Electronic Journal of Plant Breeding, 2(1):31-40 (Mar 2011)
ISSN 0975-928X

Research Article

Combining ability study in rice (*Oryza sativa* L.) under temperate conditions of Kashmir

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(Received:18 Nov 2010; Accepted:07 Jan 2011)

Abstract:
Thirty intervarietal (15 indica x indica and 15 japonica x japonica) and fifteen inter-subspecific (indica x japonica) crosses generated through half diallel and line x tester mating were subjected to combining ability analysis for various morpho-agronomic traits. The analysis of variance for combining ability revealed that variance estimates due to sca were higher in magnitude than the corresponding gca variances resulting in relatively higher non additive variance for most of the characters except for days to 50% flowering, days to maturity and grain yield/plant. The genetic components of variance revealed relatively higher estimates due to dominance deviation than corresponding estimates of additive genetic variance for most of the characters except for aforementioned characters. Average degree of dominance was in the range over dominance for most of the yield components and other traits, however maturity traits and grain yield/plant displayed partial dominance. None of the parents could be identified to possess good gca effects for all the attributes, however the parents P1 (Jehlum), P3 (SR-1), P8 (K-332), P11 (Kohsar) and P12 (K-508) were found promising combiners for most of the traits. For grain yield/plant cross combinations P1 x P5, P1 x P2, P4 x P6, P8 x P11, P11 x P12 and for early maturity P4 x P6, P1 x P5, P1 x P2, P11 x P12 and L4 x T2 demonstrated desirable and significant sca effects. Hybridization of parents with good gca effects has an ample scope of throwing promising transgressive segregants in the segregating generations to be used as commercial varieties. Similarly, cross combinations with favourable sca effects and high per se performance, besides involving good combining parents can be handled through conventional breeding programmes. In addition, desirable characters across the two sub species can be combined to derive ideal genotypes for temperate agro ecosystems within an altitude range of 5000-7500 feet amsl.

Key words: Rice (Oryza sativa L.), gca, sca, temperate ecology

Introduction

Among the various methods employed to enhance the rice productivity, hybridization of diverse parents and selecting the superior genotypes from the segregating population has been acknowledged as a time tested strategy. The principal and the most important step in successful hybridization programme is the choice of parents which produce superior crosses. However, the selection of parents on *per se* performance do not always necessarily lead to desired results as the ability of parents to nick well depends primarily on complex genetic interactions which, therefore, necessitates the evaluation of parents for their combining ability. The estimate of additive and non-additive gene action has been useful in determining the possibility of isolation of pure lines among the progenies of the good combinations in segregating generation and commercial exploitation of heterosis. Although, lot of work has been done on this aspect in rice (Chakraborty *et al*., 2009; Singh *et al*., 2007; Torres and Geraldi, 2007; Bisne and Motiramani, 2006; Singh and Kumar, 2004) but were conducted on different experimental materials and under different environmental conditions with different objectives. The experimental material comprised 12 genotypes belonging to two sub- species of rice i. e, *indica* and *japonica*. *Indica* varieties have special features of wide adaptability, good grain quality and profuse tillering while *japonica* varieties which are in vogue under higher belt of Kashmir valley (6000-7500 feet amsl) bear the characteristics of fertilizer responsiveness, high degree cold tolerance and grain boldness, socially the most acceptable character under these conditions. Hence, one more objective in addition of finding good combinations /cross combinations and breeding methodology was to combine the desirable features across the two sub-species of rice.

Material and methods

The material for the present study comprised twelve genetically diverse varieties of rice (*Oryza sativa* L.) belonging to two sub-specific groups viz. *indica* and *japonica.* The six typical *japonica* types [Koshihikari, K-332, Kohsar, GS-503, GS-504 and K-508] and six typical *indica* varieties including one wide compatibility variety (WCV) [Jehlum, SK-382, Chenab, China-1039, Shalimar rice-1 and Dular (WCV)] were selected out of the germplasm collection maintained at Rice Research and Regional Station, Khudwani. Fifteen intervarietal indica F_1 crosses were generated by six *indica* lines [Jhelum (P_1), SK-382 (P_2), Shalimar Rice-1 (P_3), China-1039 (P_4), Chenab (P_5) and Dular (P_6)] in half diallel (excluding reciprocals) in *kharif* 2008 as per the procedure described by Griffing (1956). Similarly one more set of fifteen intervarietal japonica single crosses were generated in the same season by intermating all six *japonica* varieties [Koshihikari (P_7), K-332 (P_8), GS-503 (P_9), GS-504 (P_{10}), Kohsar (P_{11}) and K-508 (P_{12})] in all possible combinations by excluding reciprocals as per the procedure of Griffing (1956).In the same season varietal set of five *indica* varieties as lines [viz. Jhelum (L_1), SK-382 (L_2), Shalimar rice-1 (L_3), China-1039 (L_4) and Chenab (L_5)] were crossed with three typical *japonica* varieties as testers [viz. Koshihikari (T_1), K-332 (T_2) and Kohsar (T_3)] in a Line x Tester fashion to generate 15 *indica*/*japonica* crosses as per Line x Tester mating design proposed by Kempthorne (1957). The materials were evaluated at two experimental farms situated under two agroecologies of Kashmir viz. Rice Research and Regional Station ,Khudwani (1650m amsl) and High Altitude Rice Research Sub-Station, Larnoo (2250m amsl) during *Kharif* 2009. The F_1 experimental progenies were grown in RBD with two replications. Each experimental progeny (F_1) was grown in two rows of 3m length with intra and inter- row spacing of 15 and 20 cm respectively, and recommended package of practices were followed to raise the good crop. The data recorded on traits related to maturity on plot basis, while as other morpho-agronomic traits were recorded on five randomly tagged plants from each experimental plot. The mean data (over two locations) were subjected to combining ability analysis as per the procedure given by Griffing (1956) and Kempthorne (1957) for respective material generated for the study. The statistical software windostat (new version) was used carrying the procedure given by Singh and Choudhary (1985).

Results and discussion

Analysis of variance for combining ability revealed significant mean square for gca and sca for all the traits except variance due to sca for days to 50% flowering, panicle length,grain yield/ plant and 100 grain weight for intervarietal *indica* (*i* x *i*) crosses. In case of intra- subspecific *japonica* crosses, traits like pollen sterility for GCA and maturity traits, panicle length, grain yield/plant and 100 grain weigh for SCA non significant. Similarly, variance due to GCA and SCA components were again significant for most of the characters for inter- sub specific crosses except for plant height and panicle length for gca and days to 50 % flowering and grain yield/plant for sca (Table-1).

The intervarietal crosses (*indica* x *indica, japonica* x *japonica*) registered higher magnitude of $\hat{\sigma}^2 s$ in relation to $\hat{\sigma}^2 g$ which implied the greater importance of non additive gene effect in the inheritance of pollen and spikelet sterility, plant height, panicle length, number of panicles/plant, biological yield and 100 grain weight. In terms of genetic components variance due to dominance deviations ($\hat{\sigma}^2 D$) were higher than that of additive genetic variance for all the characters except for maturity traits like days to 50 % flowering and maturity and grain yield/plant. Relatively higher estimates of sca component for plant height and 100 grain weight was observed in *indica x indica* in intervarietal *japonica x japonica* crosses.

Greater importance of non-additive gene effects for yield components and other morpho-agronomic traits have been reported by Singh *et al.* (200) and Torres and Geraldi, 2007. Pre-dominance of non-additive gene effects was also reported for grain yield components in rice (Ramalingam *et al*., 1997., Satyanarayana *et al*., 2000., Bisne and Motiramani, 2006). Similarly, additive gene action for maturity traits were found more important in many studies in rice (Singh and Kumar, 2004., Torres and Geraldi, 2007). There was close correspondence of the present study with earlier workers (Lavanya, 2000., Singh and Kumar, 2004 and Chakraborty *et al*., 2009) for relatively higher estimates of additive gene action regarding grain yield/plant in rice.

Estimates of average degree of dominance (dominance ratio) revealed that most of the traits were in the range of dominance to over-dominance in the intervarietal as well as inter-subspecific crosses. Partial dominance was recorded for both maturity traits and grain yield/plant in the entire tested material. Complete dominance (dominance ratio approaching unity) was recorded for spikelet sterility and biological yield in intervarietal *indica* crosses and for number of panicles/plant and panicle length in intervarietal *japonica* crosses. The traits like spikelet sterility, plant height, number of panicles/plant and biological yield/plant in inter-subspecific crosses also expressed the value of dominance ratio tending towards unity. The estimates of genetic components of variance together with the average degree of dominance revealed over-dominance for most of the traits in the entire experimental material generated for the study indicating that the present set of material were highly divergent and contained the contrasting alleles, in most of the cases in dispersion phase, which on combination through hybridization increased heterozygosity. The differential behavior of genetic material generated for the study regarding gene action and genetic components for different traits might be attributed to the different kind of material generated through different mating patterns and analyzed through different statistical procedures and evaluated under one adaptive and other non-adaptive environment.

The close examination of the results revealed that none of the parents showed significant gca effects in the desired direction simultaneously for every trait. The inter varietal and inter- subspecific cross analysis for grain yield/plant, identified parents L_2 (2.95), P11 (2.83), P12 (2.25), T2 (1.71), P1 (1.58) and P3 (1.40) as the most promising on the basis of significant positive gca effects. Hence, these parents may be presumed to have more favorable alleles for this trait (Table-2). The good *per se* performance on the basis of high mean value was recorded for all these parents except T2 showing low mean value for the trait. The genotype L2 recorded high and positive gca effects (37.01) followed by P3 (13.64), L4 (11.58), P10 (8.36) and P11 (8.17) for second important economic character i. e., biological yield/plant. Again high mean expressed in the form of high gca effects except line L4 (low *per se* performance). Simultaneously, considerations of grain yield component traits and maturity traits like days to 50% flowering and maturity suggested parent P1 to have positive and significant gca values for number of panicles/plant (1.34),significant and desirable gca estimates for days to 50% flowering (-1.12) and days to maturity (-1.46). The parent displayed desirable gca values for spikelet sterility (-4.23) but behaved as an average combiner for pollen sterility. This indicates the importance of the parent which has the favorable alleles for these traits. In all such cases good *per se* performances were realized in the form of good gca performances, whereas, in case of maturity traits and spikelet sterility it was low mean performance that expressed in the form of desirable (negative) gca effects. Similarly, among other *indica* parents P3 expressed significant positive gca effects for number of panicles (1.42).The parent depicted with undesired gca effects for traits like plant stature (2.66) and days to 50% flowering and maturity. High colinearity between good gca effects and *per se* performance observed for the parents except for 100 grain weight average performance expressed with good gca effects. For early flowering and early maturity P6 had significant and desirable gca effects (-1.16 and -3.93) while as, for rest of the characters the behavior of the parent was undesirable. Again low mean value of these traits were expressed in the form of negative gca effects. The study further observed that *indica* parents P2, P4 and P5 could not score any significant gca effect in a desired direction for any trait. The combining ability analysis in intervarietal *japonica* (*j* x *j*) crosses identified parents P11 and P12 with significant and desirable gca values for days to 50% flowering (-2.91 and -2.29) and days to maturity (-3.68 and -2.0). These genotypes also proved desirable combiners for spikelet sterility by revealing gca effects of -3.82 and -4.15 respectively. The parent P11 in addition showed significant and positive gca estimates for biological yield /plant (8.17) and 100 grain weight (0.16). The parents could not prove promising for dwarfness as depicted through significant positive gca effects of 6.73 and 4.67 respectively.

In the present study, the parents P1, P3, P11, P12 and L2 which recorded high mean value for grain yield/plant were also identified as good general combiners for this trait. Similarly, poor yielding parents namely P5, P6, P9 and P10 registered low gca effects. Suresh and Anbuselvam (2006) also reported very good correspondence between mean per se performance of the parent with their corresponding gca effects.

Table-3 gives the list of crosses having significant and positive estimates of sca effects or genetically superior combiners for grain yield/plant and their *per se* performance (mean over the locations). The table also gives the information in terms of the desirability of these cross combinations for other morpho-agronomic traits. The close observation of the table revealed the fact that the significant and desirable sca effects for the traits like early flowering and number of panicles/plant were associated with positive and significant sca effects for grain yield /plant for most of the cross combinations. However, a few crosses also showed co-association of negative sca effects for early flowering and spikelet sterility viz-a-viz positive sca effects for panicle length, biological yield/plant and 100-grain weight with positive sca effects for grain yield. For rest of the traits these elite cross combinations proved either as average or poor specific combiners. For grain yield/plant, crosses involved predominantly good x average while average x poor and average x average combinations were also observed. For other traits, good x average were the most predominant while as other kinds of combinations also came into play. Findings of Pradhan *et al*., (2006), Sanjeev *et al*., (2008) and Chakraborty *et al*., (2009) also were on similar lines.

The superiority of the crosses involving good x average and average x average combiners might possibly have resulted from the concentration and interaction of favourable alleles contributed by the parents. The potential of such crosses can be exploited through simple conventional procedures such as pedigree/bulk method of breeding and superior segregants can be thrown out in the subsequent generations. The superiority of crosses involving good x poor combiners as parents could be explained on the basis of interactions between positive alleles from good/average combiners and negative alleles from the poor combiners as parents (over-dominance and epistasis of complementary types). The crosses between good x poor general combiners resulting in significant sca effects could be used to throw superior transgressive segregants when the additive gene effects of the parents and the complementary epistatic effects in crosses act in the same direction to maximize the desirable plant attribute. The superior cross combinations involving low x low general combiners could result from over-dominance and epistasis. The high yield of such crosses is non-fixable in the subsequent generations and thus could be exploited for hetetosis breeding, which is though not currently feasible in rice under temperate Kashmir conditions because of certain apparent limitations like lack of standard emasculation systems for large scale hybrid seed production.

Thus nature and magnitude of gene action together with nature of cross combination on the basis of combining ability suggest the alternative method of breeding such as recurrent selection, diallel selective mating scheme (DSM) and biparental mating suggested as the most convenient procedures for the improvement. These methods take care of both the genetic components for crop improvement. The traits like higher yield and early maturity are the most important breeding objectives. Early maturity is the topmost priority after higher yield because of higher probability of occurrence of snowfall at early and late stages of crop growth. Spikelet sterility is very high in case of inter-subspecific crosses when compared to intervarietal crosses as was the case with present experimental material. Hence this was also one of the characters studied in the present experiment. The lodging is one of the factor that take a heavy toll of the crop more particularly when the crop reaches to dough stage. Hence medium plant height is also the desirable character. The core yield attributing traits like the number of panicles/plant and panicle length are not up `to the satisfactory level in case of *japonica* rices grown under higher belts of the Kashmir valley. So to breed for varieties having long panicles and high tillering is also the breeding target for crop improvement. Similarly, animal : man ratio is high more particularly under high altitude belts of the valley, besides the non-availability of any fodder crop during the lean season which prevail for more than five months of the year (November-March) due to the geographically remoteness location of the area. As a result the paddy straw has high demand and after the threshing operation is over and is stored and fed to the cattle during long harsh winter spell. This in fact indicates the importance of high biological yield or biomass under present study.

The Present study of the nature and magnitude of gene action simultaneously with combining ability could not identify any parent/cross suitable for all the desirable attributes. Thus hybridization of parents with good gca effects has an ample scope of throwing promising transgressive segregants in the segregating generations to be used as commercial varieties. Additional variability for selection could also be generated while crossing the material with highly promising well adopted genotypes maintained at the station. The promising crosses with desirable sca effects for most of the characters and involving good/good or average/ good as combinations will be advanced to next generations at both the agro-ecologies (research stations) to derive super segregants for most of the traits having favorable attributes from both of the sub species. The new concept for crop improvement- ideotype breeding has now been initiated under temperate agro-ecologies of Kashmir by combining the traits like lodging resistance, fertilizer responsiveness and cold tolerance of *japonica* and grain quality characteristics, high tillering, longer panicle and biological yield of *indicas*. Thus NPTs can be derived within very short spell of time.

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Table-1.1: Analysis of variance for combining ability and estimates of components of variance for various morpho-agronomic and other traits in intervarietal (i x i) crosses of rice

Source of variation	d.f.	Days to 50% flowering	Days to maturity	Pollen sterility (%)	Spikelet sterility (%)	Plant height (cm)	No. of panicles/ plant	Panicle length (cm)	Grain yield / plant (g)	100-grain weight (g)	Biological yield/plant (g)
Gca	5	34.442**	116.616**	140.908**	194.954**	39.158**	15.420*	3.88*	48.761**	0.133*	1680.323**
Sca	15	5.512	20.023**	80.174*	66.162**	18.717**	10.825*	2.319	6.150	0.093	601.50*
Error	20	3.286	4.95	35.114	20.149	5.24	4.189	1.120	4.294	0.046	204.73
Components of variance/genetic variance											
$\hat{\sigma}^2 g$		3.89	13.958	13.22	21.85	4.239	1.404	0.345	5.558	0.0108	184.449
$\hat{\sigma}^2 s$		2.226	15.07	45.06	46.013	13.47	6.636	1.19	1.856	0.047	396.77
$\hat{\sigma}^2 A$		7.78	27.916	26.44	43.70	8.479	2.807	0.69	11.116	0.0217	368.89
$\hat{\sigma}^2 D$		2.226	15.07	45.06	46.013	13.47	6.636	1.19	1.856	0.047	396.77
$[\hat{\sigma}^2 D / \hat{\sigma}^2 A]^{½}$		0.52	0.73	1.30	1.026	1.26	1.537	1.318	0.408	1.47	1.037
$2\hat{\sigma}^2 g / 2\hat{\sigma}^2 g + \hat{\sigma}^2 s$		0. 77	0.32	0.37	0.49	0.37	0.29	0.36	0.85	0.31	0.48

Electronic Journal of Plant Breeding, 2(1):31-40 (Mar 2011)
ISSN 0975-928X

Table-1.2: Analysis of variance for combining ability and estimates of components of variance for various morpho-agronomic and other traits in intervarietal (j x j) crosses of rice

Source of variation	d.f.	Days to 50% flowering	Days to maturity	Pollen sterility (%)	Spikelet sterility (%)	Plant height (cm)	No. of panicles/ plant	Panicle length (cm)	Grain yield / plant (g)	100-grain weight (g)	Biological yield/plant (g)
Gca	5	51.746**	95.88**	3.137	152.63**	293.795**	14.663**	6.145**	53.069**	0.157*	382.26**
Sca	15	8.005	13.27	5.734*	83.17**	61354**	6.123*	2.751	16.738	0.070	304.03**
Error	20	6.165	13.17	2.047	9.318	19.18	2.566	1.481	9.206	0.055	30.42
Components of variance/genetic variance											
$\hat{\sigma}^2 g$		5.697	10.33	0.136	17.91	34.32	1.511	0.583	5.482	0.0127	43.98
$\hat{\sigma}^2 s$		1.84	0.10	3.687	73.85	42.17	3.557	1.27	7.532	0.015	273.61
$\hat{\sigma}^2 A$		11.395	20.67	0.272	35.83	68.55	3.023	1.166	10.964	0.0255	87.96
$\hat{\sigma}^2 D$		1.84	0.10	3.687	73.85	42.17	3.557	1.27	7.532	0.015	273.61
$[\hat{\sigma}^2 D / \hat{\sigma}^2 A]^{½}$		0.402	0.069	3.68	1.43	0.78	1.084	1.043	0.828	0.766	1.76
$2\hat{\sigma}^2 g / 2\hat{\sigma}^2 g + \hat{\sigma}^2 s$		0.86	0.99	0.069	0.33	0.62	0.54	0.48	0.59	0.63	0.24

Table 1.3: Analysis of variance for combining ability and estimates of components of variance for various morpho-agronomic and other traits in inter-subspecific (i x j) crosses of rice

Components/ genetic components of variance	Days to 50% flowering	Days to maturity	Pollen sterility (%)	Spikelet sterility (%)	Plant height (cm)	No. of panicle s/ plant	Panicle length (cm)	Grain yield/ plant (g)	100 grain weight (g)	Biological yield/plant (g)
$\hat{\sigma}^2$ lines	27.68* ±14.12	16.94* ±7.56	530.62* ±263.81	99.418 ±58.65	58.14** ± 20.01	16.87* ±8.01	1.268 ±1.27	5.026 ±3.11	0.00064** ±0.00013	1225.95* ±593.87
$\hat{\sigma}^2$ testers	20.64 ±14.98	30.33 ±20.99	337.22 ±239.57	168.469* ±84.69	86.66 ±61.59	19.83 ±14. 40	0.905 ±1.029	1.977 ±1.550	0.000487** ±0.000104	3.30 ±3.51
$\hat{\sigma}^2$ gca (average)	22.90* ±11.20	23.63* ±11.71	433.92* ±191.55	133.94** ±28.23	72.40 ±54.10	18.35* ±9.21	1.086 ±0.855	3.501* ±1.73	0.000563* 0.000270	514.63* ±194.39
$\hat{\sigma}^2$ sca (line x testers)	15.699 ±8.29	21.12* ±10.27	760.98** ±209.72	281.29** ±84.02	156.43* ±66.47	36.41** ±6.39	7.58* ±3.70	0.595 ±0.851	0.004935* 0.002134	1121.96* ±505.33
$\hat{\sigma}^2 A$	45.80	47.26	867.84	267.88	144.80	36.70	2.172	7.002	0.001126	1029.26
$\hat{\sigma}^2 D$	15.69	21.12	760.98	281.29	156.43	36.417	7.58	0.595	0.004935	1121.96
$[\hat{\sigma}^2 A / \hat{\sigma}^2 D]^{½}$	2.919	2.237	1.140	0.952	0.92	1.007	0.286	11.76	0.228	0.917
Degree of dominance	0.585	0.668	0.936	1.024	1.039	0.996	1.868	0.29	2.093	1.044
$2\hat{\sigma}^2 g / 2\hat{\sigma}^2 g + \hat{\sigma}^2 s$	0.74	0.69	0.53	0.49	0.48	0.50	0.22	0.92	0.18	0.48

*, ** significant at 5 and 1 per cent level, respectively.

Table-2.1 : Estimates of general combining ability effects for various morpho-agronomic and other traits of parents in intervarietal (i x i) crosses of rice

Parents	Days to 50% flowering	Days to maturity	Pollen sterility (%)	Spikelet sterility (%)	Plant height (cm)	No. of panicles/ plant	Panicle length (cm)	Grain yield/plan t (g)	100-grain weight (g)
P_1 (Jhelum)	-1.1232*	-1.467*	-2.109	-4.23**	0.769	1.340*	0.002	1.584*	0.095
P_2 (SK-382)	-0.979	3.146**	3.764*	2.495	-0.240	-1.409*	-0.121	0.760	-0.193**
P_3 (SR-1)	2.522**	1.229	-2.895	0.096	2.667**	1.420*	0.174	1.403*	0.132*
P_4 (China-1039)	0.958	0.417	-1.607	-2.772	-0.241	0.150	0.522	1.136	-0.019
P_5 (Chenab)	-0.102	0.604	-0.857	-0.908	-1.314	-0.281	0.315	0.030	0.051
P_6 (Dular)	-1.167*	-3.929**	3.704	5.319**	-1.641*	-1.220	-0.892*	-4.913**	-0.066
S.E.(gi)	0.585	0.71	1.912	1.448	0.756	0.66	0.341	0.668	0.0692
S.E.(gi -gj)	0.906	1.112	2.96	2.244	1.144	1.023	0.529	1.036	0.107

Table-2.2 : Estimates of general combining ability effects for various morpho-agronomic and other traits of parents in intervarietal (j x j) crosses of rice

Parents	Days to 50% flowering	Days to maturity	Pollen sterility (%)	Spikelet sterility (%)	Plant height (cm)	No. of panicles/ plant	Panicle length (cm)	Grain yield/plant (g)	100-grain weight (g)
P_7 (Koshik)	4.396**	5.063**	0.198	4.737**	-9.344**	0.683	-1.471**	-3.308**	0.047
P_8 (K-332)	-1.979*	-2.750*	0.914*	-3.944**	1.894	0.515	0.642	1.570	-0.156*
P_9 (GS-503)	0.708	3.000*	-0.478	3.360**	1.000	-0.554	0.067	-2.403*	-0.045
P_{10} (GS-504)	2.084*	0.375	0.483	3.799**	-4.956**	-0.710	-0.508	-0.944	0.143
P_{11}(Kohsar)	-2.917*	-3.688**	-0.541	-3.806**	6.731**	-0.210	0.948*	2.833*	0.162*
P_{12} (K-508)	-2.292**	-2.000	-0.576	-4.146**	4.675**	0.277	0.323	2.252*	-0.151*
S.E.(gi)	**0.801**	**1.171**	**0.461**	**0.985**	**1.413**	**0.517**	**0.351**	**0.98**	**0.075**
S.E.(gi -gj)	**1.24**	**1.814**	**0.715**	**1.526**	**2.189**	**0.800**	**0.608**	**1.517**	**0.117**

Table-2.3 : Estimates of general combining ability effects of lines and testers for various morpho-agronomic and other traits in inter-subspecific crosses (i x j) of rice

Parents	Days to 50% flowering	Days to maturity	Pollen sterility (%)	Spikelet sterility (%)	Plant height (cm)	No. of panicles/ plant	Panicle length (cm)	Grain yield/plant (g)	100-grain weight (g)
Lines									
L_1 (Jhelum)	4.800**	1.900*	-16.157**	-9.686**	-5.681**	1.712	-2.465**	0.109	0.016
L_2 (SK-382)	-5.200**	-2.567**	16.178**	-3.071*	2.342*	1.824	1.838*	2.954**	0.383**
L_3 (SR-1)	1.800	1.933*	-4.713**	1.322	3.730**	-3.705**	1.799	0.549	-0.116**
L_4 (China-1039)	-5.367**	1.334	8.605**	4.566**	1.149	3.359**	1.157	-3.539**	-0.157**
L_5 (Chenab)	3.967**	-2.600**	-3.913*	6.869**	-1.540	-3.190**	-1.329	-0.074	-0.126**
Testers									
T_1 (Koshihikari)	5.301**	5.734**	3.498*	4.743**	9.100**	-3.464**	1.192	-2.453**	0.273**
T_2 (K332)	-3.00**	-3.067**	-8.520**	2.434*	-4.534**	2.905**	0.009	1.707**	-0.363**
T_3 (Kohsar)	-2.300**	-2.667**	5.023**	-7.177**	-4.566**	0.560	-1.201	0.746	0.090*
S.E.(gi) Lines	**0.954**	**0.775**	**1.627**	**1.475**	**0.856**	**0.951**	**0.9370**	0.605	0.039
S.E.(gi -gj) Lines	**1.349**	**1.096**	**2.301**	**2.085**	**1.211**	**1.344**	**1.325**	0.856	0.055
S.E.(gi) Testers	**0.739**	**0.600**	**1.260**	**1.142**	**0.663**	**0.73**	**0.7267**	0.469	0.030
S.E.(gi –gj) Testers	**1.045**	**0.848**	**1.782**	**1.616**	**0.937**	**1.042**	**1.026**	0.663	0.043

*, ** significant at 5 and 1 per cent level, respectively

Table-3: List of crosses with significant and positive estimates of sca effects for grain yield/plant simultaneously their desirability for other morpho-agronomic traits

Crosses with significant and desirable sca effects	Morpho-agronomic traits identified desirable on the basis of sca for respective cross combinations
P1 x P5 (3.9*) [20.5]	DFF (-3.21*), np (7.57*), pl (2.09*)
P1 x P2 (3.85*) [22.8]	DFF (-5.02), pl (1.98*), np (3.56*) , 100gw (0.38*)
P3 x P5 (3.65*) [19.9]	DM (-8.35**), np (3.77*)
P4 x P6 (3.73*) [20.0]	DFF (-3.34*), DM (10.45**), np (6.62**)
P8 x P11 (5.55*) [21.4]	DFF (-4.31*), By (10.15*)
P10 x P12 (5.34*) [22.0]	DM (-6.47*), np (6.56*), pl (2.97*), By (11.30*), 100gw (0.83**)
P11 x P12 (5.3*) [18.5]	DFF (-5.69*), np (3.0*), 100gw (0.33*)
L3 x T3 (2.06*) [16.4]	DFF (-4.2*), DM (-7.66**), ps (-13.48**), SS (-13.69**)

,* significant at 5 and 1% level respectively
(Figures in long parenthesis[ ] are *per se* performance)
DFF= Days to 50% flowering**, DM=** Days to maturity**, SS=** Spikelet sterility**, FS=**Fertile spikelets/panicle**,**
np= number of panicles/plant**, 100gw=** grain weight**, By=** biological yield, **pl** = panicle length, **ps** = pollen sterility.