Gene action and standard heterosis over environments in Rice (*Oryza sativa* L.)

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Abstract
The present study on genetic components of variance carried over individual and pooled environments for thirteen metric traits in rice revealed the greater magnitude of dominance component than corresponding additive component of variance, thereby showing greater role of dominance in genetic control for most of the traits. The net dominance effect ($\hat{h}^2$) was positively significant for the traits plant height, productive tillers per plant, spikelets per panicle, days to flowering and maturity. The $\hat{F}$ estimate was non-significant for all the traits studied. The proportion of $\hat{H}_2/4\hat{H}_1$ was less than 0.25 for all the traits. The proportion of dominance and recessive alleles (KD/KR) in the parents was greater than one for majority of the traits suggesting preponderance of dominance alleles. The study on genetic ratios revealed that proportion of average degree of dominance measured from genetic components of variance ($\hat{H}_1/\hat{D}$)$^{1/2}$ was more than unity. The estimates of $\hat{h}^2/\hat{H}_2$ were more than 0.50 for most of the characters. Low narrow sense heritability estimates were recorded for most of the traits.Thirteen cross combinations demonstrated the maximum manifestation of standard heterotic effect for grain yield plant^{-1} over check varieties Jhelum and Shalimar Rice-1. The magnitude of heterosis over Jhelum and Shalimar Rice-1 ranged from -56.07 to 35.21% and -62.69 to28.29%, respectively. The most promising cross combinations for grain yield plant^{-1} in order of merit over standard checks Jhelum and Shalimar Rice-1 included SKAU-389 x K-08-60 (35.21 and 28.29%), Jhelum x K-08-60 (32.22 and 26.20%), SKAU-389 x Pusa Sugandh-5 (30.74 and 24.14%), Jhelum x SKAU-389 (29.07 and 22.58%) and China-988 x Shalimar Rice-1 (27.08 and 22.49%). Further, these crosses revealed high heterosis in desirable direction for other economically important traits.

Key words:
Rice, Environment, gene action, heritability, standard heterosis

Introduction:
Rice (*Oryza sativa* L.) is a major food grain crop and staple food of Kashmir. The demand for rice continues to rise because of population growth and improvement in living standards. In last two decades, a number of high yielding varieties were developed and have achieved popularity in the farming community because of being high yielding, early maturing, cold tolerant and easy threshing. However, a yield plateau has been experienced for the last few years together with absence of scope for horizontal growth. Therefore, to devise a breeding methodology to unfold the genetic information for various metric traits is prerequisite. The knowledge of nature and magnitude of gene actions involvedin different quantitative traits is thus necessary for reorientation of breeding methodologies on systematic lines so that a breeder can come to the logical conclusion. The combining ability analysis gives an indication of the variance due to general and specific combining ability 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 potentialities of parent in hybrid combinations.To break the yield barriers, in the non existence of scope through horizontal growth, the development of hybrid rice is being realized as a felt need. Hybrid rice technology offer an opportunity for vertical growth through increase in productivity due to yield advantage of 15-20% over the conventional high yielding varieties (Virmani, 1996). Two temperate early, cold tolerant CMS lines SKAU-7A and SKAU-11A have been developed by SKUAST-Kashmir, but the effective restoration is still the concern. The present investigation was conducted under two diverse sets of environmental conditions to draw the valid inferences regarding the tested genotypes with respect to nature and magnitude of gene effects involved in inheritance of yield and yield attributes traits and to estimate standard heterosis among a wide array of cross combinations.

Material and methods
The present investigation was conducted during *Kharif* 2011 and 2012 at the Mountain Research Centre for Field Crops, Khudwani of Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir. In this study 36 F$_1$s were generated through half diallel by crossing nine

genotypes 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 in all possible combinations excluding reciprocals during 2011. In order to achieve good synchrony of the 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. During *kharif* 2012, 36 F1s, 9 parents and two standard checks were evaluated separately using randomized complete block design with three replications at two locations viz., Mountain research centre for Field Crops, Khudwani, Anantnag (1480 m amsl) and research Farm Of *Krishi Vighyan Kendra*, Kulgam(2000 m amsl). Jhelum and SR-1 were used as standard checks. Each experimental plot in all replication had two rows of 1m length with inter row 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 (which included N:P:K::120:60:40 kg per hectare) were followed. The observations were recorded for 13 metric traits viz., days to 50% flowering, days to maturity, number of spikelets panicle^{-1}, number of filled grains panicle^{-1},panicle length(cm), number of productive tillers plant^{-1}, plant height(cm), biological yield plant^{-1}(g), grain yield plant^{-1}(g), harvest index(%), grain length(mm), grain breadth(mm) and grain L/B ratio. The genetic components of variance, heterosis for individual and pooled data was computed through Hayman's numerical approach (1954) using *WINDOWSTAT* software.

Results and Discussions

Analysis of variance revealed significant mean squares in favour of the environments for all the characters (Table-1). Highly significant differences were found among the parents and the resulting F1s for most of the traits except grain length, grain breadth and length/breadth ratio for the individual environments and data pooled over environments, indicating that the material selected was diverse for all the traits that in turn resulted in substantial genetic variability in the crosses. The genotype x environment, parents x environments, crosses x environments and parents x crosses x environments interaction components were found significant for most of the traits, indicating that the genotypes behaved differentially under diverse environments. The analysis of variance reflected presence of adequate diversity in the genetic material chosen for the present study. Jarwar *et al.* (2012) reported significant differences among parents, hybrids and hybrids versus parents for most of the agronomic characters in rice hybrids evaluated over environments.

The studyon genetic components of variance estimated over individual environments and pooled

over environments revealed that additive component of genetic variance ($\hat{D}$) was significant for all the traits except for number of productive tillers plant^{-1}, harvest index and grain breadth. Whereas, measures of dominance component ($\hat{H}_1$ and $\hat{H}_2$) were significant for all the traits studied. This denoted the involvement of both of the components in the inheritance of those traits, however the greater magnitude of latter components of variance confirmedpredominant role of dominance in genetic control of those traits which was also established while estimating variance arising due to dominance deviation through combining ability analysis. The information regarding the distribution of alleles in the parents revealed that positive and negative alleles at different loci were not in equal proportion in parents as $\hat{H}_1$ exceeded $\hat{H}_2$ and dominance gene action resulted mainly from positive gene action (Table-2, 3).Narasimman *et al.* (2007b) and Kumar *et al.* (2011) also reported significant estimates of D (additive genetic variance) for most the traits studied.Further the values of H$_1$ and H$_2$ as well as H$_2$/4H$_1$ indicated that there were unequal frequencies of the alleles at all the loci.The net dominance effect ($\hat{h}^2$) was significant and positive for several traits except for spikelet fertility, number of filled grains panicle^{-1}, panicle length, biological yield plant^{-1}, grain yield plant^{-1}, harvest index, grain length and grain breadth indicating significant dominance effect withpositive direction over all loci in heterozygotes. The non-significant and positive value of $\hat{h}^2$ exhibited by all the above mentioned characters [except biological yield plant^{-1} were the value was negative] pointed out that the variance due to dominance deviation resulted from both dominant and recessive alleles which were equally distributed in the parents. The value of $\hat{F}$ estimate was positive and non-significant for all the traits studied except for biological yield plant^{-1} and grain breadth thus revealing contribution of more recessive alleles towards variance due to dominance deviation. On the contrary, the value of $\hat{F}$ estimate was positive and significant for grain length and grain length/breadth ratio revealing higher frequency of dominant alleles in the parents for these traits.

The dominance was due to high heterozygosity in F$_1$ indicating that parents selected were diverse. However, the discrepancy in the degree of dominance estimated from genetic components resulted mostly from G x E interaction or from sampling error, which subsequently had an influence on the estimation of genetic components. The study of proportion of various genetic components of variances revealed that the

proportion of $\hat{H}_2/4\hat{H}_1$ was less than 0.25 for all the traits revealing asymmetrical gene distribution in the parents. Mather and Jinks (1982) suggested that due to unequal gene distribution (if u = v≠ 0.5, $\hat{H}_2/4\hat{H}_1 \neq 0.25$) $\hat{H}_1$ gets inflated from $\hat{H}_2$ and results in the overestimation of dominance. Secondly the component $\hat{D}$ gets deflated in the process of additive x dominance (j type) epistasis (Pooni et al., 1984) which in turn causes inflation in the average degree of dominance. Overdominance in most of the cases may result from a particular combination of positive and negative genes or complementary type of gene action due to correlated gene distribution, which may seriously inflate mean degree of dominance and convert partial dominance into apparent overdominance (Hayman, 1954).

The genetic ratio KD/KR which gives the proportion of dominance and recessive alleles in the parents was greater than 1.0 for all the traits except grain length and grain breadth, suggesting preponderance of dominant alleles. The estimates of $\hat{h}^2/\hat{H}_2$ were more than 0.50 for most of the traits except grain length and grain breadth indicating greater proportion of dominant groups of genes for these traits and more of recessive groups of genes for the remaining ones. Any linkages among the genes reduce the estimate of an amount proportional, irrespective of its phase, to intensity of linkage. Genes lying nearer to one another on the chromosome tend to appear in a same unit of segregation whose base is thus not a single locus, but a piece of chromosome termed as effective factor (Mather and Jinks, 1982). The study of proportion of average degree of dominance measured from genetic components of variance $(\hat{H}_1/\hat{D})^{1/2}$ was more than unity thus revealing over-dominance range for all traits under study. Asymmetrical distribution of genes in the parents with importance of dominant and recessive genes has also been reported for various traits by Kumar et al. (2008). Iftekharuddaula et al. (2009) reported unequal distribution of dominant and recessive genes in parents for the characters primary branches panicle[-1] and unfilled grains/secondary branch. Raju et al. (2011) also stated that the proportion of dominant and recessive genes and genes with positive and negative effects were not in symmetry as per the estimates of H₂/4H₁ and KD/KR.

Low narrow sense heritability estimates were observed for most of the traits and was less than 0.5 except for days to 50% flowering(0.5), number of filled grains per panicle(0.5),grain length(0.6) and grain L/B ratio(0.52) indicated that in the present set of materials the genes were showing non-additive gene action and consequently,

isolation of high yielding lines would not be viable unless the non-allelic interactions and/or linkages are not dissipated through a selection procedure which can slow down the rate of attaining homozygosity in the segregating generations. Low estimates of heritability in rice have been described by several workers for sterility percentage, productive tillers hill[-1] and grain breadth (Chakraborty et al. 2009) and for number of panicles plant[-1], plumped number of grains panicle[-1], total number of grains panicle[-1] and grain weight plant[-1] (Zhou et al., 2010). Kumar et al. (2011) also reported low estimates of narrow sense heritability for eight characters he studied. Contrarily, high estimates of heritability (narrow sense) for maturity traits, morphological traits, yield and its component traits have been reported earlier by several workers for days to 50% flowering, days to maturity, plant height, and length of panicle (Kumar et al. 2008), for days to 50% flowering, grain yield hill[-1], plant height, grains panicle[-1](Chakraborty et al. 2009), and for panicle length (Gupta and Salgotra, 2006). Narasimman et al. (2007) also reported low estimates for seven and high for nine out of 16 characters studied in rice. Since the experiment was carried out over two diverse environmentsand probably might have reduced the influence due to G x E interaction. Kempthorne (1956) observed that heritability estimates would be biased upwards by the presence of G x E interaction, linkages and/or epistasis. Robinson et al. (1949) observed that differential response of genotype under different environments tended to reduce the heritability estimates and these estimates are also biased upwards if linkage disequilibrium and/or epistasis are present. The variation in the estimates of heritability usually arises because of the choice of reference population, plot size, planting density, number of replications and methods of estimation. Thus, the comparison of estimates obtained by different workers must be treated with caution (Robinson, 1963).

The second part of the study was to demonstrate the hybrid vigour or heterosis of number of cross combinations and estimates were computed for data pooled over environments. The estimates were compared against standard checks Jhelum and Shalimar Rice-1(SR-1) the most popular varieties grown on larger areas across Kashmir valley. The results revealed that wide range of heterotic patterns for all the traits studied. None of the cross combination recorded significant standard heterosis simultaneously for all the traits. These results are in agreement with the findings of Virmani et al. (1997); Tiwari et al. (2011); and Kumar et al. (2012). Heterosis for grain yield along with its components is very important consideration in heterosis breeding. In the present investigation thirteen cross combinations demonstrated the maximum manifestation of

standard heterotic effect for grain yield plant[-1] over check varieties Jhelum and SR-1 namely, Jhelum x SK-389, Jhelum x K-08-60, Jhelum x K-08-61, Jhelum x PS-5, SKAU-382 x SK-389, SKAU-382 x PS-5, SK-389 x Ch-988, SK-389 x K-08-60, SK-389 x K-08-61, SK-389 x PS-5, Ch-988 x SR-1, Ch-988 x K-08-60 and SR-1 x K-08-60. Further few more combinations were identified that showedsignificant and desirable heterosisover *Jhelum* only. On totality the spectrum of heterosis ranged from -56.07 to 35.21% over standard check *Jhelum* whileas, magnitude ranged between -62.69 to 28.29% over check SR-1. Among these the best cross combinations in order of merit in comparison to *Jhelum* and *SR-1* were SKAU-389 x K-08-60 (35.21 and 28.29%), Jhelum x K-08-60 (32.22 and 26.20%), SKAU-389 x PS-5 (30.74 and 24.14%), Jhelum x SKAU-389(29.07 and 22.58%) and China-988 x SR-1 (27.08 and 22.49%) (Table-4). The significant findings regarding standard heterosis were reported by various workers and observed more than 20% for grain yield over standard variety. Kumar *et al*. (2010) estimated standard heterosis for grain yield in the range of 22.59 to 65.32 %. Dwivedi and Pandey, (2012) reported heterosis over standard variety for grain yield in rice ranging between -64.55 to 146.15 %. Kumar *et al*. (2012) observed high standard heterosis for yield and its components.

The most promising cross combination for grain yield plant[-1]SKAU-389 x K-08-60 also revealed significant and desirable level of standard heterosis in comparison to both the standard varieties for number of spikelet panicle[-1], number of filled grains panicle[-1], plant height, panicle length, biological yield plant[-1], grain length and grain length/breadth ratio. The second most enviable cross for grain yield plant[-1]i.e. Jhelum x K-08-60 also proved significantly superior over both the check varieties for days to 50% flowering(early flowering), number of spikelets panicle[-1], number of filled grains panicle[-1], plant height, number of productive tillers plant[-1], panicle length, biological yield plant[-1], and harvest index. Other heterotic crosses for grain yield plant[-1] were also recorded significantly desirable for most of the other yield contributing traits (Table-4). Heterosis for maturity and other important yield components were both in positive and negative direction. Similar kinds of observations were also reported by Neelam *et al*. (2009) and Tiwari *et al*. (2011) for various yield components and other traits. Promising combinations for grain yield plant[-1] and all other contributing traits are given in Table-5.Malini *et al.* (2006) found standard heterosis for grain yield plant[-1]ranging from -73.71 to 129.16. Most of the hybrid combinations showed standard heterosis and heterobelitiosis for panicle length, spikelets panicle[-1], grains panicle[-1], straw yield and grain yield. Parihar and Pathak, (2008) found standard heterosis exceeding 20 % for grain yield plant[-1],

plant height, effective tillers plant[-1], 1000-grain weight, grains panicle[-1] and harvest index in rice.

Generally, long panicle is associated with high number of grains panicle[-1], results into higher product, therefore positive heterosis for panicle length is highly desirable. In the present study crosses K-08-59 x K-08-61, Jhelum x K-08-60, Jhelum x PS-5, SKAU-382 x SKAU-389, SKAU-382 x Ch-988, SKAU-382 x SR-1, SKAU-389 x K-08-60, SKAU-389 x PS-5, Ch-988 x K-08-60, SR-1 x PS-5 and K-08-60 x PS-5 were found to have significant heterosis for panicle length when compared to both the standard varieties. Further, many more cross combinations were identified positively heterotic for panicle length over standard check *Jhelum* and among them five promising combinations were SKAU-389 x K-08-61 (23.39%), Jhelum, K-08-60 (21.42%), SKAU-382 x SKAU-389 (21.26%), Jhelum x PS-5 (15.51%) and SKAU-382 x China-988 (15.28%)(Table-5). Singh *et al*. (1998) reported both positive and negative heterosis for panicle length. The taller rice genotypes are the most preferred due to due to their high economical use. It is being preservedfor the chilling winters and fed to livestock because of the fact the entire valley remains under the snow cover for three consecutive months. Further the demand of the straw has moved up because of its use as packaging material in the apple boxes. In this regard 15 combinations were found desirable for height as compared to both the standard checks, and in addition few more combinations proved heterotic over *Jhelum* only. The top five hybrid combinations in comparison to *Jhelum* were SKAU-389 x K-08-60 (18.04%), Jhelum x PS-5 (17.49%), Jhelum x K-08-60 (13.84%), SKAU-382 x SKAU-389 (11.83%) and SKAU-389 x PS-5 (9.52%). Promising combinations for grain yield and other contributing traits against the best standard check are given in Table-5.Virmani *et al.* (1981, 1982) have observed positive heterosis for number of spikelets panicle[-1], they concluded that standard heterosis in yield was primarily due to increased number of spikelets panicle[-1]. This result is in quite supporting with findings of current study as most of the crosses revealed desirable heterosis for this trait and among them five promising combinations over the best check were K-08-60 x K-08-61 (20.16%), SKAU-382 x SKAU-389 (19.20%), K-08-59 x SKAU-382 (18.83%), K-08-61 x PS-5 (18.76%) and Jhelum x PS-5 (18.44%) respectively. Furthermore, more panicle bearing tillers plant[-1] is believed to be closely associated with high yield potential. Fifteen desirable combinations for the trait were reported in this experiment and the most promising one over the best standard check was SKAU-389 x K-08-61 (33.11%) followed by K-08-59 x Jhelum (32.32%), K-08-59 x K-08-60 (30.99%), China-988 x K-08-60 (28.34%) and K-08-59 x SKAU-

382, (24.24%) (Table-5). Positive heterosis for productive tillers plant[-1] has been revealed by Neelam *et al*. (2009). Besides these yield contributing traits, both negative and positive heterosis was recorded for these cross combinations for traits like grain length and grain breadth which is in quite accordance with the findings of Rahimi *et al*. (2010).

The identified five promising heterotic cross combinations for grain yield plant[-1] and other yield contributing characters together with early maturity may be tested under across location in the target environments to verify their suitability for commercial purpose.

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Table 1: Analysis of variance for various agro-morphological traits in rice (*Oryza sativa* L.) [Pooled data]

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 length (mm)	Grain breadth (mm)	Grain L/B ratio
Environments (E)	1	171.20**	469.39**	3884.37**	4254.65**	232.04**	394.34**	346.35**	755.34**	181.55**	62.78**	2.86	0.23	4.69
Replications	1	-	-	-	-	-	-	-	-	-	-	-	-	-
Replications within Env.	2	8.03*	19.38**	44.84**	86.64**	1.72	4.05*	0.70	39.95*	28.02**	71.76**	4.31	10.03	0.81
Genotypes (G)	54	136.41**	71.47**	7548.35**	4262.93**	665.35**	11.87**	21.57**	1086.31**	273.72	333.58**	301.58**	51042**	145.87**
Parents (P)	9	151.46**	88.16**	6559.40**	2920.28**	582.61**	6.06**	16.10**	984.69**	175.75**	97.03**	555.21**	26.20**	249.68**
Crosses (C)	44	120.14**	67.15**	7612.77**	4559.57**	661.23**	12.39**	22.65**	1140.32**	301.99**	392.76**	250.66**	55.82**	121.29**
P vs C	1	557.57**	88.98**	13205.51**	4621.48**	1471.40**	40.41**	27.52**	8.82	68.10**	154.68**	54.94**	98.77**	175.77**
G x E	54	10.14**	22.35**	18.37**	23.94**	22.65**	8.52**	11.69**	18.12**	11.93**	19.65**	1.49	1.27	1.34
P x E	9	14.18**	19.21**	21.14**	29.53**	15.50**	6.57**	9.11*	26.83**	9.08**	11.64**	2.15	2.10	1.09
C x E	44	11.61**	12.38**	25.07**	18.67**	19.70**	5.48**	7.84**	13.12**	8.92**	26.93**	1.82	1.32	1.43
P x C x E	1	4.48	4.24	2.32	2.09	5.06	2.15	2.06	9.04	4.01	8.06	3.17	2.04	0.30
Pooled error	108	3.17	3.11	7.49	5.16	1.64	2.27	1.29	8.54	2.31	4.31	2.29	4.58	2.28

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

Table- 2: Estimates of genetic parameters for various agromorphological traits in rice (*Oryza sativa* L.) over individual and pooled data

G. Parameters	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 length (mm)	Grain breadth (mm)	Grain L/B ratio
$\hat{D}$	**24.28*±3.74**	**13.61*±2.40**	**1084.10*±332.32**	**482.63*±206.02**	**95.52*±36.25**	**0.58±0.52**	**2.34*±1.19**	**160.36*±51.58**	**28.48*±14.48**	**13.73±13.52**	**0.91*±0.07**	**0.001±0.06**	**0.41*±0.04**
	27.55*	13.77*	1130.93*	504.49*	100.54*	0.73	2.54*	170.39*	29.49*	11.84	0.91*	0.001	0.43*
	21.14*	13.37*	1125.32*	461.79*	90.44*	0.52	1.90*	150.03*	27.53*	15.53	0.93*		0.39*
$\hat{H}_1$	**45.04*±8.25**	**31.41*±5.30**	**3830.39*±733.49**	**2085.58*±454.76**	**442.87*±80.02**	**6.77*±1.15**	**10.52*±2.62**	**678.22*±113.84**	**138.68*±31.97**	**202.26*±29.84**	**0.97*±0.16**	**0.20*±0.13**	**0.49*±0.09**
	49.17*	32.08*	3948.91*	2147.26*	459.69*	8.05*	10.08*	741.33*	147.35*	206.33*	1.01*	0.19*	0.54*
	41.08*	30.77*	3943.25*	2027.45*	426.33*	6.00*	11.23*	622.55*	130.77*	200.00*	0.93*		0.45*
$\hat{H}_2$	**41.89*±7.10**	**28.18*±4.56**	**2847.67*±630.54**	**1601.06*±390.93**	**359.73*±68.79**	**5.95*±0.99**	**10.04*±2.25**	**557.91*±97.86**	**116.95*±27.48**	**170.63*±25.64**	**0.78*±0.14**	**0.23*±0.12**	**0.46*±0.07**
	46.27*	29.57*	2941.71*	1641.47*	373.79*	6.93*	9.42*	594.16*	124.05*	172.64*	0.82*	0.21*	0.51*
	37.81*	28.24*	2940.36*	1563.17*	345.91*	5.34*	11.04*	526.82*	110.50*	170.07*	0.76*		0.42*
$\hat{h}^2$	**40.41*±4.75**	**6.08*±3.05**	**962.50*±42.40**	**336.49±261.89**	**107.02*±46.08**	**2.79*±0.66**	**1.78±1.51**	**-0.84±65.56**	**4.66±18.41**	**10.35±17.18**	**0.04±0.09**	**0.05±0.08**	**0.13*±0.05**
	44.62*	6.76*	987.27*	346.70	108.28*	3.83*	1.98	-1.59	4.56	9.83	0.01	0.05	0.13*
	36.31*	5.38*	983.64*	326.12	105.68*	1.86*	1.48	-0.83	4.65	10.76	0.07		0.12*
$\hat{F}$	**1.88±8.73**	**6.42±5.60**	**723.85±775.24**	**163.10±480.65**	**117.02±84.58**	**0.45±1.22**	**0.24±2.77**	**158.15±120.32**	**4.95±33.79**	**1.98±31.53**	**0.48*±0.17**	**-0.05±0.14**	**0.19*±0.09**
	0.57	6.62	722.85	192.75	122.06	0.73	0.60	184.60	6.09	0.59	0.46*	-0.06	0.17*
	2.84	6.06	720.55	134.97	111.88	0.36	-0.51	150.03	4.00	3.45	0.51*		0.20*
$\hat{E}$	**0.96±1.18**	**1.08±0.76**	**9.13±105.09**	**4.08±65.16**	**1.58±11.46**	**0.43*±0.16**	**1.00±0.37**	**3.75±16.31**	**0.81±4.58**	**2.44±1.27**	**0.01±0.02**	**0.04*±0.02**	**0.01±0.01**
	1.22	1.12	11.75	4.71	1.77	0.51*	0.56	5.46	0.83	2.60	0.02	0.04*	0.01
	0.97	1.20	10.51	4.27	1.62	0.46*	0.90	3.96	1.09	2.57	0.01		0.01

*, ** Significant at 0.05 and 0.01 levels of probability, respectively. Bold figures are for pooled data and figures in normal font are for E₁ and E₂ respectively

Table 3: Estimated genetic ratios for various agromorphological traits in rice (*Oryza sativa* L.). [over individual and pooled data]

Genetic Ratio	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 length (mm)	Grain breadth (mm)	Grain L/B ratio
$(\hat{H}_1/\hat{D})^{1/2}$	**1.36**	**1.52**	**1.88**	**2.08**	**2.15**	**3.41**	**2.24**	**2.06**	**2.23**	**3.84**	**1.03**	**14.60**	**1.09**
	1.33	1.53	1.87	2.06	2.14	3.33	1.99	2.09	2.23	4.17	1.06	14.98	1.11
	1.39	1.51	1.82	2.09	2.17	3.41	2.83	2.04	2.18	3.59	1.00	7.51	1.08
$\hat{H}_2/4\hat{H}_1$	**0.23**	**0.23**	**0.19**	**0.19**	**0.20**	**0.22**	**0.24**	**0.21**	**0.21**	**0.21**	**0.20**	**0.29**	**0.23**
	0.23	0.23	0.19	0.19	0.20	0.22	0.23	0.20	0.21	0.21	0.20	0.28	0.23
	0.23	0.23	0.21	0.19	0.20	0.22	0.25	0.21	0.21	0.21	0.20	0.29	0.22
$\dfrac{KD}{KR}$	**1.06**	**1.37**	**1.43**	**1.18**	**1.79**	**1.26**	**1.05**	**1.63**	**1.08**	**1.04**	**0.68**	**-0.34**	**1.52**
	1.02	1.37	1.41	1.20	1.79	1.35	1.13	1.70	1.10	1.01	0.64	-0.33	1.43
	1.10	1.35	1.38	1.15	1.80	1.22	0.88	1.55	1.07	1.06	0.75	-0.06	1.63
$\hat{h}^2/\hat{H}_2$	**0.96**	**0.61**	**0.74**	**0.70**	**0.65**	**0.57**	**0.58**	**0.78**	**0.78**	**0.62**	**0.05**	**0.24**	**0.67**
	0.96	0.53	0.61	0.81	0.69	0.55	0.69	0.71	0.84	0.68	0.01	0.21	0.62
	0.96	0.59	0.63	0.76	0.71	0.65	0.61	0.86	0.80	0.64	0.11	0.27	0.58
Heritability (n.s)	**0.53**	**0.37**	**0.48**	**0.50**	**0.25**	**0.20**	**0.27**	**0.30**	**0.43**	**0.32**	**0.60**	**0.11**	**0.52**
	0.54	0.36	0.37	0.50	0.25	0.21	0.31	0.30	0.42	0.33	0.59	0.11	0.52
	0.51	0.37	0.37	0.50	0.25	0.20	0.22	0.29	0.43	0.31	0.60	0.11	0.50

*, ** Significant at 0.05 and 0.01 levels of probability, respectively. Bold figures are for pooled data and figures in normal font are for E$_1$ and E$_2$ respectively

Table- 4:Estimates of heterotic effects over standard checks for various agro-morphological traits in rice (*Oryza sativa* L.)[Pooleddata]

Cross Combinations	Days to 50% flowering		Days to maturity		No. of spikelet's panicle⁻¹		No. of filled grains panicle⁻¹		Plant height (cm)		Productive tillers plant⁻¹		Panicle length (cm)	
	Jhelum	SR-1	Jhelum	SR-1	Jhelum	SR-1	Jhelum	SR-1	Jhelum	SR-1	Jhelum	SR-1	Jhelum	SR-1
K-08-59 x Jhelum	-4.63**	-7.66**	-2.73**	-3.40**	17.95**	14.01**	18.42**	12.91**	-1.69	-6.42**	40.51**	32.32**	16.11*	7.24
K-08-59 x SKAU-382	-2.69*	-5.78**	2.92**	1.20	20.84**	18.83**	19.15**	16.53**	-0.69	-5.47**	31.93**	24.24**	3.41	-4.49
K-08-59 x SKAU-389	0.15	-3.03*	3.05**	1.32	15.87**	13.46**	7.99**	-5.05*	-1.73	-6.46**	17.02*	10.20	10.83	2.36
K-08-59 x Ch-988	0.75	-2.46	2.92**	1.20	14.26**	10.35**	7.85**	-5.17*	-4.02*	-8.64**	24.05**	16.82*	-10.91	-17.72**
K-08-59 x SR-1	-2.84*	-5.92**	5.12**	3.35**	7.14	-2.30	-15.41**	-25.62**	-2.88	-7.55**	16.17*	9.40	2.22	-5.59
K-08-59 x K-08-60	1.94	-1.30	1.95	0.24	12.88**	10.61**	16.31**	11.06**	12.40**	6.99**	39.10**	30.99**	15.86*	7.01
K-08-59 x K-08-61	1.79	-1.45	1.71	0.00	14.99**	12.63**	18.00**	14.31**	-1.58	-6.31**	31.93**	24.24**	21.74**	12.44*
K-08-59 x PS-5	3.13*	-0.14	1.95	0.24	17.86**	15.04**	17.23**	13.30**	-3.27*	-7.92**	22.50**	15.38*	18.24**	9.21
Jhelum x SKAU-382	1.79	-1.45	3.17**	1.44	18.39**	15.19**	10.25**	-0.42	3.95*	-1.05	6.75	0.53	18.16**	9.13
Jhelum x SKAU-389	3.58**	0.29	4.75**	2.99**	20.23**	17.51**	20.14**	18.28**	9.35**	4.09**	16.32*	9.54	16.79**	7.87
Jhelum x Ch-988	-0.60	-3.76**	1.10	-0.60	3.27	-5.82	0.86	-11.32**	-7.59**	-12.04**	23.77**	16.56*	1.53	-6.22
Jhelum x SR-1	1.19	-2.02	3.41**	1.68	15.69**	12.12**	11.94**	3.70	5.46**	0.38	6.75	0.53	7.93	-0.31
Jhelum x K-08-60	2.24**	-1.01	2.92**	1.20	20.55**	17.41**	18.00**	15.01**	19.59**	13.84**	27.99**	20.53**	31.46**	21.42**
Jhelum x K-08-61	0.45	-2.75*	-3.37**	-4.04**	12.78**	8.32*	10.91**	0.15	-2.84	-7.51**	15.75	9.01	5.88	-2.20
Jhelum x PS-5	10.30**	6.79**	6.82**	5.03**	19.23**	18.44**	22.37**	19.35**	23.43**	17.49**	3.09	-2.91	25.06**	15.51**
SKAU-382 x SK-389	2.69*	-0.58	4.26**	2.51*	22.13**	19.20**	19.21**	17.55**	17.49**	11.83**	7.88	1.59	31.29**	21.26**
SKAU-382 x Ch-988	0.60	-2.60*	0.61	-5.08**	-14.96**	-22.45**	16.20**	12.32**	-3.75*	-8.38**	3.52	-2.52	24.81**	15.28**
SKAU-382 x SR-1	-5.07**	-8.09**	-1.24	-5.92**	10.12**	4.07	0.57	-11.57**	7.81**	2.62	21.24**	14.17	22.93**	13.54*
SKAU-382 x K-08-60	-0.60	-3.76**	2.92**	1.20	17.66**	15.63**	19.49**	17.87**	7.51**	2.33	25.18**	17.88*	-0.09	-7.72
SKAU-382 x K-08-61	0.30	-2.89*	-4.37**	-3.32**	19.13**	12.11**	18.40**	15.24**	4.28**	-0.74	22.64**	15.50*	14.24*	5.51
SKAU-382 x PS-5	4.48**	1.16	2.80**	1.08	15.89**	13.39**	19.16**	16.88**	7.89**	2.70	29.54**	21.99**	14.41*	5.67
SKAU-389 x Ch-988	1.19	-2.02	2.80**	1.08	10.28**	9.36**	14.07**	8.21**	12.86**	7.43**	23.63**	16.42*	4.18	-3.78
SKAU-389 x SR-1	4.78**	1.45	1.95	0.24	13.22**	10.36**	14.31**	9.30**	5.26**	0.19	16.03	9.27	8.35	0.08
SKAU-389 x K-08-60	3.58**	0.29	2.68*	0.96	18.61**	17.37**	15.42**	12.65**	24.00**	18.04**	20.39*	13.38	33.59**	23.39**
SKAU-389 x K-08-61	1.49	-1.73	3.78**	2.04	12.81**	10.64**	18.41**	9.39**	5.17**	0.11	41.35**	33.11**	6.39	-1.73
SKAU-389 x PS-5	-1.34	-4.48**	2.68*	0.96	10.17**	8.23**	18.65**	6.08*	15.05**	9.52**	10.13	3.71	21.91**	12.60*
Ch-988 x SR-1	1.94	-1.30	0.37	-3.32**	-4.75	-13.13**	-7.83**	-18.96**	9.85**	4.57**	23.35**	16.16*	9.12	0.79
Ch-988 x K-08-60	3.13*	-0.14	0.97	-0.72	-3.75	-12.23**	-2.83	-14.56**	7.42**	2.25	36.29**	28.34**	23.61**	14.17*
Ch-988 x K-08-61	5.22**	1.88	3.17**	1.44	-9.83*	-17.78**	-11.53**	-22.21**	7.28**	2.11	13.50	6.89	16.03*	7.17
Ch-988 x PS-5	0.60	-2.60*	0.12	-4.56**	14.33**	13.02**	15.55**	1.59	14.59**	9.08**	15.75	9.01	18.76**	9.69
SR-1 x K-08-60	1.49	-1.73	2.92**	1.20	18.22**	16.10**	19.73**	15.44**	9.17**	3.91*	25.18**	17.88*	8.10	-0.16
SR-1 x K-08-61	2.54	-0.72	3.78**	2.04	5.62	-3.68	7.19*	-5.75*	9.08**	3.83*	2.81	-3.18	19.78**	10.63
SR-1 x PS-5	8.81**	-5.35**	5.12**	3.35**	12.88**	12.06**	9.56**	-3.67	11.16**	5.81**	16.03	9.27	24.72**	15.20**
K-08-60 x K-08-61	10.90**	7.37**	7.43**	5.63**	23.40**	20.16**	21.23**	19.12**	-16.41**	-20.44**	-3.80	-9.40	17.31**	8.35
K-08-60 x PS-5	11.19**	7.66**	8.40**	6.59**	18.65**	17.41**	14.39**	11.16**	-8.12**	-12.54**	-4.50	-10.07	24.30**	14.80*
K-08-61 x PS-5	10.90**	7.37**	10.35**	8.50**	19.42**	18.76**	18.13**	16.09**	10.78**	5.45**	0.42	-5.43	22.34**	12.99
SE±	1.455		1.440		4.435		2.806		1.855		0.964		1.219	

Cont'd…..

Table-4 Cont'd…..

Cross Combinations	Biological yield plant^{-1} (g)		Grain yield plant^{-1} (g)		Harvest index (%)		Grain length (mm)		Grain breadth (mm)		Grain L/B ratio	
	Jhelum	SR-1	Jhelum	SR-1	Jhelum	SR-1	Jhelum	SR-1	Jhelum	SR-1	Jhelum	SR-1
K-08-59 x Jhelum	-8.02	-12.46**	-31.95**	-42.19**	-25.75**	-33.74**	19.33**	15.97**	-7.36	-4.81	31.95**	22.11**
K-08-59 x SKAU-382	-10.53*	-14.86**	-12.90*	-26.01**	-2.86	-13.31*	2.60	-0.29	6.69	9.62*	-1.71	-9.03
K-08-59 x SKAU-389	6.24	1.11	-17.80**	-30.18**	-22.50**	-30.84**	5.01*	2.06	4.55	7.42	2.73	-4.93
K-08-59 x Ch-988	22.94**	17.00**	-30.70**	-41.13**	-43.63**	-49.69**	2.92	0.03	-4.15	-1.51	10.03**	1.83
K-08-59 x SR-1	-16.17**	-20.22**	-49.67**	-57.24**	-39.81**	-46.29**	2.33	-0.55	-6.22	-3.64	5.53	-2.34
K-08-59 x K-08-60	19.29**	13.53**	-30.70**	-41.13**	-41.90**	-48.15**	19.25**	15.89**	7.63	10.58*	13.38**	4.93
K-08-59 x K-08-61	18.07**	12.37**	-20.88**	-32.79**	-33.25**	-40.43**	22.01**	18.58**	-12.98**	-10.58*	43.34**	32.66**
K-08-59 x PS-5	-8.38	-12.80**	-16.14**	-1.34	35.17**	20.63**	14.80**	11.57**	7.89	10.86*	8.87	0.76
Jhelum x SKAU-382	4.92	-0.14	9.40*	-7.07	4.79	-6.49	4.75*	1.80	7.76	10.72*	-0.68	-8.09
Jhelum x SKAU-389	23.98**	18.00**	29.07**	22.58**	25.83**	12.29**	-0.62	-3.41	-3.28	-0.62	6.14	-1.77
Jhelum x Ch-988	-21.07**	-24.88**	-4.58	-18.94**	20.75**	7.76	2.12	-0.76	-3.01	-0.34	7.65	-0.38
Jhelum x SR-1	28.17**	21.98**	26.45**	9.96	1.22	-9.67	5.98*	3.00	4.55	7.42	3.69	-4.04
Jhelum x K-08-60	26.50**	20.39**	32.22**	26.20**	32.05**	17.84**	7.43**	4.40	5.48	8.38	4.10	-3.66
Jhelum x K-08-61	1.68	-3.24	24.19**	13.99**	32.08**	17.87**	6.60**	3.60	8.03	11.00*	2.59	-5.05
Jhelum x PS-5	33.86**	27.39**	21.69**	16.96**	3.13	-7.97	14.53**	11.31**	2.68	5.50	14.20**	5.69
SKAU-382 x SK-389	9.24*	3.96	21.04**	7.07	16.43*	3.90	6.92**	3.91	-1.07	1.65	10.51*	2.27
SKAU-382 x Ch-988	9.09*	3.82	20.01**	18.79**	29.44**	15.52**	-6.17*	-8.81**	5.42	8.32	-9.01	-15.79**
SKAU-382 x SR-1	14.29**	8.77*	12.56**	-4.38	-1.58	-12.17**	15.55**	12.30**	-7.63	-5.09	27.85**	18.32**
SKAU-382 x K-08-60	41.22**	34.40**	-4.41	-18.80**	-32.47**	-39.74**	2.95	0.05	-1.47	1.24	6.89	-1.07
SKAU-382 x K-08-61	-22.11**	-25.87**	1.91	-13.43*	30.60**	16.55**	7.10**	4.09	1.67	4.47	7.85	-0.19
SKAU-382 x PS-5	7.51	2.32	23.44**	13.36*	24.19**	10.83**	22.28**	18.84**	-6.49	-3.92	33.65**	23.69**
SKAU-389 x Ch-988	12.51**	7.08	21.77**	16.58**	25.20**	11.73**	0.19	-2.63	1.94	4.74	0.55	-6.95
SKAU-389 x SR-1	33.25**	26.81**	9.23**	-7.21	-16.79*	-25.74**	3.14	0.23	1.76	10.72*	-2.25	-9.54*
SKAU-389 x K-08-60	53.30**	45.89**	35.21**	28.29**	12.19**	0.12	9.12**	6.04**	-12.17	-9.76	26.96**	17.50**
SKAU-389 x K-08-61	33.12**	26.69**	22.27**	15.15**	5.69	-5.68	5.44*	2.48	-9.70	-7.22	19.32**	10.42*
SKAU-389 x PS-5	11.24*	5.87	30.74**	24.14**	40.97**	25.80**	19.38**	16.02**	-12.37**	-9.97*	41.64**	31.08**
Ch-988 x SR-1	16.98**	11.33*	27.08**	22.49**	28.33**	14.52**	0.27	-2.55	-1.67	1.03	4.30	-3.47
Ch-988 x K-08-60	3.60	-1.40	23.76**	17.27**	37.64**	22.83**	0.86	-1.98	-1.20	1.51	4.37	-3.41
Ch-988 x K-08-61	-19.04**	-22.95**	-24.63**	-35.97**	-6.52	-16.58**	0.80	-2.03	21.52**	17.82**	-0.07	-7.52
Ch-988 x PS-5	20.05**	14.25**	26.79**	7.70	6.09	-5.32	19.06**	15.71**	-0.40	2.34	22.18**	13.08**
SR-1 x K-08-60	32.26**	25.87**	23.17**	18.17**	9.53*	-2.25	17.32**	14.02**	6.09	9.00*	13.17**	4.74
SR-1 x K-08-61	5.84	0.72	10.32**	-6.29	4.40	-6.83	-0.80	-3.60	6.22	9.14*	-4.44	-11.56*
SR-1 x PS-5	10.41*	5.07	-36.77**	-46.29**	-42.65**	-48.82**	3.94	1.02	9.77*	12.78**	-3.00	-10.23*
K-08-60 x K-08-61	-19.29**	-23.19**	-56.07**	-62.69**	-45.41**	-51.28**	36.17**	32.33**	-11.97*	-9.55*	58.16**	46.37**
K-08-60 x PS-5	-35.00**	-38.14**	-37.02**	-46.50**	-2.78	-13.24**	39.89**	35.96**	-13.91**	-11.55*	66.42**	54.01**
K-08-61 x PS-5	-29.31**	-32.73**	-29.37**	-40.00**	0.37	-10.43**	20.27**	16.88**	-16.86**	-14.57**	48.12**	37.08**
SE±	3.005		1.240		3.005		1.240		2.05		1.482	

*, ** Significant at 0.05 and o.o1 levels of probability, respectively

Table 5. Five promising heterotic combinations for grain yield,yield component traits and traits for maturity in rice (*Oryza sativa* L.) based on pooled analysis.

Character	Five Promising Hybrids	Standard Heterosis	Character	Five Promising Hybrids	Standard Heterosis
Days to 50% flowering	SKAU-382 x SR-1	-5.07**	No. of Primary branches panicle^{-1}	Jhelum x SKAU-389	47.02**
	K-08-59 x Jhelum	-4.63**		K-08-59 x PS-5	45.04**
	K-08-59 x SR-1	-2.84**		SKAU-382 x K-08-60	42.66**
	K-08-59 x SKAU-382	-2.69*		K-08-60 x K-08-61	39.88**
	SK-389 x PS-5	-1.34		K-08-59 x K-08-61	39.29**
Days to maturity	K-08-59 x Jhelum	-2.73**	No. of secondary branches panicle^{-1}	Jhelum x PS-5	102.71**
	Jhelum x KO8-61	-3.37**		Jhelum x SKAU-389	68.80**
	SKAU-382 x KO8-61	-4.37 **		SKAU-382 x K-08-60	68.33**
	SKAU-382 x SR-1	-1.24		SKAU-382 x K-08-61	64.23**
	Ch-988 x PS-5	0.12		SKAU-382 x SKAU-389	57.14**
Number of spikelet's panicle^{-1}	KO8-60 x KO8-61	20.16**	Biological yield Plant^{-1} (g)	Jhelum x PS-5	90.71**
	SKAU-382 x SK-389	19.20**		Jhelum x SKAU-389	68.80**
	K08-59 x SKAU-382	18.83**		SKAU-382 x K-08-60	68.33**
	KO8-61 x PS-5	18.76**		SKAU-382 x K-08-61	64.23**
	Jhelum x PS-5	18.44**		SKAU-382 x SKAU-389	57.14**
Number of filled grains pancle^{-1}	Jhelum x PS-5	19.35**	Grain yield Plant^{-1} (g)	SKAU-389 x K-08-60	28.29**
	KO8-60 x KO8-61	19.12**		Jhelum x K-08-60	26.20**
	Jhelum x SK-389	18.28**		SKAU-389 x PS-5	24.14**
	SKAU-382 x KO8-60	17.87**		Jhelum x SKAU-389	22.58**
	SKAU-382 x SK-389	17.55**		China-988 x SR-1	22.49**
Plant height (cm)	SKAU-389 x K-08-60	18.04**	Harvest index (%)	SKAU-389 x PS-5	25.80**
	Jhelum x PS-5	17.49**		China-988 x SR-1	22.84**
	Jhelum x K-08-60	13.84**		K-08-59 x PS-5	20.63**
	SKAU-382 x SKAU-389	11.83**		Jhelum x K-08-61	17.84**
	SKAU-389 x PS-5	9.52**		Jhelum x K-08-60	17.87**
Number of tillers Plant^{-1}	SKAU-389 x K-08-61	37.77**	Grain length (mm)	K-08-60 x PS-5	35.96**
	K-08-59 x Jhelum	32.75**		K-08-60 x K-08-61	32.33**
	China-988 x K-08-60	26.73**		SKAU-382 x PS-5	18.84**
	K-08-59 x SKAU-382	21.83**		K-08-59 x K-08-61	18.58**
	K-08-59 x K-08-60	31.49**		K-08-61 x PS-5	16.88**
Number of productive tillers Plant^{-1}	SKAU-389 x K-08-61	33.11**	Grain breadth (mm)	Ch-988 x KO8-61	17.82**
	K-08-59 x Jhelum	32.32**		SR-1 x PS-5	12.70*
	K-08-59 x K-08-60	30.99**		Jhelum x KO8-61	11.00*
	China-988 x K-08-60	28.34**		K08-59 x PS-5	10.86*
	K-08-59 x SKAU-382	24.24**		Jhelum x SKAU-382	10.72*
Panicle length (cm)	SKAU-389 x K-08-61	23.39**	Grain L/B ratio	K-08-60 x PS-5	54.40**
	Jhelum, K-08-60	21.42**		K-08-60 x K-08-61	46.37**
	SKAU-382 x SKAU-389	21.26**		K-08-61 x PS-5	37.08**
	Jhelum x PS-5	15.51**		K-08-59 x K-08-61	32.66**
	SKAU-382 x China-988	15.28**		SKAU-389 x PS-5	31.08**

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