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Genetic consequence through combining abilities for yield and its components traits of *Brassica* species

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Abstract

The estimates of general combining ability effects suggested that among females GDM-4 and among males IC-399819 and EC-766060 were the best general combiners for seed yield and few other characters. The estimates of specific combining ability revealed that the hybrids GM-2 x EC-766437 followed by GM-2 x RH-406 and GDM-4 x EC-766378 exhibited positive sca effects in desirable direction for seed yield per plant. The hybrid GDM-4 x EC-766043 followed by GDM-4 x RH-749 and GDM-4 x EC-766495 exhibited significant negative sca effects for days to 50 per cent flowering and GM-3 x EC-766437 for days to maturity. While the hybrid GDM-4 x EC-766043 depicted significant sca effects in desired direction for oil and protein content. In general, involvement of both additive and non-additive gene effects, observed for most of the characters suggested that it would be desirable to follow cyclic method of breeding such as reciprocal recurrent selection, which would be most effective to stabilize additive genes to improve population mean and also to generate as well as to retain variability for several cycles of selection.

Keywords: Mustard, combining ability, oilseeds, *Cruciferae*, *Brassica Spp*

1. Introduction

Oilseeds occupy prime importance in Indian economy, which is evident from the impact created by yellow revolution. They are next to cereals in production of agricultural commodities in India. The genus *Brassica*, belongs to *Cruciferae* or *Brassicaceae* family and includes six cultivated species. Among those, *Brassica nigra* (n=8), *B. oleraceae* (n=9), *B. rapa* (n=10) are diploids. Rest of the three, namely *B. carinata* (n=17), *B. napus* (n=19) and *B. juncea* (n=18) are amphidiploids (Nagaheru U, 1935) [12]. Indian mustard is a natural amphidiploid (2n=36) of *Brassica campestris* (2n=20) and *Brassica nigra* (2n=16). It originated in Asia with its major center of diversity in China (Vaughan, 1977). It is largely self-pollinated crop (85-90%). However, owing to insects, especially the honeybees, the extent of cross-pollination varies from 4.0 to 16.6% (Rambhajan *et al.*, 1991) [19]. Mustard is a *Rabi* season crop of temperate region and seed is largely crushed for edible oil and cheapest source in diet. Mustard seeds contain oil, which is golden yellow, fragrant and considered among the healthiest and most nutritional cooking medium. It is also utilized as a condiment, for medicinal uses and meal or cake also nutritious (Nagraj, 1995) [13].

The major rapeseed-mustard producing countries are Canada, China, Germany and France. Rapeseed-mustard group of crops is the third most important oilseed crop after soybean and groundnut, contributing nearly 20-25% of the total oilseed production in the country. India, growing every day increasing population so could be requirement is over the production capacity of land. No one can option to fulfil need without improving genotypes for better seed yield potential per unit area. It is achieved by exploring the maximum genetic potential from the available *Brassica* genotypes. Breeders should concentrate on development of productive mustard varieties by crossing well adapter good general combining lines for seed yield and selecting transgressive segregants from the resulting hybrids.

2. Material and Methods**2.1 Germplasm**

Four of the parents as female lines (GM 1, GM 2, GM 3 and GDM 4) that were released varieties for their adaptability and high yield. Twenty three parents as male testers are collected from different places e.g. EC-766043, EC-766060, EC-766242, EC-766378, EC-766434, EC-766437, EC-766495, EC-766558, EC-766590, EC-766632 (National Bureau of

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Plant Genetic Resources, Pusa campus, New Delhi - 110012), RH-116, RH-406, RH-749, NRCHB-101, NRCDR-02, DRMR-IJ-31 (Directorate of Rapeseed-Mustard Research, Bharatpur (Rajasthan)- 321303) and NRCY-05-02, Neelam, IC-399790, IC-399819, NIRCM-120, Kiran and Pusa Swarnim (Department of Genetics and Plant Breeding, B. A. College of Agriculture, Anand-388110). The experimental material tested with 4 lines, 32 testers and their 92 F₁s developed by crossing 4 x 23 in a Line x tester mating system. The field experiment of 92 F₁ and 27 parents were produced by hand emasculation-hand pollination and selfing, respectively from Agronomy farm, B. A. College of Agriculture, Anand Agricultural University, Anand during *rabi* 2016-17.

2.2 Experimental design and management

The hybrids along with parents were evaluated in a randomized block design with 3 replications during *rabi*, 2016-17. Each genotype was represented by a single row plot of 3m length. Inter and intra row spacing was kept 45 cm and 15 cm, respectively. All the recommended package of practices was adopted to raise a good crop, while all other agronomic practices, including proper land preparation sowing at the right sowing date, thinning and three times hand weeding throughout the growing period, were applied.

2.3 Statistical analysis

Observations were recorded on five randomly selected competitive plants in each parents and hybrids every replication for collection of various characters were recorded on plot/row basis. The replication wise mean values were used in statistical analysis.

2.3.1 Analysis of variance: The technique suggested by Snedecor and Cochran (1937) [23] and reviewed by Panse and Sukhatme (1978) [17] was followed to test the differences among the genotypes for all the characters. The statistical model for randomized complete block design is as follows:

$$Y_{ij} = m + r_i + g_j + e_{ij}$$

Where, Y_{ij} = phenotypic value of the j^{th} genotype in the i^{th} replication, m = general mean, r_i = effect of the i^{th} replication, g_j = effect of the j^{th} genotype and e_{ij} = uncontrolled variation due to j^{th} genotype in the i^{th} replication.

2.3.2 Analysis of variance for combining ability: The variation among hybrids was partitioned further into sources attributed to general combining ability (gca) and specific combining ability (sca) components in accordance with the procedure suggested by Kempthorne (1957) [5]. The analysis of variances for the combining ability was based on the following statistical model.

$$Y_{ijk} = m + g_i + g_j + s_{ij} + r_k + e_{ijk}$$

Where, Y_{ijk} = Response of the progeny of the i^{th} female and j^{th} male from k^{th} replication, m = General mean, g_i = gca effect of i^{th} female parent, g_j = gca effect of j^{th} male parent, s_{ij} = sca effect of ij^{th} cross, r_k = Effect of k^{th} replication and e_{ijk} = Uncontrolled variation associated with ijk^{th} observation

3. Results

3.1 Analysis of variance for combining ability: The ANOVA for combining ability for all characters is presented

in Table 1. The variation present in the hybrids was partitioned into portions attributable to females, males and female x male and error component. Analysis of variance for combining ability revealed that mean squares due to females were highly significant for plant height, primary branches per plant, secondary branches per plant, effective length of main branch, siliquae per main branches, siliquae per plant, length of siliquae, seed per siliquae, oil content (%), protein content (%), 1000 seeds weight and seed yield per plant whereas non-significant for days to 50% flowering and days to maturity. The mean squares due to males were significant for all the characters, except for days to 50 per cent flowering, days to maturity, length of siliqua and 1000 seed weight. The variance due to female x male interaction was highly significant for all the characters except for the length of siliqua and 1000 seed weight. Thus, suggesting the importance of breeding for improvement of Indian mustard.

A comparison of variances due to females and males indicated that females showed higher magnitude of variability for days to 50% flowering, days to maturity, primary branches per plant, secondary branches per plant, effective length of main branch, siliquae on main branch, length of siliquae, seed per siliquae, oil content, protein content, 1000 seeds weight and seed yield per plant. This indicated that the contribution of females for these traits towards GCA was greater. Males showed higher magnitude of variability for days to 50% flowering, plant height and siliquae per plant. This indicated that the contribution of males for these traits towards GCA was greater. The higher magnitude of estimated component of SCA than GCA variance for all the characters except primary branches per plant, secondary branches per plant, effective length of main branch, seed per siliquae, protein content, oil content and 1000 seed weight suggested relatively greater role of non-additive genetic variance in the inheritance of all the traits except days to 50% flowering for which greater role of additive gene effect was found. The lower estimates of GCA/SCA ratio for all characters except primary branches per plant, secondary branches per plant, effective length of main branch, seed per siliquae, protein content, oil content and 1000 seed weight suggested the predominant role of non-additive gene action and greater magnitude of variance due to specific combining ability for inheritance of these traits.

3.2 Estimation of combining ability (gca and sca) effects and gene action:

The estimates of general combining ability effects of parents and specific combining ability effects of hybrids for fourteen traits are presented. The salient features of the results on combining ability effects for different characters are presented as under.

High gca effects are related to additive gene effects or additive x additive effects (Griffing, 1956) [3], which represent the fixable genetic component of variance. It may therefore, be suggested that the parents with high gca effects may be extensively used in hybridization programme for the improvement of particular traits. The SCA is the deviation from the performance predicted on the basis of general combining ability (Kempthorne, 1957) [5]. Normally SCA effects would not contribute appreciably in the improvement of self-pollinated crops except where exploitation of heterosis is feasible. However, in the production of homozygous lines, breeder's interest usually rests upon transgressive segregation shown by the crosses.

Early flowering is considered to be a more desirable character. Therefore, genotypes with negative gca and sca values are preferred for this trait. Among the female parents

GM-1 (-0.12) showed the higher negative gca effect. Whereas among the male parents, total 11 males reported negative and significant gca effect for the days to 50% flowering. The gca effects among parents, females and males ranged from -0.12 (GM-1) to 0.10 (GDM-4) and -0.75 (EC-766434) to 1.08 (EC-766558) (Table 2). Significant sca effects in the desirable direction were exhibited by 22 hybrids and it varied from -2.35 (GDM-4 x EC-766060) to 2.09 (GM-1 x Neelam), while 28 hybrids showed significant and positive sca effects. The hybrid GDM-4 x EC-766043 (-2.35) depicted highest significant sca effects in desirable direction indicating that they can be promising hybrids for exploiting earliness. The variance estimates for combining ability due to females (σ^2_f) and males (σ^2_m) were non-significant. Both general combining ability (σ^2_{gca}) and specific combining ability (σ^2_{sca}) variances were non-significant which was also reflected by less than one unity ratio of $\sigma^2_{gca}/\sigma^2_{sca}$. However, the dominance variance revealed that there was more non-additive gene action than additive gene action in the expression of this trait. These findings were in agreement with the results obtained by Macwana (2008) [9], Kumar *et al.* (2013) [7], Niranjana *et al.* (2017), Kumar *et al.* (2016) [6], Meena *et al.* (2015) [11] and Singh *et al.* (2018) [21]. All of them suggesting preponderance of non-additive gene action.

The estimates gca effects revealed that female GM-1 (-0.03) exhibited significant negative gca effects, indicating that they are good general combiners for early days to maturity (Table 4). Among male parents, Kiran (-1.26) was the best general combiner. In contrast, male and female parents, NRCHB-101 (0.74) and GM-2 (0.04) respectively, showed significant and positive gca effects (Table 2). Out of 92 hybrids, 27 hybrids showed significant negative sca effects and it varied from -1.53 (GM-3 x EC-766437) to 1.36 (GM-2 x IC-399790). The maximum estimate of sca effects was depicted by hybrid GM-3 x EC-766437 (-1.53) which was found significant and negative and can be the best hybrid for early maturity. The estimates of variance were revealed that the combining ability due to females (σ^2_f) and males (σ^2_m) were non-significant. For this trait, both σ^2_{gca} and σ^2_{sca} variances were non-significant which was also reflected by less than one unity ratio of $\sigma^2_{gca}/\sigma^2_{sca}$. The preponderance of dominance variance indicated that non-additive gene action is important than additive gene action for the expression of this trait. These results were supported by findings of Nassimi *et al.* (2006) [15], Macwana (2008) [9], Dholu *et al.* (2014) [2], Niranjana *et al.* (2017), Meena *et al.* (2015) [11], Kumar *et al.* (2016a) [6] and Singh *et al.* (2018b) [21].

Estimates of gca effects of parents revealed that none of the females or males exhibited significant negative gca effects for plant height. Among females GM-2 (-0.34) and among males RH-406 (-3.35) showed numerically high negative gca effects in desired direction indicating that they were good combiners for dwarfness (Table 4). While among the males gca effects ranged from RH-406 (-3.35) to IC-399819 (3.54) (Table 2). The significant and negative sca effects for plant height were not observed among all the hybrids. The magnitude of sca effects varied from -9.14 (GM-1 x EC-799378) to 9.08 (GDM-4 x EC-766378). Numerically maximum sca effects in desired direction for this trait was depicted by hybrid GM-1 x EC-799378 (-9.14) followed by GDM-4 x RH-749 (-8.63) and GM-1 x Kiran (-8.46). The magnitude of gca and sca variance for this trait indicated that both σ^2_{gca} and σ^2_{sca} were highly significant in desired direction, which revealed that both additive and non-additive gene action were involved for the expression of plant height. But the $\sigma^2_{gca}/\sigma^2_{sca}$ ratio was less

than unity revealing that there was preponderance of non-additive gene action in the expression of this trait. Similar results were obtained by Nassimi *et al.* (2006) [15], Macwana (2008) [9], Aghao *et al.* (2010) [1], Singh *et al.* (2010) [22], Maurya *et al.* (2012) [10], Kumar *et al.* (2013) [7], Niranjana *et al.* (2014) [16], Meena *et al.* (2015) [11], Singh *et al.* (2018) [21] and Kumar *et al.* (2018) [21].

Among female parents, GDM-4 (1.37) was the significantly superior general combiner for the primary branches per plant. While among males, EC-766434 (0.96) significant positive gca effects and were considered to be good combiners for this important yield contributing trait. Among the males, estimates of gca effect varied from -0.72 (Pusa Swarnim) to 0.96 (EC-766434) (Table 2). The perusal of sca effects revealed that 33 hybrids recorded significant positive sca effects. The sca effects for primary branches per plant ranged from -1.66 (GDM-4 x Pusa Swarnim) to 2.22 (GDM-4 x EC-766043). The cross GDM-4 x EC-766043 (2.22) had maximum significant positive sca effects followed by GDM-4 x EC-766434 (1.59) and GDM-4 x EC-766060 (1.56) and these hybrids were good combiners for primary branches per plant (Table 4). For this trait, the estimates of variance were revealed to be non-significant for combining ability due to females (σ^2_f) and males (σ^2_m). Both σ^2_{gca} and σ^2_{sca} variances were non-significant which was also reflected by less than one unity ratio of $\sigma^2_{gca}/\sigma^2_{sca}$. However, the presence of dominance variance indicated that non-additive gene action is more important than additive gene action for primary branches per plant. Similar results were obtained by Macwana (2008) [9], Singh *et al.* (2010) [22], Gupta *et al.* (2011) [4], Nasrin *et al.* (2011) [14], Yadava *et al.* (2012), Kumar *et al.* (2013) [7], Dholu *et al.* (2014) [2], Niranjana *et al.* (2014) [16], Meena *et al.* (2015) [11], Kumar *et al.* (2016) [6], Singh *et al.* (2018) [21] and Kumar *et al.* (2018) [21].

An examination of gca effects revealed that, female GDM-4 (1.35) showed significant and positive gca effects for secondary branches/plant. While among males, EC-766434 (1.42) was significantly the best desirable general combiner (Table 4). Whereas among the males gca effect varied from -0.75 (EC-766495) to 1.42 (EC-766434) and only two males recorded significant positive gca effect for this trait (Table 2). The results of sca revealed that 12 hybrids recorded significant positive sca effects. The significant positive sca effects ranged from -0.76 (GDM-4 x Pusa Swarnim) to 3.13 (GDM-4 x EC-766043). The crosses, GDM-4 x EC-766043 (3.13) GM-1 x IC-399819 (2.30) and GM-2 x NRCDR-02 (1.93) had maximum sca effects and this hybrids were good combiners for secondary branches per plant. These superior crosses involved either two good combiners or a good and a poor combiner (Table 4). Ten crosses exhibited sca effects in significant and negative direction. The magnitude of variance exposed that both combining ability estimates due to females (σ^2_f) and males (σ^2_m) were non-significant for secondary branches per plant. While both σ^2_{gca} and σ^2_{sca} variances were non-significant which also revealed less than one unity ratio of $\sigma^2_{gca}/\sigma^2_{sca}$. However, the dominance variance expressed more than additive gene variance for this trait. These results were supported by earlier studies of Macwana (2008) [9], Gupta *et al.* (2011) [4], Nasrin *et al.* (2011) [14], Yadava *et al.* (2012), Kumar *et al.* (2013) [7], Dholu *et al.* (2014) [2], Niranjana *et al.* (2014) [16], Meena *et al.* (2015) [11], Kumar *et al.* (2016) [6], Singh *et al.* (2018) [21] and Kumar *et al.* (2018) [21].

Among the parents only one female (GDM-4) and one male (IC-399819) parent exhibited significant positive estimates of

gca effects for effective length of main branch. For male parents the gca effect ranged from -2.04 (Pusa Swarnim) to 1.80 (IC-399819) for this trait. The maximum gca effect was manifested by IC-399819 (1.80) (Table 2). Out of the 92 hybrids, none of the hybrids was found to record significant positive sca effects for effective length of main branch. Magnitude of sca effects among these hybrids varied from -4.50 (GM-1 x NRCM-120) to 4.57 (GM-3 x NRCM-120). Numerically maximum estimate of positive sca effects for effective length of main branch was exhibited by hybrid GM-3 x NRCM-120 (4.57). The variance estimates for combining ability due to females (σ^2_f) and males (σ^2_m) were non-significant. The estimates of general combining ability (σ^2_{gca}) variances were non-significant, while specific combining ability (σ^2_{sca}) variances were significant. The ratio $\sigma^2_{gca}/\sigma^2_{sca}$ was also less than unity which revealed that there was non-additive gene action in the expression of this trait. Similar studies were conducted earlier and results were supported by Macwana (2008)^[9], Gupta *et al.* (2011)^[4], Yadava *et al.* (2012), Kumar *et al.* (2013)^[7], Dholu *et al.* (2014)^[2], Niranjana *et al.* (2014)^[16], Meena *et al.* (2015)^[11] and Kumar *et al.* (2016)^[6] which suggested role of non-additive gene action

The estimates of gca effects of parents revealed that females GDM-4 (1.42) and five males exhibited significant positive gca effects in desirable direction for the siliquae on main branch (Table 2). Out of 92 hybrids evaluated, only 4 hybrids exhibited significant positive sca effects for siliquae on main branch. The magnitude of sca effects among these hybrids varied from -3.57 (GDM-4 x IC-399790) to 3.21 (GDM-4 x EC-766434). The variance estimates for combining ability due to females (σ^2_f) and males (σ^2_m) were both non-significant. The estimates of general combining ability (σ^2_{gca}) variances were non-significant, while the significance of specific combining ability (σ^2_{sca}) variance indicated the involvement of non-additive gene action in the expression of number of siliquae on main branch. The ratio $\sigma^2_{gca}/\sigma^2_{sca}$ was also less than unity which revealed that there was non-additive gene action for this trait. The present findings are in agreement to those of Yadav *et al.* (2011)^[25], Yadava *et al.* (2012), Meena *et al.* (2015)^[11], Kumar *et al.* (2016)^[6] and Singh *et al.* (2018)^[21]. The literature available suggested role of non-additive gene action for the expression of this trait.

An examination of gca effects of parents revealed that, none of the parents were found significant for siliquae per plant. Numerically high magnitude of gca effect were observed for female GM-1 (8.11). Among males, EC-766242 (28.59) recorded positive gca effects and hence were considered as good general combiners (Table 4). GM-1 (8.11) and EC-766242 (28.59) had higher but non-significant and positive gca effects among females and males respectively (Table 3). The results of sca revealed that none of the hybrids recorded significant positive sca effects. The sca effects of hybrids ranged from -58.32 (GM-1 x E-766242) to 54.14 (GM-4 x EC-766242). The most superior cross combinations exhibited numerically higher sca effects in desired direction and confirmed their highly positive sca effects. The variance estimates for combining ability due to females (σ^2_f) were non-significant while combining ability due to males (σ^2_m) were significant. The magnitude σ^2_{gca} and σ^2_{sca} variances revealed that both variances were highly significant, which indicated that additive and non-additive gene action were involved for the expression of total siliquae per plant. The ratio $\sigma^2_{gca}/\sigma^2_{sca}$ were also less than unity which revealed

that there was preponderance of non-additive gene action for this trait. These results were supported by earlier studies Macwana (2008)^[9], Agao *et al.* (2010)^[11], Lal *et al.* (2011), Nasrin *et al.* (2011)^[14], Kumar *et al.* (2013)^[7], Saeed *et al.* (2013)^[20], Dholu *et al.* (2014)^[2], Niranjana *et al.* (2014)^[16], Meena *et al.* (2015)^[11], Kumar *et al.* (2016)^[6], Tomar *et al.* (2017)^[24], and Kumar *et al.* (2018)^[21].

An examination of gca effects of parents revealed that two females and eleven males recorded significant and positive gca effects for length of siliquae. The maximum positive gca effect was manifested by female GDM-4 (0.29) and among males, IC-399819 (0.48) (Table 3). The significant sca effects ranged from -0.91 (GDM-4 x Pusa Swarnim) to 1.01 (GM-3 x Pusa Swarnim). The results revealed that 23 hybrids recorded significant sca effects in desirable direction. The highest sca effects was observed in crosses GM-3 x Pusa Swarnim (1.01). The estimates of variance for combining ability due to females (σ^2_f) and males (σ^2_m) were both non-significant. Both general combining ability (σ^2_{gca}) variance and specific combining ability (σ^2_{sca}) variance were non-significant which was also reflected by less than one unity ratio of $\sigma^2_{gca}/\sigma^2_{sca}$. However, the dominance variance revealed a preponderance of non-additive gene action in the expression of length of siliquae. These results were supported by earlier studies of Monpara and Dobariya (2007), Macwana (2008)^[9], Niranjana *et al.* (2014)^[16], Meena *et al.* (2015)^[11], Kumar *et al.* (2016)^[6] and Singh *et al.* (2018)^[21] which suggested a role of non-additive gene action in the expression of this character. The estimates of gca effects of parents revealed that three females and eight males parents exhibited significant positive gca effects in desirable direction for the seed per siliquae. The maximum gca effect was manifested by female GDM-4 (1.36) and among males, EC-766434 (0.59). The gca effect ranged from -1.09 (Pusa Swarnim) to 0.59 (EC-766434) for males (Table 3). Total 23 hybrids exhibited significant positive sca effects for seed per siliquae. The magnitude of sca effects among hybrids varied from -1.90 (GDM-4 x Pusa Swarnim) to 1.84 (GDM-4 x EC-766378). Maximum sca effects for this trait was depicted by hybrid GDM-4 x EC-766378 (1.84) indicating that these hybrids are good combiners for this trait (Table 4). The variance estimates for combining ability due to females (σ^2_f) and males (σ^2_m) were both non-significant. Both general combining ability (σ^2_{gca}) variance and specific combining ability (σ^2_{sca}) variance were non-significant which exposed more σ^2_{sca} than σ^2_{gca} , indicating presence of dominance variance. These results are in agreement with those of Monpara and Dobariya (2007), Macwana (2008)^[9], Kumar *et al.* (2013)^[7], Niranjana *et al.* (2014)^[16], Meena *et al.* (2015)^[11] and Kumar *et al.* (2016)^[6].

Among females, significant positive gca effects were depicted by GDM-4 (1.40). Among males, maximum gca effects in desirable direction was depicted by EC-766434 (0.68) for oil percentage. In contrast, among females GM-2 (-0.67) and male Pusa Swarnim (-1.0) showed highest significant negative gca effects and thus, they were poor combiners for this trait (Table 4). The significant and positive sca effects for oil percentage ranged from -2.69 (GDM-4 x Pusa Swarnim) to 2.28 (GDM-4 x EC-766043). Out of 92 hybrids, 26 hybrids showed significant positive sca effects. The maximum significant positive sca effect was depicted by hybrid GDM-4 x EC-766043 (2.28) and were the best three cross combinations for this trait. The analysis of data revealed that combining ability due to females (σ^2_f) and males (σ^2_m) variance were both non-significant. For this trait, both σ^2_{gca}

and σ^2_{sca} variances were non-significant which was also less than one unity ratio of $\sigma^2_{gca}/\sigma^2_{sca}$. However, the presence of dominance variance *viz* additive genetic variance indicated that non-additive gene action was involved in the expression of oil content. Macwana (2008) [9], Kumar *et al.* (2013) [7], Dholu *et al.* (2014) [2], Niranjana *et al.* (2014) [16], Meena *et al.* (2015) [11], Kumar *et al.* (2016) [6] and Singh *et al.* (2018) [21] reported non-additive gene action in the expression of this trait which suggested role of non-additive gene action

Out of four females, one female GDM-4 (1.36) had positive and significant gca effects and proved to be a good combiner for protein content (Table 4). Among males, highest gca effects were depicted by EC-766434 (0.83) which suggested them to be good general combiners for protein content. Estimates of gca effect had varied from -0.85 (Pusa Swarnim) to 0.83 (EC-766434) for males (Table 3). The results of sca revealed that 14 hybrids recorded significant and positive sca effects. The significant and positive sca effects of hybrids ranged from -1.95 (GDM-4 x Pusa Swarnim) to 2.60 (GDM-4 x EC-766.43). The hybrid GDM-4 x EC-766.43 (2.60) were the best crosses having positive and significant sca effects for this quality trait. The estimates of variance for combining ability due to females (σ^2_f) and males (σ^2_m) were both non-significant and both σ^2_{gca} and σ^2_{sca} variances also non-significant. The ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ suggested that non-additive gene action could be responsible for the expression of this character. In case of protein content (%) in mustard not much research have been conducted so far. The results are supported by studies by Patel (2011) [18], Dholu *et al.* (2014) [2] and Niranjana *et al.* (2014) [16], who suggested role of non-additive gene action.

A perusal of data on gca effects revealed that female parents GM-3 (1.05) and males RH-116 (0.57) showed significant positive gca effects for 1000 seed weight proving to be good combiners for this character (Table 4). The gca effects of male parents ranged from -0.57 (RH-116) to -1.45 (Pusa Swarnim) for this trait (Table 3). Out of the 92 hybrids tested, 36 hybrids showed significant positive sca effects for 1000 seed weight. The gca effects of hybrids ranged from -1.71 (GDM-4 x Pusa Swarnim) to 1.24 (GDM-4 x EC-766378) for the 1000 seed weight. The hybrids, GDM-4 x EC-766378 (1.24) were the best three crosses which had positive and significant sca effects for 1000 seed weight. The estimates of variance for combining ability due to females (σ^2_f) and males (σ^2_m) and specific combining ability (σ^2_{sca}) variance were non-significant. The less than one unity ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ suggested that non-additive gene action could be responsible for the expression of 1000 seed weight of seed. Monpara and Dobariya (2007), Makwana (2008) [9], Yadava *et al.* (2012), Kumar *et al.* (2013) [7], Saeed *et al.* (2013) [20], Niranjana *et al.* (2014) [16], Meena *et al.* (2015) [11], Kumar *et al.* (2016) [6] and Singh *et al.* (2018) [21] reported non-additive gene action in the expression of this trait.

Among females, *viz*. GDM-4 (1.50) exhibited positive gca value indicating that it is a good general combiner for seed yield per plant (Table 4). While among the male parents, IC-399819 (1.06) showed significant positive gca value hence could be considered as the best general combiner for seed yield per plant. The magnitude of gca effects of males for seed yield per plant ranged from -1.45 (Pusa Swarnim) to 1.06 (IC-399819) (Table 3). The results of sca revealed that none of the hybrids recorded significant positive sca effects. The sca effects of hybrids ranged from -3.42 (GDM-4 x Neelam) to 2.61 (GDM-4 x EC-766437). The GM-2 x EC-766437 (2.61) superior cross combinations were found to exhibit

numerically higher sca effect in desired direction. The estimates of variance for combining ability due to females (σ^2_f) and males (σ^2_m) were non-significant. However variance due to σ^2_{sca} was highly significant, indicating that non additive gene action is playing a role in the expression of this character. As the $\sigma^2_{gca}/\sigma^2_{sca}$ ratio is less than unity, it was confirmed that non additive gene action was operating for expression of yield. The results are in akin with Monpara and Dobariya (2007), Makwana (2008) [9], Singh *et al.* (2010) [22], Gupta *et al.* (2011) [4], Nasrin *et al.* (2011) [14], Yadava *et al.* (2012), Kumar *et al.* (2013) [7], Saeed *et al.* (2013) [20], Dholu *et al.* (2014) [2], Niranjana *et al.* (2014) [16], Meena *et al.* (2015) [11], Kumar *et al.* (2016) [6] and Singh *et al.* (2018) [21]. All of them suggested role of non-additive gene action in the expression of this character.

4. Discussion

The Analysis of variance for combining ability revealed that mean squares due to females were highly significant for all the traits whereas non-significant for days to 50% flowering and days to maturity. The mean squares due to males were significant for all the characters, except for days to 50 per cent flowering, days to maturity, length of siliqua and 1000 seed weight. The variance to female x male interaction was highly significant for all the characters except for the length of siliqua and 1000 seeds weight. Thus, suggesting the importance of heterosis breeding for improvement of mustard. A comparison of variances due to females and males indicated that females showed higher magnitude of variability for all the traits except for plant height and seeds per siliquae. This indicated that the contribution of females for these traits towards gca was greater. Males showed higher magnitude of variability for days to 50% flowering, plant height and siliquae per plant. This indicated that the contribution of males for these traits towards gca was greater. The higher magnitude of estimated component of sca than gca variance for all the characters except primary branches per, secondary branches per plant, effective length of main branches, seeds per siliqua, protein content, oil content and test weight suggested relatively greater role of non-additive genetic variance in the inheritance of all the traits except days to per cent flowering for which greater role of additive gene effect was observed. The lower estimates for the ratio of gca/sca for most of the characters except primary branches per plant, secondary branches per plant, effective length of main branch, seeds per siliqua, protein content, oil content and 1000 seed weight suggested the predominant role of non-additive gene action. Most of the characters confirmed that non additive gene action were operating for expression which can be improved by heterosis breeding or cyclic method of breeding.

5. Conclusion and Future Research Use

The general combining ability effects enabled the identification of desirable female and male parents. The estimates of gca effects revealed that the female parent GDM-4 was found good general combiner for seed yield per plant and yield attributing characters except siliquae per plant. Whereas male parent EC-766434 was a good general combiner for all the characters except for seed yield per plant, plant height, siliquae per plant, siliquae on main shoot and effective length of main branch. Therefore, above parents can be considered as a good source of favorable genes for increasing seed yield along with other yield attributes. Therefore, it would be worthwhile to use the above parental lines in the hybridization programme for improvement of

mustard. Among the male parents, EC-766060, EC-766558 and IC-399819 were found good general combiners for seed yield per plant and majority of characters under study. Among crosses, the hybrids GM-2 X EC-766437, GM-2 x RH-406 and GDM-4 x EC-766434 exhibited positive sca effects for seed yield per plant. The hybrid GDM-4 x EC-766043 also depicted significant positive sca effects for primary branches per plant, secondary branches per plant, Oil content and protein content. GDM-4 x EC-766043 and GM-3 x EC-

766437 exhibited significant negative sca effects for days to 50 per cent flowering and days to maturity respectively. Whereas the hybrid GM-1 x NRCM-120 for Length of main branch, GDM-4 x EC-766434 for siliquae per main branch, GM-3 x EC-766242 for siliquae per plant, GM-3 x Pusa Swarnim for length of siliqua, GDM-4 x EC-766378 for seeds per siliqua and 1000 seed weight, depicted positive sca effects in desired direction.

Table 1: Analysis of variance (mean squares) and variance components for combining of

Source	d.f.	DF	DM	PH	PBP	SBP	LMP	SMB
Replications	2	53.32**	116.40**	4237.02**	0.26	384.61**	4378.65**	1750.57**
Lines (L)	3	0.62	0.05	11.34**	60.28**	58.51**	71.69**	68.81**
Testers (T)	22	3.45**	2.33**	46.17**	1.88**	3.48**	15.35**	9.22**
Lines x Testers	66	5.11**	2.56**	112.38**	2.23**	5.28**	19.40**	12.45**
Error	182	1.15	0.82	46.64	0.32	2.05	10.27	4.23
σ^2_{gca} (Lines)	-	-0.07	-0.04	-1.46	0.84	0.77	0.76	0.82
σ^2_{gca} (Testers)	-	-0.14	-0.02	-5.52	-0.03	-0.15	-0.34	-0.27
σ^2_{gca}	-	-0.15	-0.07	-4.13	1.42	1.27	1.19	1.31
σ^2_{sca}	-	1.32	0.58	21.92	0.64	1.07	3.04	2.74
$\sigma^2_{gca}/\sigma^2_{sca}$	-	-0.11	-0.12	-0.19	2.23	1.18	0.39	0.48
Source	d.f.	SPP	LS	SPS	OC	PC	TW	SY
Replications	2	57279.93**	0.59	25.09**	170.77**	36.77**	19.21**	306.70**
Lines (L)	3	2415.98**	4.38**	59.42**	62.02**	58.66**	36.24**	72.94**
Testers (T)	22	6248.68**	0.61	1.92*	2.06**	1.73*	1.22	4.77**
Lines vs Testers	66	2385.50**	0.57	2.37**	2.68**	2.18**	1.02	10.05**
Error	182	1589.51	0.06	0.67	0.69	0.97	0.26	4.31
σ^2_{gca} (Lines)	-	0.44	0.06	0.83	0.86	0.82	0.51	0.91
σ^2_{gca} (Testers)	-	321.93	0.01	-0.04	-0.05	-0.04	0.02	-0.44
σ^2_{gca}	-	96.14	0.09	1.40	1.45	1.38	0.87	1.42
σ^2_{sca}	-	265.33	0.17	0.57	0.66	0.40	0.26	1.91
$\sigma^2_{gca}/\sigma^2_{sca}$	-	0.36	0.56	2.47	2.19	3.44	3.43	0.74

*, ** Significant at 5 % and 1% levels, respectively.
 DF= Days to 50% flowering, DM= Days to maturity, PH=Plant height, PBP= Primary branches/ plant, SBP= Secondary branches / plant, LMB=Effective length of main branch, SMB= Siliquae/main branch, SPP= Silique /plant, LS= Length of siliquae, SPS= Seed/siliquae, OC= Oil content, PC=Protein content, TW= Test weight, SY=Seed yield/plant,

Table 2: Estimation of general combining ability effects of parents for days to 50 % flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, effective length of main branch and siliquae per main branch

Sr. No.	Parents	Days to 50% flowering	Days to maturity	Plant height	Primary branches/ plant	Secondary branches / plant	Effective length of main branch	Siliquae/ main branch
Lines								
1	GM-1	-0.12**	-0.03**	0.12	-0.46**	-0.44**	-0.66**	-0.63**
2	GM-2	-0.03	0.04**	-0.34	-0.7**	-0.68**	-0.81**	-0.76**
3	GM-3	0.05**	0.00	0.52	-0.21**	-0.23**	0.06	-0.03
4	GDM-4	0.10**	0.00	-0.30	1.37**	1.35**	1.42**	1.42**
Testers								
5	EC-766043	0.29**	-0.24**	-0.74	0.08**	-0.25	0.81	0.32
6	EC-766060	0.90**	0.46**	3.22	0.24**	-0.03	1.66	1.34**
7	EC-766242	0.45**	0.44**	1.42	-0.03	-0.16	0.36	0.50
8	EC-766378	-0.36**	-0.61**	-0.15	-0.13**	0.10	-1.30	-0.94**
9	EC-766434	-0.75**	-0.17*	-1.04	0.96**	1.42**	-0.36	0.02
10	EC-766437	-0.69**	0.19**	-2.95	0.12**	0.17	-0.33	-0.33
11	EC-766495	0.07	0.02	-0.41	-0.43**	-0.75**	0.30	-0.18
12	EC-766558	1.08**	0.43**	2.77	0.12**	-0.15	1.54	1.22**
13	EC-766590	0.60**	0.19**	1.59	0.06*	-0.07	0.45	0.59
14	EC-766632	-0.25**	-0.53**	-0.57	-0.39**	-0.15	-1.56	-1.19**
15	RH-116	-0.65**	-0.06	-0.71	0.95**	1.41**	-0.36	0.02
16	RH-406	-0.30**	0.01	-3.35	-0.36**	-0.31	-0.81	-0.81*
17	RH-749	0.16	0.06	-0.34	-0.1**	-0.43*	0.62	0.14
18	NRCHB-101	0.58**	0.74**	2.84	-0.3**	-0.58**	1.12	0.79*
19	NRCDR-02	0.54**	0.24**	1.52	0.15**	0.02	0.54	0.68
20	DRMR-IJ-31	-0.50**	-0.19**	-1.91	0.04	0.21	-1.22	-0.68
21	NRCY-05-02	-0.54**	-0.05	-1.54	-0.21**	0.25	-1.52	-1.14**
22	Neelam	-0.35**	0.16*	-2.78	0.040	0.10	-0.40	-0.40
23	IC-399790	0.08	-0.32**	-0.21	-0.40**	-0.72**	0.33	-0.15
24	IC-399819	0.44**	0.67**	3.54	0.40**	0.12	1.80*	1.49**

25	NIRCM-120	0.14	0.05	0.80	-0.13**	0.01	1.45	1.1**
26	Kiran	-0.39**	-1.26**	0.38	0.06*	0.30	-1.11	-0.74*
27	Pusa Swarmim	-0.55**	-0.22**	-1.39	-0.72**	-0.51**	-2.04*	-1.66**
	S.E. (Si)	0.13	0.11	0.82	0.07	0.17	0.39	0.25
	S.E. (Sj)	0.31	0.26	1.97	0.16	0.41	0.93	0.59
	GCA range of lines	-0.12 to 0.10	-0.03 to 0.04	-0.34 to 0.52	-0.70 to 1.37	-0.68 to 1.35	-0.81 to 1.42	-0.76 to 1.42
	GCA range of testers	-0.75 to 1.08	-1.26 to 0.74	-3.35 to 3.54	-0.72 to 0.96	-0.75 to 1.42	-2.04 to 1.82	-1.66 to 1.49

*, ** indicate level of significance at 5% and 1%, respectively.

Table 3: Estimation of general combining ability effects of parents for siliqua per plant, length of siliqua, seeds per siliqua, oil content, protein content, 1000 seed weight and seed yield per plant

Sr. No.	Parents	Siliqua /plant	Length of siliqua	Seeds/ siliqua	Oil content	Protein content	1000 seed weight	Seed yield/plant
Lines								
1	GM-1	8.11	-0.11**	-0.47**	-0.49**	-0.44**	-0.38**	-0.47**
2	GM-2	-6.01	-0.29**	-0.69**	-0.67**	-0.66**	-0.58**	-0.79**
3	GM-3	-1.72	0.10**	-0.21**	-0.24**	-0.26**	-0.09**	-0.24**
4	GDM-4	-0.37	0.29**	1.36**	1.40**	1.36**	1.05**	1.50**
Testers								
5	EC-766043	21.9	-0.29**	0.26**	0.47**	0.16	-0.33**	0.70
6	EC-766060	26.33	-0.06**	0.36**	0.19**	0.10	0.03	0.90*
7	EC-766242	28.59	-0.12**	0.14*	-0.09	0.03	-0.04	-0.35
8	EC-766378	-17.47	-0.28**	-0.09	-0.35**	0.09	-0.11**	-0.30
9	EC-766434	5.88	0.31**	0.59**	0.68**	0.83**	0.55**	0.65
10	EC-766437	27.27	0.05**	-0.06	0.44**	0.06	0.31**	-0.39
11	EC-766495	5.31	-0.05**	-0.25**	-0.04	-0.35**	-0.09**	0.19
12	EC-766558	11.83	-0.21**	0.25**	0.08	-0.01	-0.08**	0.78*
13	EC-766590	4.53	-0.14**	0.23**	0.00	0.12	-0.30**	-0.26
14	EC-766632	-9.04	-0.12**	-0.35**	-0.61**	-0.17*	-0.36**	-0.56
15	RH-116	-1.46	0.26**	0.58**	0.67**	0.82**	0.57**	0.64
16	RH-406	-7.17	-0.17**	-0.54**	-0.04	-0.43**	-0.17**	-0.87*
17	RH-749	-12.79	0.11**	0.08	0.29**	-0.02	0.24**	0.51
18	NRCHB-101	-12.77	-0.04**	-0.18**	-0.35**	-0.44**	-0.17**	0.36
19	NRCDR-02	-39.47	0.14**	0.32**	0.09	0.22**	0.23**	-0.17
20	DRMR-IJ-31	-20.5	0.14**	0.01	-0.20**	0.20*	0.08**	-0.05
21	NRCY-05-02	-33.26	-0.07**	-0.58**	-0.49**	-0.34**	-0.28**	-0.52
22	Neelam	-44.64	0.07**	-0.13*	0.37**	-0.02	0.24**	-0.46
23	IC-399790	-23.25	0.07**	-0.21**	0.00	-0.32**	-0.05*	0.22
24	IC-399819	26.85	0.48**	0.52**	0.35**	0.26**	0.44**	1.06**
25	NIRCM-120	27.00	0.09**	0.02	-0.33**	-0.23**	0.00	-0.52
26	Kiran	16.54	0.33**	0.10	-0.16**	0.28**	0.09**	-0.11
27	Pusa Swarmim	19.78	-0.50**	-1.09**	-1.00**	-0.85**	-0.80**	-1.45**
	S.E. (Si)	4.80	0.03	0.10	0.10	0.12	0.06	0.25
	S.E. (Sj)	11.51	0.07	0.24	0.24	0.28	0.15	0.60
	GCA range of lines	-6.01 to 8.11	-0.29 to 0.29	-0.69 to 1.36	-0.67 to 1.40	-0.66 to 1.36	-0.58 to 1.05	-0.79 to 1.50
	GCA range of testers	-44.64 to 28.59	-0.50 to 0.48	-1.09 to 0.59	-1.00 to 0.68	-0.85 to 0.83	-0.80 to 0.57	-1.45 to 1.06

*, ** indicate level of significance at 5% and 1%, respectively.

Table 4: Classification of parents with respect to general combining effect for different characters.

Sr. No.	Parents	DF	DM	PH	PBP	SBP	LMB	SMB	SPP	LS	SPS	OC	PC	TW	SY
1	GM-1	G	G	A	P	P	P	P	A	P	P	P	P	P	P
2	GM-2	A	A	A	P	P	P	P	A	P	P	P	P	P	P
3	GM-3	G	A	A	P	P	A	A	A	G	P	P	P	P	P
4	GDM-4	P	A	A	G	G	G	G	A	G	G	G	G	G	G
5	EC-766043	P	G	A	G	A	A	A	A	P	G	G	A	P	A
6	EC-766060	P	P	A	G	A	A	G	A	P	G	G	A	A	G
7	EC-766242	P	P	A	A	A	A	A	A	P	G	A	A	A	A
8	EC-766378	G	G	A	P	A	A	P	A	P	A	P	A	P	A
9	EC-766434	G	G	A	G	G	A	A	A	G	G	G	G	G	A
10	EC-766437	G	P	A	G	A	A	A	A	G	A	G	A	G	A
11	EC-766495	A	P	A	P	P	A	A	A	P	P	A	P	P	A

12	EC-766558	P	P	A	G	A	A	G	A	P	G	A	A	P	G
13	EC-766590	P	P	A	G	A	A	A	A	P	G	A	A	P	A
14	EC-766632	G	G	A	P	A	A	P	A	P	P	P	P	P	A
15	RH-116	G	A	A	G	G	A	A	A	G	G	G	G	G	A
16	RH-406	G	A	A	P	A	A	P	A	P	P	A	P	P	P
17	RH-749	A	A	A	P	A	A	A	A	G	A	G	A	G	A
18	NRCHB-101	P	A	A	P	A	A	G	A	P	P	P	P	P	A
19	NRCR-02	P	A	A	G	A	A	A	A	G	G	A	G	G	A
20	DRMR-IJ-31	G	G	A	A	A	A	A	A	G	A	P	G	G	A
21	NRCY-05-02	G	A	A	P	A	A	P	A	P	P	P	P	P	A
22	Neelam	G	P	A	A	A	A	A	A	P	P	G	A	G	A
23	IC-399790	A	G	A	P	P	A	A	A	G	P	A	P	P	A
24	IC-399819	P	P	A	G	A	A	P	A	G	G	G	G	G	G
25	NIRCM-120	A	A	A	P	A	A	G	A	G	A	P	P	A	A
26	Kiran	G	G	A	G	A	A	P	A	G	A	P	G	G	A
27	Pusa Swarnim	G	G	A	P	P	P	P	A	G	P	P	P	P	P
No. of good combiner		13	9	0	11	3	1	5	0	14	10	9	7	10	4
No. of average combiner		5	10	27	3	18	23	13	27	0	6	7	9	3	18
No. of poor combiner		9	8	0	13	6	3	9	0	13	11	11	11	14	5

DF= Days to 50% flowering, DM= Days to maturity, PH=Plant height, PBP= Primary branches/ plant, SBP= Secondary branches / plant, LMB=Effective length of main branch, SMB= Silique/main branch, SPP= Silique /plant, LS= Length of silique, SPS= Seed/silique, OC= Oil content, PC=Protein content, TW= Test weight, SY=Seed yield/plant, A = Average parent having either positive or negative but non-significant gcs effect, G = Good parent having significant gcs effect in desired direction, and P = Poor parent having significant gcs effect in undesired direction.

Table 5: Top three parents with respect to their magnitude of gca effects of lines and testers and sca effects of have top hybrids for various traits.

Traits	Rank	gca effect				sca effect	
		Lines		Testers		Hybrids	
DF	1 st	GM-1	-0.12**	EC-766434	-0.75**	GDM-4 x EC-766043	-2.35**
	2 nd	GM-2	-0.30	EC-766437	-0.69**	GDM-4 x RH-749	-2.22**
	3 rd	GM-3	0.05**	RH-116	-0.65**	GDM-4 x EC-766495	-2.21**
DM	1 st	GM-1	-0.03**	Kiran	-1.26**	GM-3 x EC-766437	-1.53**
	2 nd	GM-3	0.01	EC-766378	-0.61**	GM-3 x Neelam	-1.47**
	3 rd	GDM-4	0.01	EC-766632	-0.53**	GM-3 x Kiran	-1.45**
PH	1 st	GM-2	-0.34	RH-166	-3.35	GM-1 x EC-766378	-9.14
	2 nd	GDM-4	-0.30	EC-766437	-2.95	GDM-4 x RH-116	-8.63
	3 rd	GM-1	0.12	Neelam	-2.78	GM-1 x Kiran	-8.46
PBP	1 st	GDM-4	1.37**	EC-766434	0.96**	GDM-4 x EC-766043	2.22**
	2 nd	GM-3	-0.21**	RH-116	0.95**	GDM-4 x EC-766434	1.59**
	3 rd	GM-1	-0.46	IC-399819	0.40**	GDM-4 x EC-766060	1.56**
SBP	1 st	GDM-4	1.35**	EC-766434	1.42**	GDM-4 x EC-766043	3.13**
	2 nd	GM-3	-0.23**	RH-116	1.41**	GM-1 x IC-399819	2.30**
	3 rd	GM-1	-0.44**	Kiran	0.30	GM-2 x NRCR-02	1.93**
LMB	1 st	GDM-4	1.42**	IC-399819	1.80	GM-1 x NIRCM-120	4.57
	2 nd	GM-3	0.06	EC-766060	1.66	GM-1 x RH-406	3.70
	3 rd	GM-1	-0.66**	EC-766558	1.54	GM-1 x Neelam	3.59
SMB	1 st	GDM-4	1.42**	IC-399819	1.49**	GDM-4 x EC-766434	3.21*
	2 nd	GM-3	-0.03	EC-766060	1.34**	GM-1 x RH-406	3.19*
	3 rd	GM-1	-0.63	EC-766558	1.22**	GM-1 x Neelam	3.08*
SPP	1 st	GM-1	8.11	EC-766242	28.59	GM-3 x EC-766242	54.14
	2 nd	GDM-4	-0.37	EC-766437	27.27	GM-1 x EC-766558	49.46
	3 rd	GM-3	-1.72	IC-399819	28.85	GM-3 x NIRCM-120	49.07
LS	1 st	GDM-4	0.29**	IC-399819	0.48**	GM-3 x Pusa Swarnim	1.01**
	2 nd	GM-3	0.10**	Kiran	0.33**	GM-2 x EC-766437	0.88**
	3 rd	GM-1	-0.11**	EC-766434	0.31**	GM-2 x NRCR-02	0.57**
SPS	1 st	GDM-4	1.36**	EC-766434	0.59**	GDM-4 x EC-766378	1.84**
	2 nd	GM-3	-0.21**	RH-116	0.58**	GDM-4 x EC-766043	1.68**
	3 rd	GM-1	-0.47**	IC-399819	0.52**	GM-1 x EC-766495	1.43**
OC	1 st	GDM-4	1.40**	EC-766434	0.68**	GDM-4 x EC-766043	2.28**
	2 nd	GM-3	-0.24**	RH-116	0.67**	GDM-4 x EC-766590	1.97**
	3 rd	GM-1	-0.49**	EC-766043	0.26**	GDM-4 x EC-766060	1.44**
PC	1 st	GDM-4	1.36**	EC-766434	0.83**	GDM-4 x EC-766043	2.60**
	2 nd	GM-3	-0.26**	RH-116	0.82**	GM-3 x Neelam	1.69**
	3 rd	GM-1	-0.44**	IC-399819	0.26**	GM-3 X Pusa Swarnim	1.53**
TW	1 st	GDM-4	1.05**	EC-766434	0.57**	GDM-4 x EC-766378	1.24**
	2 nd	GM-3	-0.09**	RH-116	0.55**	GM-3 x Neelam	1.69**
	3 rd	GM-1	-0.38**	IC-399819	0.44**	GM-3 X Pusa Swarnim	0.94**
SY	1 st	GDM-4	1.50**	IC-399819	1.06**	GM-2 X EC-766437	2.61
	2 nd	GM-3	-0.24**	EC-766060	0.90**	GM-2 x RH-406	2.30

	3 rd	GM-1	-0.47**	EC-766558	0.78**	GDM-4 x EC-766434	2.25
*, ** Significant at 5 % and 1% levels, respectively.							
Note: DF= Days to 50% flowering, DM= Days to maturity, PH=Plant height, PBP= Primary branches/ plant, SBP= Secondary branches/plant, LMB= Effective length of main branch, SMB= Siliquae/main branch, SPP= Siliquae /plant, LS= Length of siliqua, SPS= Seeds/siliqua, OC= Oil content, PC=Protein content, TW= 1000 seed weight, SY=Seed yield/plant.							

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