COMBINING ABILITY FOR YIELD RELATED TRAITS IN BRASSICA JUNCEA

NAUSHAD ALI TURI¹, RAZIUDDIN¹, FARHATULLAH¹, NAQIB ULLAH KHAN¹, GHULAM HASSAN¹, JEHAN BAKHT², SAJID KHAN¹ AND MOHAMMAD SHAFI³

¹Department of Plant Breeding and Genetics, KPK Agricultural University, Peshawar, Pakistan ²Institute of Biotechnology & Genetic Engineering, KPK Agricultural University, Peshawar, Pakistan ³Department of Agronomy, KPK Agricultural University, Peshawar, Pakistan

Abstract

A diallel experiment was conducted to determine better general and specific combiners in 8x8 Brassica juncea L., genotypes for seed yield and its associated traits. Analysis of variance revealed highly significant (p≤0.01) differences among all the genotypes for pod length, 1000 seed weight and seed yield plant⁻¹ while significant ($p \le 0.05$) differences were noted for pods plant⁻¹ and seeds pods⁻¹. According to combining ability analysis, the general combining ability (GCA) mean squares was highly significant ($p \le 0.01$) for seed yield plant⁻¹ and significant ($p \le 0.05$) for 1000 seed weight, while found non significant for pods plant⁻¹, pod length and seeds pod⁻¹. The specific combining ability (SCA) and reciprocal combining ability (RCA) mean squares were highly significant $(p \le 0.01)$ for all the traits except seeds pod⁻¹. GCA effects were of greater magnitude than SCA and RCA for pods plant⁻¹, pod length and seed yield plant⁻¹ indicating that these traits were controlled by additive type of gene action. Reciprocal effects were found greater than GCA and SCA for seed pod⁻¹ and 1000 seed weight showing that maternal effects were also active and need due attention for the said traits. The parental genotypes MYT009, MYT113, MYT123, MYT120 and MYT117 were found the best general combiners, while hybrids MYT117 x MYT123, MYT113 x MYT009, MYT123 x MYT113, MYT124 x MYT117, MYT105 x MYT103 and MYT113 x MYT120 were found the best specific combiners for majority of the traits and could be exploited through further selection in segregating population. Results revealed the importance of both additive and nonadditive genetic variability suggesting the use of integrated breeding strategies which can efficiently utilize the additive as well as non-additive genetic variations.

Introduction

For faster advances and getting tangible results in plant breeding, it is necessary to know the existing genetic variability and combining abilities of the breeding materials. In quantitative genetics, the study of different type of gene actions helps in the identification and selection of suitable parental lines to be included in hybridization to develop superior F_1 hybrids. This technique can be exploited for hybrids development and or the genotypes can be studied through intensive selection in the segregating generations.

Diallel analysis provides a mating design whereby the selected parents are crossed in all possible combinations. The mean values are used for predicting combining ability of the parents (GCA) and hybrids (SCA) to enlighten the nature of gene action involved in the inheritance of traits (Khan *et al.*, 2009a). Combining ability is a statistical procedure used for analysis of diallel crosses in a universal theoretical form (Griffing, 1956). It works as a principal method for screening of germplasm and to determine the ability of the different genotypes to be included or not in a future breeding programme on the basis of their GCA, SCA and reciprocal effects. The yield advancement in brassica requires

information regarding the nature of different combining abilities of parents and also know how about the nature of gene action involved in expression of different quantitative and qualitative traits of economic importance is also a prerequisite to develop and design desirable lines. Zhang (1987) reported that selection of parent cultivars for intraspecific hybridization is greatly facilitated by the utilization of GCA and SCA. In breeding programs, the GCA and SCA are usually used for parents and their cross combinations selection, respectively for improvement of crop production (Singh *et al.*, 2003). Therefore, desirable GCA and SCA are needed to achieve higher yield with heterosis (Marinkovi & Marjanovic, 2004).

Many studies have been conducted to address the effects of GCA and SCA for yield and yield components in different crops (Khan *et al.*, 2009a & b; Muraya *et al.*, 2006; Jan *et al.*, 2005; Attia *et al.*, 2001; Sameena *et al.*, 2000; Juma *et al.*, 1999; Islam *et al.*, 1999). But the research studies regarding gene action for yield and yield components in brassica is unsolved and needs consideration. However, studies on combining ability in relation to other yield related traits have been reported (Abercrombie *et al.*, 2005; Satwinder *et al.*, 2000; Singh 2003). The present study aims to identify the best general combiners and their F_1 hybrids on the basis of their general, specific and reciprocal combining ability for yield and its contributing traits.

Materials and Methods

Plant material and experimental design: Eight *Brassica juncea* L. genotypes of MYT (MYT stands for Mustard Yield Trail on National Level) series viz; MYT103, MYT009, MYT124, MYT113, MYT123, MYT117, MYT105 and MYT120 were crossed manually in 8x8 full diallel fashion at KPK Agricultural University, Peshawar, Pakistan. Fifty six hybrids and their eight parental lines were sown next year in a randomized complete block (RCB) design with two replications. Each replication contained 64 sub-plots and each sub-plot with four rows of four meters length having inter- and inta-row spacing of one meter and 15 cm respectively. All recommended cultural practices were followed uniformly in all entries from sowing till the harvesting.

Traits measurement and statistical analysis: The data were recorded on pods plant⁻¹, pod length, seeds pod⁻¹, 1000 seed weight and seed yield plant⁻¹. All the data were subjected to analysis of variance (ANOVA) technique according to Steel & Torrie (1980) using MstatC computer software to test the null hypothesis of no differences between various F_1s and their parental lines. The data were further subjected to combining ability analysis as outlined by Griffing (1956) Method-I, based on Eisenhart's Model-II to assess the genetic variances due to GCA and SCA and maternal effects.

Results and Discussion

Mean performance revealed that parental lines and their F_1 hybrids have highly significant differences (p \leq 0.01) for all traits studied i.e., pods plant⁻¹, pod length, seeds pod⁻¹, 1000 seed weight and seed yield plant⁻¹ (Table 1). To obtain the information regarding gene action involved in these traits, the genetic variations were further partitioned into components of variance i.e., GCA, SCA and RCA effects (Table 2).

Samuel of		Mean squares						
Source of variance	df	Pods plant ⁻¹	Pod length	Seeds pod ⁻¹	1000 seed weight	Seed yield plant ⁻¹		
Replications	1	52.53*	0.22**	7.03*	0.02**	2.00**		
Genotypes	63	1469.43**	0.45**	4.48**	1.28**	3.43**		
Error	63	92.34	0.02	1.60	0.01	0.13		

Table 1. Mean squares for pods plant⁻¹, pod length, seeds pod⁻¹, 1000 seed weight and seed yield plant⁻¹ in *B. juncea* L.

**, * = Significant at $p \le 0.01$ and $p \le 0.05$ reepctively.

Table 2. Analysis of variance for combining ability for pods plant⁻¹, pod length, seeds pod⁻¹, 1000 seed weight and seed yield plant⁻¹ in *B. juncea* L.

G 6	df	Mean squares						
Source of components		Pods plant ⁻¹	Pod length	Seeds pod ⁻¹	1000 seed weight	Seed yield plant ⁻¹		
GCA	7	1813.56 ^{ns}	1893.42 ^{ns}	1.61 ^{ns}	0.21*	3.87**		
		(45.18)	(46.35)	(17.52)	(16.03)	(61.92)		
SCA	28	956.96**	938.41**	1.59 ^{ns}	0.06**	0.15**		
		(23.84)	(22.97)	(17.30)	(4.58)	(2.40)		
RCA	28	1243.33**	1249.13**	4.46**	1.03**	2.00**		
		(30.97)	(30.58)	(48.53)	(78.63)	(32.00)		
Error	63	0.53	4.24	1.53	0.01	0.23		
		(0.01)	(0.10)	(16.65)	(0.76)	(3.68)		

**, * = Significant at p \leq 0.01 and p \leq 0.05 respectively, ns = Non-significant

Upper values denote variance components while lower values denote variance estimate in percentage

Pods plant⁻¹: The mean squares indicated that the effects due to SCA and RCA were highly significant ($p \le 0.01$), while non-significant (p > 0.05) differences were observed for GCA (Table 2). According to GCA, out of 8 parents, 5 parents showed positive GCA while remaining 3 showed negative GCA effects for pods plant⁻¹. Maximum positive GCA effects (8.80) was recorded in genotype MYT009 whereas maximum negative GCA effects (-14.33) were noted in MYT117 (Table 3). Out of 28 crosses, 10 F₁ hybrids showed positive SCA effects and remaining 18 indicated negative effects (Table 4). The best specific performance with maximum positive SCA effects (16.39) were observed in cross combination MYT009 x MYT120 while maximum negative effects (-25.86) were recorded for the F₁ hybrid MYT103 x MYT105. In case of RCA effects, 17 out of 28 crosses showed positive while remaining 11 F_1 hybrids had negative RCA effects for pods plant⁻¹ (Table 5). Maximum positive reciprocal effect (44.0) was recorded in the reciprocal cross MYT120 x MYT117. Zhang et al., (1987) reported significant GCA for pods plant⁻¹ pod length, seeds pod⁻¹, seed yield plant⁻¹ and 1000-seed weight. Sachan et al., (2003), Gupta et al., (1991) also obtained significant GCA for the same trait. Similarly, Noshin et al., (2007) also reported significant GCA effects for pods main raceme⁻¹.

1000-seed weight and seed yield plant in D. junceu D.						
Genotypes	Pods plant ⁻¹	Pod length	Seeds pod ⁻¹	1000 seed weight	Seed yield plant ⁻¹	
MYT103	8.17	-0.16	-0.23	0.03	-0.40	
MYT009	8.80	-0.20	-0.67	0.07	0.30	
MYT124	3.23	0.08	0.39	0.06	0.14	
MYT113	4.05	-0.23	-0.30	-0.03	0.31	
MYT123	-12.27	0.03	0.14	-0.16	-0.51	
MYT117	-14.33	0.01	-0.23	0.15	-0.61	
MYT105	5.61	0.07	0.70	-0.08	0.39	
MYT120	-3.27	0.35	0.20	-0.04	0.38	

Table 3. General combining ability effects for pods plant ⁻¹ , pod length, seeds pod ⁻¹ ,
1000-seed weight and seed yield plant ⁻¹ in <i>B. juncea</i> L.

Table 4. Specific combining ability effects for pods plant⁻¹, pod length, seeds pod⁻¹, 1000-seed weight and seed yield plant⁻¹ in *B. juncea* L.

	Pods Pod Seeds 1000 seed Seed yield						
Genotypes	plant ⁻¹	length	pod ⁻¹	weight	plant ⁻¹		
MYT103 x MYT009	-16.05	-0.11	0.23	0.13	-0.30		
MYT103 x MYT124	-1.48	0.06	-0.83	-0.18	0.36		
MYT103 x MYT113	-1.30	-0.28	-0.14	-0.15	-0.26		
MYT103 x MYT123	-10.48	-0.21	-0.58	-0.17	-1.39		
MYT103 x MYT117	-2.9.29	0.10	-1.20	-0.17	0.01		
MYT103 x MYT105	-25.86	-0.03	0.86	0.06	-0.43		
MYT103 x MYT120	14.52	-0.01	-0.14	-0.18	-0.38		
MYT009 x MYT124	-0.11	-0.12	-0.39	-0.17	0.31		
MYT009 x MYT113	-12.42	-0.23	-0.70	-0.23	-0.26		
MYT009 x MYT123	-18.11	-0.07	-0.14	-0.00	0.69		
MYT009 x MYT117	6.95	0.02	-0.77	-0.01	0.19		
MYT009 x MYT105	-2.98	-0.24	-1.70	-0.23	-1.23		
MYT009 x MYT120	16.39	0.01	0.80	0.03	-0.63		
MYT124 x MYT113	-21.36	-0.17	-0.77	-0.02	-0.91		
MYT124 x MYT123	9.45	-0.03	0.80	0.01	-0.04		
MYT124 x MYT117	-19.48	-0.14	-1.83	-0.05	0.16		
MYT124 x MYT105	14.08	-0.07	-0.77	-0.07	-1.28		
MYT124 x MYT120	-20.55	0.10	1.23	-0.26	0.08		
MYT113 x MYT123	-13.36	0.03	-0.52	-0.00	-0.01		
MYT113 x MYT117	12.70	0.04	0.86	-0.11	-0.91		
MYT113 x MYT105	13.27	-0.00	1.08	-0.18	0.56		
MYT113 x MYT120	-12.36	-0.34	0.43	0.08	-0.19		
MYT123 x MYT117	5.02	-0.14	-0.58	-0.03	-0.09		
MYT123 x MYT105	4.08	-0.07	-0.52	0.30	-0.13		
MYT123 x MYT120	-22.05	-0.20	-1.52	0.01	-0.27		
MYT117 x MYT105	-22.36	-0.33	0.86	0.05	-0.28		
MYT117 x MYT120	5.52	0.06	-1.14	-0.15	-0.52		
MYT105 x MYT120	-18.92	-0.23	0.42	-0.27	-0.06		

pod ⁻ , 10	pod ⁻¹ , 1000-seed weight and seed yield plant ⁻¹ in <i>B. juncea</i> L.							
Com others on	Pods	Pod	Seeds	1000 seed	Seed yield			
Genotypes	plant ⁻¹	length	pod ⁻¹	weight	plant ⁻¹			
MYT009 x MYT103	11.00	0.05	0.00	0.25	-1.30			
MYT124 x MYT103	-10.00	0.05	0.00	0.15	-0.50			
MYT124 x MYT009	22.00	0.20	2.00	0.00	0.15			
MYT113 x MYT103	-21.00	-0.10	0.00	-0.10	-0.65			
MYT113 x MYT009	-0.50	0.55	-1.00	-0.05	0.25			
MYT113 x MYT124	26.00	0.15	0.00	0.25	-1.15			
MYT123 x MYT103	9.50	-0.05	-2.00	-0.05	-0.10			
MYT123 x MYT009	33.50	0.10	0.00	0.15	1.50			
MYT123 x MYT124	1.50	0.05	0.00	0.35	-1.00			
MYT123 x MYT113	-0.50	0.01	2.00	-0.05	0.20			
MYT117 x MYT103	-21.00	-0.10	1.00	0.25	-0.40			
MYT117 x MYT009	1.50	-0.30	-3.00	-0.05	-0.90			
MYT117 x MYT124	25.50	0.00	-1.00	0.10	0.10			
MYT117 x MYT113	-7.50	-0.30	-1.00	-0.25	1.30			
MYT117 x MYT123	2.50	0.15	0.00	-0.70	0.90			
MYT105 x MYT103	-28.00	0.15	0.00	-0.25	-1.05			
MYT105 x MYT009	0.50	0.05	-1.00	-0.50	-1.05			
MYT105 x MYT124	10.00	-0.15	-1.00	-0.35	-0.15			
MYT105 x MYT113	11.00	0.00	2.00	0.05	-1.35			
MYT105 x MYT123	-8.50	-0.10	1.00	-0.30	-1.95			
MYT105 x MYT117	-15.00	0.30	0.00	-0.25	-0.10			
MYT120 x MYT103	-23.50	-0.35	0.50	-0.05	0.00			
MYT120 x MYT009	1.00	-0.30	1.00	-0.01	-1.45			
MYT120 x MYT124	-15.50	-0.50	0.50	0.00	0.10			
MYT120 x MYT113	12.50	-0.25	-1.00	0.05	-0.10			
MYT120 x MYT123	1.50	-0.45	-0.50	0.05	0.00			
MYT120 x MYT117	44.00	-0.45	1.50	0.20	-0.35			
MYT120 x MYT105	4.50	0.15	0.00	0.15	0.00			

Table 5. Reciprocal combining ability effects for pods plant⁻¹, pod length, seeds pod⁻¹, 1000-seed weight and seed yield plant⁻¹ in *B. juncea* L.

Pods length: Mean squares presented in Table 2 shows that effect due to GCA were nonsignificant (p>0.05) while the effects of SCA and RCA were highly significant (p ≤ 0.01) for pods length. Longer pods are considered one of the major yield contributing components in brassica, therefore, positive GCA and SCA are desirable. Results revealed that out of 8 parents, 5 showed positive GCA effects for pod length, where maximum positive effects (0.35) were observed for MYT120 (Table 3). Maximum negative GCA effects (-0.23) were observed in MYT113. Regarding SCA effects, out of 28 F₁ hybrids, 8 crosses showed positive SCA effects, where the best specific performance (0.10) was observed in cross combinations of MYT103 x MYT117 and MYT124 x MYT120 (Table 4). Maximum negative SCA effects (-0.34) were recorded in cross MYT113 x MYT120. Out of 28 crosses, 3 crosses indicated positive RCA effects, maximum positive effects (0.55) being observed in MYT113 x MYT009 (Table 5) while minimum RCA effects (-0.45) were found in F₁ hybrids MYT120 x MYT123 and MYT120 x MYT117. The present results are supported by the earlier findings of Nassimi et al., (2006) who observed higher GCA effects in comparison to SCA and RCA effects for pod length in B. napus genotype indicating that these traits were controlled by additive gene action. Similarly, Hu et al., (1996) also reported that both GCA and SCA were significant $(p \le 0.05)$ for pod length and other yield contributing traits.

Seeds pod⁻¹: Mean square showed that the effects due to GCA and SCA were nonsignificant (p>0.05), while the effects of RCA were highly significant (p<0.01) on seeds pod⁻¹ (Table 2). Seeds pod⁻¹ is the major yielding contributing component of seed yield in brassica, hence positive combining ability is preferred for this trait. The data revealed that the effects due to RCA were highest in its magnitude (48.53%) whereas variance due to GCA was 17.52% and for SCA was 17.30% (Table 2). Data concerning GCA effects (Table 3) indicated that out of 8 parents, 4 showed positive and 4 indicated negative GCA effects. Maximum positive GCA effects (0.70) were presented by MYT105, while maximum negative GCA effects (-0.67) were noted in MYT009. Out of 28 F₁ hybrids, 10 showed positive SCA effects where maximum SCA effects (1.23) were observed in the cross combination of MYT124 x MYT120 (Table 4). Maximum negative SCA effects (-1.83) were recorded in cross of MYT124 x MYT117. RCA effects for seeds pod⁻¹ showed that 19 crosses attained positive RCA effects where maximum positive effects (2.00) were recorded in MYT124 x MYT009 and MYT123 x MYT113 crosses and least value was observed in reciprocal cross of MYT117 x MYT009 (-3.00). Nassimi et al., (2006) reported significant (p \leq 0.05) GCA, SCA and RCA effects for seed pod⁻¹ in brassica. Significant (p≤0.05) GCA effects were also found by Hu et al., (1996) and Davik (1997) for pod length, seeds pod⁻¹, 1000-seed weight and seed yield plant⁻¹.

1000-seed weight: 1000-seed weight is considered as one of the yield contributing components in brassica, hence positive effects of GCA, SCA and RCA are desirable. Mean square values for GCA were significant ($p \le 0.05$) and highly significant ($p \le 0.01$) for both SCA and RCA (Table 2). However, the RCA effects were enormous in magnitude (78.63%) in comparison to GCA (16.03%) and SCA (4.58%) indicating the importance of reciprocal effects for this trait and that type of cytoplasmic effects should not be ignored. In GCA effects, four parents showed positive GCA effects, where the maximum (0.15) being observed in MYT117 (Table 3). The negative GCA effects were maximum (-0.16) in genotype MYT123. The SCA effects indicated that out of 28 F₁ hybrids, 8 crosses showed positive SCA effects, where best specific performance with the maximum positive SCA effects (0.30) was observed in cross combination of MYT123 x MYT105. The maximum negative SCA effects (-0.27) were found in F₁ hybrid MYT105 x MYT120. Positive reciprocal effects were noted in 14 crosses where maximum positive RCA effects (0.35) were recorded in reciprocal cross of MYT123 x MYT124 (Table 5). Our findings are in line with the results of Nassimi *et al.*, (2006) and Yadav *et al.*, (1991) who reported significant ($p \le 0.05$) GCA and SCA effects for yield and yield components indicating that both additive and non-additive gene actions were important in the inheritance of these traits. Our results are also in conformity with the reports of Teklewold & Becker (2005) who mentioned significant (p≤0.05) SCA effects for yield and vield associated traits.

Seed yield plant⁻¹: The combining ability mean square values were highly significant ($p \le 0.01$) for GCA, SCA and RCA in case of seed yield plant⁻¹. From these results it can be seen that GCA effects were greater in magnitude (61.92%) followed by RCA (32.00%) and SCA (2.40%) indicating the importance of additive type of gene action for seed yield plant⁻¹. Table 3 indicated that 5 parental lines showed positive GCA effects for seed yield plant⁻¹, whereas maximum GCA values were observed in MYT105 (0.39). The negative GCA effects were maximum (-0.61) in MYT117. In case of SCA, out of 28 crosses, 8 F₁ hybrids showed positive SCA effects, where the best specific performance with maximum positive SCA (0.69) was recorded in cross combination of MYT009 x MYT123 (Table 4). Maximum negative SCA effects (-1.39) were found in F₁ hybrid

(MYT103 x MYT123). Positive reciprocal effects were noted in 11 crosses where maximum value (1.50) was recorded in MYT123 x MYT009 while the minimum value (-1.35) was obtained in MYT105 x MYT113 (Table 5).

Seed yield is the final outcome of all the yield contributing components in brassica, therefore, positive combining ability effects are desirable. Highest significant and positive GCA effects in comparison to SCA and RCA were recorded for seed yield plant⁻¹. Similarly, Noshin *et al.*, (2007) reported significant ($p \le 0.05$) GCA, SCA and RCA for seed yield plant⁻¹ in brown mustard. Our results are also in conformity with the findings of Mcharo *et al.*, (1995), who reported significant ($p \le 0.05$) GCA effects for seed yield, oil content and flowering traits. Diwakar & Singh (1993), Gupta *et al.*, (1991) and Yadav *et al.*, (1991) observed significant GCA and SCA effects for yield and yield component indicating the importance of both additive and non-additive genes.

Conclusion

From the present investigation it could be concluded that GCA effects were higher in magnitude for pods plant⁻¹, pod length and seed yield plant⁻¹ indicating that these trait were governed by additive type of gene action. RCA effects were of higher magnitude for seeds pod⁻¹ and 1000 seed weight manifesting that maternal effect play crucial role for these traits. The importance of both additive and non-additive variability could not be ignored and the use of integrated breeding strategies is needed for the improvement of these traits in *Brassica juncea* genotypes.

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