



ESTIMATION OF GENE ACTION AND COMBINING ABILITY IN RICE (*Oryza sativa* L.) THROUGH LINE x TESTER ANALYSIS CARRIED OVER ENVIRONMENTS

Sajad Hussain Dar*, A.G. Rather, S. Najeeb, M. Ashraf Ahangar and Z.A. Bhat

Mountain Research Centre for Field Crops, S.K. University of Agricultural Sciences & Technology
of Kashmir, Khudwani, Anantnag 192 102, Jammu & Kashmir (India)

*e-mail: dar.sajad@rediffmail.com

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ABSTRACT

Line x tester analysis over environments was carried out in rice during 2011 and 2012, with 9 lines, 3 testers and 27 hybrids thus generated. Analysis of variance revealed significant differences among genotypes for most of the characters studied. Mean squares due to G x E interaction and environmental component was observed to be significant for all the traits. Analysis of variance further revealed significant mean squares for general and specific combining ability for all traits. The mean sum of squares due to environments was also significant for most of the traits. The variances of SCA were higher than GCA variances for some of the characters but reverse was true for other characters, thus showing importance of both additive and non-additive genetic components. The GCA estimates for grain yield plant⁻¹ suggested that the parents 'K-08-60', 'K-08-61' and 'Pusa Sugand-5' as promising on the basis of significant positive GCA effects at pooled levels.

Key words: Combining ability, environmental interaction, gene action, hybrid rice, line x tester

INTRODUCTION

Exploitation of hybrid vigour is considered one of the outstanding achievements of plant breeders in 20th century. The hybrids in rice have shown a yield advantage of 1.0-1.5 t ha⁻¹ (20-30%) over the conventionally bred modern varieties (Yuan *et al.*, 1998). A number of hybrid varieties have been developed and released for commercial cultivation in India but all these varieties are related to tropical conditions and do not perform well under temperate agro-ecological conditions of Kashmir (Sanghera *et al.*, 2003, 2010). Hence developing hybrids suitable for temperate conditions hold a great promise. Assessing the combining ability of identified restorer and maintainer lines are prerequisite in heterosis breeding especially when many prospective lines are available. A rice cultivar with excellent performance in itself may not be a good parental line in hybrid rice breeding which necessitates the evaluation of its combining ability. Parental lines with high general combining ability (GCA) effects generally increase the probability of obtaining better heterotic combinations (Saidaiyah *et al.* 2010; Ghara, *et al.* 2012; Dwivedi and Pandey, 2012), however it is limited to the tropical and subtropical conditions. Concerted efforts in this direction are desired in temperate India particularly in Kashmir valley. The expression of quantitative traits is greatly

influenced by the environment and the degree of such influence increases with increase in the number of genes governing the expression of a trait. Therefore, exclusion of G x E variance from the estimates of genetic variance forms integral part of any attempt to estimate genetic variances without bias (Jarwar *et al.*, 2012). The present study was aimed to assess the general and specific combining ability effects of parents and crosses for seed yield and its component traits and to determine the nature and magnitude of gene action using components of genetic variance analysis.

MATERIALS AND METHODS

The present investigation was conducted under two diverse environments *viz.*, Mountain Research Centre for Field Crops, SKUAST-Kashmir, Khudwani (1580 m amsl) [E₁], and at the Experimental Farm of Krishi Vigyan Kandra (KVK) Pombay, Kulgam (2000 m amsl) [E₂] during *kharif* 2011 and 2012. The number of favourable days available for the crop growth in these two locations/environments ranges from 140 to 150 and 120 to 130, respectively. Similarly there is a great variation with respect to photo- and thermal-periods with more number of sunny days and less number of cold spells at different stages of crop growth in case of former and reverse in case of latter. The lines namely Jhelum, Pusa Sughandh-5 (PS-5), China-988, Shalimar Rice-1 (SR-1), SKAU-382, SKAU-389, K-08-59, K-08-60 and K-08-61 were crossed with three CMS lines *viz.*, SKAU-7A, SKAU-11A and IR-68888A in a line x tester fashion to generate 27 cross combinations. In order to achieve good synchrony of male and female parents staggered sowing was made of at 10 days interval. The genetic material was chosen from a broad array of germplasm maintained at Mountain Research Centre for Field Crops, Khudwani. The crosses were generated in *kharif* 2011. During *kharif* 2012, 27 F₁s, 12 parents and two standard checks were evaluated separately using randomized complete block design with three replications at each location. 'Jhelum' and 'SR-1' were used as standard checks. Each experimental plot in each replication had a single row of 1 m length with inter- and intra-row spacing of 20 cm and 15 cm, respectively. Thirty days old seedlings were transplanted with single plant hill⁻¹. Recommended packages of practices were followed to raise a good crop. The observations were recorded on 15 metric traits *viz.*, days to 50% flowering, pollen fertility, spikelet fertility, days to maturity, number of spikelets panicle⁻¹, panicle length, number of productive tillers plant⁻¹, plant height, biological yield plant⁻¹, grain yield plant⁻¹ and grain L/B ratio by following the Standard Evaluation System of Rice (IRRI, 2002). Analysis of variance was carried out as per Singh and Choudhary (1985). Combining ability analysis was carried out as per Kempthorne (1957) following new version of *Windowstat* software.

RESULTS AND DISCUSSION

The individual environments and pooled data over environments revealed significant mean squares due to line x tester interaction for most of the traits (Table 1). The variances due to lines and testers was significant for majority of the traits, however mean squares for lines in case of productive tillers plant⁻¹ (E₁, E₂ and pooled) and grain breadth under E₁ and E₂ were non-significant. The genotype x environment interaction was significant for all the traits indicating that the genotypes under study behaved differently under diverse environments. The cross x environment, line x environment, tester x environment and line x tester x environment interaction components were significant for most of the traits, suggesting that F₁s did not have the same performance across locations. Waghmode (2011) and Jarwar *et al.* (2012) also reported significant G x E interaction for

Table 1: Analysis of variance for various agro-morphological traits in rice (*Oryza sativa* L) [only pooled data over environments]

Source of variation	d.f.	Mean squares										
		Days to 50% flowering	Pollen fertility (%)	Spikelet fertility (%)	Days to maturity	Spikelets panicle ⁻¹	Plant height (cm)	Productive tillers plant ⁻¹	Panicle length (cm)	Biological yield (g plant ⁻¹)	Grain yield (g plant ⁻¹)	Grain L/B ratio
Replications	2	5.5	4.2	0.5	3589.8*	24.1	14.6	1.7	29.8*	81.0*	47.8*	3.4*
Environments (E)	1	164.0*	175.0*	32.6*	2246.2*	2536.4*	62.1*	157.2*	182.9*	234.4*	69.3*	3.6*
Rep. within E	2	0.7	7.2	1.7	4269.2*	3.8	0.5	0.2	0.1	3.3	0.3	2.6*
Genotypes (G)	2	172.7*	4442.9*	4867.7*	4149.7*	4411.7*	609.3*	4.3*	23.7*	496.4*	246.1*	3.4*
Parents (P)	11	65.8*	25.3*	46.8*	13476.7*	3563.6*	596.4*	5.8*	14.6*	675.2*	84.4*	3.4*
Parent vs crosses	1	988.6*	53424.3*	63600.6*	8606.9*	43216.3*	171.2*	39.0*	3.4	14.8	916.1*	1.3
Crosses (C)	26	60.6*	4428.0*	4648.4*	32.2*	3278.0*	631.7*	2.3*	28.4*	439.4*	314.1*	7.3*
Lines (L)	8	110.3*	12124.7*	13118.6*	71.1*	7664.3*	773.2*	2.3	60.9*	834.2*	857.6*	3.0*
Testers (T)	2	199.9*	316.7*	56.3*	14.6*	5893.4*	1760.9*	9.9*	7.9	580.7*	34.6*	2.5
L x T	16	18.3*	1093.6*	987.3*	14.9*	757.9*	419.8*	1.3	14.8*	223.8*	78.9*	5.2*
T x E	38	89.4*	823.8*	882.9*	4262.3*	4594.9*	831.4*	5.5*	9.9*	481.5*	97.5*	3.4*
P x E	11	22.7*	29.9*	41.9*	13812.0*	3736.3*	594.1*	1.9	8.1*	492.7*	99.7*	0.6
P X C x E	1	10.6*	3.6	27.6*	9438.8*	1458.6*	11.1	2.6	0.2	3.3	0.9	1.4
C x E	26	102.2*	1191.2*	1271.5*	23.0*	5078.8*	963.4*	7.1*	11.1*	495.2*	100.2*	6.6*
L x E	8	1.5	807.3*	747.0*	1.36	975.5*	328.6*	1.1	21.1*	283.7*	131.9*	7.4*
T x E	2	733.3*	1435.9*	233.4*	43.0*	21880.2*	5393.0*	31.2*	2.4	2459.5*	63.7*	3.1*
L X T x E	16	73.6*	1352.5*	1663.5*	31.3*	5030.3*	777.1*	7.2*	14.7*	455.4*	134.0*	8.4*
Pooled error	233	5.2	4.2	3.4	3.9	30.2	8.4	1.3	2.1	14.9	22.9	0.6

*= Significant at 0.05 level of probability

most of the traits they studied. Analysis of variance for combining ability revealed significant mean squares for GCA and SCA for all the traits for data pooled over environments. However, the traits like productive tillers plant⁻¹ and length/breadth ratio proved non-significant (Table 2). GCA x environment and SCA x environment interactions were reported significant for most of the traits for data pooled over environments. Saidaiyah (2010), Ghara *et al.* (2012) and Zeinab *et al.* (2014) reported significant interaction of parents x locations, crosses x locations and parents x crosses x locations for different traits in rice.

The estimate of combining ability revealed that variances due to SCA were higher than GCA variances for some of the characters namely, pollen fertility, days to maturity, number of spikelets panicle⁻¹, plant height, productive tillers plant⁻¹, panicle length, biological yield plant⁻¹ and grain length/breadth ratio for the data pooled over environments, but reverse was true for the remaining characters, thus showing importance of both additive and non-additive genetic components. The magnitude of $\hat{\sigma}^2D$ was higher than their corresponding $\hat{\sigma}^2A$ for the traits like days to maturity, panicle length and length/breadth ratio, thereby revealing the importance of non-additive gene action for inheritance of these traits, but reverse was true for the remaining traits (Table 2). Sharifi *et al.* (2012), Ashfaq *et al.* (2012) and Habib *et al.* (2012) observed significant variance due to GCA and SCA for yield traits in rice and reported that additive and non-additive genes play significant role in controlling the expression of various traits. The estimates of average degree of dominance $[\hat{\sigma}^2D/\hat{\sigma}^2A]^{1/2}$ for pooled data revealed that most of the traits viz., days to maturity, panicle length, biological yield plant⁻¹ and grain yield plant⁻¹ and length/breadth ratio showed over-dominance. However, partial dominance was observed for days to 50% flowering, pollen fertility, spikelet fertility, plant height and productive tillers plant⁻¹. Dominance was reported complete for the number of spikelets panicle⁻¹. Partial dominance as well as complete dominance for some traits in rice has also been reported by Yadav (2007). The estimates of genetic components of variance ($\hat{\sigma}^2A$ and $\hat{\sigma}^2D$) together with the average degree of dominance revealed over-dominance for most of the traits indicating that the present set of material were highly divergent and contained contrasting alleles, in most of the cases in dispersion phase, which on combination through hybridization increased heterozygosity.

Table 2: Analysis of variance for combining ability and estimates of components of genetic variance for various agro-morphological traits in rice (*Oryza sativa* L.) [pooled data over environments]

Source of variation	Mean squares										
	Days to 50% flowering	Pollen fertility (%)	Spikelet fertility (%)	Days to maturity	Spikelets panicle ⁻¹	Plant height (cm)	Productive tillers plant ⁻¹	Panicle length (cm)	Biological yield plant ⁻¹ (g)	Grain yield plant ⁻¹ (g)	Grain L/B ratio
σ^2 Lines	5.8*	673.3*	728.7*	3.8*	424.3*	42.4*	0.1	3.2*	45.5*	44.4*	-0.1
	±3.1	±303.6	±328.4	±1.9	±213.8	±25.9	±0.1	±1.6	±22.9	±21.5	±0.2
σ^2 Testers	3.6	5.7	1.0	0.2	108.6	32.4	0.2	0.1	10.4	-0.4	-0.1
	±9.9	±22.1	±12.4	±0.6	±298.4	±74.5	±0.4	±0.2	±33.2	±1.5	±0.1
σ^2 GCA	12.2*	172.7*	182.9*	1.1*	287.6*	54.9*	0.13	0.9*	49.2*	12.8*	-0.1
	±5.5	±77.8	±82.6	±0.7	±120.1	±26.2	±0.32	±0.4	±12.6	±2.5	±0.1
σ^2 SCA	6.2*	181.5*	164.2*	2.03*	171.9*	68.4*	-0.02	2.08*	44.5*	13.5*	0.2
	±2.2	±96.6	±67.5	±1.9	±82.6	±29.1	±0.41	±1.2	±18.2	±3.6	±0.4
σ^2 E	1.4*	0.8*	-0.0	1.8*	33.8*	0.5*	0.8*	1.0*	1.0*	-0.3	0.0
	±0.0	±0.0	±0.0	±0.0	±0.1	±0.0	±0.0	±0.0	±0.1	±0.2	±0.0
σ^2 Lines x E	-5.4*	139.2*	182.7*	-7.2*	195.5*	74.4*	1.1*	2.4*	37.4*	11.8*	-0.1
	±2.7	±64.2	±71.9	±1.2	±142.5	±30.9	±0.3	±0.6	±17.1	±5.4	±0.3
σ^2 Testers x E	26.9*	53.0	8.6	3.5*	809.4*	199.4*	1.1	1.0*	90.5*	8.2*	-0.0
	±19.2	±41.2	±21.4	±1.2	±576.4	±141.6	±0.8	±0.2	±64.6	±2.4	±0.1
σ^2 GCA x E	20.1*	68.1*	27.1	2.1*	733.4*	185.9*	2.8*	0.4*	93.7*	8.3*	-0.1
	±14.4	±34.8	±24.1	±0.9	±434.9	±76.4	±0.6	±0.2	±48.7	±2.2	±0.1
σ^2 SCA x E	22.8*	449.3*	553.7*	9.5	1668.1*	255.9*	1.9	4.1*	146.2*	25.3*	0.4
	±8.2	±100.3	±184.8	±3.5	±558.9	±86.4	±0.8	±1.7	±50.6	±16.8	±0.8
σ^2 A	8.3	345.3	365.8	2.2	375.2	69.9	0.3	1.8	38.4	21.6	-0.1
σ^2 D	2.2	181.5	164.2	4.1	121.9	68.40	-0.0	2.1	34.5	3.4	0.2
$\hat{\sigma}^2 A / \hat{\sigma}^2 D$	3.8	1.9	2.2	1.1	3.1	1.0	0.2	0.9	1.1	6.3	-0.6
Degree of dominance	0.5	1.1	0.7	0.9	0.9	1.0	0.3	1.1	1.2	1.4	1.3

* = Significant at 0.05 level of probability

The proportionate contribution of lines, testers and their interaction to the total variance showed that lines played an important role by giving greater contribution towards the trait signifying their predominant influence on the traits (Table 3). The greater contributions of lines x testers interaction than testers for all the characters, except days to 50 % flowering, pointed out higher estimates of specific combining ability variance effects. These results are in agreement with the findings of Rashid *et al.* (2007). Greater contribution of Line x tester interactions than that of lines and testers except for number of spikelets panicle⁻¹ was also reported by Ghara, *et al.* (2012).

Table 3: Percent contribution of different components (lines, testers and lines x testers) towards the hybrid sum of squares for pooled over analysis for various agro-morphological traits in rice (*Oryza sativa* L.)

Characters	Line	Tester	Line x tester
Days to 50% flowering	56.02	25.37	18.61
Pollen fertility (%)	84.25	0.55	15.20
Spikelet fertility (%)	86.84	0.09	13.07
Days to maturity	67.93	3.50	28.56
Spikelets panicle ⁻¹ (No.)	71.94	13.83	14.23
Plant height (cm)	37.66	21.44	40.89
Productive tillers plant ⁻¹ (No.)	40.21	22.48	38.51
Panicle length (cm)	65.82	2.13	32.04
Biological yield plant ⁻¹ (g)	58.48	10.17	31.35
Grain yield plant ⁻¹ (g)	83.74	0.84	15.41
Grain L/B ratio	23.99	0.67	75.34

Table 4: Estimates of general combining ability effects for various agro-morphological traits in rice (*Oryza sativa* L.) [Pooled data over environments]

Parent	Days to 50% flowering	Pollen fertility (%)	Spikelet fertility (%)	Days to maturity	Spikelet panicle ⁻¹	Plant height (cm)	Product- ive tillers plant ⁻¹	Panicle length (cm)	Biologi- cal yield plant ⁻¹ (g)	Grain yield plant ⁻¹ (g)	Grain L/B ratio
Lines											
K-08-59	-1.5*	25.4*	30.6*	-3.3*	-33.0*	-8.9*	0.3	0.4	-9.5*	-1.6	0.1
Jhelum	-3.6*	-24.3*	-23.5*	0.5	18.1*	0.5	-0.2	-0.7*	-0.3	-5.9*	0.8
SKAU-382	-0.4	-16.6*	-11.7*	-0.8	5.8*	4.1*	-0.2	0.3	-0.9	-5.7*	-0.4
SKAU-389	-2.5*	-15.2*	-23.0*	-1.3*	-35.1*	-4.6*	-0.2	-0.2	10.1*	-6.2*	-0.2
China-988	1.2*	-30.2*	-26.4*	-1.9*	10.3*	-9.0*	0.9*	-2.0*	-1.1	-1.2	-0.2
SR-1	1.7**	-25.6*	-26.9*	1.4*	-1.9	-4.2*	-0.4	-3.0*	-7.8*	-5.5*	-0.5
K-08-60	-0.7	29.9*	32.5*	2.1*	-2.3	4.8*	-0.2	1.2*	-4.2*	8.4*	-0.1
K-08-61	1.2*	32.1*	31.6*	2.7*	7.1*	11.0*	0.2	2.9*	5.6*	10.4*	0.4
PS-5	4.6**	29.5*	28.9*	0.7	15.6*	5.7*	0.2	2.1*	8.2*	10.2*	0.1
Testers											
SKAU-7A	1.2*	-5.1*	-2.1*	0.1	-7.4*	6.9*	0.8*	0.7*	-0.5	0.6	-0.2
SKAU-11A	-4.7*	6.2*	0.7*	-0.7*	-21.0*	7.6*	0.4*	0.1	1.6*	1.0	0.2
IR-68888A	3.6*	-1.1*	1.5*	0.5*	28.4*	-	-0.4*	-0.4*	-7.6*	-0.9	-0.1
						14.5*					
SE (gi) Lines	0.5	0.5	0.4	0.4	1.2	0.7	0.3	0.4	0.9	1.8	0.5
SE (gi-gj) Lines	0.8	0.7	0.5	0.5	1.7	1.0	0.4	0.5	1.4	2.5	0.7
SE (gi) Testers	0.3	0.3	0.2	0.2	0.7	0.4	0.2	0.2	0.6	1.0	0.3
SE (gi-gj) testers	0.4	0.4	0.3	0.3	1.0	0.6	0.2	0.3	0.8	1.5	0.4
Parents with desirable gca effects	4	5	6	5	6	6	3	4	4	3	0

*Significant at 0.05 level of probability

None of the parents showed significant GCA effect simultaneously in the desired direction for all the traits studied (Table 4). To find the best parent for subsequent hybrid rice development, variation in GCA effects was estimated among lines and testers for all the traits. The GCA estimates for grain yield plant⁻¹ suggested that the parents K-08-60, K-08-61 and PS-5 were promising on the basis of significant positive GCA effects at individual and pooled levels. Hence, these parents may be presumed to have more favourable alleles for grain yield plant⁻¹. The good *per se* performance on the basis of high mean value was recorded for K-08-61, while K-08-60 and PS-5 exhibited poor *per se* performance. The genotypes SKAU-389, K-08-61 and PS-5 revealed highest GCA effect for biological yield plant⁻¹ for data pooled over environments. In general, higher *per se* performance for most of the traits was associated with higher GCA except for pollen fertility, spikelet fertility and plant height. Correspondence between *per se* performance and GCA effects for different traits in rice has been observed by Faiz *et al.* (2006) and Selvaraj *et al.* (2011).

Furthermore, the parents K-08-59 and SKAU-389 were the top most performers for maturity traits i.e. days to 50% flowering and days to maturity. The lines K-08-61 and PS-5 were observed to have significant GCA effects for yield and other traits like pollen fertility, spikelet fertility and number of spikelets panicle⁻¹, plant height, panicle length and biological yield plant⁻¹ for data pooled over environments. Also, the line K-08-60 was observed to have significant GCA effects for yield and most of the other contributing traits. However, for rest of the characters behaviour of all these parents was either average or poor (Table 4). Further, pooled environmental data identified none of the CMS lines or female parent to be good general combiner for all the traits studied. The female parent SKAU-11A was noticed as good combiner due to high GCA effects for most of the traits studied (Table 4). Also the CMS lines SKAU-7A and IR-68888A were observed to be good general combiners for some of the traits studied. In a similar kind of research, IR-64, Ujala Depama

and MALIDA were identified as good general combiners (Shiva Prasad *et al.* 2013). Thus the present investigation on GCA effects revealed that among lines and testers there were good general combiners for grain yield and other traits. Hence, these good general combiners of males and females may be extensively used in multiple crossing programmes to identify superior genotypes for hybrid rice development.

Table-5: Estimates of specific combining ability effects for various agro-morphological traits in rice (*Oryza sativa* L.) [Pooled data]

Cross combination	Days to 50% flowering	Pollen fertility (%)	Spikelet fertility (%)	Days to maturity	Spikelets panicle ⁻¹	Plant height (cm)	Productive tillers plant ⁻¹	Panicle length (cm)	Biological yield plant ⁻¹ (g)	Grain yield plant ⁻¹ (g)	Grain L/B ratio
SKAU-7A x K-08-59	3.2*	2.6*	0.9	4.9*	29.2*	1.2	-1.4*	1.3	-2.9	-4.5	2.9*
SKAU-11A x K-08-59	-3.9*	-8.3*	-2.7*	-2.3*	-59.1*	8.4*	0.8	-0.5	-1.4	1.0	-1.3*
IR-68888A x K-08-59	0.9	5.8*	1.8*	-2.7*	29.9*	-9.6*	0.5	-0.7	4.4	3.5	-1.6*
SKAU-7A x Jhelum	-0.9	-1.9	-1.9*	0.5	-7.7*	-7.4*	0.6	0.1	10.2*	0.5	0.4
SKAU-11A x Jhelum	-2.5	-3.5*	-4.4*	2.2*	38.9*	-6.6*	0.1	-0.2	-8.6*	0.9	1.2*
IR-68888A x Jhelum	3.5*	5.3*	6.1*	-2.8*	-31.3*	13.9*	-0.8	0.1	-1.6	-1.4	-1.6*
SKAU-7A x SKAU-382	-5.3*	-17.1*	-21.8*	-0.8	0.1	-28.4*	-0.3	-1.6	-9.7*	-4.7	-0.7
SKAU-11A x SKAU-382	5.6*	26.3*	34.4*	0.7	44.1*	18.7*	0.2	2.7*	0.7	1.6	0.7
IR-68888A x SKAU-382	-0.3	-9.2*	-12.6*	0.1	-44.2*	9.0*	0.0	-0.5	8.9*	3.1	0.0
SKAU-7A x SK-389	-1.4	-6.6*	-13.3*	-1.6	-7.3*	9.7*	-0.8	0.0	4.5	0.0	-1.2*
SKAU-11A x SK-389	-1.6	9.6*	-16.3*	0.3	-19.5*	-9.9*	1.5*	0.1	10.0*	0.5	0.2
IR-68888A x SK-389	3.1*	13.1*	27.1*	1.3	26.8*	0.3	-0.2	-0.2	-14.5*	-0.6	1.0*
SKAU-7A x Ch-988	-2.3	7.6*	1.6	-2.8*	8.9*	-1.3	-0.0	0.5	-6.9*	11.7*	-1.7*
SKAU-11A x Ch-988	3.7*	-5.0*	2.5*	0.4	-26.7*	-12.3*	0.2	-0.7	6.9*	-10.0*	-0.2
IR-68888A x Ch-988	-1.3	-2.6*	-4.1*	3.1*	17.8*	13.6*	-0.1	2.8*	-0.2	-1.7	1.8*
SKAU-7A x SR-1	-1.1	15.9*	20.3*	1.9	-26.4*	0.1	-1.6*	1.2	-9.1*	2.4	0.9
SKAU-11A x SR-1	3.5*	-2.9*	-7.5*	-1.9	-0.1	-3.8*	-0.4	-0.6	1.0	-1.2	-0.8
IR-68888A x SR-1	-2.3	-13.0*	-12.8*	-0.1	26.5*	3.7*	1.6*	-0.6	8.1*	-1.1	-0.1
SKAU-7A x K-08-60	0.2	5.3*	5.7*	-1.9*	7.7*	-0.3	0.0	-3.4*	-6.5*	9.7*	-1.2
SKAU-11A x K-08-60	-1.2	-5.5*	-4.5*	1.7	31.3*	5.9*	-0.1	3.5*	-8.8*	9.6*	1.3*
IR-68888A x K-08-60	0.2	0.2	-1.2	0.2	-38.9*	-5.7*	0.1	-0.7	15.4*	9.9*	-0.2
SKAU-7A x K-08-61	6.3*	4.2*	4.3*	-1.3	-2.2	16.2*	0.2	-0.5	10.9*	10.4*	-0.4
SKAU-11A x K-08-61	-5.4*	-4.3*	-1.7	0.6	2.5	-3.9*	0.2	-1.0	-8.7*	9.7*	-0.1
IR-68888A x K-08-61	-0.9	0.3	-2.6*	0.7	-0.3	-12.0*	-0.4	0.0	-2.2	8.6*	0.4
SKAU-7A x PS-5	0.7	6.5*	1.5	1.7	-2.3	10.3*	1.5*	2.4*	9.2*	10.1*	1.1*
SKAU-11A x PS-5	2.1	-6.5*	0.2	-1.9	-11.3*	3.7*	0.2	-0.1	9.1*	8.9*	-1.1*
IR-68888A x PS-5	-0.1	-0.3	-1.7	0.1	13.6*	-13.9*	-0.3	-2.3*	-18.3*	-3.9	0.1
S.E $\pm$ (S _{ij})	1.3	1.2	0.9	0.9	2.9	1.7	0.5	0.6	1.3	4.4	0.5
S.E $\pm$ (S _j - S _{ik})	2.4	2.3	1.3	1.8	5.3	3.2	1.3	1.6	4.3	8.1	0.1
No. of crosses showing desirable sca effects	3	11	8	5	11	11	3	4	9	9	6

*Significant at P_{0.05}

On basis of estimates of specific combining ability affects none of the cross combinations exhibited significant and desirable SCA effect for all the characters studied. Yield plant⁻¹ is ultimate goal of rice breeding and hybrid development programme. In the present experiment for grain yield plant⁻¹, seven hybrid combinations viz. SKAU-7A x China-988, SKAU-7A x K-08-60, SKAU-11A x K-08-60, IR-68888A x K-08-60, SKAU-7A x K-08-61, SKAU-11A x K-08-61 and SKAU-7A x PS-5 were found good specific combinations based on high and significant SCA effects. The cross combination SKAU-7A x PS-5 was the best specific combination for acceptable and significant SCA effects for grain yield plant⁻¹ and other desirable characters like pollen fertility %, plant height, number of productive tillers plant⁻¹, panicle length, biological yield plant⁻¹, and length/breadth ratio (Table 5). SKAU-7A x K-08-61 was second best specific combination for grain yield plant⁻¹ and most of the other desirable characters. Similarly, all the remaining cross combinations identified with significant SCA effect for grain yield plant⁻¹ were also observed with desirable and significant SCA effects for other agro-morphological traits. High SCA effects for grain yield using line x tester analysis have earlier been reported (Thakare *et al.* 2010; Saidaiah *et al.* 2010; Mirarab *et al.* 2011; Shiva Prasad *et al.* 2013). For biological yield plant⁻¹ some of the promising cross combinations identified on the basis of significant and positive SCA effects at individual and pooled over

environments were IR-68888A x K-08-60, SKAU-7A x K-08-61, SKAU-11A x SKAU-389, SKAU-7A x PS-5 and SKAU-11A x PS-5. Similarly for early maturity promising cross combinations identified were IR-68888A x Jhelum, SKAU-11A x K-08-59, IR-68888A x K-08-59, SKAU-7A x Ch-988 and SKAU-7A x K-08-6.

The perusal of SCA effects along with *per se* performance revealed that some of the crosses showing desirable SCA effects were also having superior *per se* performance for most of the traits for data pooled over environments. For example, for grain yield the promising cross combinations based on high SCA effect and high *per se* performance were SKAU-7A x PS-5, SKAU-7A x K-08-60, SKAU-11A x K-08-61 and SKAU-11A x K-08-60. For biological yield IR-68888A x PS-5 and SKAU-7A x SKAU-389 cross combinations were identified most promising and for plant height the potential combinations were SKAU-11A x SKAU-382 and SKAU-7A x PS-5. These results are in line with those of Saleem *et al.* (2010), and Najeeb *et al.* (2011a).

Conclusion: The identified cross combinations on the basis of significant and desirable sca effects for yield and yield based traits validate the performance of a heterotic combination on the genetic basis and nullify the chance heterotic event in any cross combination. Furthermore the detection of genotype x environment interaction for these traits emphasizes the need for multi-environment testing of the material both spatially as well as temporally to help draw valid conclusions.

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