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COMBINING ABILITY STUDIES FOR QUANTITATIVE TRAITS IN *BRASSICA JUNCEA*

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ABSTRACT

Combining ability was determined in an 8 × 8 F_1 diallel cross of *Brassica juncea* L. genotypes for various quantitative traits during 2010-2011 at the University of Agriculture, Peshawar, Pakistan. Genotypes revealed highly significant ($p \leq 0.01$) differences for days to maturity, plant height, primary branches plant^{-1}, pods main raceme^{-1} and seed yield plant^{-1} while significant ($p \leq 0.05$) variations were noted for days to 50% flowering. According to combining ability analysis, mean squares due to general combining ability (GCA) were significant ($p \leq 0.01$) for all the traits except days to 50% flowering and maturity. Mean squares due to specific combining ability (SCA) and reciprocal combining ability (RCA) were significant ($p \leq 0.01$) for all the traits except SCA mean squares for seed yield plant^{-1}. Mean squares due to RCA were even greater than GCA/SCA for some variables, and therefore maternal effects cannot be ignored. The variations among genotypes for earliness and plant height were controlled by non-additive gene action, while morphological and seed yield traits were governed by additive gene action. Genotypes MYT120, MYT124 and MYT105 and F_1 hybrids MYT117 × MYT123, MYT103 × MYT124, MYT009 × MYT123, MYT123 × MYT009 and MYT117 × MYT113 were identified as best general and specific combiners and could be exploited through selection in early segregating populations. Results suggested the use of integrated breeding strategies which can efficiently utilize the additive as well as non-additive genetic variations.

Keywords: *Brassica juncea* L., combining ability, diallel analysis, general and specific combining ability, quantitative traits.

INTRODUCTION

Pakistan is facing huge shortage of edible oil since long. Rapid rise in population and improvement in living standard of people are the major reasons for shortage of edible oil in the country. Pakistan is an agro-based country and crops genetic diversity is required to be studied due to their consequence on agricultural economics. Crucifer Brassica encompasses highly diverse group of crop plants that have great economic value. Over the past couple of decades, rapeseed and mustard have become most important world sources of vegetables oil, which constitute an important part of the human diet. In Pakistan, oilseed Brassica crops annually occupy about 234,600 hectares with a production of 185,000 metric tons with average yield of 789 kg ha^{-1} (PBS, 2012). In order to save foreign exchange, government has encouraged the cultivation of different oilseed crops in the country. Genetic potential of the traditional oil seed crops about production is limited; therefore, efforts are being made to develop new high yielding and better quality lines.

Brassica species (*B. napus, B. campestris, B. juncea*) are grown world wide as a source of edible oil. Although widely and extensively grown as a vegetable, mustard is being grown more for its seeds, which yield an essential oil and condiment. Its oil content varies between 28.6 to 45.7%. In addition to edible purposes, it also used as hair oil and lubricant. Seed residue is used as cattle feed and in fertilizers. Mustard (*B. juncea*) is one of the major oil seed crop in Indian sub-continent, and is widely grown throughout the rain-fed areas of Pakistan. It has greater yield potential for semi-arid conditions and known to be more drought tolerant and shattering resistant than *B. napus* and *B. campestris*. It matures earlier than *B. napus* and consequently escapes the attack of aphids and hairy caterpillars. It is more lodging resistant as compared to rapeseeds (*B. napus* and *B. campestris*). There is much scope of developing new mustard varieties, containing low levels of erucic acid and glucosinolates. However, there are some limitations in *B. juncea* as the available genotypes contain higher glucosinolates and erucic acids contents. Erucic acid is a fatty acid found primarily in genus Brassica and some other oil seed crops. In *B. juncea* genotypes, erucic acid constitutes 60-65% of the total fatty acids.

Feeding experiments with animals have demonstrated that rapeseed oil, which is rich in erucic acid, interferes in myocardial conductance and peripheral vascular system, increases blood cholesterol and shorten coagulation time (Renard and McGregor, 1992), and thus, restricting their use as edible oil crop. On the other hand, defatted Brassica oilseed meal contains about 40% protein with a well-balanced amino acid composition. It is used in human and animal nutrition; however, its use is limited due to glucosinolate content. Glucosinolate studies revealed that its all kinds are derived from amino acids and most of them are the product of a common biosynthetic pathway. Intact glucosinolate (without myrosinases: an enzyme which break down the glucosinolate) are capable of causing significant anti-nutritional and toxic effects (Bille *et al*., 1983). In addition, oil contents of these species are also lower than would be desired. Therefore, there is great need to screen out breeding lines for lower levels of erucic acid and glucosinolates with higher yield potential.

Diallel mating design has been extensively used to analyze the combining ability effects of *B. napus* L. genotypes and to provide information regarding genetic mechanisms controlling seed yield and other traits. Such concerted breeding efforts need critical evaluation of parental genotypes for their combining ability to get synthetics development (Sood *et al*., 2000). For improvement of any desirable trait in a genotype, collection of certain genetic information related to this character is prerequisite. For this, necessary data on various agronomic traits and there analyses through combining ability and heritability is required. Combining ability is the process which is used to evaluate the impending performance of genotype(s) to combine with other desirable genotype(s). This technique can be exploited for hybrids development and populations can be studied through intensive selection in segregating generations.

In various crops, many studies have been conducted to address the effects of GCA, SCA and RCA for yield and yield components. In past studies, gene action regarding yield and yield components in Brassica needs to be considered. However, studies on combining ability in relation to other yield related traits have been reported (Satwinder *et al*., 2000; Singh and Sachan, 2003; Sincik *et al*., 2011). In combining ability analysis, the mean squares due to GCA, SCA and RCA were found significant for majority of morphological and yield traits (Sincik *et al*., 2011).

The variance for GCA includes the additive portion of the total variance, whereas that for SCA includes the non-additive portion, arising not largely from dominance and epistatic deviations. Information on the relative importance of additive and non-additive gene actions within a breeding population can determine that which breeding procedure will efficiently improve the performance of the traits of interest. Most of the previous studies on combining abilities have shown significant GCA and SCA effects for morphological, yield and yield related traits (Teklewold and Becker, 2005; Nassimi *et al.*, 2006a, b; Marjanovic-Jeromela *et al.*, 2007; Sincik *et al*., 2011). Both additive and non-additive gene action were found important in inheritance of yield and its components (Sheoran *et al.*, 2000; Sood *et al*., 2000; Singh *et al.*, 2002; Rameah *et al.*, 2003; Cheema and Sadaqat, 2004; Tuncturk and Ciftci, 2007; Akbar *et al.*, 2008; Huang *et al*., 2010). In present studies, an effort was made to ascertain the credentials of suitable parental genotypes of *B. juncea* and their F_1 hybrids through GCA, SCA and RCA for various earliness, morphological and yield related traits.

MATERIALS AND METHODS

Eight Brassica genotypes of MYT (Mustard Yield Trial) including MYT009, MYT103, MYT105, MYT113, MYT123, MYT117, MYT120 and MYT124 were crossed in an 8 × 8 diallel fashion during 2010 at The University of Agriculture, Peshawar, Pakistan. The 56 F_1 hybrids and their eight parental lines were sown during 2011 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 100 and 15 cm of rows and plants spacing, respectively and maintained 26 plants in each row. Recommended cultural practices were followed uniformly in all entries from sowing to harvesting.

Data were recorded on ten randomly selected plants for days to 50% flowering, days to maturity, primary branches plant^{-1}, pods raceme^{-1}, plant height and seed yield plant^{-1}. All the recorded data were subjected to analysis of variance technique according to Steel *et al*. (1997). Data were further analyzed through 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 RCA effects.

RESULTS

Mean squares revealed that parental lines and their F_1 hybrids had significant ($p \leq 0.01$) differences for days to maturity, plant height, primary branches plant^{-1}, pods main raceme^{-1} and seed yield plant^{-1} and significant ($p \leq 0.05$) for days to 50% flowering (Table 1). These significant genotypic variations were further partitioned into variations due to GCA, SCA and reciprocal effects.

Days to 50% flowering: Mean squares due to components of combining ability were significant ($p \leq 0.01$) for SCA and RCA, while GCA was non-significant among parental accessions for days 50% flowering (Table 1). Greater SCA mean square revealed that time to 50% flowering was controlled non-additively. Early flowering result in sufficiently larger grain filling period, which will ultimately results into bolder grain and more seed yield. Therefore, negative combining ability effects for flowering are desirable. In case of GCA effects, two out of eight parental accessions showed desirable negative GCA effects for days to 50% flowering i.e. MYT105 (-0.53) followed by MYT124 (-0.09) (Table 2). Maximum positive GCA effects were recorded in MYT117 (0.28) and MYT009 (0.16). Twelve

F_1 hybrids revealed negative SCA effects for days to 50% flowering (Table 3). Best specific performance was observed in F_1 hybrids MYT105 × MYT123 (-2.00), MYT009 × MYT124 (-1.45) and same SCA value of -1.00 was shown by crosses MYT105 × MYT113 and MYT120 × MYT123. Parental genotypes with greater GCA i.e. MYT105 and MYT124 were involved in majority of desirable specific F_1 hybrids. Eleven F_1 hybrids revealed positive SCA effects for days to 50% flowering, and remaining hybrids showed zero SCA effects. Maximum positive SCA effects were found in F_1 hybrids viz., MYT120 × MYT124 (2.00), MYT009 × MYT113 (1.41) and MYT103 × MYT117 (1.28). Fourteen F_1 hybrids showed desirable negative reciprocal effects which were maximum in MYT123 × MYT117 (-1.78) followed by MYT120 × MYT009 (-1.50) and MYT117 × MYT103 (-1.00) (Table 4).

Days to maturity: Mean square due to GCA were non-significant while were significant ($p \leq 0.01$) for SCA and RCA (Table 1), and days to maturity were managed by non-additive gene action. Since early maturity is one of the major objectives of Brassica breeding programs, therefore, negative effects of GCA, SCA and RCA are preferred. Four parental accessions displayed negative GCA effects, and being maximum in MYT105 (-0.25) followed by MYT117 and MYT120 with similar value of -0.13 (Table 2). Maximum positive GCA effects were found in parental accession MYT113 (0.38) followed by MYT103 (0.13). Six F_1 hybrids showed negative SCA effects (Table 3), whereas with earliness the best specific combinations were MYT009 × MYT103, MYT009 × MYT120, MYT113 × MYT124, MYT117 × MYT123 and MYT123 × MYT124 with same SCA value of -0.50 followed by MYT103 × MYT113 (-0.19). Positive SCA effects with expected delayed maturity were recorded in sixteen F_1 hybrids, and greater SCA values were observed in hybrids MYT120 × MYT123 (1.00), MYT103 × MYT105 (0.94) and MYT009 × MYT123 (0.81). Data referring to RCA effects showed that ten F_1 reciprocal hybrids revealed desirable negative reciprocal effects (Table 4). However, maximum negative maternal effects were recorded in F_1 hybrids MYT113 × MYT103 and MYT117 × MYT113 with same value of -1.00, followed by MYT124 × MYT103, MYT120 × MYT105 and MYT123 × MYT113 with similar value of -0.50. In desirable F_1 hybrids, the high × low GCA parents were involved for best specific combinations.

Plant height: Mean squares for GCA, SCA and RCA were significant ($p \leq 0.01$) for plant height (Table 1). Plant height was controlled both by additive and non-additive gene actions, however, dominance was predominant due to greater SCA value. In Brassica, taller plants are susceptible to lodging, thus, medium/short stature plants are desirable and therefore, negative components of combining ability are desirable for plant height. Four parental genotypes viz., MYT113, MYT103 and MYT123 and MY117 showed negative GCA effects of -14.09, -7.41, -3.53 and -0.53, respectively (Table 2). Positive GCA effects were observed in parental genotypes i.e. MYT120, MYT124, MYT105 and MYT009 with values of 9.47, 5.91, 4.97 and 2.41, respectively. In case of SCA effects, 15 F_1 hybrids revealed negative effects and best specific performance was presented by F_1 hybrids MYT103 × MYT113 (-39.16), MYT103 × MYT123 (-15.22), MYT009 × MYT120 (-11.53) and MYT117 × MYT123 (-11.00) (Table 3). The 13 F_1 hybrids revealed positive SCA effects, and maximum positive SCA effects of 22.34, 21.00, 18.50 and 14.50 were exhibited by F_1 hybrids MYT103 × MYT124, MYT105 × MYT113, MYT120 × MYT123 and MYT113 × MYT124, respectively. In case of RCA effects, eighteen F_1 hybrids showed negative and desirable reciprocal effects and being maximum in F_1 hybrids MYT117 × MYT113 (-33.50), MYT123 × MYT103 (-27.00), MYT124 × MYT117 (-25.34) and MYT120 × MYT117 (-16.50) (Table 4). Involvement of best general combiners in combination with low GCA parents performed well in specific crosses.

Primary branches per plant: Mean squares due to GCA, SCA and RCA were significant ($p \leq 0.01$) for primary branches per plant (Table 1), and the said trait was controlled both by additive and non-additive gene actions, however, additive genes were predominant due to greater GCA. The primary branches per plant are positively correlated with seed yield in Brassica, therefore, positive combining ability effects are considered desirable. Eleven F_1 hybrids showed positive SCA effects for primary branches per plant (Table 3), and the best specific performance was revealed by three crosses MYT113 × MYT124, MY117 × MYT124, MYT123 × MYT124 with same SCA value of 1.00, followed by MYT009 × MYT120 and MYT103 × MYT117 with similar SCA value of 0.56. In F_1 hybrids, 15 cross combinations showed negative SCA effects, and the poor performers were MYT103 × MYT123 (-2.00), MYT120 × MYT123 (-1.00), and MYT103 × MYT105 and MYT113 × MYT120 with similar SCA value of -0.94. In case of reciprocals, eight cross combinations showed positive RCA effects and maximum effects were recorded in F_1 hybrid MYT120 × MYT103 (1.50) followed by three other F_1 crosses i.e. MYT113 × MYT009, MYT123 × MYT103 and MYT120 × MYT113 with similar RCA value of 1.00 (Table 4). High × low general combiners performed well in specific crosses.

Pods per main raceme: Mean squares due to components of combining ability i.e. GCA, SCA and RCA were significant ($p \leq 0.01$) for pods per main raceme (Table 1). The said trait was controlled by both additive and non-additive gene actions, however, due to prominent GCA the variable was inclined to additive gene action. In case of GCA effects for eight parental accessions, four genotypes revealed positive GCA effects, and being maximum in accession MYT120 (4.58) followed by MYT124 (2.27), MYT123 (1.58) and MYT009 (0.64) (Table 2). Maximum negative GCA effects were noted in genotype MYT105 (-5.30) followed by MYT103 (-2.48). In case of SCA effects (Table 3), sixteen F_1 hybrids showed positive SCA effects for pods per main raceme. Best performance was recorded in F_1 hybrid MYT009 × MYT120 (15.89) followed by MYT105 × MYT124 (11.50), MYT105 × MYT123 (8.00) and MYT113 × MYT124 (7.50). Negative SCA effects were exhibited by 11 F_1 hybrids, and maximum in MYT103 × MYT123 (-8.27) followed by MYT103 × MYT113 (-8.14) and MYT113 × MYT117 (-6.81). In case of maternal effects (Table 4), nine F_1 hybrids exhibited positive RCA effects, and being maximum in F_1 hybrid MYT120 × MYT113 (12.00) followed by MYT105 × MYT009 (11.00), MYT117 × MYT009 (8.00) and MYT120 × MYT009 (5.50).

Seed yield per plant: Mean squares due to GCA and RCA were highly significant while SCA was nonsignificant in seed yield per plant (Table 1). The GCA mean squares were greater in magnitude than RCA and SCA indicating preponderance of additive gene action for seed yield per plant. Five parental lines showed positive GCA effects (Table 2), and being maximum in MYT105 (0.39) and MYT120 (0.38) followed by MYT113 (0.31) and MYT109 (0.30). Negative GCA effects were maximum in accessions MYT117 (-0.61) and MYT123 (-0.51). In case of SCA effects (Table 3), eight F_1 hybrids showed positive SCA effects. The best specific performance was noted in cross combinations viz., MYT117 × MYT123 (0.90), MYT009 × MYT123 (0.69), MYT103 × MYT124 (0.36) and MYT009 × MYT124 (0.31). Nineteen cross combinations showed negative SCA effects for seed yield per plant, however, maximum negative SCA effects of -1.95, -1.39 and -1.35 were observed in F_1 hybrids MYT105 × MYT123, MYT103 × MYT123 and MYT105 × MYT113, respectively. Positive and desirable reciprocal effects were noted in eight F_1 hybrids (Table 4), whereas the maximum positive maternal effects were noted in F_1 hybrids MYT123 × MYT009 (1.50), MYT117 × MYT113 (1.30) and MYT113 × MYT105 (0.56). However, maximum negative reciprocal effects revealed by F_1 hybrids MYT120 × MYT009 (-1.45), MYT124 × MYT105 (-1.28), followed by two crosses (MYT105 × MYT009 and MYT105 × MYT103) with similar RCA value (-1.05).

Genotypes revealed greater genetic variability by having highly significant differences for all the traits. According to combining ability analysis, the component variations due to GCA, SCA and RCA were highly significant for majority traits, which confirmed that there is a sufficient scope for identification of desirable general and specific combiners to be used in future breeding for improvement in said variables. In present studies, variations among genotypes for earliness and plant height were controlled non-additively due to greater SCA mean squares. Morphological and seed yield traits were governed by additive gene action due to maximum GCA mean squares. Mean squares due to RCA were even greater than GCA/SCA for some variables, and therefore maternal effects cannot be ignored. Parental genotypes MYT120, MYT124 and MYT105 were identified as best general combiners by having desirable GCA for majority traits. The F_1 hybrids MYT117 × MYT123, MYT103 × MYT124, MYT009 × MYT123, MYT123 × MYT009 and MYT117 × MYT113 showed best specific performance for majority traits and could be further exploited through selection in early segregating populations.

DISCUSSION

Majority of the traits exhibited significant GCA, SCA and RCA mean squares, and manifested importance of additive, non-additive gene action and maternal effects. Similarly, Teklewold and Becker (2005) and Noshin *et al.* (2007) also reported significant mean squares due to GCA, SCA and RCA for various morphological and seed yield traits in brown mustard. Genetic variations attributable to components of combining ability (GCA, SCA and RCA) were highly significant for earliness, yield and its related traits (Sheoran *et al.*, 2000; Singh *et al.*, 2002; Tuncturk and Ciftci, 2007). In present studies, GCA, SCA and RCA contribution to the total sums of squares revealed that earliness traits and plant height were controlled by non-additive gene action, while morphological and seed yield traits were governed by additive gene action. Maternal effects were also found significant and cannot be ignored. Nassimi *et al.* (2006a, b) reported significant GCA and SCA effects, and reported both additive and non-additive gene actions for inheritance of morphological, yield and yield components. Rameah *et al.* (2003) and Sincik *et al.* (2011) observed significant mean squares due to SCA for morphological, and yield traits, and reported that direction of crosses was important for yield and its contributing traits.

Early flowering provides sufficient time for seed filling which could help in yield enhancement. Similarly, early maturity and reduced plant height are the most desirable traits in Brassica as to escape the crop from pest losses and lodging, respectively and eventually to get the increased seed yield. In Brassica (grown for seed yield), the taller plants are susceptible to lodging, and therefore, medium or short-statured plants are desirable, and accordingly negative GCA and SCA values are sought for plant height. Hence, negative combining ability effects for earliness traits and plant height are required to get higher yields as to discourage the late maturity and tallness. Plant height is an important agronomic character with respect to the risks of wind damage and lodging (Sincik *et al*., 2011). In general, small and medium plant height is preferred in Brassica because these plants can tolerate heavy winds and can be prevented from lodging; therefore, negative combining ability effects are desirable characteristic for producing plants of suitable height (Nassimi *et al.*, 2006a). In present studies, negative GCA, SCA and RCA effects were recorded for earliness and plant height in parental accessions and F_1 hybrids indicating that these populations could be used for developing early maturing short stature genotypes with higher yields. Amiri-Oghan *et al.* (2009) recorded significant negative combining ability effects for days to flowering and identified fourteen F_1 hybrids with early maturity and three F_1 hybrids with short stature plants. Turi *et al.* (2011) reported significant SCA for days to flowering, secondary branches and pods per plant, while GCA was significant for seed yield. Similarly, significant SCA and GCA effects were noted for days to flowering, early maturity, primary branches, secondary branches and pods per raceme (Nassimi *et al.*, 2006b; Noshin *et al.*, 2007; Shiva, 2011). Sincik *et al.* (2011) findings revealed significant GCA and SCA effects for flowering traits, seed yield and oil content.

Higher seed yield is the main aim of breeding programs, hence, improvement in yield and its components is the prerequisite. Desirable GCA, SCA and RCA effects were recorded in parental genotypes and their F_1 hybrids, respectively, for earliness, morphological and yield related traits which might be responsible for improvement in yield contributing traits and eventually seed yield in Brassica. Therefore, positive combining ability effects are considered desirable for yield and associated traits. Nassimi *et al.* (2006a) findings revealed that GCA was highly significant for 50% flowering, primary branches and pods per main raceme. However, Marjanovic-Jeromela *et al.* (2007) and Sincik *et al*. (2011) reported nonsignificant GCA differences in genotypes for seed yield. Low GCA effects for seed yield and agronomic traits did not make it possible to identify good general combiners (Sincik *et al*., 2011). Contradiction in above findings might be due to different genetic make-up of the breeding material and the environments in which studied.

Parental genotypes MYT120, MYT124 and MYT105 were identified as best general combiners by having desirable GCA for majority traits. The F_1 hybrids MYT117 × MYT123, MYT103 × MYT124, MYT009 × MYT123, MYT123 × MYT009 and MYT117 × MYT113 were noted as best specific cross combinations for majority traits and could be further exploited through selection in early segregating populations. Good general combiners and specific cross combinations for early maturity and short stature have also been reported in past studies (Teklewold and Becker, 2005; Marjanovic-Jeromela *et al*., 2007; Akbar *et al.*, 2008). Earlier studies have determined good general combiners with significant GCA effects for morphological and yield traits (Rameah *et al.*, 2003; Nassimi *et al.*, 2006a, b; Huang *et al.*, 2010). Davik *et al.* (1997) mentioned best performance of inbred lines in F_1 hybrids for plant height, primary branches, pod length, seeds per pod and 1000-seed weight and that were controlled non-additively. Present results were supported by findings of Iqbal *et al.* (2003), who reported significant GCA and SCA for primary branches and yield related traits, and identified 24 F_1 hybrids with higher yield. Both additive and non-additive gene actions were reported in parental accessions and F_1 hybrids for pods per main raceme, seed yield and its components (Sood *et al.*, 2000; Qian *et al.*, 2003). Results suggested the use of integrated breeding strategies which can efficiently utilize the additive as well as non-additive genetic variations. Therefore, in present studies, the simple selection in early segregating generation would be more effective for the traits controlled by additive genes, whereas for those traits controlled by non-additive gene action, the selection in later segregating generation would be more effective (Cheema and Sadaqat, 2004).

Table 1. Mean squares for various traits in 8 × 8 F_1 diallel cross of *Brassica juncea* L.

Variables	**Mean Squares**						
	ANOVA			**Combining ability**			
	Reps.	**Genotypes**	**Error**	**GCA**	**SCA**	**RCA**	**Error**
Days to 50% flowering	0.13^{NS}	1.64*	0.01	0.92^{NS}	1.60**	1.34**	1.56
Days to maturity	0.00	1.69**	0.00	0.77^{NS}	0.78**	1.04**	0.01
Plant height	0.07^{NS}	1073.27**	3.8	248.25**	642.26**	631.07**	6.84
Primary branches plant^{-1}	0.63*	7.67**	0.93	6.39**	2.63**	1.63**	0.91
Pods main raceme^{-1}	19.02**	57.39**	5.43	143.19**	137.62**	251.15**	5.61
Seed yield plant^{-1}	2.00**	3.43**	0.13	3.87**	0.15^{NS}	2.00**	0.23

**, *= significant at $p \leq 0.01$ and $p \leq 0.05$ respectively, N.S. = Non-significant

Table 2. General combining ability effects of genotypes for various traits in *B. juncea* L.

Parental genotypes	Days to 50% flowering	Days to maturity	Plant height	Primary branches plant^{-1}	Pods main raceme^{-1}	Seed yield plant^{-1}
MYT009	0.16	-0.06	2.41	0.44	0.64	0.30
MYT103	0.03	0.13	-7.41	0.63	-2.48	-0.40
MYT105	-0.53	-0.25	4.97	-0.63	-5.30	0.39
MYT113	0.03	0.38	-14.09	-0.19	-0.55	0.31
MYT117	0.28	-0.13	-0.53	-0.13	-0.74	-0.61
MYT120	0.03	-0.13	9.47	0.19	4.58	0.38
MYT123	0.09	0.06	-3.53	-0.56	1.58	-0.51
MYT124	-0.09	0.00	5.91	0.25	2.27	0.14

Table 3. Specific combining ability effects of F_1 hybrids for various traits in *B. juncea* L.

F_1 hybrids	Days to 50% flowering	Days to maturity	Plant height	Primary branches plant^{-1}	Pods main raceme^{-1}	Seed yield plant^{-1}
MYT009 × MYT103	0.00	-0.50	7.00	0.00	0.00	-1.30
MYT009 × MYT105	0.47	0.63	11.97	0.25	5.48	-1.23
MYT009 × MYT113	1.41	0.50	-00.69	-0.19	-4.27	-0.26
MYT009 × MYT117	-0.34	0.00	-5.34	-0.75	0.92	0.19
MYT009 × MYT120	0.91	-0.50	-11.53	0.56	15.89	-0.63
MYT009 × MYT123	-0.66	0.81	-1.03	-0.81	-0.39	0.69
MYT009 × MYT124	-1.45	0.38	-10.97	-0.13	-4.01	0.31
MYT103 × MYT105	-0.41	0.94	-0.72	-0.94	-4.39	-0.43
MYT103 × MYT113	-0.09	-0.19	-39.16	-0.38	-8.14	-0.26
MYT103 × MYT117	1.28	0.31	2.28	0.56	-0.45	0.01
MYT103 × MYT120	1.03	0.31	-0.72	-0.25	-1.77	-0.38
MYT103 × MYT123	0.47	0.13	-15.22	-2.00	-8.27	-1.39
MYT103 × MYT124	-0.34	0.69	22.34	0.19	3.55	0.36
MYT105 × MYT113	-1.00	0.00	21.00	0.50	5.50	-1.35
MYT105 × MYT117	0.50	0.50	5.00	0.50	-1.00	-0.10
MYT105 × MYT120	0.59	0.19	-6.59	-0.50	1.55	-0.06
MYT105 × MYT123	-2.00	0.00	-1.50	0.00	8.00	-1.95
MYT105 × MYT124	0.00	0.00	12.00	0.50	11.50	-0.15
MYT113 × MYT117	0.78	0.06	-0.84	-0.63	-6.81	-0.91
MYT113 × MYT120	-0.97	0.06	1.97	-0.94	2.78	-0.19
MYT113 × MYT123	-0.53	0.38	-1.53	-0.69	-2.20	-0.01
MYT113 × MYT124	0.00	-0.50	14.50	1.00	7.50	-1.15
MYT117 × MYT120	-0.22	0.56	-0.22	0.00	5.48	-0.52
MYT117 × MYT123	0.00	-0.50	-11.00	-0.50	5.00	0.90
MYT117 × MYT124	0.50	0.00	5.00	1.00	4.50	0.10
MYT120 × MYT123	-1.00	1.00	18.50	-1.00	4.00	0.00
MYT120 × MYT124	2.00	0.00	5.50	-0.50	4.50	0.10
MYT123 × MYT124	0.00	-0.50	2.00	1.00	1.00	-1.00

Table 4. Reciprocal combining ability effects of F_1 hybrids for various traits in *B. juncea* L.

F_1 hybrids	Days to 50% flowering	Days to maturity	Plant height	Primary branches plant^{-1}	Pods main raceme^{-1}	Seed yield plant^{-1}
MYT103 × MYT009	0.41	-0.25	-0.16	0.01	-0.33	-0.30
MYT105 × MYT009	0.50	1.00	1.50	-1.00	11.00	-1.05
MYT113 × MYT009	1.00	0.50	0.50	1.00	0.00	0.25
MYT117 × MYT009	-0.50	0.50	9.50	0.50	8.00	-0.90
MYT120 × MYT009	-1.50	0.00	-2.50	0.00	5.50	-1.45

MYT123 × MYT009	1.00	-0.50	-10.00	0.00	-10.00	1.50
MYT124 × MYT009	0.00	0.00	-4.50	-1.50	-1.00	0.15
MYT105 × MYT103	-0.50	0.50	-3.00	-1.00	1.00	-1.05
MYT113 × MYT103	-0.50	-1.00	9.50	0.00	-6.00	-0.65
MYT117 × MYT103	-1.00	0.00	16.00	0.00	1.50	-0.40
MYT120 × MYT103	-0.50	0.00	7.50	1.50	1.50	0.00
MYT123 × MYT103	1.00	0.00	-27.00	1.00	-4.00	-0.10
MYT124 × MYT103	0.00	-0.50	2.00	0.00	-5.50	-0.50
MYT113 × MYT105	0.09	0.19	-7.03	-0.63	-2.82	0.56
MYT117 × MYT105	-0.66	0.19	-5.91	-1.69	-8.14	-0.28
MYT120 × MYT105	-0.50	-0.50	5.00	0.00	-15.00	0.00
MYT123 × MYT105	0.03	0.50	-0.09	0.25	-0.45	-0.13
MYT124 × MYT105	-0.78	-0.44	-11.03	-1.06	-5.64	-1.28
MYT117 × MYT113	-0.50	-1.00	-33.50	-1.00	-1.00	1.30
MYT120 × MYT113	-0.50	0.00	4.50	1.00	12.00	-0.10
MYT123 × MYT113	0.00	-0.50	-10.00	-0.50	-24.00	0.20
MYT124 × MYT113	2.66	0.44	-3.47	-1.00	6.61	-0.91
MYT120 × MYT117	0.50	0.00	-16.50	0.00	-16.50	-0.35
MYT123 × MYT117	-1.78	-0.13	-5.91	0.25	1.98	-0.09
MYT124 × MYT117	-0.09	0.44	-25.34	-2.06	-12.23	0.16
MYT123 × MYT120	-0.53	0.38	-16.59	-0.56	-12.33	-0.27
MYT124 × MYT120	0.66	0.44	2.97	-0.13	-4.52	0.08
MYT124 × MYT123	0.59	-0.20	-0.53	-0.63	-5.02	-0.04

Conclusion: For combining ability components, parental accessions and their F_1 hybrids revealed greater genetic variability for various traits. Variations among genotypes for earliness and plant height were managed non-additively, while morphological and seed yield traits were governed by additive gene action. Maternal effects in reciprocal hybrids were also significant and cannot be ignored. Genotypes MYT120, MYT124 and MYT105 and F_1 hybrids MYT117 × MYT123, MYT103 × MYT124, MYT009 × MYT123, MYT123 × MYT009 and MYT117 × MYT113 were identified as best general and specific combiners and could be exploited through selection in early segregating populations.

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