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ESTIMATION OF HETEROSIS AND COMBINING ABILITY IN RAPESEED (BRASSICA NAPUS L.) KEEPING WITH THE VIABILITY OF CREATING F1 HYBRID IN LINE X TESTER MATING DESIGN

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ABSTRACT
The presented study was carried out at Mata Gujri College, Fatehgarh Sahib's experimental farm, Department of Agriculture during 2020-2021, 2021-2022. The experimental material consisted of 8 parents(IC 571662, IC 311734, IC 571697, IC 589680, IC 589670) and three testers (EC 338978, EC 338975, EC 338976) and 1 check were collected from NBPGR (National Bureau of Plant Genetic Resources, New Delhi) and fifteen f1's using line x tester mating design were grown in randomized block design. The analysis of variance different for all the genotypes for all of the features tested, showing at the all of the qualities have considerable genetic variability. The crosses IC 311734 x EC 338976 was the most promising hybrid for seed yield per plant based on performance and heterosis estimation. The largest positive significant in the GCA and PCV is siliquae length and it is followed by number of siliquae per plant, yield per plant and number of primary branches.

INTRODUCTION
Brassica napus is sometimes referred to as canola or oilseed rape. Brassica napus is an allotetraploid species, having 38 chromosomes. According to Song et al. (1994), Brassica napus is descended from crosses between Brassica rapa and Brassica oleracea, with some lines bearing Brassica rapa as the maternal parent and others Brassica oleracea. Because Brassica napus is a relatively new species, having a 500–2000 year European origin, its range of forms is restricted. By mating the two parent species and tripling the chromosome count, numerous contemporary cultivars of Brassica napus have been created *(Tsunoda et al., 1980)*. Because of historical chromosomal rearrangements in the earlier forms of Brassica napus (Paterson et al., 2000), there may be some sterility in crosses between these two groups. As a result, these two groups may differ slightly at the chromosome level.

India accounts for 16% of global mustard production and 35% of all mustard cultivated land worldwide. India ranks fourth in the world for mustard consumption and fifth in the world for mustard production. It produces 8.00 million tonnes and 1194 kg/hectare on 6.70 million hectares of land in India (Economic year 2013).

Is mostly grown in the states of Rajasthan, which accounts for 49% of the nation's total mustard production. Uttar Pradesh, Haryana, Madhya Pradesh, West Bengal, Gujarat, and other districts follow with 11%, 11%, and 7% of the total. (Reddy and others, 2019)

The Solvent Extractors Association of India (SEA 2018) has estimated that the greatest output estimate for rapeseed-mustard for the current Rabi season is down 3.7% due to a reduction in seeding and productivity. The yield in terms of kg/hectare decreased by 7.5%, while the average fell by 0.06%. In India, mustard is produced on 6.41 million hectares, with a production of 6.57 million tonnes and a productivity of 7399 kg/hectare during 2016–17. This compares to the total output of 6.57 million tonnes in the country during 2016–2017, which is 6.53 million tonnes for the present year (SEA, 2018). According to SEA (2018), Rajasthan is the largest state in India in terms of both area (2.56 million hectares) and output (2.95 million tonnes), followed by Eastern India, West Bengal, Uttar Pradesh, Haryana, and others. The utilisation of heterosis may be a key factor in raising Indian brassica's output and productivity.

One of the most practical methods for breeding past the current yield barrier is heterosis breeding. as a crossbred organism exhibits greater size, vigour, fruitfulness, development speed, resistance to disease, bug and pest infestation, or climatic vigour as compared to other inbreds, it is said to exhibit heterosis (Shull, 1952 and jinks and jones, 1958).

A crucial stage in the creation of new kinds is identifying parental material combinations with secure heterosis for yield and obtaining genetic data. Knowing whether combinations of parents are appropriate and capable of exhibiting a high degree of heterotic response is important. Production costs could be reduced by increasing output levels and improving input usage efficiency by taking use of heterosis in F1 hybrids (Pingali, 1997).

One of the most effective methods for determining the worth of parental lines to generate lucrative recombinants and hybrids of higher quality is combining ability analysis (Singh et al., 2013). Furthermore, selecting suitable parents is crucial for using hybridisation to create improved genotypes.

MATERIALS AND METHOD

1. Experimental Site and Condition

The studies were carried out at the Mata Gujri College Experimental Farm in Fatehgarh Sahib. It is located at 30°27' and 30°46' north latitude and 76°04' and 76°38' east longitude, at a height of 246 meters above mean sea level. It is located 35 kilometres from Patiala and 42 km from Chandigarh. In the winter, fog is common, and in the summer, hot, dry winds blow. The three distinct seasons of Sri Fatehgarh Sahib's climate are hot and dry summer, monsoon, and chilly winter. The region has a subtropical semi-arid climate. December through January might see a low of 40 degrees Celsius, while May and June could see a high of 420 degrees Celsius.

2. Experimental materials

There were fifteen F1 hybrids and eight genotypes of mustard in the experimental material. In the 2020–21 Rabi season, the parents were crossed in the Line tester mating design.

Table 2.1: Parents used in crossing programme with line × tester mating design.

Sr. no.	Genotypes	Sources
Lines (Females)		
1.	IC 571662	NBPGR
2.	IC 311734	Do
3.	IC 571697	Do
4.	IC 589680	Do
5.	IC 589670	Do
Tester (Males)		
6.	EC338978	Do
7.	EC338975	Do
8.	EC338976	Do

3. Plan of work

The experiment was carried out in the Experimental Farm, Department of Agriculture, Mata Gujri College, Fatehgarh Sahib (Punjab) during the winter seasons of 2020–21 and 2021–22.

Ist year (winter): 2020-21

1. Using line tester mating design, five elite lines of mustard were produced in the field with three replications in RBD, yielding F1.
2. There were 15 crosses produced in all (5 × 3). To retain pure seed, each parent plant will self-pollinate.
3. F1 seeds were gathered individually for additional analysis.

IInd year (winter): 2021-22.

1. Three replications of 15 F1s with eight genotypes and one check were produced in RBD, with a population size of 20 plants per treatment and standard spacing.
2. Information on yield characteristics was documented.
3. F2 seeds were gathered individually for additional analysis.

METHODS

1. Field layout

Eight genotypes, or five parents and three testers, made up the experimental material that was cultivated in a randomised block design with three replications.

2. Observation

From each replication, five competing plants will be chosen at random to record the observations for every character. For various statistical studies, the average of the data from each replication with regard to distinct characters will be employed.

We kept track of observations for the following quantitative parameters

1. Days to first flowering

The number of days between the date of the mustard crop's sowing and the following date on which the plants began to bloom was noted.

2. Days to 50% flowering

Days to 50% flowering is the number of days from the date of sowing until 50% of the plants in the field have flowered.

3. Number of primary Branches/ Plant
When the plants in each replication reached maturity, the number of branches growing from the main stem was recorded for each plant that was chosen.

4. Number of secondary Branches/Plant
At maturity, the secondary branches that grew from the primary branches of each plot's chosen plants were counted in each replication.

5. Plant height (cm)
All of the tagged plants' mature plant heights, including the inflorescence, were measured using a metre scale and centimetres to measure from the base of the axis to the top.

6. Number of Siliquae/Plant
All of the siliquae, which were abundant in seeds and found on both the primary and secondary branches, were counted from each plot's selected trousers in each replication at maturity.

7. Siliquae length (cm)
Only ten siliquae of each chosen plant in each plot, measured from the upper base to the top, were randomly selected.

8. Number of seeds/siliquae
The number of seeds from each genotype's ten randomly chosen siliquae of each selected plant was counted. and employed to calculate the siliquae length.

9. Days to maturity
The date of sowing to the date of maturity, or the point at which every plant in the line appeared to have turned yellow, was used to record the number of days till maturity.

10. Biological yield/plant (g)
The eight plants in each row were harvested at the designated spot, attached to the ground, collected, and then sun-dried until their weight remained constant.

11. Seed yield/plant (g)
When the plants reached maturity, every genotype's chosen plants in each replication were mechanically threshed separately and thoroughly cleaned in the lab. The yield was measured in grammes using an electric balance to weigh the grains.

12. Harvested index (%)
The harvested index was taken as a ration of grain yield to the total biomass expressed as percent: Harvest index = Grain yield (g) × 100/Biological yield (g)

13. Test weight (g)
Every chosen plant had its 1000 seeds randomly collected, and the seeds were then weighed in grammes using an electronic scale in the lab.

Hybridization programme
Using the line tester mating design, each of the eight lines was crossed, resulting in the production of fifteen hybrids. The following day, the healthy flower bids from the fresh flush were open to being chosen for emasculation and pollination. The chosen buds were manually emasculated between 4:00 and 5:00 p.m. with forceps and needles. In order to prevent contamination from other or foreign pollen, the emasculated blooms are then covered with butter paper sheets and stapled to both sides. The pollination of the emasculated bloom was completed between 7.30 and 10.30 am the next day. The male father selected the well-opened flowers with dehisced anther, carefully removed the butter paper beg, and contacted the stigma with the male flower's anther. Because they were simple to identify and prevented pollen contamination, the female flower was likewise quickly covered in another shade of butter paper beg. Every pollinated flower had a label attached to its petal that included the date of crossing, the names of the male and female parents, and other identification information.

3.7. Statistical analysis
The mean values of nine plants in each parent and F1 plot over all three replications were used for statistical analysis. Hyderabad-based Indo Stat conducted data analysis.

3.7.1. Analysis of variance
The purpose of the analysis of variance is to determine whether or not there is a significant difference between the treatments. For every genotype, it was conducted using the Randomised Block design (RBD) analysis method (Panse and Sukhatme, 1989). Three sources of variance were identified: replication, treatment, and error. These accounted for half of the overall variance.

The model of ANOVA is given as:
$Y_{ij} = \mu + t_i + r_j + e_{ij}$,
Here,
i = 1, 2, 3……..55;
j= 1, 2, 3;
Null hypothesis,
H_o = $t_1 = t_2 \ldots\ldots\ldots t_{55}$

Table 3.7.1. Analysis of variance (Anova).

Source	D.F.	Sum of Square	Mean square	F- Value
Replication	(r-1)	RSS	RSS/(r-1)= Mr	Mr/Me
Treatment	(g-1)	GSS	GSS/(g-1)= Mg	Mg/Me
Error	(r-1) (g-1)	ESS	ESS/(r-1)(g-1)= Me	
Total	(rg-1)	TSS		

The standard error and critical difference were calculated as standard error(SE. d±)=√(2.MSE)/r critical difference (CD)= SEd × t value at 5% or 1% level significance at error degree of freedom, or vice versa, if F calculated value > F tabulated value, indicating that respective source of variation is significant at 5% or 1% level of significance, or vice versa.

Test of significance

A difference between treatments was deemed statistically significant if the calculated value was higher than the tabulated value of F for n1 and n2 degrees of freedom at the 5% or 1% level of significance. However, it was deemed statistically insignificant if it was less than the tabulated value, indicating that there isn't a true difference between the genotypes.

3.7.2. Line x tester analysis

Using the approach described by Kempthorne (1957) and further developed by Arunachalam (1974), the "line x tester" analysis was performed to estimate the variances of general and particular combining abilities and their consequences.On a small scale, line tester analysis was utilised to ascertain the GCA and SCA of various lines. In this design, random sample of 'l' lines is taken and each line is mated to each of the't'testers (Singh and Chaudhary 1977). This is how analysis of variance is formatted:

Table 3.7.2 Line x Tester analysis.

Source of variation	DF	SS	MSS	Expected MSS
Replications	(r-1)	-	-	-
Lines (Females)	(l-1)	SS (l)	M (l)	$\sigma^2e+r(Cov.FS–2.Cov.HS) + rt.Cov.H.S.$
Testers (Males)	(t-1)	SS (t)	M (t)	$\sigma^2e+r(Cov.FS–2.Cov.HS) + l.Cov.H.S.$
Lines x Tester	(l-1)(t-1)	SS (lt)	M (lt)	$\sigma^2e+r(Cov.FS–2.Cov.HS)$
Error	(r-1)(T-1)	SS (e)	M (e)	σ^2e

3.7.3. Estimation of heterosis

Using the formulas (Kempthorne, 1957), heterosis in F1s was determined as the difference in hybrid performance between the better parent (heterobeltiosis) and the standard check (standard heterosis).The percentage rise or reduction in the mean values of the hybrids (F1s) over the standard check (SC) and better parent (BP) was used to calculate the kind and extent of heterosis:

Heterobeltiosis = $\frac{(\bar{F}_1 - \overline{BP})}{\overline{BP}} \times 100$

Standard heterosis = $\frac{(\bar{F}_1 - \overline{SC})}{\overline{SC}} \times 100$

Average heterosis = $\frac{(\bar{F}_1 - \overline{MP})}{\overline{BP}} \times 100$

3.7.3.1. Test of the significance of heterosis

After the 't' test, the significance of heterosis was determined. Comparing the computed "t" value to the table value of "t" at the error degree of freedom from the ANOVA with parents and F1sP = 0.05 and P = 0.01 was done. The estimated "t" value is provided below:

t (H) = $\frac{\bar{F}_1 - \overline{MP} \text{ or } \overline{BP} \text{ or } \overline{SC}}{SE\ (H) \text{ over } MP \text{ or } BP \text{ or } SC}$

SE (H) for BP or SC = $\sqrt{\frac{2Mse}{r}}$

3.7.4. Estimation of combining ability

Kempthorne's (1957) line-x tester method was used to estimate the combining ability variances and effects. Analysis of variance was applied to the experimental data collected on twelve characters. The combining ability was estimated using the line tester analysis.

3.7.4.1. Estimation of combining ability effects

The model of Kempthorne (1957) was used for the estimation of the combining ability effects of ijk[th] observations are as follows:

$X_{ijk} = \mu + g_i + g_j + s_{ij} + e_{ijk}$

The individual effect was estimated as follow:

(i) Grand mean

$$\mu = \frac{X...}{rlt}$$

Where,

X… = Total of all hybrid combinations.

μ = General mean

(ii) Gca lines

$$g_i = \frac{Xi..}{tr} - \frac{X...}{rlt}$$

(iii) Gca testers

$$g_j = \frac{X.j.}{lr} - \frac{X...}{rlt}$$

(iv) Sca effects

$$s_{ij} = \frac{Xij.}{r} - \frac{Xi..}{rt} - \frac{X.j.}{lr} + \frac{X...}{rlt}$$

3.7.4.2. Standard errors for combining ability estimates

SE (gca lines) = (Me/rt)½

SE (gca testers) = (Me/lr) ½

SE (sca effects) = (Me/r)½

SE (gi-gj) lines = (2Me/rt)½
SE (gi-gj) testers = (2Me/lr)½
SE (s_{ij}-s_{kl}) = (2Me/r)½
Critical difference (C.D.) was calculated as:
C.D. = SEd× t at 5% or 1% level at error d.f.
The significance of GCA lines, GCA testers and sca effects were tested by comparing with respective C.D. values.

DISCUSSION

Prior to initiating an efficient and successful breeding program, it is imperative to identify superior parents and ensure that the various qualities are inherited (Dhillon and Singh 1979). Desirable F1s or segrements are not necessarily produced by parents with good mean performance for yield and other qualities. Because it would be impractical, if not impossible, to analyse and handle a large number of crossings resulting from various parents available in crop collection, it is crucial to pick a small number of parents with high genetic potential in accordance with breeding objectives. In plant breeding, the idea of combining ability has gained significance as a formidable tool for determining suitable parents for hybridisation and particular crosses for additional exploitation. The GCA measures additive gene effects, whereas, SCA measures non-additive gene effects such as. The most effective breeding plan might be determined with the help of this knowledge on the type of gene action in the population. One of the many methods for combining ability analysis is line x tester analysis (Kempthorne, 1957). It is frequently used for germplasm screening in many crops, such as Indian mustard, to find prospective crosses and valued donor parents. The current study uses the Line x Tester design to examine the capacity of parents and crosses to combine, as well as the gene action for seed yield per plant and its constituent parts. The following headings provide a detailed discussion of the study's findings.

The nature and Magnitude of heterosis
Combining ability
The nature and Magnitude of heterosis

Understanding heterosis's direction and size is essential to taking use of it. The type and degree of heterosis in determining the best cross-combination and investigate them to find the more effective transgressive segregants. The most significant concepts for the application and understanding of hybrid in self-pollinated crops are those presented by Singh and Singh (1984) in their discussion of the dominant gene theory.

The improved application of genetic concepts to the field for crop breeding is the basis for the commercial exploitation of heterosis. Because they can readily counteract the negative effects of a crop, hybrids are crucial to modern agriculture. Additionally, with the use of breeding phenomena, they can produce F1 hybrid seed, which enhances plant growth and productivity. They can be found in the study's calculations of the standard check, better parents, midparent, and relative of heterosis (Moll et al, 1974). The percentage rise or decrease in the F1value over the relative heterosis, heterobeltiosis, and standard check indicates the degree of heterosis. While negative values were considered ideal for days to 50% flowering, days to maturity, and plant height, all desirable features exhibit positive significant values. Below the provided paragraphs, each trait's results are explained:

Days before the first blooming, the heterosis over the midparents showed that no cross exhibited positive significance, and the largest negative significant value was (IC 571662 x EC 338975). When it comes to heterosis over better parents, there are no positive significant crosses, and the lowest negative significant cross is (IC 311734 x EC 338975). These results are consistent with those of Bhinda et al. (2020).

For days to 50% blooming, the cross combination (IC 589680 x EC 338975) displayed the highest negative significant value, and in the mid parent, better parent, and standard check, every characteristic displayed a negative significant value.

The maximum negative significant value in the standard check (IC 589670 x EC 338975) and the heterobeltiosis (IC 589670 x EC 338975). Aher et al. (2009) noted the cross combination's equivalent value.

For days to maturity, the cross combination with the largest negative significant value over the mid parent was IC 571662 x EC 338976. In the better parent, all the crosses except one (IC 571697 x EC 338978) displayed negative significant values. Both in the conventional check (IC 571662 x EC 338976) and the heterobeltiosis (IC 571662 x EC 338976) have the largest negative significant value. In cross combination, Patel et al. (2012) and Dholu et al. (2014) noted a similar value.

The greatest positive significant value for average heterosis, better parent, and standard check for the number of primary branches per plant is (IC 311734 x EC 338976), whereas the least signification value is (IC 589680 x EC 338978). Meena et al. (2014) noted the cross combination's equivalent value.

The greatest positive significant value for average heterosis, better parent, and standard check for the number of secondary branches per plant is (IC 571662 x EC 338978), whereas the minimum signification value is (IC 571662 x EC 338975). In cross combination, Singh et al. (2007) and Aher et al. (2009) noted a similar value.

The most positive significant value for plant height, better parent, and midparent is (IC 311734 x EC 338975), while the least signification value is (IC 571662 x EC 338978). Meena et al. (2014) noted the cross combination's equivalent value.

The average heterosis, better parent, and standard check for the number of siliquae per plant revealed that the least signification value is (IC 589680 x EC 338975) and the maximum positive significance is (IC 571662 x EC 338976). Bharti et al. (2018) noted that the cross combination had a comparable value.

The greatest positive significant value for the siliquae length is (IC 311734 x EC 338976), whereas the least signification value is (IC 571662 x EC 338976). These values are supported by the mid parent, better parent, and standard check. Singh et al. noticed a similar value in the cross combination (2007).

The greatest positive significant value for average heterosis, better parent, and standard check for test weight is (IC 311734 x EC 338978), whereas the least signification value is (IC 589670 x EC 338976). Sikarwar et al. (2017) noted the cross combination's equivalent value.

The maximum positive significant value for biological yield, as shown by the better parent and standard check, is 28.19 (IC 571662 x EC 338976), while the minimum signification value is 8.84 (IC 589670 x EC 338976). Gami et al. reported a comparable result in a cross combination (2013).

The greatest positive significant value for average heterosis, better parent, and standard check for harvest index is (IC 311734 x EC 338976), whereas the least signification value is (IC 571662 x EC 338976). Furthermore, (IC 5719697 x EC 338976) is the negative significant maximum value. Patel et al. (2015) noted the cross combination's equivalent value.

Average heterosis, better parent and standard check for yield per plant all the traits shows positive significant and the maximum positive significant is (IC 311734 x EC 338976) and the minimum signification value is (IC 589670 x EC 338975). Tomar et al. (2018) noted the cross combination's equivalent value.

General and Specific combining ability

All eleven of the qualities' significant variances were revealed by the line effect analysis of the variances in general and particular combining ability. The tester displays several variances for plant height, siliquae length, biological yield, test weight, and days to 50% blooming. For each of the eleven attributes, the line x tester design was employed. Two components make up the genotypic mean of square: the general combining ability and the specialised combining ability. Also, they could begin with the general combining ability line in a sequence of cross and particular combining ability utilised to account for variations in cross combination performance. (Spraue and Tatum, 1942).

With the exception of the number of secondary branches, test weight, biological yield, days to first flowering, and days to 50% blooming, parent IC 571662, demonstrated a positive significant value in general combining ability for all the parameters. With the exception of test weight, biological yield, days to first flowering, days to 50% blooming, and days to maturity, genotype IC 311734 demonstrated a significant value in general combining ability for all the traits. For all the parameters except days to 50% flowering, number of primary branches, number of secondary branches, plant height, test weight, and biological yield, genotype IC 571697 demonstrated a significant value in general combining ability. For every characteristic except days to first flowering, days to 50% flowering, days to maturity, number of secondary branches, plant height and siliquae length, test weight, biological yield, harvest index, and yield per plant, genotype IC 589680 demonstrated a significant value in general combining ability. With the exception of days to first flowering, days to 50% flowering, days to maturity, number of primary branches, number of secondary branches, plant height, test weight, and biological yield, genotype IC 589670 demonstrated a significant value in general combining ability for all the variables. With the exception of days to first flowering, days to 50% flowering, days to maturity, number of primary branches, number of secondary branches, plant height, siliquae length, test weight, and biological yield per plant, genotype EC 338978 demonstrated a significant value in general combining ability for all the traits. With the exception of the number of secondary branches, plant height, siliquae length, test weight, biological yield, and days to first flowering, 50% blooming, and maturity, genotype EC 338975 demonstrated a significant value in general combining ability for all the parameters. In terms of overall combining ability, genotype EC 338978 demonstrated a significant value for every trait with the exception of the number of primary and secondary branches, days to maturity, days to first flowering, days to 50% flowering, plant height, siliquae length, test weight, and biological yield per plant. In terms of overall combining ability, genotype EC 338975 demonstrated a significant value for every parameter with the exception of the number of secondary branches, plant height, siliquae length, test weight, and biological yield.

The fifteen crosses are all compared to their parents in order to estimate the specific combining ability. Cross IC 571662 x EC 338976 displays significant positive values for harvest index and yield per plant, while cross IC 571662 x EC 338975 displays significant positive values for biological yield and yield per plant. The important values for the number of siliquae per plant are displayed by IC 571662 x EC 338976. None of the IC 311734 x EC 338978 values exhibit positive significant values. Only the quantity of siliquae per plant and the harvest index exhibit positive significant correlations (IC 311734 x EC 338976). The positive significant values for days to first flowering, siliquae length, harvest index, and yield per plant are displayed in IC 311734 x EC 338976. The positive significant values for the number, length, and yield of siliquae per plant are displayed by IC 571697 x

EC 338978. None of the values for IC 571697 x EC 338975 exhibit a positive significant value. The only biological yield that exhibits a positive significant value is IC 571697 x EC 338976. The positive significant values for the number of siliquae per plant and the days to 50% flowering are displayed in IC 589680 x EC 338978. EC 338975 x IC 589680 The only length with a positive significant value is siliquae length. The harvest index and yield per plant have positive significant values, as indicated by IC 589680 x EC 338976. The positive significant values for the harvest index and yield per plant are displayed by IC 589670 x EC 338978. Only for siliquae length does IC 589670 x EC 338975 exhibit a positive significant value. EC 338976 x IC 589670 Not a single one displays the positive significant value.

CONCLUSION

Thirteen characters were observed, including days to first flowering, days to 50% flowering, days to maturity, number of primary and secondary branches, plant height, number of siliquae per plant, length of siliquae, biological yield, test weight, and harvest index. These data were recorded on five competitive, healthy plants that were randomly chosen from each plot, and flowering was observed at the base of the row.

When Brassica napus seed yield per plant and its constituents were analysed, the mean sum of squares resulting from genotype showed extremely significant values for every trait. Two F1 hybrids for the seed yield per plant in the better parents is (IC 311734 x EC 338976) and (IC 311734 x EC 338975). And none of the crosses shows negative significant.

The combining ability of both GCA and SCA is substantial across all attributes according to the analysis of variance. Three of the five lines—IC 571697, IC 589680, and IC 589670—show negative significant values for the seed yield per plant, whereas the other two lines—IC 311734 and IC 571662—show positive significant values. Furthermore, only one of the three testers—EC 338978—shows a statistically significant negative value in the GCA for the seed production per plant; the other two—EC 338975 and EC 338976—show positive values. Out of fifteen hybrids in the SCA for seed yield per plant only seven crosses shows highly significant value that is namely IC 571662 x EC 338978, IC 571662 x EC 338975, IC 311734 x EC 338975, IC 311734 x EC 338978, IC 571697 x EC 338978, IC 589680 x EC 338976 and IC 589680 x EC 338978 and the eight crosses show negative significant value that is ranging from -2 (IC 589680 x EC 338978) to -9.50 (IC 311734 x EC 338978).

List of Abbreviation

Yij = Phenotypicobservationin the ith treatment of jth replication;
μ = Overall mean;
ti = Effect of the ith treatment;
rj = Effect of jth replication;
ei = Random error associated with ith genotype and jthreplication;
r = number of replications
t = number of treatments
l = number of lines
t = number of testers
σ^2e = variance due to error
Cov.HS = Covariance between half-sibs
Cov.FS = Covariance between Full-sibs
$\overline{F_1}$ = mean value of F_1
$\overline{BP}$ = mean value of better parent
$\overline{SC}$ = mean value of check variety
Me = error variance obtained by ANOVA comprising parents
r = Number of replication
μ = Population mean
g_i = gca effect of the i^{th} line
g_j = gca effect of the j^{th} tester
s_{ij} = sca effect of the ij^{th} combination
e^{ijk} = Error associated with ij^{th} observation at k^{th} plots
I = 1, 2, 3, ……, l
j = 1, 2, 3, ……, t
r =Number of replications (1, 2, 3, ……., r)
g_j = general combining ability effect of j^{th}tester.
$X_{.j.}$ = Total of j^{th} tester over all lines and replications
Sij = specific combining ability effect of ith line and jth tester.

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