

Combining ability and gene action analysis in a half-diallel cross of *Brassica rapa* L.

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ABSTRACT: Fifteen hybrids along with six parents were tested to identify good combiners through analyzing combining ability and gene action for yield and its attributes. The experiment was conducted in randomized complete block design with three replications during 2010/11 at research farm of Sher-e-Bangla Agricultural University (SAU), Dhaka. Data for days to 50% flowering and 80% maturity, plant height, number of primary and secondary branches, number of pods per plant, number of seeds per pod, pod length, seed yield and 1000-seed weight was recorded for analysis. The results showed that mean squares for parents, hybrids, parent vs hybrid were significantly different ($p < 0.01$ or $p < 0.05$) for most of the traits. Highly significant mean squares due to general combining ability (GCA) were found for all the traits except for length of pod, whereas highly significant mean squares due to specific combining ability (SCA) were also found for days to 50% flowering, number of secondary branches per plant, number of pods per plant, length of pod and seed yield per plant. This indicated that both additive and non-additive gene effects were important but additive gene effects were predominant for the expression of most of the measured traits. Estimates of GCA and SCA effects for yield and its attributes suggested that parent BARI Sarisha-6, BARI Sarisha-15 and Tori-7 was good combiners for different traits. Hayman's graphical analysis indicated both over- and partial-dominance for growth and yield attributes. As dominant (non-fixable) variation was high for most of the attributes, substantial improvements of these traits may be possible by transferring complementary gene into non-epistatic high-dominance crosses or eliminating duplicate genes from high-dominance crosses. Considering GCA, SCA and *per se* performance BARI Sarisha-6, BARI Sarisha-15 and Tori-7 might be good parents towards an effective breeding programme.

Keywords: Gene action, general combining ability, rapeseed, specific combining ability, yield component.

INTRODUCTION

Rapeseed (*Brassica rapa* L.) is an obligate out-crossing, and self-incompatible crop with high genetic diversity within the cultivars (Zhao et al., 2005). It is the number one oilseed crop in Bangladesh and occupies an important portion of cultivable land (Pervin et al., 2017). Although mustard and rapeseed contribute lion share of oil requirement in Bangladesh, total production is still low due to poor yield performance of the existing varieties

(Chowdhury et al., 2014). So, genetic improvement of rapeseed is necessary for yield and its attributes towards developing high yielding varieties. However, scopes of genetic improvement for this crop are limited because of the bottleneck of germplasm, whereas diverse germplasm is considered an asset for a successful breeding programme of rapeseed. In Bangladesh, genetic improvement is mostly focused on phenotype selection.

The selection of parents in a breeding program on the basis of *per se* performance is a very common strategy which does not necessarily lead to fruitful results always (Allard, 1960). Therefore, breeding methods of genetic improvement can be selected based on the analysis of combining ability and gene action (Habib et al., 2005).

The combining ability analysis is usually employed to identify the better combiners, which can be hybridized to explore better crosses for direct use or further breeding work. The variances of general combining ability (GCA) and specific combining ability (SCA) depends on the type of gene action involved. The variance for GCA includes the additive portion of the total variance, whereas SCA includes the non-additive portion of the total variance, arising mostly from dominance and epistatic deviations (Malik et al., 2004; Mohan et al., 2011; Sincik et al., 2011). Estimation of additive (GCA) and non-additive (SCA) gene actions within a breeding population is imperative; it is used to determine which breeding procedures efficiently improve the performance of the traits of interest (Dudley and Moll, 1969). Most of the past studies on combining abilities have shown significant GCA and SCA effects for yield and its component traits (Rameah et al., 2003; Akbar et al., 2008; Huang et al., 2010; Shiva, 2011; Amiri-Oghan et al., 2012; Azizinia, 2016; Meena et al., 2016; Naheed et al., 2017). However, intra-species hybridization is considered one of the best ways of combining desired traits and generating variation within the population (Dar et al., 2016). Therefore, the project was aimed at identifying the best parents by hybridizing *Brassica rapa* L. varieties for the future breeding programme through the estimation of GCA and SCA and the nature of gene action in controlling yield and its related traits.

MATERIALS AND METHODS

Plant materials

Six open pollinated *Brassica rapa* varieties: SAU Sarisha-1, SAU Sarisha-2, SAU Sarisha-3, BARI Sarisha-6, BARI Sarisha-15 and Tori-7 were selected for the study based on seed yield potential and related agronomic traits as described by Liton et al. (2017). Using these six varieties, 15 F₁ hybrids was produced following 6×6 half-diallel cross (Table 1) and the F₁ seeds were kept for next year field trial. Hybrid seed was produced by the emasculation and hand pollination of immature buds during October 2009 to February 2010 at the research farm of Sher-e-Bangla Agricultural University (SAU) Dhaka, Bangladesh. Approximately 20 plants from each variety were utilized in the crossing. Fifteen F₁ populations from a 6×6 half-diallel cross along with their parents were evaluated in 2010 to 2011.

Experimental design and field preparation

The field experiment was conducted at the Research Farm

of SAU, Dhaka, Bangladesh from October 2010 to February 2011. The experimental site experienced an average annual rainfall of 713 mm and a mean monthly temperature of 14.4°C. The soil of the site was moderately fertile and classified as clay loam. The field plots were organized in a randomized complete block design with three replications. Seeds were sown on 30 October 2010 in line with the spacing of 40 cm×10 cm and at a soil depth of 2.5 to 3.5 cm. Land preparation, fertilizer application and other agronomic practices were done as described by Liton et al. (2017).

Data collection and statistical analyses

Agronomic traits such as plant height, days to 80% maturity, number of primary branches per plant, number of pods per plant and length of pod were recorded just prior to harvest from 10 randomly selected plants per plot (row) and considered as one replication. After harvesting, number of seeds per pod, seed yield per plant and 1000-seed weight was recorded for each plot. Days to 50% flowering was recorded during flowering time. Analysis of variance was performed according to Gomez and Gomez (1984). The diallel analysis for combining ability was conducted using mean values following Model I (fixed effect) Method II of Griffing (1956). All statistical analyses were performed using Microsoft Excel and Statistix 8.0 software. A diallel table was prepared from the averages of three replications for all the traits studied followed by analysis of Wr-Vr graphs as described by Hayman (1954 and 1958). Components of genetic parameters were calculated following numerical approach of Jinks (1955 and 1983) based on Mather's notation (Mather and Jinks, 2013).

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) and combining ability

The preliminary ANOVA showed that the mean squares for all the traits except 1000-seed weight were highly significant (Table 2). The results indicated significant difference among the genotypes in this study ($p < 0.05$ or $p < 0.01$), which was stressed out further analysis of combining ability and gene action. Mean sum of squares of genotypes were further partitioned into parent, cross and parent vs cross. Parent and cross showed highly significant variances for days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, length of pod, seeds per pod and seed yield per plant (Table 2), indicating the presence of variability in the plant materials. Variances due to interaction of parent vs cross was also significant for the traits viz days to 50% flowering, number of secondary branches per plant, length of pod, seeds per

Table 1. Cross combinations in developing F₁'s by a half-diallel fashion

Parents	SAU Sarisha-1	SAU Sarisha-2	SAU Sarisha-3	BARI Sarisha-6	BARI Sarisha-15	Tori-7
SAU Sarisha-1	-	SAU Sarisha-1 x SAU Sarisha-2 (Hybrid1)	SAU Sarisha-1 x SAU Sarisha-3 (Hybrid2)	SAU Sarisha-1 x BARI Sarisha-6 (Hybrid3)	SAU Sarisha-1 x BARI Sarisha-15 (Hybrid4)	SAU Sarisha-1 x Tori-7 (Hybrid5)
SAU Sarisha-2		-	SAU Sarisha-2 x SAU Sarisha-3 (Hybrid6)	SAU Sarisha-2 x BARI Sarisha-6 (Hybrid7)	SAU Sarisha-2 x BARI Sarisha-15 (Hybrid8)	SAU Sarisha-2 x Tori-7 (Hybrid9)
SAU Sarisha-3			-	SAU Sarisha-3 x BARI Sarisha-6 (Hybrid10)	SAU Sarisha-3 x BARI Sarisha-15 (Hybrid11)	SAU Sarisha-3 x Tori-7 (Hybrid12)
BARI Sarisha-6				-	BARI Sarisha-6 x BARI Sarisha-15 (Hybrid13)	BARI Sarisha-6 x Tori-7 (Hybrid14)
BARI Sarisha-15					-	BARI Sarisha-15 x Tori-7 (Hybrid15)
Tori-7						-

Table 2. Analysis of variances (MS) for seed yield and its component traits in a 6x6 half-diallel cross of *Brassica rapa* L.

Source of variation	Df	Plant height	Days to 50% flowering	Primary branch/plant	Secondary branch/plant	Pods/plant	Length of pod	Seeds/pod	Seed yield/plant	1000-seed weight
Replication	2	128.198	0.015	0.509	3.732	629.447	0.046	5.238	4.615	0.943
Genotype	20	93.241	45.530**	3.893**	33.937**	11438.79**	0.797**	48.992**	8.388*	0.391
Parent	5	58.577	48.9**	5.538**	27.276**	9900.612**	0.521**	36.556**	3.988	0.322
Cross	14	71.994	44.784**	3.485*	38.030**	12800.51**	0.766**	49.584**	9.423*	0.439
Parent vs Cross	1	564.024**	39.125**	1.381	9.931*	65.669	2.606**	102.890**	15.904**	0.065
Error (P)	40	72.095	0.032	1.572	5.456	3219.394	0.152	3.821	4.052	0.253
GCA	5	41.143	21.492**	2.879**	24.480**	4978.376**	0.044	14.178**	4.761**	0.221*
SCA	15	27.726	13.071**	0.770	6.922**	3424.448**	0.339**	17.048**	2.141	0.1001
GCA/SCA	--	1.483	1.644	3.738	3.536	1.453	0.129	0.831	2.223	2.207
Error (CA)	40	24.031	0.010	0.524	1.818	1073.131	0.050	1.273	1.350	0.084

Df = degrees of freedom; * = $p < 0.05$; ** = $p < 0.01$; P = Preliminary; CA = Combining ability.

pod and seed yield per plant. Highly significant mean squares due to GCA were found for all the traits except for length of pod. On the other hand, highly significant mean squares due to SCA were also found for days to 50% flowering, number of secondary branches per plant, number of pods per plant, length of pod, and seed yield per plant (Table

2). ANOVA of combining ability reflected that both GCA and SCA mean squares were highly significant for most of the parameters studied. This indicated that both additive and non-additive gene effects were important for these traits. The higher magnitude of GCA variance was observed than that of SCA variance for plant height, days to 50%

flowering, primary branches per plant, secondary branches per plant, pods per plant, seed yield per plant and 1000-seed weight suggesting the presence of additive gene action. The involvement of additive gene effects link to yield and yield contributing traits in oilseed crops has been previously reported in many studies (Brandle

and McVetty, 1990; Sheoran et al., 2000; Rameah et al., 2003; Cheema and Sadaqat, 2004; Yadav et al., 2005; Akbar et al., 2008; Shiva, 2011; Patel et al., 2015; Azizinia, 2016; Meena et al., 2016; Singh et al., 2016; Naheed et al., 2017). On the other hand, researchers have also emphasized the value of non-additive gene effects for other traits such as number of branches and number of pods per plant in this crop (Brandle and McVetty, 1990; Rameah et al., 2003). In addition to that, both additive and non-additive gene action for the major traits including seed yield have been found to be involved in Indian mustard (Farshadfar et al., 2013; Muhammad et al., 2014). However, the higher magnitude of SCA variance was also observed than that of GCA variance for length of pod, and seeds per pod in this study suggesting the presence of dominant gene action in the parental populations. In an earlier study, Verma (2000) reported higher SCA variance than that of GCA variance for seed yield per plant. Therefore, significant items of SCA established the validity of further analysis of Vr-Wr graph.

Analysis of genetic components

E, the environmental component revealed significant values for all the traits except days to 50% flowering and days to 80% maturity, indicating influence of environmental factors in the expression of these traits (Table 3). Similar environmental influence in the expression of the traits reported in *Brassica napus* (Azizinia, 2016) and *Brassica rapa* (Chowdhury et al., 2004; Rahman et al., 2011). However, the magnitude of E for each trait was much lower than the respective value of D (additive genetic variance) and H1 (dominance genetic variance) excluding pods per plant. This indicated that the expression of traits was influenced less by the environment. These results were in good agreement with the previous findings from *Brassica juncea* for seed yield per plant, 1000-seed weight, length of pod and pods per plant (Rahman et al., 2011).

The average degree of dominance as indicated by the proportion $(H_1/D)^{0.5}$ was more than the unity, suggesting that over dominance was effective in the expression of most of the components of seed yield. Over-dominance of seed yield and its attributes was reported in past studies in *Brassica juncea* (Swarnkar et al., 2002; Singh et al., 2002; Gupta et al., 2010) and *Brassica rapa* (Chowdhury et al., 2004). The ratio of $H_2/4H_1$ usually provides an estimation of the average frequency of positive and negative alleles from all the parents. The traits plant height and 1000-seed weight had an asymmetrical distribution of the alleles because of their lowest value respectively. Most of the traits studied indicated unequal distribution of positive and negative alleles whereas the value of days to 50% flowering (0.33) was closer to 0.25 suggesting equal distribution of alleles (Table 3). Similar type of findings was reported by Chowdhury et al. (2004) in *Brassica rapa*.

The ratio of $[(4DH_1)^{0.5} + F]/[(4DH_1)^{0.5} - F]$ estimates the relative proportion of dominant and recessive alleles

from the parents. In the present study, the ratio for all the traits except pod length and seed yield were greater than the unity suggesting majority of dominant alleles and minority of recessive alleles i.e., an asymmetrical distribution for the dominant and recessive alleles has been observed in the parents for these two traits. These findings were also in an agreement with the study of Chowdhury et al. (2004) for days to flowering, plant height and 1000-seed weight in *Brassica rapa*. The estimation of effective factors (h^2/H_2) was less than the unity for all the attributes. The proportion of genes showed dominance which could be owing to either the predominant concealing effects or non-isodirectional distribution of polygene as reported in previous study (Brar et al., 2006; Sharma et al., 2008). Heritability in narrow sense was higher ($> \pm 2$) for days to flowering, plant height, pods per plant, seed yield per plant and seeds per pod indicated that these traits were highly heritable whereas rest of the traits had low to very low heritability. These were also consistent with the studies of Singh et al. (2002) and Chowdhury et al. (2004).

General combining ability (GCA) effects

The GCA effects for parents (Table 4) indicated that none of the parents were super general combiner for all the traits studied. However, BARI Sarisha-15, BARI Sarisha-6, SAU Sarisha-1, SAU Sarisha-2, SAU Sarisha-3 and Tori-7 were observed to be good combiners for days to 50% flowering; BARI Sarisha-15, BARI Sarisha-6, SAU Sarisha-3 and Tori-7 for the number of seeds per pod; BARI Sarisha-15, and SAU Sarisha-3 for number of primary branches; BARI Sarisha-15, BARI Sarisha-6 and Tori-7 for number of secondary branches; Tori-7 was also for number of pod per plant and seed yield per plant. Therefore, the prediction is that these varieties can be used in a crop breeding program aimed at the improvement of respective traits. Some of the parents were used already in a crossing programme which showed a satisfactory agreement with the predictions (Liton et al., 2017). The data in this study showed that BARI Sarisha-15, BARI Sarisha-6 and Tori-7 revealed significant desirable GCA effects for most of the traits and also had remarkable *per se* performance for the traits. Consideration of *per se* performance in combination with the combining ability estimates usually provides a better choice of superior parents in a hybridization programme (Abro et al., 2009). GCA effects for earliness, plant height, number of branches, number of pods, length of pods, number of seeds, seed yield and 1000-seed weight were also reported in the previous studies in different *Brassica* species (Singh et al., 1996; Verma, 2000; Chowdhury et al., 2004; Shiva, 2011; Khan et al., 2014; Azizinia, 2016; Meena et al., 2016; Naheed et al., 2017; Singh et al., 2017).

Specific combining ability (SCA) effects

The SCA effects signify the role of non-additive (dominance

Table 3. Estimation of genetic components of variation and their ratios for growth and yield contributing traits in *Brassica rapa* L.

Source of variation	Days to 50% flowering	Days to 80% maturity	Plant height	Primary branches	Secondary branches
D	16.29 ^{***} ± 0.04	23.05 ^{***} ± 0.31	-5.40 ^{***} ± 0.08	1.34 ^{***} ± 0.01	7.30 ^{***} ± 0.03
F	28.39 ^{***} ± 0.10	25.01 ^{***} ± 0.75	-24.24 ^{***} ± 0.19	0.49 ^{***} ± 0.01	0.27 ± 0.09
H ₁	27.97 ^{***} ± 0.10	22.51 ^{***} ± 0.78	-52.61 ^{***} ± 0.20	-0.52 ^{***} ± 0.01	4.37 ^{***} ± 0.09
H ₂	36.82 ^{***} ± 0.09	101.15 ^{***} ± 0.70	33.25 ^{***} ± 0.18	1.60 ^{***} ± 0.01	19.17 ^{***} ± 0.08
h ²	-5.82 ^{***} ± 0.06	0.81 ^{ns} ± 0.47	-35.92 ^{***} ± 0.12	-1.37 ^{***} ± 0.01	1.93 ^{***} ± 0.05
E	0.01 ^{ns} ± 0.01	0.02 ^{ns} ± 0.12	24.92 ^{***} ± 0.03	0.51 ^{***} ± 0.01	1.79 ^{***} ± 0.01
(H ₁ /D) ^{0.5}	1.31	0.99	3.12	0.62	0.77
H ₂ /4H ₁	0.33	1.12	-0.16	-0.77	1.10
$\frac{[(4DH_1)^{0.5} + F]}{[(4DH_1)^{0.5} - F]}$	4.970	3.435	0.163	1.827	1.050
h ² (ns)	1.02	1.12	-0.08	0.57	0.39

Table 3 Continued.

Source of variation	Pods /plant	Pod length	Seeds /pod	Seed yield/plant	1000-seed weight
D	2268.12 ^{***} ± 19.1	0.13 ^{***} ± 0.01	10.89 ^{***} ± 0.10	-0.03 ± 0.01	0.01 ^{***} ± 0.00
F	4441.68 ^{***} ± 46.6	0.35 ^{***} ± 0.01	16.72 ^{***} ± 0.24	-1.31 ^{***} ± 0.02	-0.10 ^{***} ± 0.00
H ₁	3563.08 ^{***} ± 48.4	0.15 ^{***} ± 0.01	12.08 ^{***} ± 0.25	-1.09 ^{***} ± 0.02	-0.21 ^{***} ± 0.00
H ₂	8473.75 ^{***} ± 43.3	1.02 ^{***} ± 0.01	54.02 ^{***} ± 0.22	3.99 ^{***} ± 0.02	0.19 ^{***} ± 0.00
h ²	-565.16 ^{***} ± 29.1	-1.53 ^{***} ± 0.01	-10.15 ^{***} ± 0.15	-4.46 ^{***} ± 0.01	0.18 ^{***} ± 0.00
E	1032.02 ^{***} ± 7.2	0.05 ^{***} ± 0.00	1.30 ^{***} ± 0.04	1.36 ^{***} ± 0.01	0.10 ^{***} ± 0.00
(H ₁ /D) ^{0.5}	1.25	1.11	1.12	6.00	4.20
H ₂ /4H ₁	0.60	1.66	6.38	-0.92	-0.22
$\frac{[(4DH_1)^{0.5} + F]}{[(4DH_1)^{0.5} - F]}$	8.141	-8.566	6.377	-0.567	0.005
h ² (ns)	0.41	1.00	0.95	-0.01	0.04

^{ns}/^{ns}= not significant; * = $p < 0.05$; * * * = $p < 0.001$.

and/or epistatic) gene action in the expression of a specific trait. It denotes the highly specific combining ability which leads to the highest performance of a specific hybrid. SCA effects for earliness, plant height, secondary branches,

number of pods, length of pods, seeds per pod, and seed yield were observed at either 1% or 5% level of probability (Table 5). Hybrid 12 (-4.73) and Hybrid 14 (-4.31) produced significant negative value for days to 50% flowering, whereas Hybrid 1,

Hybrid 2, Hybrid 3, Hybrid 4, and Hybrid 11 produced significant positive value (Table 5). Thus, the parents Tori-7, BARI Sarisha-6 and SAU Sarisha-3 showed the potentiality for developing early flowering hybrids. Earliness was also

Table 4 General combining ability (GCA) effects for seed yield and its component traits in a 6x6 half-diallel cross of *Brassica rapa* L.

Parents	Days to 50% flowering	Days to 80% maturity	Primary branch / plant	Secondary branch / plant	Pods / plant	Seeds / pod	Seed yield / plant	1000-seed weight
SAU Sarisha-1	2.361**	-2.542	0.140	-0.738	-2.256	-0.070	-0.253	0.087
SAU Sarisha-2	-1.514**	0.833	-0.060	0.821	-0.176	-0.141	-0.744	-0.217
SAU Sarisha-3	-1.931**	-6.667**	-0.901**	1.042	0.628	-1.274**	-0.770	-0.050
BARI Sarisha-6	0.653**	3.083	0.007	-2.338***	-24.297	1.409**	0.349	0.254*
BARI Sarisha-15	1.028**	2.708	0.969**	-1.238**	-19.926	1.654***	0.144	-0.121
Tori-7	-0.597**	2.583	-0.156	2.450***	46.028***	-1.578***	1.274*	0.046
SE (gi)	0.033613	2.394949	0.233681	0.435286	10.57282	0.364272	0.375126	0.093789
SE (sij)	0.092316	6.577551	0.641789	1.195482	29.03747	1.000445	1.030256	0.257583

* = $p < 0.05$; ** = $p < 0.01$.**Table 5.** Specific combining ability (SCA) effects for seed yield and its component traits in *Brassica rapa* L.

Hybrids	Plant height	Days to 50% flowering	Days to 80% maturity	Secondary branches/plant	Pods/plant	Length of pod	Seeds/pod	Seed yield/plant
Hybrid1	-4.45	4.90**	7.80	-1.98	-42.56	0.06	2.57*	-0.57
Hybrid2	0.90	3.98**	-20.70**	1.46	46.14	-0.59*	-3.23**	0.28
Hybrid3	-2.17	1.73**	4.55	-0.26	-17.41	-0.04	-1.04	0.37
Hybrid4	-4.88	1.36**	-0.07	-1.16	-76.08*	0.66**	5.05**	-1.19
Hybrid5	-5.07**	-2.02	4.05**	-1.28	-5.86**	-0.60	-2.96	-1.21
Hybrid6	-1.16	-0.14	-12.07	4.34**	1.29	0.44*	2.34*	-0.16
Hybrid7	-4.86	-0.39**	-1.82	-1.52	-27.95	-0.01	-1.84	-0.58
Hybrid8	-4.14	-1.77**	-0.45	-3.72**	-69.06*	0.74**	5.72**	-0.67
Hybrid9	1.64	-2.14**	-2.32	-0.50	-0.91	-0.51*	-4.82**	-1.77
Hybrid10	-2.61	-0.98**	3.68	-0.10	20.51	-0.30	-3.27**	-0.17
Hybrid11	-2.12	0.65**	10.05	-0.60	7.04	-0.96**	-4.45**	-2.66*
Hybrid12	-6.65	-4.73**	4.18	1.28	-12.01	0.23	2.25*	0.15
Hybrid13	-3.32	-2.93**	0.30	0.38	4.33	-0.31	-2.80*	0.14
Hybrid14	4.55	-4.31**	-2.57	2.82*	110.31**	-0.17	-0.47	2.44*
Hybrid15	5.98	-0.68**	-3.20	4.62**	71.91*	-0.58*	-5.18**	0.84
SEd(gi-gj)	2.4511	0.0520	3.7102	0.6743	16.3793	0.1127	0.5643	0.5811
SEd(Sij-Sik)	6.4850	0.1377	9.8163	1.7841	43.3356	0.2983	1.4930	1.5375
SEd(Sij-Skl)	6.0039	0.1275	9.0881	1.6517	40.1210	0.2762	1.3823	1.4235

* = $p < 0.05$; ** = $p < 0.01$.

observed in *Brassica juncea* (Singh et al., 1996; Khan et al., 2014) and *Brassica campestris* (Singh et al., 2017) in the previous studies. Hybrid 2 showed the highest significant negative SCA effects (-20.70) for days to 80% maturity, whereas hybrid 5 showed the highest significant positive SCA effects (4.05) indicated that SAU Sarisha-1 and SAU Sarisha-3 could be useful for developing early maturing varieties (Table 5). Early maturity was also observed in hybrids derived from different *Brassica* species (Acharya and Swain, 2004; Chowdhury et al., 2004; Singh et al., 2017). Only hybrid 5 produced statistically significant negative SCA value (-5.07) for their height. So, either Tori-7 or SAU Sarisha-1 can be used to develop dwarf variety. Similar SCA effect was observed in previous studies (Acharya and Swain, 2004; Chowdhury et al., 2004). The highest significant positive values of SCA effects for the secondary branches were revealed by the hybrid 15 (4.62) and hybrid 6 (4.34), whereas the highest significant negative SCA effect (-3.72) was provided by the hybrid 8 (Table 5). Therefore, BARI Sarisha-15, Tori-7, SAU Sarisha-2 and SAU Sarisha-3 were the best specific combiners to improve plants with more secondary branches. On the contrary, BARI Sarisha-15 and SAU Sarisha-2 was the best specific combiner to develop varieties with minimum secondary branches. These results were very identical with the previous studies in *Brassica* (Acharya and Swain, 2004; Chowdhury et al., 2004; Singh et al., 2017). Among the hybrids, hybrid 14 showed the highest (110.31) significant positive SCA effects for pods per plant followed by hybrid 15 (71.91). On the other hand, hybrid 4 showed the highest (-76.08) significant negative SCA effects for pods per plant followed by hybrid 8 (-69.06). The data were in line with the study of Acharya and Swain (2004) and Chowdhury et al. (2004). SCA effects for length of pod indicated that none of the parents were super specific combiner for their hybrids but statistically significant effect was observed from hybrid 2, hybrid 4, hybrid 6, hybrid 8, hybrid 11 and hybrid 15 (Table 5). Similar results were reported by Singh et al. (1996) and Acharya and Swain (2004) in different *Brassica* species. Among the hybrids, hybrid 8 exhibited the highest (5.72) significant positive SCA effects followed by hybrid 4 (5.05) for seeds per pod, whereas significant positive moderate values were showed by hybrid 1 (2.57), hybrid 6 (2.34), and hybrid 12 (2.25). The other cross combinations showed either insignificant or negative SCA effects. Hence, the parents BARI Sarisha-15 and SAU Sarisha-2 of hybrid 8 were the best specific combiner to increase the number of seeds in the pod. Only the hybrid 14 exhibited significant positive SCA effects (2.44) for seed yield and the other hybrids showed either significant negative or insignificant SCA effects (Table 5). Thus, the parents BARI Sarisha-6 and Tori-7 of hybrid 14 was the best specific combiner for the improvement of seed yield in *Brassica rapa*. Similar SCA effects were reported in *B. juncea* (Acharya and Swain, 2004); *B. rapa* (Chowdhury et al., 2004) and *B. campestris* (Singh et al., 2017). The SCA

effects may arise not only on cross involving high \times high combinations, but also from low \times high or from low \times low. In practice, some of the low combiners could also be accommodated in the hybridization programmes. However, the magnitude and direction of the significant effects for six parents and 15 hybrids provided meaningful comparisons and a clue to the future breeding programmes.

Gene action

Vr-Wr graphs, a two-dimensional depiction made based on the parental variance (Vr) and parent offspring co-variance (Wr) were presented here (Figure 1). The regression line intersected the Wr-axis below the point of origin suggesting over-dominance gene action for controlling flowering, plant height, production of secondary branches, production of pods, production of seeds and seed yield (Figure 1A-H except 1B and 1F). The distribution of the array points indicated two parents: BARI Sarisha-15 (P1) and SAU Sarisha-1 (P5) have the most dominant alleles as they are closer to the point of origin. The parents BARI Sarisha-6 (P2), SAU Sarisha-3 (P3) and SAU Sarisha-2 (P4) fall on the middle indicating equal frequencies of dominant and recessive alleles, whereas rest of the parents are far away from the origin indicating that they possess maximum frequency of recessive alleles. Such serious inflation of dominance has been postulated by Hayman (1958) and Jinks (1955). Besides, the existence of pseudo-over dominance was seen in the estimation of D and H components. It was also seen in the variance component of GCA and SCA effects. However, the over dominance may not be an index of a real over-dominance at a gene level. It could cause higher inflation in particularly combinations of unidirectional dominance which might have resulted in an over-estimation of partial dominance as reported in earlier studies (Comstock and Robinson, 1948; Hayman, 1958; Hallauer et al., 2010). The presence of over dominance in the various components of seed yield in the present study has been confirmed by the previous studies in *Brassica juncea* (Trivedi and Mukharjee, 1986; Kumar et al., 2013; Saeed et al., 2013), *Brassica carinata* (Alemayehu and Becker, 2005) and *Brassica rapa* (Chowdhury et al., 2004). The regression line intersected the Wr-axis above the point of origin suggesting partial dominance of gene action controlling maturity and length of pods (Figure 1B and 1F). The parents BARI Sarisha-15 (P1), BARI Sarisha-6 (P2), SAU Sarisha-1 (P5) and Tori-7 (P6) have the maximum dominant alleles as they lay closer to the point of origin. The parent SAU Sarisha-3 (P3) and SAU Sarisha-2 (P4) have the maximum frequency of recessive alleles as they exist far from the origin. The results confirmed the results of Chowdhury et al. (2004) where they also observed partial dominance in *Brassica rapa*.

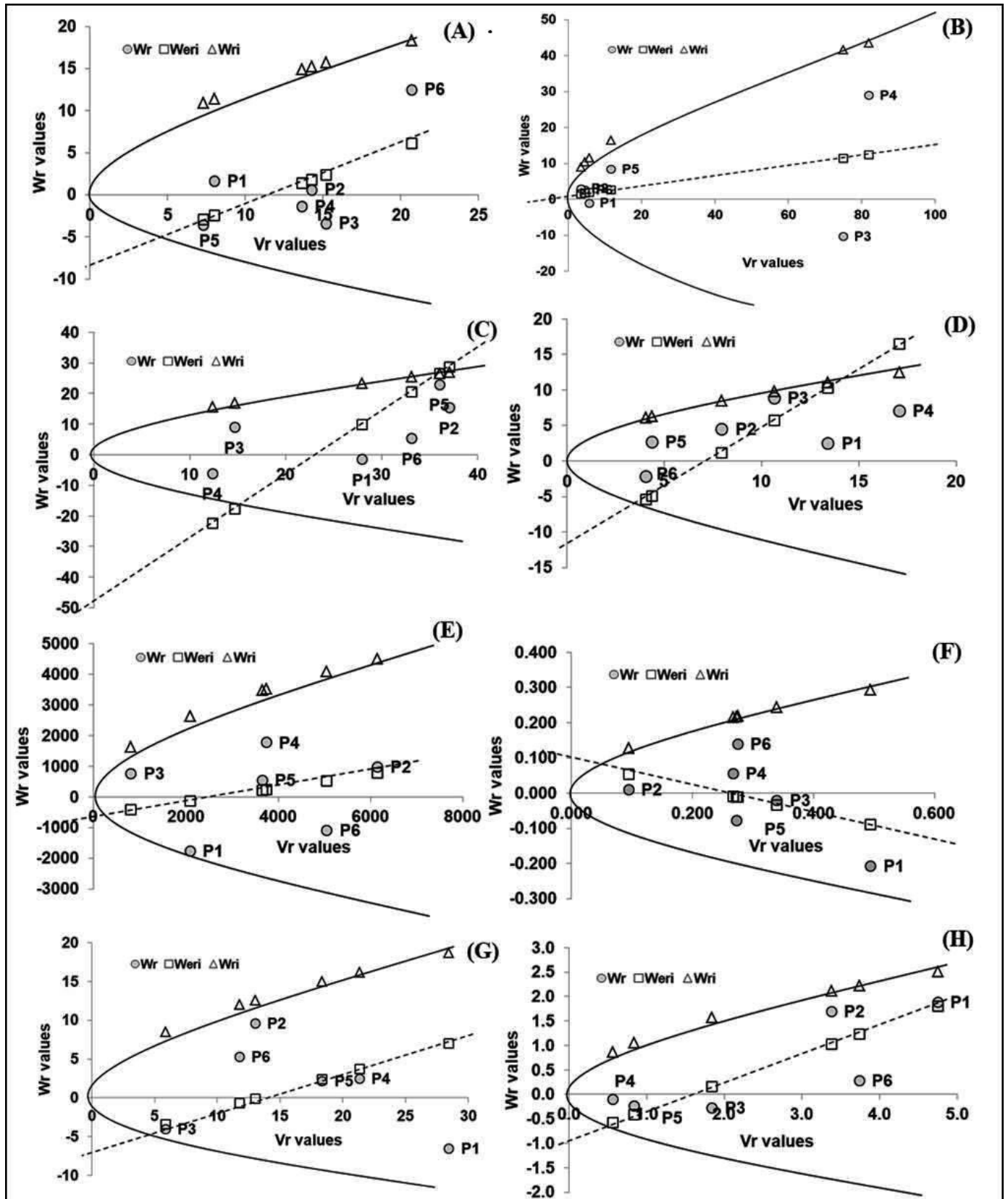


Figure 1. Vr-Wr graph for yield and yield attributing traits of *Brassica rapa* L. Traits are: (A) days to 50% flowering; (B) Days to 80% maturity; (C) plant height; (D) secondary branches; (E) pods per plant; (F) length of pod; (G) seeds per pod and (H) seed yield. Noted that P1: BARI Sarisha-15; P2: BARI Sarisha-6; P3: SAU Sarisha-3; P4: SAU Sarisha-2; P5: SAU Sarisha-1 and P6: Tori-7.

Conclusion

The highest yielding hybrids with considerable portions of both GCA and SCA effects could be the best choice for rapeseed breeders. Analysis of combining ability following Griffing's approach showed significant GCA and SCA variance for all the traits studied, indicating the role of both additive and non-additive components controlling the traits. Estimates of GCA effects for different traits suggested that parent BARI Sarisha-6, BARI Sarisha-15 and Tori- 7 was a good general combiner for different traits. The higher magnitude of GCA variance was observed than that of SCA variance which indicated the superiority of additive components in their expression. The SCA estimates of various traits revealed that the cross combinations of BARI Sarisha-6×BARI Sarisha-15 (Hybrid 13), BARI Sarisha-6×Tori-7 (Hybrid 14) and BARI Sarisha-15×Tori-7 (Hybrid 15) showed statistically significant performance in this study indicating these hybrids can be used towards variety development. The Vr-Wr graph indicated both over and partial dominance for growth and yield attributes. Furthermore, additional studies on epistatic components would be beneficial towards an efficient breeding programme.

CONFLICT OF INTEREST

The authors declare that there are no conflicts of interest.

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