

Genetic analysis over environments in rice (*Oryza Sativa L.*) under temperate agroecology

Sajad Hussain Dar^{*1}, Faheem Ameen¹, N.R. Sofi², F.A. Sheikh² and M. Ashraf Ahanger²

¹Division of Plant Breeding and Genetics, SKUAST-Kashmir, Shalimar, Srinagar, 190025 India.

²MRCFC, Khudwani, SKUAST-Kashmir, Shalimar, Srinagar, 190025 India.

Corresponding author: dar.sajad@rediff

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Abstract

Rice is one of the crucial staple food crops and holds two third of world population. In order improve its production and productivity a diallel study was carried out over two diverse environments in 2012 by generating 36 F1hybrids using 9 parents. Analysis of variance revealed significant differences among the genotypes together with significant G x E interaction for most of the characters studied. Estimates of $\hat{\sigma}^2_g$ and $\hat{\sigma}^2_s$ revealed that, the latter component of variance was greater in magnitude for most of the traits for pooled data over environments. The magnitude of $\hat{\sigma}^2_D$ was higher than corresponding, $\hat{\sigma}^2_A$ indicating non-additive gene action was of greater importance. Significant and positive estimates of GCA over pooled data for grain yield/plant identified the parents, SKAU-389, Jhelum, SKAU-382, and SR-1as promising. Likewise 15 potential hybrid combinations for grain yield/plant were observed on the basis of high and significant SCA effects. The hybrids, Jhelum x K-08-60, SKAU-389 x K-08-60, SR-1 x K-08-60, K-08-59 x PS-5 and China-988 x SR-1 were prospective combinations for grain yield/plant and other desirable characters. Results would indicate that the parental lines are genetically diverse and could contribute to the improvement of hybrid rice productivity.

Highlights

- 36 hybrid and 9 parents were analysed for their general and specific combining abilities over environments.
- Significant differences among the genotypes together with significant G x E interaction.
- Non-additive gene action was found of greater magnitude.

Keywords: combining ability, diallel, gene action, G x E interaction, GCA, SCA, temperate ecology

Rice (*Oryza sativa L.*) is the world's most important food crop providing more than 20% of the caloric intake for over 3.5 billion people. Globally one billion people depend on rice cultivation for their livelihoods (Anonymous, 2013). The demand continues to rise because of increases in population and improving living standards shifting food habits towards rice. However, yield stagnation has been observed over the past decade. To break the yield plateau through increase in production and productivity levels, coherent breeding efforts on sound and systematic lines need to be devised. Choice of suitable parents is of paramount importance. The combining ability analysis gives

an indication of the variance due to GSA and SCA which represents a relative measure of additive and non-additive gene actions, respectively. Breeders use these variance components to measure the gene action and to assess the genetic potential of parents in hybrid combinations. Diallel analysis (Griffing, 1956a, b) provides reliable information about the general and specific combining ability of parents. The present investigation was, therefore, conducted under two varied environmental conditions to draw the valid inferences regarding genetically diverse set of genotypes with respect to combining ability and nature and magnitude of gene action involved in inheritance of yield, maturity, and related traits.

Materials and methods

The study was conducted during the 2012 *Kharif* season at the Mountain Research Centre for Field Crops, (MRCFC) Khudwani (1650 m amsl) and at the Experimental Farm of Krishi Vigyan Kandra (KVK) Pombay, Kulgam (2000 m amsl) of Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir. Thirty-six F_1 hybrids were generated by crossing nine genotypes, 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 in half diallel mating. The 36 F_1 hybrids and 9 parents were evaluated using a randomized complete block design with three replications at each location. Thirty days old seedlings were transplanted with single plants per hill. Each experimental plot in each replication had two rows of 1 m length with inter-row and intra-row spacing of 20 cm and 15 cm, respectively and recommended practices were followed for rice production in the regions. Observations were recorded on 11 metric traits days to 50 % flowering, days to maturity, number of spikelet's per panicle, number of filled grains per panicle, panicle length (mm), number of productive tillers per plant, plant height (cm), biological yield per plant (g), grain yield per plant (g), harvest index (%), and grain length/breadth ratio following Standard Evaluation System of Rice (IRRI, 1998). Analysis of variance for pooled data was carried out following Singh and Chowdhary, (1985). Combining ability analysis for GCA and SCA of parents and crosses was done by following Model-I Method-II of Griffing, (1956b), using WINDOW STATE software (source).

Results and discussion

Highly significant differences were found among the parents and the resulting F_1 hybrids for all the traits on pooled data over environments except length/breadth ratio, indicating that the parents were diverse for most of the traits resulting in substantial genetic variability in the crosses (Table 1). The simple and complex interactions such as genotype x environment, parents x environments, crosses x environments and components were found significant for the majority of the traits, indicating that the genotypes behaved differentially under diverse environments. Jarwar *et al.* (2012) also reported significant differences among parents,

hybrids and hybrids vs parents over environments for most of the agronomic characters in rice. The results further revealed significant mean squares for general and specific combining ability for all traits (Table 2). The mean squares due to environments were also significant for all the traits except for panicle length and grain L/B ratio demonstrating that the environments were significantly diverse. The interaction components of GCA x environment and SCA x environment recorded significance for all the traits except for no. of spikelet's per panicle and no. of filled grains per panicle.

The results pertaining to the estimation of combining ability for pooled data revealed that mean squares due to GCA were relatively greater in magnitude than mean squares due to SCA except for 50% flowering (Table 2). Estimates of σ^2_g and σ^2_s revealed that, the latter component of variance was greater in magnitude for all the traits except for days to 50% flowering and grain length /breadth ratio. Magnitude of σ^2_D was observed greater than their corresponding σ^2_A , except for days to 50% flowering and grain length/breadth ratio, thereby indicating the involvement of both additive and non-additive genetic components in the inheritance of these trait with greater importance of non-additive gene effects (Table 2). Involvement of both additive and non-additive genetic components with preponderance of latter component for expression of yield and its components have also been reported by Najeeb *et al.* (2011), Dwivedi and Pandey (2012), Gopikannan and Ganesh (2013) . Chaturvedi *et al.* (2010), Saidaiah *et al.* (2010), Savitha and Usha Kumari (2015) also observed predominance of non-additive gene action for grain yield and other important traits over environments. Estimates of average degree of dominance $[\sigma^2_D/\sigma^2_A]^{1/2}$ for pooled data revealed over-dominance for days to maturity, number of spikelet's/panicle, number of filled grains/panicle, plant height, productive tillers/plant, panicle length, biological yield/plant, grain yield/plant and harvest index. Partial dominance was noticed only for grain length/breadth ratio whereas, days to 50% flowering demonstrated complete dominance divergent parental lines with contrasting alleles in dispersion phase, which on combination through hybridization increased heterozygosity would contribute to over-dominance. Kumar and Reddy (2011) also reported over dominance for most of the traits in rice.

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

Source of variation	d.f	Mean Squares										
		Days to 50% flowering	Days to maturity	No. of spikelets panicle ⁻¹	No. of filled grains panicle ⁻¹	Plant height (cm)	Productive tillers plant ⁻¹	Panicle length (cm)	Biological yield plant ⁻¹ (g)	Grain yield plant ⁻¹ (g)	Harvest index (%)	Grain L/B ratio
Environments (E)	1	171.2**	469**	3884.4**	4254.7**	232.1**	394.3**	346.5**	755.3**	181.5**	62.8**	4.7
Replications	2	-	-	-	-	-	-	-	-	-	-	-
Replications within Env.	2	8.0*	19.4**	44.8**	86.6**	1.7	4.1*	0.7	39.9*	28.0**	71.8**	0.8
Genotypes (G)	46	136.4**	71.5**	7548.4**	4262.9**	665.4**	11.9**	21.7**	1086.3**	273.7	333.6**	145.9**
Parents (P)	8	151.4**	88.2**	6559.4**	2920.3**	582.6**	6.1**	16.1**	984.7**	175.8**	97.0**	249.7**
Crosses (C)	35	120.2**	67.2**	7612.8**	4559.6**	661.2**	12.4**	22.7**	1140.3**	302.0**	392.9**	121.3**
P vs C	1	557.5**	89.0**	13205.5**	4621.5**	1471.4**	40.4**	27.5**	8.8	68.1**	154.7**	175.8**
G x E	46	10.2**	22.4**	18.4**	23.9**	22.7**	8.5**	11.7**	18.1**	11.9**	19.7**	1.3
P x E	8	14.2**	19.2**	21.1**	29.5**	15.5**	6.6**	9.1*	26.8**	9.1**	11.6**	1.1
C x E	35	11.6**	12.4**	25.1**	18.7**	19.7**	5.5**	7.8**	13.1**	8.9**	26.9**	1.4
P x C x E	1	4.5	4.2	2.3	2.1	5.1	2.2	2.1	9.0	4.0	8.1	0.3
Pooled error	108	3.2	3.1	7.5	5.2	1.6	2.3	1.3	8.5	2.3	4.3	2.3

*, ** Significant at 0.05 and 0.01 levels of probability, respectively

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.) [data pooled over environments]

Source of variation	d.f	Mean Squares										
		Days to 50% flowering	Days to maturity	No. of spikelets panicle ⁻¹	No. of filled grains panicle ⁻¹	Plant height (cm)	Productive tillers plant ⁻¹	Panicle length (cm)	Biological yield plant ⁻¹ (g)	Grain yield plant ⁻¹ (g)	Harvest index (%)	Grain L/B ratio
Environments (E)	1	85.6**	234.7**	1942.2**	3710.0**	116.0**	197.2**	173.2	377.0**	90.8**	31.4**	2.3
GCA	8	138.0**	56.8**	6335.9**	2127.3**	307.0**	4.8**	13.0**	618.4**	215.5**	186.4**	155.2**
SCA	35	24.9**	16.5**	1667.3**	912.3**	202.8**	3.8**	5.9**	305.2**	63.6**	94.5**	24.9**
GCA x E	8	3.1**	6.2**	5.4	1.9	6.3**	1.2**	3.2**	23.2**	7.2**	12.5**	2.8**
SCA x E	35	4.2**	4.1**	1.4	1.2	5.2**	1.2**	2.2**	17.6**	4.4**	9.6**	1.4**
Error	88	-	-	-	-	-	-	-	-	-	-	-
Pooled	269	1.1	1.0	9.8	3.8	1.7	0.5	0.7	4.5	0.8	2.1	0.8
$\hat{\sigma}^2 g$	-	6.2	2.5	287.6	168.5	13.9	0.2	0.6	27.9	9.8	8.4	7.0
$\hat{\sigma}^2 s$	-	11.9	7.7	828.7	454.2	100.6	1.7	2.6	150.6	31.4	46.2	12.1
$\hat{\sigma}^2 A$	-	12.5	5.1	575.1	336.9	27.7	0.4	1.1	55.8	19.5	16.8	14.0
$\hat{\sigma}^2 D$	-	11.9	7.7	828.7	454.2	100.6	1.7	2.6	150.6	31.4	46.2	12.1
$\hat{\sigma}^2 A \hat{\sigma}^2 D$	-	1.0	0.6	0.7	0.7	0.8	0.2	0.8	0.4	0.6	0.4	1.2
$2\hat{\sigma}^2 g 2\hat{\sigma}^2 s$	-	0.5	0.4	0.4	0.4	0.2	0.8	0.3	0.3	0.4	0.3	0.5
$\hat{\sigma}^2 D \hat{\sigma}^2 A$	-	1.0	1.1	1.2	1.2	1.9	2.2	1.5	1.6	1.3	1.7	0.9

*, ** Significant at 0.05 and 0.01 levels of probability, respectively

Table 3: Estimates of general combining ability effects for various agro-morphological traits in rice (*Oryza sativa* L.) [Data pooled over environments]

Parent	Days to 50% flowering	Days to maturity	No. of spikelets panicle ⁻¹	No. of filled grains panicle ⁻¹	Plant height (cm)	Productive tillers plant ⁻¹	Panicle length (cm)	Biological yield plant ⁻¹ (g)	Grain yield plant ⁻¹ (g)	Harvest index (%)	Grain L/B ratio
K-08-59	-2.67**	-1.01**	-9.68**	-11.74**	-4.63**	0.57**	-1.05**	-3.91**	-5.88**	-6.40**	0.64**
Jhelum	-1.30**	-1.02**	5.07**	4.37**	0.02	-0.07	-0.40*	1.83**	2.13**	2.10**	-2.04**
SKAU-382	-2.42**	-1.35**	4.78**	4.79**	0.89**	-0.12	0.08	2.03**	1.74**	2.026**	-1.82**
SKAU-389	-0.87**	-0.19	8.40**	7.18**	6.65**	0.42**	0.23	8.95**	4.95**	2.84**	-0.99**
China-988	-1.09**	-0.88**	-31.97**	-23.12**	0.26	0.41**	-0.75**	-3.29**	0.40*	2.12**	-2.97**
SR-1	-1.21**	-0.81**	-18.60**	-13.17**	2.44**	-0.05	-0.35*	3.72**	0.67**	-1.08**	-2.50**
K-08-60	2.80**	1.74**	17.84**	15.76**	-1.43**	0.10	0.89**	1.28**	-0.69**	-1.97**	3.17**
K-08-61	2.59**	1.77**	4.57**	3.84**	-5.72**	-0.50**	0.49*	-9.75**	-3.25**	-0.36	2.46**
PS-5	4.18**	2.59**	19.59**	12.09**	1.32**	-0.83**	1.35**	-0.85	-0.08	0.72*	4.05**
SE± (g)	0.21	0.21	0.63	0.40	0.26	0.14	0.17	0.43	0.18	0.29	0.17
SE± (g-g)	0.31	0.31	0.94	0.60	0.40	0.21	0.26	0.64	0.26	0.44	0.26
No. of desirable parents for trait	6	5	6	6	4	3	3	5	5	5	4

*, ** Significant at 0.05 and 0.01 level of probability, respectively



General Combining Ability

The GCA effects represent the additive nature of gene action. A good general combiner is distinguished by higher better breeding value when used in hybrid combinations. None of the parent's possessed significant GCA effects in the desired direction simultaneously for all the traits studied (Table 3). The genotypes Jhelum, SKAU-382, SKAU-389 and SR 1 were found as the good general combiners for grain yield and biological yield. Regarding harvest index all parents except K-08-59, SR-1 and K-06-60, whereas for grain length/breadth only K-08-59, K-06-60, K-06-61 and PS-5 proved promising combiners. Habib *et al.* (2012) and Ashfaq *et al.* (2012) reported some good combiners for yield and yield components. SKUA-382 and Jhelum revealed association between desirable GCA effects and good performance for earliness and grain yield revealing the possibility of very promising alleles for such traits (Table 4). Correspondence between *per se* performance and GCA effects for different traits in rice has been observed by Selvaraj *et al.* (2011), however the contrast findings of Sharma and Mani (2008) showed no connection between GCA effects and *per se* performance. The pooled data analysis thus demonstrated the parent SKAU-389 to have significant GCA effects for yield, earliness and for most of yield components. Similarly, genotypes like Jhelum, SKAU-382 and SR-1 were also observed to have significant GCA effects for yield and other characters. For rest of the traits the behavior of all these parents was either average or poor. Thus in the present investigation the progenies of the crosses involving identified good general combiners could serve as a potential source of promising segregants having higher yielding potential together with earliness.

Specific combining ability

Breeding for higher yield potential is a major goal of all breeding programmes and 15 hybrid combinations K-08-59 x K-08-61, K-08-59 x PS-5, Jhelum x K-08-60, Jhelum x K-08-61, Jhelum x PS-5, SKAU-382 x China-988, SKAU-382 x PS-5, SKAU-389 x K-08-60, SKAU-389 x K-08-61, SKAU-389 x PS-5, China-988 x SR-1, China-988 x K-08-60, China-988 x PS-5, SR-1 x K-08-60 and SR-1 x K-08-60 were found suitable for grain yield/plant based on positive and significant SCA effects (Table 5) Jhelum x K-08-60 was

also identified as the better specific combination for days to 50 per cent flowering (earliness), number of filled grains panicle⁻¹, plant height, number of productive tillers plant⁻¹, panicle length, biological yield plant⁻¹ and harvest index. High SCA effects for grain yield have been reported by Chakarborty *et al.* (2009), Patil *et al.* (2012), Ghara *et al.* (2012) and Ashfaq *et al.* (2012). Hybrid combinations with desirable SCA effects and performance along with GCA effect of their parent for different traits are presented in Table-6. For grain yield the promising cross combinations based on *per se* performance and significant and desirable SCA effects were SKAU-389 x K-08-60, Jhelum x K-08-60 and Ch-988 x SR-1. The results of pooled data analysis of Saidaiyah *et al.* (2010) and Muthuramu (2010) reported parallelism between *per see* performance and SCA effects for grain yield and other traits in rice. The 4 top ranking crosses for grain yield plant⁻¹ involved good x poor, poor x average, good x good and good x average combinations. The superiority of SCA effects may be due to complementary type of gene action or involvement of non-allelic interaction of fixable and non-fixable genetic variances. The crosses involving poor combiners suggest the epistatic gene action which could mainly be due to genetic diversity in the form of heterozygous loci. Furthermore, the majority of cross combinations were involved with good/poor or average/poor type of gene interactions which substantiate the operation of non-additive gene action expression of these traits. Besides these interactions, involvement of good x good, poor x poor and average x average were also evident from the study such as K-08-59 x Jhelum for early maturity, Jhelum x PS-5, Jhelum x SKAU-389, K-08-60 x K-08-61 for number of spikelet's panicle⁻¹ and Jhelum x SKAU-389, Jhelum x PS-5, SKAU-382 x PS-5 for number of filled grains panicle⁻¹. Involvement of both the poor general combiners as parents also produced superior hybrids as evident from the combinations K-08-59 x Ch-988 for number of spikelet's panicle⁻¹, K-08-61 x PS-5 for plant height, K-08-59 x K-08-61 for biological yield plant⁻¹. Involvement of both the combiners with low GCA has been attributed to dominance x dominance interaction, which have been suggested by Singh *et al.* (2005), and Dalvi and Patel (2009) and Saleem *et al.* (2010) in rice. Furthermore, hybrid combinations which show non-significant SCA effects (average effects) but originated from parents having high

Table 5: Estimates of SCA effects for various agro-morphological traits in rice (*Oryza sativa* L.) [Data pooled over environments]

Cross combination	Days to 50% flowering	Days to maturity	No. of spikelets panicle ⁻¹	No. of filled grains panicle ⁻¹	Plant height (cm)	Productive tillers plant ⁻¹	Panicle length (cm)	Biological yield plant ⁻¹ (g)	Grain yield plant ⁻¹ (g)	Harvest index (%)	Grain L/B ratio
K-08-59 x Jhelum	-4.56**	-3.53**	16.20**	9.02**	-2.86**	2.11**	1.84**	-8.76**	-4.47**	-3.75**	5.23**
K-08-59 x SKAU-382	-1.28	1.97**	23.84**	19.16**	-2.71**	1.03*	-1.12*	-10.61**	-0.26	3.31**	-3.21**
K-08-59 x SKAU-389	0.34	0.97	5.87*	-13.53**	-9.74**	-1.12*	0.12	-6.52**	-4.45**	-3.50**	-2.95**
K-08-59 x Ch-988	1.22	2.50**	39.80**	16.64**	-5.81**	-0.16	-3.16**	16.68**	-2.49**	-9.22**	0.81
K-08-59 x SR-1	-2.65**	4.42**	-5.94*	-15.77**	-6.66**	-0.80	-1.00	-16.01**	-6.56**	-4.86**	-0.75
K-08-59 x K-08-60	-1.34*	-2.45**	-18.51**	-4.41**	14.99**	1.76**	0.43	9.71**	-1.40*	-4.61**	-4.51**
K-08-59 x K-08-61	-1.29	-2.82**	-3.96	11.08**	3.01**	1.58**	2.34**	19.95**	3.13**	-3.58**	3.52**
K-08-59 x PS-5	-1.38*	-3.30**	13.09**	12.71**	-5.99**	0.73	0.44	-6.31**	7.38**	16.21**	-6.49**
Jhelum x SKAU-382	2.36**	2.15**	-13.17**	-22.16**	-1.61	-1.12*	1.18*	-6.19**	-3.81**	-2.86**	-0.27
Jhelum x SKAU-389	2.82**	3.15**	60.59**	54.23**	-1.48	-0.37	0.69	-0.60	2.33**	2.74*	0.57
Jhelum x Ch-988	-1.63*	-0.15	-11.77**	-6.22**	-14.61	0.63	-1.30*	-17.95**	-5.27**	1.91*	2.91**
Jhelum x SR-1	0.48	1.94**	20.23**	0.34	-1.61	-1.09*	-0.46	7.38**	1.27*	-0.84	1.48*
Jhelum x K-08-60	-2.37**	-1.27	4.34	13.49**	18.71**	1.28*	2.90**	8.71**	10.00**	9.45**	-4.10**
Jhelum x K-08-61	-4.15**	-5.80**	-30.46**	-20.58**	-3.10**	0.43	-1.34*	3.45*	6.15**	7.85**	3.75**
Jhelum x PS-5	5.25**	3.21**	58.15**	37.31**	20.42**	-0.74	1.19*	15.70**	3.68**	-2.06*	-2.51**
SKAU-382x SK-389	2.94**	2.98**	40.04**	24.44**	7.11**	-1.44**	3.04**	-10.48**	-3.30**	-0.06	1.41*
SKAU-382x Ch-988	0.81	-8.32**	-32.46**	-23.12**	-11.02**	-1.83**	2.76**	1.65	4.25**	4.64**	-1.38*
SKAU-382x SR-1	-5.40**	-2.56**	-12.36**	-16.86**	0.25	0.57	1.99**	-1.94	-1.72**	-1.63	7.16**

SKAU-382x K-08-60	-4.41**	-0.77	16.26**	14.01**	3.77**	0.88*	-3.75**	18.18**	-3.76**	-10.16**	-3.64**
SKAU-382x K-08-61	-3.20**	-3.30**	16.26**	14.25**	4.31**	1.18*	-0.19	-12.37**	0.07	7.47**	-2.69**
SKAU-382x PS-5	-0.12	-1.79*	20.53**	30.88**	1.47	2.33**	-1.38*	-1.81	3.22**	4.44**	2.02**
SKAU-389 x Ch-988	-0.06	1.51*	21.73**	12.42**	2.36*	0.17	-1.49*	-3.02*	1.00	2.42*	0.13
SKAU-389 x SR-1	4.06**	-0.73	-5.52*	3.67*	-8.67**	-0.43	-1.08	3.59*	-5.59**	-7.09**	-1.02
SKAU-389 x K-08-60	-1.29	-2.27**	2.22	4.78**	17.01**	-0.06	2.61**	19.19**	8.36**	2.64*	0.44
SKAU-389 x K-08-61	-3.41**	-0.80	-24.56**	-13.24**	-0.61	3.02**	-1.95**	16.98**	4.55**	-0.95	-0.71
SKAU-389 x PS-5	-8.17**	-3.12**	-42.61**	-25.13**	3.84**	-0.35	-0.13	-6.28**	4.68**	8.74**	3.14**
Ch-988 x SR-1	1.10	-1.20	2.69	2.93*	3.28**	0.56	0.06	5.14**	7.14**	7.40**	2.56**
Ch-988 x K-08- 60	-2.08**	-2.91**	-32.62**	-21.12**	4.30**	1.94**	1.65*	-1.20	7.03**	11.13**	-3.10**
Ch-988 x K-08- 61	0.97	0.06	-26.35**	-17.66**	8.43**	-0.16	0.92	-5.04**	-3.90**	-3.95**	-3.47**
Ch-988 x PS-5	-5.79**	-4.92**	2.54	0.24	9.99**	0.44	0.24	11.73**	3.23**	-1.18	0.37
SR-1 x K-08-60	-3.29**	-1.32*	27.63**	29.31**	4.16**	0.92*	-1.79**	10.60**	7.45**	5.75**	-1.41*
SR-1 x K-08-61	-2.42**	-0.18	-21.94**	-9.52**	8.35**	-1.13*	1.25*	4.29**	2.83**	2.58*	-4.99**
SR-1 x PS-5	3.50**	0.83	-17.09**	-15.48**	3.72**	0.77	1.00	-1.61	-9.78**	-12.86**	-6.24**
K-08-60 x K-08- 61	3.41**	2.27**	32.29**	10.88**	-17.45**	-2.06**	-0.47	-9.77**	-9.12**	-11.73**	4.61**
K-08-60 x PS-5	2.15**	2.79**	-8.91**	-20.44**	-14.84**	-1.81**	-0.33	-28.99**	-8.47**	0.20	5.03**
K-08-61 x PS-5	2.03**	5.42**	9.84**	-2.00	11.45**	-0.63	0.05	-14.22**	-4.37**	-0.45	1.28*
S.E $\pm(S_{ij})$	0.66	0.66	2.03	1.28	0.85	0.44	0.56	1.37	0.568	0.94	0.56
S.E $\pm(S_{ij} - S_{ik})$	0.98	0.97	2.99	1.89	1.25	0.65	0.82	2.03	0.837	1.38	0.83
No. of crosses showing desirable SCA effects	13	14	16	18	18	11	11	15	17	15	14

*, ** Significant at 0.05 and 0.01 levels of probability, respectively.

Table 6: Promising crosses in respect of SCA effects, per se performance and GCA effect of parents in rice (*Oryza sativa* L.) [Pooled data]

Character	Promising parents in respect of		GCA effect of parents	Character	Promising parents in respect of		GCA effect of parents
	Per se performance	SCA effects			Per se performance	SCA effects	
Days to 50% flowering	SKAU-382 x SR-1 (106)	SKAU-389 x PS-5 (-8.170)	good x poor	Panicle length (cm)	SKAU-389 x K-08-60 (26.11)	SKAU-382 x SKAU-389 (3.042)	average x average
	K-08-59 x Jhelum (106.5)	Ch-988 x PS-5 (-5.791)	good x good		Jhelum x K-08-60 (25.7)	SKAU-382 x Ch-988 (2.763)	average x poor
	K-08-59 x SR-1 (108.5)	SKAU-382 x SR-1 (-5.397)	good x poor		SKAU-382 x SKAU-389 (25.67)	SKAU-389 x K-08-60 (2.609)	average x good
	K-08-59 x SKAU-382 (108.67)	SKAU-382 x K-08-60 (-4.412)	good x poor		Jhelum x PS-5 (24.45)	Jhelum x K-08-60 (2.898)	poor x good
	SKAU-389 x PS-5 (110.16)	SKAU-389 x K-08-6 (-3.412)	good x poor		SR-1 x PS-5 (24.38)	K-08-59 x K-08-61 (2.341)	average x good
Days to maturity	K-08-59 x Jhelum (135.83)	SKAU-382 x Ch-988 (-8.318)	good x good	Biological yield Plant ⁻¹ (g)	SKAU-389 x K-08-60 (100.67)	K-08-59 x K-08-61 (19.949)	Poor x poor
	Jhelum x K-08-61 (136.33)	Jhelum x K-08-61 (-5.803)	good x poor		SKAU-382 x K-08-60 (92.73)	SKAU-389 x K-08-60 (19.196)	Good x good
	SKAU-382 x SR-1 (136.5)	Ch-988 x PS-5 (-3.121)	good x poor		Jhelum x PS-5 (87.90)	SKAU-382 x K-08-60 (18.182)	Good x good
	Ch-988 x PS-5 (137)	K-08-59 x Jhelum (-3.530)	good x good		SKAU-389 x SR-1 (87.5)	SKAU-389 x K-08-60 (16.981)	Good x poor
	SKAU-382 x K-08-61 (137.33)	K-08-59 x PS-5 (-3.303)	good x poor		SK-389 x KO8-61 (87.41)	K-08-59 x Ch-988 (16.684)	Poor x good
Number of spikelet's panicle ⁻¹	Jhelum x PS-5 (232.33)	Jhelum x SKAU-389 (60.586)	good x good	Grain yield Plant ⁻¹ (g)	SKAU-389 x K-08-60 (34.5)	Jhelum x K-08-60 (10.001)	Good x poor
	Jhelum x SKAU-389 (231.58)	Jhelum x PS-5 (58.152)	good x good		Jhelum x K-08-60 (33.3)	SKAU-389 x K-08-60 (8.365)	Good x poor
	K-08-60 x K-08-61 (212.21)	SKAU-382 x SKAU-389 (40.044)	good x average		SKAU-389 x PS-5 (31.40)	SR-1 x K-08-60 (7.445)	Poor x average
	SKAU-382 x SKAU-389 (210.75)	K-08-59 x Ch-988 (39.797)	poor x poor		Jhelum x SKAU-389 (31.26)	K-08-59 x PS-5 (7.379)	Good x good
	SKAU-382 x PS-5 (202.41)	K-08-60 x K-08-61 (32.289)	good x good		Ch-988 x SR-1 (30.06)	Ch-988 x SR-1 (7.138)	

Number of filled grains panicle ¹	Jhelum x SKAU-389 (188.18)	Jhelum x SKAU-389 (54.231)	good x good	Harvest index (%)	SKAU-389 x PS-5 (43.01)	K-08-59 x PS-5 (16.214)	Poor x good
	Jhelum x PS-5 (176.16)	Jhelum x PS-5 (37.305)	good x good		Ch-988 x K-08-61 (28.52)	Ch-988 x K-08-60 (11.134)	Good x poor
	SKAU-382 x PS-5 (170.16)	SR-1 x K-08-60 (29.314)	poor x good		Jhelum x K-08-61 (40.29)	Jhelum x K-08-60 (9.451)	Good x poor
	SKAU-382x SKAU-389(158.81)	SKAU-382 x SKAU-389(24.440)	good x good		Jhelum x K-08-60 (40.20)	SKAU-389 x PS-5 (8.736)	Good x good
	SKAU-382 x K-08-60 (156.96)					Ch-988 x SR-1 (7.401)	
Plant height (cm)	SKAU-389 x K-08-60 (144.3)	Jhelum x PS-5 (20.425)	average x poor	Grain L/B ratio	K-08-60 x PS-5 (4.06)	SKAU-382 x SR-1 (7.157)	Poor x poor
	Jhelum x PS-5 (143.63)	SKAU-389 x K-08-60 (17.014)	average x poor		K-08-60 x K-08-61 (3.86)	K-08-59 x Jhelum (5.234)	Good x poor
	Jhelum x K-08-60 (139.16)	K-08-59 x K-08-60 (14.991)	good x average		K-08-59 x K-08-61 (3.50)	K-08-60 x PS-5 (5.030)	Good x good
	SKAU-382 x SKAU-389 (136.71)	K-08-61 x PS-5 (11.446)	poor x average		SKAU-389 x PS-5 (3.45)	K-08-60 x K-08-61(4.607)	Poor x good
	SKAU-389 x PS-5 (133.88)		poor x poor			SKAU-389 x PS-5 (3.145)	
Number of productive tillers Plant ¹	SKAU-389 x K-08-61 (16.75)	SKAU-389 x K-08-61(3.016)	poor x average				
	K-08-59 x Jhelum (16.65)	SKAU-382 x PS-5 (2.335)	poor x average				
	K-08-59 x SKAU-382 (15.63)	K-08-59 x Jhelum (2.106)	poor x average				
	Ch-988 x K-08-60 (16.15)	Ch-988 x K-08-60 (1.944)	average x poor				
	K-08-59 x SKAU-382 (15.63)	K-08-59 x K-08-60 (1.765)	good x average				



GCA effects (additive gene effects) can be used for recombination breeding with easy selection of desirable segregants. The number of such hybrid combinations in the present study was however low.

Conclusion

Presence of both additive and non-additive variances with preponderance of latter for most of the traits reveals the emphasis on hybrid rice breeding programme by transferring elite CMS from different sources. Parents SKAU-389, Jhelum, SKAU-382 and SR-1 were good general combiners for grain yield and other important traits suggest a multiple crossing programme to derive superior genotypes as varieties or parents in future for hybrid rice breeding programme. Detection of genotype x environment interaction for different traits emphasizes the need for multi-environment testing of the material to help draw valid conclusions and identify cultivars for specific agro-ecological situations.

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