



Combining ability and gene action for yield in indigenous accessions of Indian mustard (*Brassica juncea* L.)

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Abstract

Seed yield improvement in Indian mustard (*Brassica juncea*) needs the information about the nature of gene action and both type of combining ability involved in expression of various useful traits that are responsible for yield improvement. Combining ability analysis helps to identification of the suitable parents for hybrids development. Present study was conducted to determine combining ability of 23 genotypes (8 parents and 15 F₁s) of Indian mustard. Line × tester analysis including 5 lines and 3 testers exhibited the operation of additive (fixable) and non-additive (non-fixable) gene actions with predominance of non-additive gene action in controlling yield components. Only one genotype, namely, IC317528 was identified the best general combiner possessing highly significant positive GCA (General Combining Ability) and IC335858 × IC571648, IC589669 × IC571655 were exhibit high SCA (Specific Combining Ability) effects for seed yield. Genotypes IC571655, IC589670, IC571683 were significant negatively for early flowering. Significant SCA effect for earliness, plant height, seed yield and other contributing characters in desirable direction were recorded in a series of hybrids.

Keywords: *Combining ability, gene action, Indian mustard, seed yield*

Introduction

Seed yield in mustard is correlated with different yield contributing characters. These characters are also correlated between themselves. Therefore, various quantitative characters contribute seed yield and the correlation between seed yield as well as various contributing traits establishes a complex chain. Genetic diversity play basic and important role for genetic improvement (Ambaw and Dessalegn, 2017; Kumar *et al.*, 2019). It is widely accepted that information about genetic diversity in germplasm (Mukhtar *et al.*, 2002) and in self-pollinated crops, genetic improvement of yield depends on nature of genetic diversity (Joshi and Dhawan, 1966). Genetic diversity among the populations can be examined using morphological, molecular and biochemical approaches (Mohammadi and Prasanna, 2003). Various researchers evaluated earlier genetic diversity in brassica using quantitative traits (Vaishnav *et al.*, 2006; Singh *et al.*, 2010; Kumar *et al.*, 2018).

Combining ability analysis is the most powerful method for selection of suitable parents to develop superior and stable hybrids (Singh *et al.*, 2013) and evaluation of various possible manifestations and inheritance of yield characters in heterosis (Allard, 1958). The combining ability will help for identification of the suitable parents for hybrids development particularly yield improvement.

Combining ability (Griffing, 1956) studies emphasized the preponderance effect of GCA on yield and the GCA and SCA variances are used to assess the contribution of additive and non-additive gene actions involved in the inheritance of characters (Wos *et al.*, 1999; Channa *et al.*, 2018).

Brassica juncea being an autogamous species, line × tester mating design (Kempthorne, 1957) for general and specific combining ability analysis is most important for identifying of lines with rapidity. It is necessary to identify the stable inbred lines suitable for wide range of climatic conditions. Several experiments have been conducted earlier for this purpose (Brandle and McVetty, 1989; Sincik *et al.*, 2014; Sabaghnia *et al.*, 2010).

Materials and Methods

A set of eight genetically diverse mustard parents was used in the present study. Five winter type indigenous mustard accessions/lines were used as female parents (IC 589669, IC 589670, IC 317528, IC 335852, IC 335858) and three accessions/lines (IC 571648, IC 571655, IC 571683) were used as male parents (testers). These lines were crossed in a line × tester mating design given by Kempthorne (1957).

F₁ seeds generated during 2016-17 were used for evaluation in the field during winter seasons 2017-18 and

2018-19. Eight parents and their 15 F_1 combinations were evaluated with randomized block design replicated thrice at the Experimental Farm, Mata Gujri College, Fatehgarh Sahib, India. Row to plant spacing of 70 × 25 cm was maintained and proper plant population maintained by thinning. The entire recommended package required for a healthy crop was given for raising a good crop.

Five selected plants were taken from each genotype for recording data on different characters viz., first flowering, primary branches, plant height (cm), siliquae per plant, siliqua length (cm), seeds per siliqua, days to maturity, biological yield (g), seed yield/plant (g), harvest index (%) and test weight (g) respectively. The data pertaining to various traits were analyzed as per the procedure of RBD given by (Panse and Sukhatme, 1967). Statistical analyzes for agronomical data on yield and its traits were conducted using Windostat Version 9.3 from Indostat Services, Hyderabad, India.

Results and Discussion

General effects

The analysis of variance (ANOVA) exhibited highly significant differences among all the treatments for all the 11 quantitative traits, exhibited considerable genetic differences among parents and their cross combinations. The success of any plant breeding programme relies on genetic variation present in the germplasm. Among different biometrical tools, line × tester analysis is used for estimating GCA and SCA effects for parents and their crosses as well as revealing information about the nature of gene actions (Kempthorne, 1957; Esposito *et al.*, 2014).

The GCA effects of five lines (female) and three testers (male) are summarized in Table 1. The results revealed that the female parents showed desirable GCA effects for all the traits except harvest index, whereas all three testers showed poor GCA values for siliqua length, seeds per plant and biological yield per plant. Among the eight parents, only line IC589670 ($p \leq 0.01$) negative and IC335858 exhibited positive significant ($p \leq 0.05$) GCA effects for days to first flowering, thus other parental lines were poor general combiners for this trait. For the trait primary branches/ plant, female parents IC335858 and IC589669 showed highly significant ($p \leq 0.01$) positive GCA effects while IC335852 ($p \leq 0.01$) and IC317528 ($p \leq 0.05$) expressed significant negative GCA effects whereas among testers, only IC571683 exhibited highly significant ($p \leq 0.01$) positive GCA effect, indicating that these parental lines were good general combiner for this trait. The female parent IC335858 revealed significant ($p \leq 0.01$) positive GCA effects for plant height, indicating that parental accessions were good general combiners

for this trait, however, among the testers IC571648 and IC571655 showed significant ($p \leq 0.01$) positive GCA effects, thus considered as good general combiners for this trait (Table 1). For siliquae / plant, GCA effects were positive and highly significant ($p \leq 0.01$) for parental line IC317528 and IC589669 showed significant positive ($p \leq 0.05$) GCA effect while only one tester IC571655 exhibited highly significant positive ($p \leq 0.01$) GCA effect, therefore above two female and one male parents were good general combiners for siliquae per plant. For siliqua length, the GCA effects were positive and significant ($p \leq 0.05$) for the accession IC335858, which revealed that the accession was good general combiner for this trait. However, the accession IC589669 displayed negative ($p \leq 0.05$) GCA effects for this trait. None of the testers showed positive significant effects for this trait. In the case of seeds/siliqua, the only parental line IC335858 showed positive and significant ($p \leq 0.01$) GCA effects, whereas the line IC335852 displayed negative and significant ($p \leq 0.01$) GCA effects. For days to maturity, only accession IC335852 indicated highly significant ($p \leq 0.01$) positive GCA effects, whereas none of these showed negative GCA effects.

Among the testers the GCA effects were positive and significant ($p \leq 0.01$) only for IC571648 which revealed that this male parent was a good general combiner for earliness. As regards biological yield/ plant, all the accessions apart from IC317528 exhibited significant ($p \leq 0.01$) positive or negative GCA effect while, parent IC589670 and IC589669 exhibited significant ($p \leq 0.01$) negative GCA effects for this trait. Among testers, none of the parent showed significant positive or negative GCA effects for biological yield per plant. For seed yield / plant, the GCA effects were positive and significant ($p \leq 0.01$) for the accession IC317528, which revealed that the accession were good general combiner for this trait. However, the accession IC589670 displayed negative ($p \leq 0.01$) GCA effects for this trait. None of the tester showed positive significant effects for this trait. In case of harvest index none of the parental line showed significant positive or negative GCA effects for this trait, whereas among the three testers one exhibited significant ($p \leq 0.01$) positive and one significant ($p \leq 0.01$) negative GCA effects (Table 1). For test weight, the female accession IC335858 expressed highly significant positive ($p \leq 0.01$) and accession IC571683 as tester showed positive significant ($p \leq 0.01$) GCA effects and can be regarded as good general combiners for this trait. Since higher yields in F_1 combination may be due to fixable (additive) and/or non-fixable (non-additive) gene action, the total effect of F_1 progeny split into general combining ability (GCA) and specific combining ability (SCA) effects deciphers the

Table 1: Estimation for general combining ability (GCA) effects for various characters in Indian mustard

Genotypes	Days to first Flowering	Primary Branches/Plant	Plant Height (cm)	Siliqua /Plant	Siliqua Length (cm)	Seeds /siliqua	Days to maturity	Biological Yield/Plant (g)	Seed yield /Plant (g)	Harvest Index (%)	Test weight (g)
IC589669	-0.508	1.091 **	0.789	17.314 *	-0.174 *	0.094	-1.600	-10.845 *	1.662	-1.350	0.001
IC589670	-1.754 **	-0.165	2.478	-22.192 **	-0.082	-0.206	-1.378	-18.936 **	-7.011 **	0.391	0.086
IC317528	0.685	-0.601 *	-8.789 **	121.524 **	0.118	-0.310	0.622	45.695 **	5.357 **	-1.524	-0.488
IC335852	0.560	-1.658 **	-4.511 **	-30.184 **	-0.048	-0.806 **	4.178 **	-10.215	-2.870	2.361	-0.048
IC335858	1.017 *	1.333 **	10.032 **	-86.462 **	0.186 *	1.229 ***	-1.822	-5.699	2.861	0.123	0.450 **
IC571648	1.581 **	-0.020	4.448 **	-18.772 **	0.021	-0.234	-7.378 **	-1.013	2.700	-3.408 **	-0.128
IC571655	-0.921 **	-0.730 **	6.432 **	57.965 **	0.032	0.026	3.689 **	-0.360	1.907	4.039 **	-0.102
IC571683	-0.661 *	0.749 **	-10.879 **	-39.193 **	-0.053	0.209	3.689 **	1.373	-4.607 **	-0.632	0.230 *
CD 95%	0.816	0.477	2.515	13.008	0.172	0.500	2.211	10.281	3.768	2.365	0.230
GCA (Line)											
CD 95%	0.632	0.370	1.948	10.076	0.133	0.387	1.713	7.963	2.918	1.832	1.78
GCA (Tester)											

**= Highly significant (Pd^{0.01}), *= Significant (Pd^{0.05})

causes of heterosis. In this study, the variance of SCA exhibited a higher value than the variance of GCA in most of the yield characters. Similar results were reported by (Nasim *et al.*, 2014; Shehzad *et al.*, 2015; Singh *et al.*, 2019) in Indian mustard.

In the present study, the highly significant GCA effects of parents in desirable direction also showed potentiality of parental lines in generating encouraging breeding populations and for the specific yield and yield related traits are due to the predominance of additive genetic effects of genes and additive × additive interactions (Dey *et al.*, 2014). Therefore in future, attempts must be done to broaden the genetic base for important characters. Considering the useful traits, parents IC317528, IC571648 and IC335852 may be considered as good general combiners for seed yield and IC571648, IC589670 and IC571683 for earliness. However statistically, for seed yield one parents IC317528 showed significant GCA effect. The similar findings were also discussed by (Maurya and Singh, 2018).

SCA effects

Estimation of specific combining ability for 15 cross combinations are presented in Table 2. None of the cross combination was found to be a common combiner for all the characters under study. Cross combination IC335852 × IC571648 (-6.44) showed highly significant ($p \leq 0.01$) desirable negative specific combining ability (SCA) effects and cross combination IC335852 × IC571683 (5.24) exhibited highly significant ($p \leq 0.01$) positive SCA effect for days to first flowering. Cross combination IC589669 × IC571648 (-2.57) showed highly significant ($p \leq 0.01$) negative specific combining ability (SCA) effects and cross combination IC589669 × IC571683 (3.83) exhibited highly significant ($p \leq 0.01$) desirable positive SCA effect for primary branches. For plant height, cross IC335852 × IC571655 (-27.8) exhibited highly significant ($p \leq 0.01$) negative SCA effects and cross IC335858 × IC571655 (35.3) exhibited highly significant ($p \leq 0.01$) positive SCA effect. Cross combination IC335858 × IC571655 (-174.2) showed highly significant ($p \leq 0.01$) negative SCA effects and cross IC589670 × IC571655 (157.2) exhibited highly significant positive SCA effect for siliqua per plant. For siliqua length, none of the crosses combination showed positive or negative significant SCA effect. In case of seed per siliqua cross combination IC335858 × IC571648 (-0.91) exhibit highly significant ($p \leq 0.01$) desirable negative SCA effects and cross combination IC335858 × IC571683 (1.27) exhibited highly significant ($p \leq 0.01$) positive SCA effect. For days to maturity, only cross combination IC335852 × IC571648 (4.32) exhibited significant ($p \leq 0.05$) positive SCA effect. For biological yield per plant, cross combination

Table 2: Estimation of specific combining ability (SCA) effects for various characters in Indian mustard

Genotypes	Days to first Flowering	Primary Branches/Plant	Plant Height (cm)	Siliqua /Plant	Siliqua Length (cm)	Seeds /Siliqua	Days to maturity	Biological Yield/Plant (g)	Seed yield/Plant (g)	Harvest Index (%)	Test weight (g)
IC589669×IC571648	3.32**	-2.57**	-3.66	84.31**	0.11	0.38	-2.40	2.01	2.45	-6.30**	0.11
IC589669×IC571655	0.06	-1.26**	-3.08	28.34*	-0.20	-0.02	1.20	0.67	8.34*	9.39**	-0.26
IC589669×IC571683	-3.37**	3.83**	6.75**	-112.65**	0.09	-0.37	1.20	-2.68	-10.78**	-3.09	0.15
IC589670×IC571648	3.56**	0.17	-4.16	-136.66**	-0.19	-0.49	-0.96	-21.91*	-9.32**	2.63	0.54*
IC589670×IC571655	-1.81*	0.69	-5.26*	157.23**	0.06	0.68	-1.52	22.74*	5.83	-2.08	0.13
IC589670×IC571683	-1.75*	-0.86*	9.42**	-20.56	0.13	-0.19	2.48	-0.83	3.49	-0.55	-0.66**
IC317528×IC571648	0.06	0.56	11.34**	12.44	0.08	-0.07	-1.29	-12.53	-8.32*	-1.22	0.08
IC317528×IC571655	-0.46	0.36	0.78	-36.73**	-0.16	0.51	3.48	-4.58	2.89	1.33	0.22
IC317528×IC571683	0.40	-0.91*	-12.12**	24.29*	0.08	-0.45	-2.19	17.10	5.42	-0.11	-0.30
IC335852×IC571648	-6.44**	-0.40	12.02**	-26.93*	0.20	1.08*	4.32*	2.86	-0.96	4.15*	0.63**
IC335852×IC571655	1.19	0.39	-27.77**	25.33*	0.08	-0.82	-3.58	-3.79	-5.80	-6.38**	-0.21
IC335852×IC571683	5.24**	0.01	15.75**	1.60	-0.28	-0.26	0.74	0.93	6.75*	2.23	0.84**
IC335858×IC571648	-0.50	2.24**	-15.54**	66.84**	-0.20	-0.91*	0.32	29.57**	16.14**	0.75	-0.09
IC335858×IC571655	1.02	-0.18	35.34**	-174.17**	0.22	-0.35	0.42	-15.05	-11.26**	-2.26	0.12
IC335858×IC571683	-0.52	-2.06**	-19.80**	107.324**	-0.02	1.27**	-0.74	-14.52	-4.88	1.52	-0.03
CD 95% SCA	1.41	0.83	4.36	22.53	0.30	0.87	3.89	17.81	6.53	4.10	0.40

**= Highly significant (Pd<0.01), *= Significant (Pd<0.05)

IC589670 × IC571670 (-21.91) showed highly significant ($p \leq 0.05$) negative SCA effects and cross combination IC335858 × IC571648 (29.57) exhibited highly significant ($p \leq 0.01$) desirable positive SCA effect.

For seed yield per plant cross combination IC335858 × IC571655 (-11.261) showed highly significant ($p \leq 0.01$) negative SCA effects and cross combination IC 335858 × IC571648 (16.14) exhibited highly significant ($p \leq 0.01$) desirable positive SCA effect. This type of SCA value for seed yield is according with the results of (Patel *et al.*, 2016) in Indian mustard. The results revealed that most of the genotypes had relatively high degree of correspondence between mean performance and GCA effects for the observed characters. This can be ascribed to the predominant role of additive and additive × additive gene action for the inheritance of these traits. The estimates of specific combining ability effects revealed that as many as only one hybrid exhibited significant and SCA in positive effects for seed yield. The findings are also in agreement with (Bhusan *et al.*, 2014). Three F_1 crosses IC335852 × IC571683, IC335852 × IC571648 and IC589670 × IC571648 had desirable magnitude of expression for test weight. The similar findings were reported by (Dey *et al.*, 2014).

In the present study, one of the top four crosses which exhibited high SCA effects for seed yield, the cross, IC589670 × IC571655 involved one good general combiner (IC571655) indicating additive × dominance type of gene interaction which is expected to produce desirable

transgressive segregants in subsequent generations. (Falk *et al.*, 2014) have revealed the involvement of additive × additive (A × A), additive × dominance (A × D) and epistasis gene action in expression of yield and other supported characters in mustard. Similar findings were reported by Mohammadi and Prasanna (2003). GCA effects revealed that IC 317528 having significant and positive GCA effects was found to be the top combiner for most of the yield contributing traits, while on the basis of SCA, IC335858 × IC571648 was recorded best specific F_1 hybrid for most of the yield contributing traits. It may be concluded that IC317528 is good general combiner and IC335858 × IC571648 is a best specific combination for higher yield (Table 3).

Considering mean performance, heterosis and combining ability, none of the F_1 hybrid was found promising for commercial exploitation. This may be due the presence of genetic variation in the form of dispersed genes for these characters by (Dar *et al.*, 2012; Arashida *et al.*, 2017).

It represents a desirable gene flow in high frequency from parents to off spring and these parents lines exhibiting highly significant GCA for the particular traits in desirable direction can be utilized to accumulate favorable alleles via recombination and selection (Gao *et al.*, 2013; Brandle and McVetty, 1989; Kaur *et al.*, 2019). Further, our findings revealed that none of the parents was good general combiner for studied yield and yield related traits. Few crosses with significantly high SCA in desirable direction for various traits had both parents with good GCA.

Table 3: List of best specific combinations and good general combiners

Traits	Good specific combinations	Good general combiners
Days to first flowering	IC335852 × IC571648, IC589669 × IC571683	IC589670, IC571655, IC571683
Primary Branches/ Plant	IC335858 × IC571648, IC589669 × IC571683	IC589669, IC335858, IC571683
Plant Height (cm)	IC335858 × IC571655, IC335852 × IC571683, IC335852 × IC571648, IC317528 × IC571648, IC589670 × IC571683, IC589669 × IC571683	IC335858, IC571648, IC571655
Siliquae / Plant	IC589670 × IC571655, IC335858 × IC571683, IC589669 × IC571648, IC335858 × IC571648	IC317528, IC571655, IC589669
Siliqua Length(cm)	—	IC335858
Seeds/Siliqua	IC335858 × IC571683, IC335852 × IC571648	IC335858
Days to maturity	—	IC571648
Biological Yield/ Plant (g)	IC335858 × IC571648, IC589670 × IC571655	IC317528
Seed yield / Plant (g)	IC335858 × IC571648, IC589669 × IC571655	IC317528
Harvest Index (%)	IC589669 × IC571655, IC335852 × IC571648	IC571655
Test weight (g)	IC335852 × IC571683, IC335852 × IC571648	IC335858, IC571783

Conclusion

GCA effects revealed that IC 317528 was the best combiner for most of the yield contributing traits, with significant and optimistic GCA effects, while SCA revealed that IC335858 × IC571648 was the best F1 hybrid for most of the yield traits. It may be concluded IC317528 is a decent general combiner and IC335858 × IC571648 is the best individual combination for higher yield and included in future breeding scheme to obtain desirable segregants for the evolution of superior hybrid/genotypes.

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