-0.11	-0.001	9.96
G-902 × G-909	2.07	3.19	-0.03	0.003	9.76
G-902 × G-1500	-0.56	2.27	0.14	-0.011	-3.37
G-909 × G-1500	0.45	6.71	-0.24	-0.027	8.82
S.E (*Sij*) ±	1.39	3.12	0.079	0.0124	3.91
S.E (*Sik-Skl*) ±	1.84	4.15	0.105	0.0164	5.20

S.E (S*ij*): Standard error of SCA of cross *ith x jth*; S.E (Sik-Skl): Standard error of difference of SCA of *cross ith x kth* and *kth x lth*

Table 5. Reciprocal combining ability effects for primary branches plant^{-1}, pods main raceme^{-1}, pod length, 100-seed weight and seed yield plant^{-1} traits in *B. rapa* (L.) *ssp. dichotoma* (Roxb.) Hanelt.

F1 Hybrids	Primary branches plant^{-1}	Pods main raceme^{-1}	Pod length	100-seed weight	Seed yield plant^{-1}
G-403 × G-265	2.30	-7.00	-0.15	0.017	7.35
G-902 × G-265	0.20	1.70	-0.14	0.029	8.35
G-902 × G-403	1.75	-0.60	-0.14	-0.026	5.70
G-909 × G-265	3.15	0.20	0.19	-0.014	-3.90
G-909 × G-403	1.85	-5.10	-0.24	-0.030	0.70
G-909 × G-902	0.85	7.15	0.01	-0.024	12.35
G-1500 × G-265	-1.35	2.15	0.06	-0.040	-7.80
G-1500 × G-403	0.70	3.65	0.12	-0.002	8.85
G-1500 × G-902	2.90	-3.20	-0.10	0.008	21.40
G-1500 × G-909	2.75	8.20	0.06	-0.009	2.85
S.E (*rij*) ±	1.68	3.79	0.096	0.0150	4.75
S.E (*rij-rkl*) ±	2.38	5.36	0.136	0.0212	6.71

S.E (r*ij*): Standard error of RCA of cross *ith x jth*; S.E (rik-rkl): Standard error of difference of RCA of *cross ith x kth* and *kth x lth.*

Table 6. Estimates of variances due to general combining ability (σ^2_{GCA}), specific combining ability (σ^2_{SCA}), reciprocal combining ability (σ^2_{RCA}) and error (σ^2_e) for selected traits in *B. rapa* (L.) *ssp. dichotoma* (Roxb.) Hanelt.

Plant traits	σ^2_{GCA}	σ^2_{SCA}	σ^2_{RCA}	σ^2_e	$\sigma^2_{GCA}/\sigma^2_{SCA}$
Primary branches plant^{-1}	-0.750	6.664	1.240	5.669	-0.113
Pods main raceme^{-1}	17.89	35.77	8.126	28.72	0.500
Pod length	-0.002	0.031	0.009	0.019	-0.079
100-seed weight	-0.0001	0.0005	0.0003	0.0005	-0.2056
Seed yield plant^{-1}	-27.88	180.6	70.44	45.07	-0.154

Table 7. Mid (MP) and high (HP) parent hetrosis (H) for yield and ts attributing traits in *B. rapa ssp. dichotoma* (Roxb.) Hanelt.

Hybrids	Primary branches plant^{-1}		Pods main raceme^{-1}		Pod length (cm)		100 seed weight (g)		Seed yield plant^{-1}(g)	
	MPH	HPH	MPH	HPH	MPH	HPH	MPH	HPH	MPH	HPH
G-265 x G-403	57.1*	34.4	22.5**	9.8	16.5**	11.6*	-30.1**	-31.3**	96.7**	65.7*
G-265 x G-902	46.3*	38.2	15.6	4.9	13.3**	12.5**	-39.5**	-41.9**	97.8**	87.4**
G-265 x G-909	25.7	18.8	-3.6	-18.0*	-3.1	-4.2	-13.9	-12.9	109.8**	102.6**
G-265 x G-1500	40.9*	39.8	-6.2	-7.4	-7.6	-11.8**	20.8*	14.1	48.6*	34.7
G-403 x G-265	99.1**	70.3**	1.1	-9.3	7.7	3.2	-16.7	-18.2	157.7**	117.1**
G-403 x G-902	44.7*	18.1	-14.9	-16.0	15.3**	11.2*	-5.8	-8.0	110.6**	85.9**
G-403 x G- 909	35.3	10.4	-2.7	-8.3	18.4**	14.7**	6.5	3.4	79.7**	47.2
G-403 x G-1500	57.6*	35.7	-24.3**	-31.3**	-7.0	-14.8**	-6.2	-13.0	61.7*	25.9
G-902 x G-265	49.3**	41.0*	20.9*	9.7	5.1	4.4	-16.7	-20.0*	159.4**	145.8**
G-902 x G-403	74.5**	42.4*	-16.6*	-17.6*	7.0	3.2	-26.3**	-28.0**	161.1**	130.5**
G-902 x G-909	39.6*	39.6*	-2.1	-8.9	2.5	2.1	-3.3	-8.2	76.2**	61.6*
G-902 x G-1500	-0.7	-6.9	9.9	0.8	5.8	0.3	-18.9*	-26.3**	-26.3	-36.4
G-909 x G-265	72.1**	62.5**	-3.1	-17.5*	8.1	6.9	-25.9**	-26.7*	83.5**	77.2**
G-909 x G-403	66.8**	36.1	-15.8*	-20.7**	3.6	0.4	-18.4*	-20.8*	85.3**	51.8
G-909 x G-902	51.4**	51.4**	16.4*	8.3	3.0	2.6	-22.6*	-26.5**	163.9**	142.0**
G-909 x G-1500	8.1	1.4	-2.7	-16.3*	-13.6**	-18.4**	-15.6	-19.5	66.0**	55.4*
G-1500 x G-265	19.7	18.8	1.1	-0.2	-4.2	-8.6*	-14.0	-18.8	-0.3	-9.7
G-1500 x G-403	70.5**	46.8*	-13.3	-21.3*	0.1	-8.3	-8.0	-14.6	126.3**	76.1**
G-1500 x G-902	42.2*	33.3	0.1	-8.1	0.2	-5.0	-11.7	-19.8*	114.5**	85.2**
G-1500 x G-909	48.9**	39.6*	20.4**	3.5	-10.3**	-15.3**	-23.9*	-27.3*	83.3**	71.6**

** Significant at $p \leq 0.01$, * Significant at $p \leq 0.05$

Pods main raceme^{-1}: The 2 out of 5 parental lines viz., G-902 and G-909 exhibited desirable positive GCA effects of 3.01 and 7.37, respectively (Table 3). However, 5 out of 10 crosses exhibited positive SCA effects. The maximum positive effects were noted for the F_1 cross combination G-265 × G-403 (9.24) followed by G-265 × G-902 (6.80), whereas the maximum negative SCA effects were noted for the F_1 hybrid G-403 × G-902 (-8.56) (Table 4). RCA effects for 6 out of 10 crosses were positive, ranged 0.20 (G-909 × G-265) to 8.20 (G-1500 × G-909). The highest positive RCA effects were noted for hybrid G-1500 × G-909 (8.20) followed by G-909 × G-902 (7.15). However, the maximum negative RCA effects (-7.00) were noted for F_1 hybrid G-403 × G-265 (Table 5). Both additive and non-additive genes were operative in managing the said trait due to significant GCA and SCA mean squares (Table 2). However, relative magnitude of σ^2_{GCA} (17.89), σ^2_{SCA} (35.77), σ^2_{RCA} (8.126) and $\sigma^2_{GCA}/\sigma^2_{SCA}$ (0.500) revealed more importance of non-additive genetic control (Table 6). Results were in accordance with findings of Sincik *et al.,* (2011) who reported highly significant GCA and SCA with non-significant reciprocal effects. Our results were also in continuity with early reports in Indian mustard (Acharya & Swain, 2004; Singh *et al.,* 2010; Gupta *et al.,* 2011; Vaghela *et al.,* 2011) and rapeseed (Rameeh, 2010) as they reported significant GCA and SCA mean squares. Suchindra & Singh (2006) and Noshin *et al.,* (2007) reported highly significant GCA, SCA and reciprocal effects. Acharya and Swain (2004) reported predominant role of additive genetic effects, while Gupta *et al*., (2011) and Vaghela *et al.,* (2011) reported prevalence of non-additive genetic control for the said variable. Table 7 showed that 9 hybrids exhibited positive heterosis over mid parent ranged 0.1 (G-1500 x G-902) to 22.5 % (G-265 x G-403) whereas 6 hybrids had positive high parent heterosis ranged 0.8 (G-902 x G-1500) to 9.8 % (G-265 x G-403). Only 4 of the positive mid parent and none of the positive high parent heterotic values were significant (Table 7). Positive significant mid parent heterosis (Gupta *et al.,* 2011) and heterobeltiosis (Rameah *et al.,* 2003; Gupta *et al.,* 2011) were reported. These results were not in conformity for high parent heterosis.

Pod length: Positive combining ability effects for pod length are desirable, and longer pods are likely to host more seeds. The two parental genotypes exhibited positive GCA effects. However, maximum positive GCA effects were recorded for parental line G-902 (0.08) followed by G-265 (0.05). Maximum negative GCA effect of -0.09 was recorded for genotype G-909 (Table 3). The 6 out of 10 crosses reveled positive SCA effects, ranged 0.02 to 0.21. The highest positive SCA effect was recorded in F_1 hybrid G-403 × G-909 (0.21) followed by G-265 × G-403 (0.16). The maximum negative SCA effect was noted for F_1 hybrid G-909 × G-1500 (-0.24) (Table 4). RCA effects for five out of ten crosses were positive, the highest being 0.19 (G-909 × G-265) followed by 0.12 (G-1500 × G-403). The maximum negative RCA effect was noted for hybrid G-909 × G-403 (-0.24) (Table 5). Significant SCA indicated that only non-additive genetic control is important (Table 2), which was also evident from the relative magnitudes of -0.002, 0.031, 0.009, and -0.079 for σ^2_{GCA}, σ^2_{SCA}, σ^2_{RCA} and $\sigma^2_{GCA}/\sigma^2_{SCA}$, respectively (Table 6). Sabaghnia *et al.,* (2010) reported non-significant GCA and highly significant SCA effects. Turi *et al.,* (2011) reported non-significant GCA whereas highly significant SCA and RCA effects for pod length. Acharya & Swain (2004) in Indian mustard, Teklewold & Becker, (2005) in Ethiopian mustard and Rameeh (2010) in rapeseed reported highly significant GCA and SCA effects. Earlier reports of significant GCA, SCA (Singh *et al.,* 2001; Nassimi *et al.,* 2006a) and RCA (Nassimi *et al.,* 2006a) were also in conformity. Prevalence of non-additive genetic control was also reported by Akbar *et al.,* (2008), whereas Acharya & Swain (2004) reported more importance of additive genetic effects. Data perusal for heterosis revealed that 14 hybrids had positive mid parent heterosis ranged 0.1 (G-1500 x G-403) to 18.4 % (G-403 x G-909) whereas 12 hybrids had positive heterobeltiosis ranged 0.3 (G-902 x G-1500) to 14.7 % (G-403 x G-909) (Table 7). However, only 4 hybrids had positive significant mid and high parent heterosis. Rameah *et al.,* (2003) reported positive non-significant and significant negative high parent heterosis for length of pod.

100-seed weight: Positive combining ability effects for 100 seed weight is desirable, heavier the seed higher will be the yield. Parental lines G-403 and G-902 exhibited positive GCA effects of 0.0071 and 0.0029, respectively. The maximum negative GCA effects were recorded for genotype G-265 (-0.0051) followed by G-1500 (-0.0029) (Table 3). The three F_1 hybrids revealed positive SCA effects. The maximum positive effect was noted for the cross combination G-265 × G-1500 (0.031) followed by G-403 × G-909 (0.011) and G-902 × G-909 (0.003). The maximum negative SCA effect was noted for the F_1 hybrid G-265 × G-902 (-0.029) (Table 4). RCA effects for three F_1 crosses were positive. The highest positive RCA effect of 0.029 was noted for F_1 hybrid G-902 × G-265 followed by 0.017 (G-403 × G-265). The highest negative RCA effect was noted for cross combination G-1500 × G-265 (-0.040) (Table 5). Significant SCA and RCA mean squares (Table 2) indicated that non-additive and maternal genes were involved. The variance estimates σ^2_{GCA} (-0.0001), σ^2_{SCA} (0.0005), σ^2_{RCA} (0.0003) and $\sigma^2_{GCA}/\sigma^2_{SCA}$ (0.0003) revealed preponderance of non-additive genetic control (Table 6). Suchindra & Singh (2006); Turi *et al.,* (2011) reported highly significant SCA and RCA effects. In Indian mustard (Acharya & Swain 2004; Gupta *et al.,* 2011; Nasrin *et al.,* 2011; Vaghela *et al.,* 2011), Ethiopian mustard (Teklewold & Becker, 2005) and rapeseed (Shen *et al.,* 2005; Sabaghnia *et al.,* 2010; Rameeh, 2011) were in partial agreement and reported significant GCA and SCA effects. Aghao *et al.,* (2010) in Indian mustard and Akbar *et al.,* (2008) in rapeseed reported non-significant GCA and SCA effects. Non-additive genetic control was also elucidated in some earlier investigations (Nassimi *et al.,* 2006a; Akbar *et al.,* 2008; Aher *et al.,* 2009; Parmar *et al.,* 2011; Vaghela *et al.,* 2011) still others (Rameah *et al.,* 2003; Acharya & Swain, 2004; Gupta *et al.,* 2011) revealed preponderance of additive genetic effects. Positive heterosis was recorded for 2 hybrids viz. 6.5 (G-403 x G-909); 20.8 % (G-265 x G-1500) over mid parent, with the later differing significantly from its mid parent, whereas 3.4 and 14.1% over better parent by the same hybrids, respectively (Table 7). None of the hybrids with positive heterobeltiosis was significant. Rameah *et al.,* (2003) reported positive non-significant and significant negative heterobeltiosis which is in conformity. Rameeh (2011) reported both positive and negative significant better parent heterosis and thus in partial agreement with the findings of the present study. Mahto &

Haider, (2004) reported positive significant mid parent heterosis. Gupta *et al.,* (2011) reported positive significant heterosis over both mid and better parent.

Seed yield plant^{-1}: The three parental lines viz., G-265, G-902 and G-909 exhibited desirable positive GCA effects of 0.63, 1.31 and 2.87, respectively. Maximum negative GCA effect was recorded for G-403 (-2.67) (Table 3). The seven crosses exhibited positive SCA effects, ranged 6.65 to 12.00 The maximum positive SCA effects were noted for F_1 hybrid G-265 × G-902 (12.0) followed by G-403 × G-1500 (9.96), whereas the maximum negative SCA effect was noted for the F_1 cross G-265 × G-1500 (-6.89) (Table 4). RCA effects for eight crosses were positive, ranged 0.70 to 21.40. The highest positive RCA was noted in F_1 hybrid G-1500 × G-902 (21.40) followed by G-909 × G-902 (12.35). The maximum negative RCA effect was noted for cross combination G-1500 × G-265 (-7.80) (Table 5). Significant SCA and RCA mean squares indicated that non-additive and reciprocal genes were involved in the expression seed yield per plant (Table 2). Predominance of non-additive genetic control is obvious from relative estimates of -27.88, 180.6, 70.44 and -0.154 for σ^2_{GCA}, σ^2_{SCA}, σ^2_{RCA} and $\sigma^2_{GCA}/\sigma^2_{SCA}$, respectively (Table 6). In Indian mustard (Acharya & Swain 2004; Vaghela *et al.,* 2011) and rapeseed (Shen *et al.,* 2005; Akbar *et al.,* 2008; Amiri-Oghan *et al.,* 2009) highly significant GCA and SCA effects were reported. The present results are in agreement for SCA but in contrast for GCA effects for the concerned trait. Nassimi *et al.,* (2006a) reported non-significant GCA effects, highly significant SCA and RCA effects. Teklewold & Becker, (2005) reported significant GCA and non-significant SCA mean squares. Some earlier studies (Rameah *et al.,* 2003; Gupta *et al.,* 2006; Akbar *et al.,* 2008; Aher *et al.,* 2009; Gupta *et al.,* 2011; Parmar *et al.,* 2011; Vaghela *et al.,* 2011) also reported non-additive genetic control. Huang *et al.,* (2010) reported predominance of additive genetic effects whereas Nassimi *et al.,* (2006a) reported prevalence of maternal effects. Positive heterosis was recorded for 18 hybrids; all of these were significant for heterosis over mid parent however for better parent heterosis only 14 of these were significantly different from respective high parent. Mid parent heterosis ranged 48.6 (G-265 x G-1500) to 163.9 % (G-909 x G-902) with heterosis recorded however, heterobeltiosis varied from 25.9 (G-403 x G-1500) to 145.8 % (G-902 x G-265) (Table 7). Earlier investigations reported positive significant heterosis over mid parent (Cheema & Sadaqat, 2004; Mahto & Haider, 2004; Qian *et al*., 2007; Gupta *et al.,* 2011) and over better parent (Rameah *et al.,* 2003; Gupta *et al.,* 2011; Rameeh, 2011) which is in conformity with the present study. However, Gupta *et al.,* (2006) reported non-significant positive better parent heterosis.

Conclusions

Parental line G-909 was found as best general combiner for primary branches plant^{-1}, pods main raceme^{-1} and seed yield plant^{-1}. Based on combing ability and heterosis the F_1 hybrids G-909 × G-265 (primary branches plant^{-1}), G-265 × G- 403, G-1500 × G-909 (pods main raceme^{-1}), G-403 × G-909 (pod length), G-265 × G-1500 (100-seed weight) and G-1500 × G-902, G-909 × G-902 (seed yield plant^{-1}) can be utilized in future breeding endeavors. Non-additive genetic control, as predominant mechanism, implicates that parental selection based on known performance of parent is likely to fetch better results and further improvement can be made by subsequent family selection. The use of schemes like bi-parental mating design, diallel selective mating followed by recurrent or reciprocal recurrent selection can be beneficial.

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