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Gene action and combining ability analysis for yield and yield contributing traits in rice (O*ryza sativa* L.) over environment

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Abstract
Line × tester experiment was conducted to evaluate the performance of 54 F_1 hybrids alongwith 18 parents in rice. Analysis of variance revealed highly significant differences among treatments, parents, crosses and lines × testers for number of panicle bearing tillers per plant, panicle length, spikelets per panicle, and grains per panicle, spikelets fertility, biological yield per plant, harvest index and grain yield per plant under both normal and saline conditions. Parents vs. crosses were significant for panicle bearing tillers per plant, spikelets per panicle, grains per panicle, spikelets fertility, biological yield per plant and grain yield per plant in normal condition while in saline condition for spikelets per panicle, grains per panicle, spikelets fertility, biological yield per plant and harvest index. Lines were significant for panicle length, biological yield per plant and harvest index in normal condition but in case of saline condition panicle length and grain yield per plant were found significant. Testers were non-significant for all the traits in both conditions. The estimates of variance of specific combining ability effects, ratio of variance of general combining ability to specific combining ability and degree of dominance indicated preponderance of non-additive gene effects for each trait. On over all bases, role of lines in the expression of most of the yield components was more than testers and line × tester interaction under both conditions.

Keywords: PCV, GCV, GCA, SCA, standard heterosis and rice

Introduction
India is the world's second largest producer of rice, wheat and other cereals. The huge demand for cereals in the global market is creating an excellent environment for the export of Indian cereal products. According to the final estimate for the year 2014-15 by Ministry of Agriculture of India, the production of rice stood at 105.48 million tonnes. (According to APDEA report 2016).

The high food quantities of rice grain at one hand, and the intensive growth of population in the developing countries on the other, have predetermined the wide cultivation of this crop practically in all situations including saline-alkali soils. However, considering the current rate of population growth at the global level and in our country, the requirement of rice by 2020 AD is estimated to be around 800 and 140 million tonnes, respectively. This increased productivity therefore, must come from less land, water, labour and other inputs. This reducing trend of agricultural land availability would be overcome with utilization of an area estimated at more than 22 m ha in Asia alone. Both saline and alkali soils are wide spread in inland areas as that in U.P. Line × tester technique (Kempthorne, 1957) [8] is useful in deciding the relative ability of female and male lines to produce desirable hybrid combinations. It also provides information on genetic components and enables the breeder to choose appropriate breeding methods for hybrid variety or cultivar development programme. Information on general and specific combining ability for yield and its components will prove very useful in selection of appropriate parents for the development of superior hybrids. The knowledge of heritability and genetic advance of yield attributes may be helpful in the selection of some promising material from the existing population, which would be of almost importance. The present research work was therefore, carried out with the objective to assess combining ability based on mean performance, genetic components and heterosis controlling some economic traits in rice. The information obtained thus will be used in selection of suitable parents and choice of appropriate breeding methods to develop high yielding rice cultivar(s) or hybrid variety(s).

Materials and Methods
The present investigation was conducted at Genetics and Plant Breeding Research Farm and Student Instructional Farm of N.D. University of Agriculture and Technology, Narendra

Nagar (Kumarganj), Faizabad. The crosses were made during *Kharif*, 2013 and the hybrids along with parental lines and checks were evaluated during *Kharif*, 2014.

A line × tester set of 54 hybrids (F₁s) were derived by crossing 18 lines (female) with three high yielding testers (male) *viz.,* Narendra Usar Dhan- 2, Narendra Usar Dhan- 3 and Narendra Usar Dhan-2009 during *Kharif* 2013. The eighteen lines were NDRK-5014, NDRK-5016, NDRK-5030, NDRK-5032, NDRK-5035, NDRK-5043, NDRK-5062, NDRK-5071, NDRK-5081, NDRK-5092, NDRK-50001, CSR – 23, CSR – 28, IR SST-N 27, IR 74095 AC 64, IR 72579-B-2R, HPU-CIJ, and LD 183-4. The 54 F₁s along with their parents and check varieties (NDR 359 for normal condition and Narendra Usar Dhan 2009 for saline condition) were evaluated in randomized complete block design with three replications during *Kharif*, 2014. Single row plots of 3m length were used for transplanting single seedling per hill for each genotype (treatment) in each replication following intra and inter-row spacing of 15 cm and 20 cm, respectively. Recommended cultural practices were followed to raise a good crop.

The pH, EC and ESP were 8.9, 0.28 dSm^{-1} and 68%, respectively for saline soil. The data were recorded on yield contributing traits like panicle bearing tillers per plant, panicle length (cm), spikelets per panicle, grains per panicle, spikelets fertility (%), biological yield per plant (g), harvest index (%) and grains yield per plant (g). The analysis of variance for randomized complete block design was carried out following Panse and Sukhatme (1967) [9]. The combining ability analysis was carried out following line × tester mating design outlined by Kempthorne (1957) [8] and further elaborated by Arunachalam (1974) [1]. Line × tester analysis was used to estimate general combining ability (GCA) and specific combining ability (SCA) variances and their effects using the observations taken on F₁ generation of the line × tester sets of crosses. In this mating system, a random sample of 'l' lines is taken and each line is mated to each of the 't' testers (Singh and Chaudhary, 1985) [12]. Phenotypic (PCV) and genotypic (GCV) coefficients of variation for different characters were estimated by following formulae suggested by Burton and de Vane (1953) [3]. Heritability in broad sense (h²b) was calculated as suggested by Hanson *et al.* (1956) [6]. The expected genetic advance (Ga) was estimated using formula suggested by Johnson *et al.* (1955) [7].

Proportional contribution of lines, testers and their interactions was calculated by these formulae

$$\text{Contribution of lines (\%)} = \frac{\text{S.S. (lines)}}{\text{S.S. (crosses)}} \times 100$$

$$\text{Contribution of testers (\%)} = \frac{\text{S.S. (testers)}}{\text{S.S. (crosses)}} \times 100$$

$$\text{Contribution of lines} \times \text{testers (\%)} = \frac{\text{S.S. (lines x testers)}}{\text{S.S. (crosses)}} \times 100$$

The standard heterosis was computed as per cent increase or decrease of the mean values of crosses (F₁'s) over standard variety.

$$\text{Heterosis over standard variety (Standard heterosis)} = \frac{\overline{F_1} - \overline{SV}}{\overline{SV}} \times 100$$

Where,

$$F_1 = \text{Mean of } F_1$$

$$\overline{SV} = \text{Mean of standard variety or check variety}$$

The test of significance was applied to determine the significance of heterosis by using the following formula:

$$\text{'t' (Standard heterosis)} = \frac{\overline{F_1} - \overline{SV}}{\text{S.E.}}$$

S.E. of heterosis over standard variety $= \sqrt{2Me/r}$

Where,

Me = Mean error variance
r = Number of replications.

Thus, C.D. = SE ×'t' value at error d.f. at 5 or 1% probability level.

Results and Discussion

Analysis of variance revealed highly significant differences among treatments, parents, crosses and lines × testers for all traits under both normal and saline conditions. Parents vs. crosses were significant for most of the characters except panicle length and harvest index under normal comdition, while, in saline condition for spikelets per panicle, grains per panicle, spikelets fertility, biological yield per plant and harvest index. Lines were significant for panicle length, biological yield per plant and harvest index in normal condition but in case of saline condition panicle length and grain yield per plant were found significant. The success of selection in improving plant characters depends mainly on presence of substantial genetic variability and nature of heritability and genetic advance. The genetic variability is the raw material of plant breeding programme on which selection acts to evolve superior genotypes.

Estimates of SCA variance were higher than the corresponding estimates of GCA variance for all the traits under both conditions. The analysis of variance for combining ability revealed no significant differences among the testers for all the characters under study. The mean sum of squares due to lines × tester interactions was found to be highly significant for all the characters representing importance of specific combining ability and non-additive gene effects. The above results suggested importance of both additive and non-additive gene effects for majority of characters.

The phenotypic and genotypic coefficients of variation can be used for assessing and comparing the nature and magnitude of variability existing for different characters in the breeding materials. Heritability in broad sense quantifies the proportion of heritable genetic variance to total phenotypic variance, while heritability in narrow sense represents the ratio of fixable additive genetic variance to total phenotypic variance. Estimates of heritability help in estimating expected progress through selection. The genetic advance in per cent of mean provides indication of expected selection response by taking into account the existing genetic variability and heritability of the character. The estimates of direct selection parameters, coefficients of variation, heritability and genetic advance in per cent of mean were computed for eight characters of 54 crosses and their parents (Table 1 and 2 for normal and saline conditions, respectably).

The high estimates of genotypic and phenotypic coefficient of variation, heritability in broad sense along with genetic

advance in per cent of mean were recorded for spikelets per panicle and grains per panicle. Grains yield per plant were recorded high estimates for GCV, heritability in broad sense and genetic advance in per cent of mean, while, moderate for PCV. Panicle length showed moderate estimates for PCV, GCV and genetic advance in per cent of mean, while, high estimates for heritability. Biological yield per plant showed high estimates for heritability in broad sense and genetic advance in per cent of mean, while, moderate for PCV and GCV. Panicle bearing tillers per plant showed high PCV and genetic advance in per cent of mean but had low estimate for GCV and moderate for heritability in broad senesce. Harvest index recorded low estimates for PCV, genetic advance in per cent of mean and moderate for heritability and GCV, while, spikelet fertility showed low heritability, PCV and genetic advance but moderate for GCV. The high to very high estimates of direct selection parameters for above mentioned characters indicated that these would be ideal traits for improvement through selection in context of materials evaluated due to existence of high genetic variability represented by high coefficients of variation and high transmissibility denoted by high heritability for them. This indicated that improving trait through selection in context of present material would be straightforward due to comprise of genetic variability for these traits under normal condition. The high estimates of direct selection parameters observed for the above characters are broadly in agreement with earlier reports in rice (Basavaraja*etal.* 2013 and Sathya and Jebaraj, 2013) [11].

The high estimates of genotypic and phenotypic coefficient of variation and high heritability in broad sense along with high genetic advance in per cent of mean were recorded for grains per panicle. Biological yield per plant, harvest index and grains yield per plant recorded high heritability and genetic advance in per cent of mean, while moderate for PCV and GCV. Panicle bearing tillers per plant possessed high PCV and genetic advance in per cent of mean, while, moderate for GCV and heritability. Panicle length showed moderate PCV and genetic advance in per cent of mean, while, high for heritability in broad sense and low for GCV. Spikelet fertility possessed low PCV, GCV and genetic advance in per cent of mean, while, high for heritability. The high to very high estimates of direct selection parameters for above mentioned characters indicated that these would be ideal traits for improvement through selection in context of materials evaluated due to existence of high genetic variability represented by high coefficients of variation and high transmissibility denoted by high heritability for them. The high estimates of direct selection parameters observed for the above characters are broadly in agreement with earlier reports in rice (Basavaraja*etal.* 2013 and Sathya and Jebaraj, 2013) [11].

Proportional contribution of lines, testers and lines × testers interaction for 8 characters have been presented in table 1 for normal condition and in table 2 for saline condition.

The maximum contribution of females (lines) was recorded for grain yield per plant (56.12%) followed by biological yield per plant (44.24%), panicle length (43.54%), harvest-index (40.17%), panicle bearing tillers per plant (34.16%), spikelet fertility (31.91%), grains per panicle (21.61%) and spikelets per panicle (19.70%) for normal condition. Under saline condition the maximum contribution of females (lines) was recorded for grain yield per plant (59.48) followed panicle length (47.41), harvest-index (%) (39.50), biological yield per plant (34.37), spikelet fertility (33.34), spikelets per panicle (32.13), grains per panicle (28.00) and panicle bearing

tillers per plant (22.32)

Maximum contribution of male (testers) in normal condition was recorded for spikelets per panicle (9.32%) followed by grains per panicle (9.10), panicle length (6.87%), panicle bearing tillers per plant (3.47%), harvest-index (2.50%), grain yield per plant (1.42%), spikelet fertility (0.85%) and biological yield per plant (0.85%), while in saline condition maximum contribution of male lines (testers) was recorded for biological yield per plant (6.23%), followed by grains per panicle (5.03), spikelets per panicle (4.61%), panicle length (3.09%), panicle bearing tillers per plant (2.20%), grain yield per plant (2.20%), harvest-index (1.10%) and spikelet fertility (0.72%).

Proportional contribution of lines × testers was found maximum for the spikelets per panicle (70.97%), followed by grains per panicle (69.28), spikelet fertility (67.23%), panicle bearing tillers per plant (62.36%), harvest-index (57.32%), biological yield per plant (54.89%), panicle length (49.58%), and grain yield per plant (42.45%) under normal condition. Proportional contribution of lines × testers was found maximum for the character panicle bearing tillers per plant (75.47%) followed by grains per panicle (66.98%), spikelet fertility (65.95%), spikelets per panicle (63.26%), harvest-index (59.41%), biological yield per plant (59.40%), panicle length (49.50%) and grain yield per plant (38.32%) under saline condition.

Identification of parents based on mean performance and GCA effects

Mean performance and GCA effects of the parents have been given in table 3 for normal and in table 4 for saline conditions.

The significant and positive GCA effects for grain yield per plant were exhibited by NDRK 5014, NDRK 5035, NDRK 5071, NDRK50001, IR 74095AC -64, IR 72579-2-2R, HPU-CIJ and LD 183-4 among line and by Narendra Usar Dhan-3 among testers. The parent NDRK 5014, with highest GCA effects for grain yield per plant also showed significant and desirable GCA effects for panicle length and biological yield per plant. Parent NDRK 5035 recorded significant and desirable GCA effects for spikelets per panicle and biological yield per plant. Line NDRK 5071 emerged as good general combiner for spikelets per panicle and biological yield per plant. Line NDRK 50001 emerged as good general combiner for panicle length and spikelet fertility. IR 74095 AC 64 was identified as good general combiner for panicle length and biological yield per plant. HPU-CIJ recorded significant and desirable GCA effects for panicle bearing tillers per plant, spikelets per panicle, grains per panicle and biological yield per plant. LD 183-4 emerged as good general combiner for panicle length and biological yield per plant under normal condition.

The significant and positive GCA effects for grain yield per plant were exhibited by NDRK 5014, NDRK 5016, NDRK 5035, NDRK 50001, CSR 28, IR 74095AC -64, HPU-CIJ and LD 183-4 among line and by Narendra Usar Dhan-3 among testers. The parent NDRK 5014, with highest GCA effects for grain yield per plant also showed significant and desirable GCA effects for panicle length, spikelets per panicle, grains per panicle, biological yield per plant and harvest index. Parent NDRK 5016 recorded significant and desirable GCA effects for panicle bearing tillers per plant, panicle length and harvest index. Line NDRK 5035 emerged as good general combiner for spikelets per panicle, grains per panicle and spikelet fertility. Line NDRK 50001 emerged as good general combiner for panicle bearing tillers per plant, panicle length,

spikelets per panicle, grains per panicle and biological yield per plant. CSR 28 was identified as a good general combiner for biological yield per plant and harvest index. IR 74095 AC 64 was identified as good general combiner for panicle bearing tillers per plant, spikelets per panicle, grains per panicle and biological yield per plant. HPU-CIJ recorded significant and desirable GCA effects for panicle length, grains per panicle, spikelet fertility and biological yield per plant. LD 183-4 emerged as good general combiner for panicle length, spikelets per panicle, grains per panicle, spikelet fertility and harvest index under saline condition.

The nine parents for normal and eight parents for saline conditions showing positive and significant GCA effects for grain yield and other important traits as mentioned above may serve as valuable parents for hybridization programme or multiple crossing programme for obtaining high yielding hybrid varieties. Dwivedi et al., (1999) [4, 5] have also reported Narendra 359 and Sarjoo 52 as good general combiner for yield and its associated traits over environments.

Identification of hybrids based on SCA effects, mean performance and standard heterosis

The SCA effects represent dominance and epistasis gene actions and can be used as an index to determine the worth of a particular cross combination in the exploitation of heterosis. Thirteen crosses, NDRK 5014 × Narendra Usar Dhan-2, NDRK 5071 × Narendra Usar Dhan-2, NDRK 5032 × Narendra Usar Dhan-3, NDRK 5071 × Narendra Usar Dhan-3, NDRK 50001 × Narendra Usar Dhan-3, IR 74095 AC 64 × Narendra Usar Dhan-3, LD 183-4 × Narendra Usar Dhan-3, CSR 23 × Narendra Usar Dhan-2009, IR SST N 27 × Narendra Usar Dhan-2009, CSR 23 × Narendra Usar Dhan-2, NDRK 5030 × Narendra Usar Dhan-3, NDRK 5014 × Narendra Usar Dhan-2009 and HPU-CIJ × Narendra Usra Dhan 2009 exhibited significant and positive SCA effects for grain yield per plant, as well as for some other yield components (Table 5 and 6 for normal condition). Perusal of data on the top hybrids having the highest SCA effects for grain yield per plant indicated that crosses involved high×high (IR 27579-B-2R × Narendra Usar Dhan 3, IR 74095 AC 64 × Narendra Usar Dhan 3, NDRK 50001 × Narendra Usar Dhan 3, NDRK 5071 × Narendra Usar Dhan 3 and LD 183-4 × Narendra Usar Dhan 3), high × average (NDRK 5071 × Narendra Usar Dhan 2, NDRK 5071 × Narendra Usar Dhan 2 and NDRK 5032 × Narendra Usar Dhan 3), high × low (NDRK 5071 × Narendra Usar Dhan 2009, HPU-CIJ × Narendra Usar Dhan 2009, NDRK 5014 × Narendra Usar Dhan 2009 and NDRK 5030 × Narendra Usar Dhan 3), low × average (CSR 23 × Narendra Usar Dhan 2), low × low (IR SST N 27 × Narendra Usar Dhan 2009 and CSR 23 × Narendra Usar Dhan 2009) general combining parents. These results are in agreement with the findings of Ram et al. (1994) and Dwivedi et al., (1999) [4,5]. However, in self-pollinated crops, the additive × additive type of interaction is also fixable in later generations if the crosses showing high SCA effects involved parents which are good general combiners. Such crosses are expected to through some useful transgressive segregates in the breeding program for pedigree method of selection. Moreover, if the hybrids showing high SCA effects involved high × low general combiner parents (Table 5), the high SCA effect was attributed due to the interaction between positive effect allele from the good combiners and negative alleles from the poor combiners. The high yield from such crosses would be non-fixable in subsequent generations. If high × high GCA combiners would be involved in high heterosis, it would be due to interaction

between positive × positive alleles and can be fixable in the subsequent generation if repulsion phase linkage were involved. Combining ability studies indicated that crosses with significant and positive SCA effects involved parents with high×high general combiner 33.33% and high×low with 13.33% in F_1. Thus, it is evident from the SCA effects of crosses for grain yield per plant were attributed almost equally due to dominance and epistasis gene interaction or due to additive×additive interaction. Young (1987) [13] indicated that, in majority of the crosses, the high SCA effects of grain yield were attributed to dominance and epistasis effects under normal condition.

The estimates of standard heterosis ranged between -34.38 to 64.05%. The top hybrids recording the high SCA effects for grain yield were shown to manifest high standard heterosis. The hybrids IR 74095AC64 × Narendra Usar Dhan 3, NDRK 50001 × Narendra Usar Dhan 3, NDRK 5071 × Narendra Usar Dhan 3. LD 183-4 × Narendra Usar Dhan 3, NDRK 5071 × Narendra Usar Dhan 2, NDRK 5014 × Narendra Usar Dhan 2 and NDRK 5032 × Narendra Usar Dhan 3 with high SCA effects for grain yield revealed significant standard heterosis and high mean performance involved both parents as high general combiner or one parent high and other as average combiner. High performances of such combinations are due to interaction of additive genes contributed by the parents. These crosses can be exploited through conventional breeding methods to isolate high-yielding pure lines. The higher heterosis in hybrids, HPU-CIJ × Narendra Usar Dhan 2009, NDRK 5030 × Narendra Usar Dhan 3, CSR 23 × Narendra Usar Dhan 2 and CSR 23 × Narendra Usar Dhan 2 resulted from high × low or average × low and in crosses IRSSTN 27 × Narendra Usar Dhan 2009 and CSR 23 × Narendra Usar Dhan 2009 resulted from low × low general combiner, probably due to dominance and epistatic interaction with non-additive and non-fixable genetic component for grain yield. Random mating and selection among the segregates would lead to transgressive segregation in later generations. These hybrids can be exploited directly for hybrid breeding.

A closer examination of SCA effects of top crosses (Table 6) showing the maximum SCA effects for grain yield indicated that most of the crosses also displayed significant and high SCA effects for some major yield contributing characters such as panicle bearing tillers per plant, panicle length, spikelets per panicle, grains per panicle, spikelet fertility (%), biological yield per plant and harvest index. In general, the reports in the literature (Ram et al., 1994) [10] also supported the present findings. Some crosses, specifically NDRK 50001 × Narendra Usar Dhan 3, CSR 23 × Narendra Usar Dhan 2, NDRK 5032 × Narendra Usar Dhan 3, NDRK 5014 × Narendra Usar Dhan 2 and HPU-CIJ × Narendra Usar Dhan 2009 exhibited high SCA, mean performance and standard heterosis were suggested for exploitation in the breeding program to create high-yielding pure lines by pedigree selection and/or directly for hybrid breeding.

In saline condition, none of the crosses showed significant SCA effects in desirable direction for all the characters under study. Several crosses exhibited significant and desirable SCA effects for one or more characters but none of them emerged as good specific combination for more than six characters. Nine crosses, NDRK 5071 × Narendra Usar Dhan-2, IR 27579-B-2R × Narendra Usar Dhan-2, NDRK 5032 × Narendra Usar Dhan-3, NDRK 5043 × Narendra Usar Dhan-3, NDRK 5071 × Narendra Usar Dhan-3, NDRK 50001 × Narendra Usar Dhan-3, CSR 23 × Narendra Usar Dhan-3, NDRK 5030 × Narendra Usar Dhan-2009 and NDRK 5071 × Narendra Usar Dhan-2009 showed highly significant and

positive SCA effects for grains yield per plant, while, two crosses CSR 23 × Narendra Usar Dhan-2009 and HPU-CIJ × Narendra Usar Dhan 2009 exhibited significant and positive SCA effects for yield and some yield components.

Perusal of data on the hybrids having the high SCA effects for grain yield per plant under saline condition (Table 7 and 8) indicated that crosses involved high× high (NDRK 50001 × Narendra Usar Dhan 3), high × low (HPU-CIJ × Narendra Usar Dhan 2009 and NDRK 5043 × Narendra Usar Dhan 3), and low × low (NDRK 5071 × Narendra Usar Dhan 2 and IR 27579-B-2R × Narendra Usar Dhan 2) general combining parent. These results are in agreement with the findings of Ram et al. (1994) [10]. In self-pollinated crops, the additive × additive type of interaction component is fixable if the crosses showing high SCA effects involved parents with high general combiners. If high × high GCA combiners would be involved in high heterosis, it would be due to interaction between positive × positive alleles and can be fixable in the subsequent generation if repulsion phase linkage were involved. Such crosses are expected to through some useful transgressive segregates in the breeding program for pedigree method of selection. Moreover, if the hybrids showing high SCA effects involved high × low or low × low parents (Table 7), the high yield from such crosses would be non-fixable in subsequent generations. It is evident from the SCA effects of crosses for grain yield per plant were attributed almost equally due to dominance and epistasic gene interaction or due to additive×additive interaction. Young (1987) [13] indicated that, in majority of the crosses, the high SCA effects of grain yield were attributed to dominance and epistasic effects.

The estimates of standard heterosis ranged between -52.52 to 48.64%. The hybrids NDRK 50001 × Narendra Usar Dhan 3, IR 27579-B-2R × Narendra Usar Dhan 2, NDRK 5043 × Narendra Usar Dhan 3, HPU-CIJ × Narendra Usar Dhan 2009 and NDRK 5071 × Narendra Usar Dhan 2 with high SCA effects for grain yield revealed significant standard heterosis and per se performance and involved both parents as a high general combiner (NDRK 50001 × Narendra Usar Dhan 3), one high and other low combiner (NDRK 5043 × Narendra Usar Dhan 3 and HPU-CIJ × Narendra Usar Dhan 2009) and both low combiners (HPU-CIJ × Narendra Usar Dhan 2009 and NDRK 5071 × Narendra Usar Dhan 2). The cross having both high general combiner parents can be exploited to isolate high-yielding pure lines and crosses involving high × low and low × low general combining parents can be exploited directly for hybrid breeding.

A closer examination of SCA effects of top crosses (Table 7) showing the maximum SCA effects for grain yield indicated that most of the crosses also displayed significant and high SCA effects for some major yield contributing characters such as panicle bearing tillers per plant, panicle length, spikelet per panicle, grains per panicle, spikelet fertility (%), biological yield and harvest index. In general, the reports in the literature (Ram et al., 1994) [10] also supported the present findings.

Table 1: Mean square for analysis of variance, estimates of genetic components and contribution of line, tester and line X tester to the total variance in rice genotypes under normal condition

Source	d.f.	Plant bearing tillers per plant	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	Biological yield per plant (g)	Harvest index (%)	Grains yield per plant(g)
Replication	2	0.59	0.27	32.58*	3.94	9.04	7.59	7.09	0.5
Treatment	74	18.85**	18.65**	2016.38**	1794.30**	13.53**	238.04**	30.17**	36.48**
Parents	20	30.55**	17.31**	1062.69**	959.37**	8.17*	121.55**	24.49**	18.92**
Parent vs crosses	1	45.42**	0.52	7301.85**	7279.45**	36.77**	29.91**	4.73	11.62**
Crosses	53	13.93**	19.49**	2276.54**	2005.87**	15.11**	285.92**	32.79**	43.57**
Line	17	14.84	26.46*	1398.34	1351.46	15.03	394.40*	41.06	76.24**
Tester	2	12.84	35.5	5622.74	4838.59	3.42	65.13	21.76	16.43
L×T	34	13.54**	15.07**	2518.81**	2166.45**	15.84**	244.66**	29.30**	28.83**
Error	148	1.95	2.24	7.24	8.31	5.32	3.6	5.4	1.47
σ^2GCA		0.004	-0.078	-2.589	-1.716	-0.008	0.441	0.037	0.158
σ^2SCA		3.913	27.623	1067.282	932.165	2.065	75.392	8.298	12.418
σ^2GCA/σ^2SCA		0.001	-0.003	-0.002	-0.002	-0.004	0.006	0.004	0.013
σ^2A		0.008	0.095	-5.179	-3.432	-0.016	0.882	0.075	0.315
σ^2D		3.913	7.635	1067.282	932.165	2.065	75.392	8.298	12.418
$(\sigma^2A/\sigma^2D)^{1/2}$		0.0010	0.0062	-0.0024	-0.0018	-0.0039	0.0058	0.0045	0.0127
PCV		34.68	11.72	20.4	20.81	3.07	16.4	8.24	14.74
GCV		29.88	9.87	20.3	20.66	1.79	16.04	6.41	13.89
$h^2_{(b.s.)}$ ±SE		74.26 ±1.14	70.94 ±1.22	98.93 ±2.20	98.62 ±2.35	33.96 ±1.88	95.6 ±1.55	60.48 ±1.90	88.78 ±0.99
GA		53.12	17.11	41.62	42.33	2.15	32.3	10.27	26.95
Contribution % of Lines		34.16	43.54	19.7	21.61	31.91	44.24	40.17	56.12
Testes		3.47	6.87	9.32	9.1	0.85	0.85	2.5	1.42
Line×Tester		62.36	49.58	70.97	69.28	67.23	54.89	57.32	42.45

*, ** Significant at 5% and 1% probability levels, respectively

Table 2: Mean square for analysis of variance, estimates of genetic components and contribution of line, tester and line X tester to the total variance in rice genotypes under saline condition

Source	d.f.	Plant bearing tillers per plant	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	Biological yield per plant(g)	Harvest index (%)	Grains yield per plant(g)
Replication	2	0.3	1.78	1.7	7.37	6.76	5.61	3.41	2.48
Treatment	74	5.38**	15.46**	2146.21**	1789.41**	62.52**	268.72**	101.38**	50.56**
Parents	20	6.17**	9.52**	1293.56**	1214.18**	26.41**	172.51**	65.67**	46.36**
Parent vs crosses	1	1.77	3.08	6185.30**	2837.40**	120.06**	235.94**	88.73**	0.65
Crosses	53	5.15**	17.93**	2391.75**	1986.70**	75.07**	305.64**	115.09**	53.09**
Line	17	3.58	26.51*	2395.73	1733.99	78.01	327.52	141.73	98.45*
Tester	2	3.01	14.67	2919.79	2645.87	14.3	504.84	33.4	31
L×T	34	6.06**	13.84**	2358.70**	2074.29**	77.17**	282.98**	106.58**	31.71**
Error	148	0.59	1.4	7.11	7.99	4.99	5.22	4.92	1.36
σ^2GCA		-0.010	-0.005	0.353	-0.936	-0.022	0.242	0.091	0.229
σ^2SCA		1.247	14.775	848.996	717.976	17.252	121.278	29.322	16.597
σ^2GCA/ σ^2SCA		-0.008	0.000	0.000	-0.001	-0.001	0.002	0.003	0.014
σ^2A		-0.019	0.088	0.706	-1.872	-0.045	0.484	0.182	0.457
σ^2D		1.247	5.480	848.996	717.976	17.252	121.278	29.322	16.597
$(\sigma^2$A/ σ^2D$)^{1/2}$		-0.008	0.008	0.000	-0.001	-0.001	0.002	0.003	0.014
PCV		21.92	10.83	19.43	20.2	5.59	19.52	13.92	19.65
GCV		18.75	9.5	19.33	20.06	4.98	18.97	12.97	18.88
h^2 (b.s.) ±SE		73.17 ±0.63	76.94 ±0.97	99.01 ±2.18	98.67 ±2.31	79.34 ±1.82	94.39 ±1.87	86.74 ±1.81	92.34 ±0.95
GA		33.02	17.17	39.55	40.98	9.14	37.91	24.84	37.32
Contribution % of Lines		22.32	47.41	32.13	28	33.34	34.37	39.5	59.48
Testes		2.2	3.09	4.61	5.03	0.72	6.23	1.1	2.2
Line×Tester		75.47	49.5	63.26	66.98	65.95	59.4	59.41	38.32

*,** Significant at 5% and 1% probability levels, respectively

Table 3: Mean performance and general combining ability (GCA) effects of parents (lines and testers) for 8 characters in rice under normal condition

S.N.	Line	Plant bearing tillers per plant		Panicle length (cm)		Spikelet per panicle		Grains per panicle		Spikelet fertility (%)		Biological yield per plant(g)		Harvest index (%)		Grains yield per plant(g)	
		Mean	GCA	Mean	GCA	MEAN	GCA	Mean	MEAN	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
1	NDRK-5014	10.6	-0.72	23.9	2.14**	46.13	-7.53**	21.22	-10.68**	93.89	-3.14**	132.78	3.90**	124.65	0.63	93.89	2.16**
2	NDRK-5016	7.73	2.38**	27.83	0.61	43.15	11.66**	16.02	12.85**	95.88	1.49	147.24	-3.51**	141.12	0.92	95.88	-0.97*
3	NDRK-5030	11.8	1.27**	21.1	-0.15	48.28	20.43**	33.16	18.06**	91.76	-0.78	126.84	-14.18**	116.39	0.44	91.76	-5.99**
4	NDRK-5032	13.06	2.14**	22.1	-1.70**	44.44	-16.99	26	-14.24**	92.61	1.03	214.8	-3.30**	198.88	3.71**	92.61	0.55
5	NDRK-5035	7.2	0.10	25.77	-1.65**	47.13	0.15**	20.65	-0.87**	87.80	-0.57	106.98	4.22**	93.92	-0.92	87.8	1.37**
6	NDRK-5043	6.53	-1.39**	22.7	0.13	44.54	7.43**	19.41	7.28**	94.31	0.83	111.38	-1.87**	104.99	-2.84**	94.31	-2.51**
7	NDRK-5062	11.06	-0.57	20.5	-0.97	49.19	7.25	19.12	7.11**	95.33	0.33	106.71	-7.72**	101.72	-0.98	95.33	-3.91**
8	NDRK-5071	7.46	-0.33	22.9	-1.79**	49.55	0.21**	20.23	0.39	90.02	0.09	81.44	4.59**	73.32	0.94	90.02	2.73**
9	NDRK-5081	10.86	0.94*	22.5	-0.70	47.19	7.13**	24.54	5.41**	94.80	-0.23	132.76	-3.99**	125.85	0.95	94.8	-1.34**
10	NDRK-5092	6.21	-0.59	21.64	-2.38**	45.75	-4.75**	30.6	-5.21**	90.78	-0.97	146.96	-4.64**	133.42	1.12	90.78	-1.32**
11	NDRK-50001	7.74	-0.45	22.97	3.40**	44.64	11.42**	22.35	13.80**	90.15	2.52**	119.81	10.18**	107.99	-1.52	90.15	2.97**
12	CSR – 23	9.34	0.78	21.44	-0.64	41.64	13.55**	22.5	14.67**	94.41	1.52**	105.55	-5.65**	99.59	-5.04**	94.41	-4.81**
13	CSR – 28	6.01	-0.81	25.33	-1.22*	37.68	-19.70**	32.31	-19.39**	89.98	-1.16	165.43	0.76	148.83	2.25**	89.98	1.72**
14	IR SST-N 27	5.34	-0.22	23.9	0.68	47.81	9.24**	24.13	8.10**	95.02	-0.25	75.29	-3.65**	71.53	2.05**	95.02	-0.45
15	IR 74095 AC 64	7.47	-1.17*	22.17	1.78**	40.8	-14.31**	14.29	-13.90**	94.54	-0.70	153.45	10.58**	145.07	0.34	94.54	4.80**
16	IR 72579-B-2R	7.67	-1.35**	20.84	-1.49**	46.98	-22.30**	16.64	-21.38**	95.54	-0.46	123.77	-0.11	118.23	1.42	95.54	0.85*
17	HPU-CIJ	7.47	1.93**	22.84	1.01*	43.96	4.38**	22.32	5.50**	89.15	1.12	122.76	6.41**	109.43	-0.25	89.15	2.50**
18	LD 183-4	6.14	-1.91**	24.44	2.95**	40.93	-7.27**	31.94	-7.50**	93.34	-0.69	147.12	7.97**	137.27	-3.21**	93.34	1.63**
	GM	8.32		23.05		44.99		23.19		92.74		128.95		119.57		92.74	
	SE (gi) line		0.47		0.50		0.90		0.96		0.77		0.63		0.77		0.40
	Tester																
1	Narendra Usar Dhan 2	5.34	0.14	24.12	0.81**	46.5	9.53**	31.95	8.67**	89.56	0.00	107.5	-0.58*	96.26	0.73*	89.56	0.17
2	Narendra Usar Dhan 3	7.14	-0.54**	28.39	0.00	41.04	-10.77**	29.04	-10.10**	90.29	-0.25	125.28	1.27**	113.06	-0.29	90.29	0.44**
3	Narendra Usar Dhan 2009	8.34	0.40*	24.91	-0.81**	49.16	1.24**	23.21	1.43**	87.78	0.25	116.51	-0.68**	102.25	-0.44	87.78	-0.62**
	GM	6.94		25.81		45.57		28.07		89.21		116.43		103.86		89.21	
	SE(gi) tester		0.19		0.20		0.37		0.39		0.31		0.26		0.32		0.17

*, ** Significant at 5% and 1% probability levels, respectively

Table 4: Mean performance and general combining ability (GCA) effects of parents (lines and testers) for 8 characters in rice under saline condition

S.N.	Line	Plant bearing tillers per plant		Panicle length (cm)		Spikelets per panicle		Grains per panicle		Spikelet fertility (%)		Biological yield per plant (g)		Harvest index (%)		Grains yield per plant(g)	
		Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
1	NDRK-5014	9.32	0.45	23.65	0.89*	45.94	4.84**	19.31	17.72**	135.51	-0.24	120.42	2.01**	88.91	4.84**	24.42	3.60**
2	NDRK-5016	7.52	0.59*	22.85	1.74**	40.58	1.79*	19.2	-18.84**	127.72	1.01	110.53	2.86**	86.56	1.79*	22.31	2.34**
3	NDRK-5030	5.32	0.09	26.85	-0.51	48.89	-2.58**	31.89	-5.22**	92.85	-1.19	83.53	-15.55**	89.97	-2.58**	24.73	-7.28**
4	NDRK-5032	7.99	-0.28	21.88	-2.10**	41.38	2.98**	17.75	0.50	144.98	3.87**	129.6	-3.52**	89.39	2.98**	13.05	0.09
5	NDRK-5035	6.2	-0.59*	22.88	-1.42**	45.12	1.70*	21.02	26.42**	143.17	3.10**	122.03	4.68**	85.25	1.70*	18.26	3.16**
6	NDRK-5043	6.47	0.30	21.84	-2.58**	35.8	2.10**	22.53	-11.46**	123.2	-1.45	103.68	-3.49**	84.22	2.10**	11.28	-0.44
7	NDRK-5062	8.2	-0.38	19.34	-2.48**	47.71	0.43	18.28	-17.78**	160.95	0.37	144.68	-4.72**	89.95	0.43	22	-1.77**
8	NDRK-5071	5	-0.07	22.58	-0.71	46.95	-5.13**	20.43	2.03*	97.8	1.50*	88.22	-2.54**	90.23	-5.13**	23.47	-2.97**
9	NDRK-5081	6.34	1.16**	19.92	-0.29	44.3	-5.66**	24.25	-13.13**	148.79	1.16	139.6	3.44**	93.83	-5.66**	19.24	-2.81**
10	NDRK-5092	5.34	-0.48	19.93	-1.23**	45.33	1.09	21.11	-12.49**	187.83	-4.14**	170.91	-6.27**	90.99	1.09	22.23	-1.77**
11	NDRK-50001	7.2	0.93**	22.65	3.36**	46.89	-1.11	30.62	12.07**	165.81	-3.06**	149.43	11.29**	90.12	-1.11	26.73	3.99**
12	CSR – 23	6.07	-0.76**	21.27	-0.05	42.9	1.56*	31.24	16.22**	143.55	-5.35**	129.92	-0.72	90.6	1.56*	24.95	0.67
13	CSR – 28	6	0.05	18.97	-0.64	48.18	4.13**	16.46	-6.20**	141.68	1.16	125.36	1.59*	88.49	4.13**	22.44	2.99**
14	IR SST-N 27	6.76	-0.54*	19.97	0.14	47.79	-11.18**	18.98	-15.51**	121.37	-0.11	105.19	1.66*	86.65	-11.18**	20.01	-6.11**
15	IR 74095 AC 64	8.53	0.87**	21.44	2.05**	40.37	0.31	32.65	5.99**	127.91	0.58	106.05	7.62**	82.91	0.31	20.68	3.45**
16	IR 72579-B-2R	6.76	-1.14**	20.26	1.22**	45.94	1.74*	20.24	-2.12*	132.86	-5.12**	124.25	-3.82**	93.51	1.74*	18.5	-0.67
17	HPU-CIJ	6.33	-0.40	21.55	-0.08	45.55	-0.14	21.23	2.70**	136.07	4.35**	121.39	5.67**	89.21	-0.14	20.33	1.92**
18	LD 183-4	6.17	0.19	18.88	2.69**	39.81	3.13**	22.07	19.12**	89.16	3.54**	72.02	-0.19	80.8	3.13**	20.3	1.63**
	GM	6.75		21.48		44.41		22.74		134.51		119.27		88.42		20.83	
	SE (gi) line		0.26		0.39		0.74		0.94		0.74		0.76		0.74		0.39
1	Narendra Usar Dhan 2	6.85	0.27*	23.33	0.54**	47.42	0.25	24.72	7.75**	204.77	0.58	174.35	-1.62**	85.18	0.25	25.1	-0.57**
2	Narendra Usar Dhan 3	6.18	-0.10	22.57	-0.04	48.37	-0.88**	21.13	-5.87**	146.61	-0.40	133.03	3.53**	90.74	-0.88**	25.19	0.86**
3	Narendra Usar Dhan 2009	8.72	-0.17	24.9	-0.50**	48.75	0.63*	19.72	-1.88**	136.11	-0.18	116.75	-1.91**	85.79	0.63*	24.95	-0.29
	GM	7.25		23.6		48.18		21.86		162.5		141.38		87.23		25.08	
	SE(gi) tester		0.10		0.16		0.30		0.38		0.30		0.31		0.30		0.16

Table 5: Specific combining ability effects, mean performance, heterosis of crosses and general combining ability of parents involved in crosses for grain yield per plant in rice under normal condition.

S.N.	Line	SCA	Mean	Standard heterosis	GCA
1	IR SST N 27 × Narendra Usar Dhan 2009	5.73**	24.83	13.55 **	L×L
2	IR 74095 AC 64 × Narendra Usar Dhan 3	4.04**	24.75	21.50 **	H×H
3	NDRK 5071 × Narendra Usar Dhan 2	4.01**	27.3	34.04 **	H×A
4	CSR 23 × Narendra Usar Dhan 2009	3.67**	23.13	13.55 **	L×L
5	NDRK 50001 × Narendra Usar Dhan 3	3.44**	33.42	64.05 **	H×H
6	NDRK 5071 × Narendra Usar Dhan 3	3.41**	24.29	19.23 **	H×H
7	LD 183-4 × Narendra Usar Dhan 3	2.69**	23.42	14.96 **	H×H
8	NDRK 5032 × Narendra Usar Dhan 3	2.54**	30.43	49.40 **	A×H
9	NDRK 5014 × Narendra Usar Dhan 2	2.07**	30.19	48.21 **	H×A
10	HPU-CIJ × Narendra Usra Dhan 2009	1.66**	28.55	40.16 **	H×L
11	NDRK 5014 × Narendra Usa rDhan 2009	1.53*	23.47	15.22 **	H×L
12	CSR 23 × Narendra Usar Dhan 2	1.49*	31.13	52.84 **	L×A
13	NDRK 5030 × Narendra Usar Dhan 3	1.49*	23.67	16.18 **	L×H

*, ** Significant at 5% and 1% probability levels, respectively

Table 6: Estimates of specific combining ability effects of significant crosses for grain yield and associated traits in rice under normal condition

S.N.	Line	Plant bearing tillers per plant	Panicle length (cm)	Spikelet per panicle	Grains per panicle	Spikelet fertility (%)	Biological yield per plant (g)	Harvest index (%)	Grains yield per plant (g)
1	IR SST N 27 × Narendra Usar Dhan 2009	-2.38**	-1.37	6.79**	5.72**	-0.25	18.02**	-3.14*	5.73**
2	IR 74095 AC 64 × Narendra Usar Dhan 3	0.22	-0.80	-2.21	-0.77	0.85	20.35**	-6.44	4.04**
3	NDRK 5071 × Narendra Usar Dhan 2	-1.19	2.24**	-26.64**	-28.58**	-3.52**	6.77**	0.2	4.01**
4	CSR 23 × Narendra Usar Dhan 2009	-0.55	1.24	25.04**	20.71**	-2.01	6.44**	1.09	3.67**
5	NDRK 50001 × Narendra Usar Dhan 3	-0.56	-0.42	-14.37**	-16.24**	-2.91*	6.09**	1.28	3.44**
6	NDRK 5071 × Narendra Usar Dhan 3	-0.7	-0.92	-43.27**	-38.12**	1.36	11.04**	-2.77*	3.41**
7	LD 183-4 × Narendra Usar Dhan 3	-1.94*	1.00	-4.11**	-8.52**	-3.40*	1.99	3.69**	2.69**
8	NDRK 5032 × Narendra Usar Dhan 3	-0.27	0.76	-17.20**	-15.58**	0.3	6.00**	-0.39	2.54**
9	NDRK 5014 × Narendra Usar Dhan 2	-1.74*	-2.50**	-18.46**	-16.26**	0.35	4.05**	0.2	2.07**
10	HPU-CIJ × Narendra Usra Dhan 2009	0.75	4.00**	-21.67**	-19.12**	0.76	0.36	2.28	1.66*
11	NDRK 5014 × Narendra Usar Dhan 2009	-0.23	-1.07	-38.94**	-35.86**	-0.42	4.83**	-1.25	1.53*
12	CSR 23 × Narendra Usar Dhan 2	0.66	1.35	24.56**	24.12**	1.16	4.06**	-1.01	1.49*
13	NDRK 5030 × Narendra Usar Dhan 3	-1.36	2.55**	14.67**	14.19**	0.41	6.12**	-2.59	1.49*

*,** Significant at 5% and 1% probability levels, respectively

Table 7: Specific combining ability effects meanper formance, heterosis of crosses and general combining ability of parents involved in crosses for grain yield per plant in rice under saline condition

S.N.	Line	SCA	Mean	Standard heterosis	GCA
1	NDRK 5071 × Narendra Usar Dhan 2009	6.23**	18.37	-14.73 **	L×L
2	NDRK 5032 × Narendra Usar Dhan 3	6.06**	18.77	-12.88 **	A×H
3	NDRK 5030 × Narendra Usar Dhan 2009	3.87**	23.05	7.01	L×L
4	NDRK 5071 × NarendraUsar Dhan 3	3.51**	20.30	-5.76	L×H
5	NDRK 5071 × NarendraUsar Dhan 2	3.20**	23.47	8.94 *	L×L
6	CSR 23 × NarendraUsar Dhan 3	2.92**	22.67	5.23	A×H
7	NDRK 50001 × NarendraUsar Dhan 3	2.90**	24.36	13.11 **	H×H
8	NDRK 5043 × NarendraUsar Dhan 3	2.22**	24.00	11.42 **	L×H
9	IR 27579-B-2R × NarendraUsar Dhan 2	1.96**	25.00	16.06 **	L×L
10	CSR 23 × NarendraUsar Dhan 2009	1.66*	21.70	0.74	A×L
11	HPU-CIJ × Narendra Usra Dhan 2009	1.45*	21.70	9.87 *	H×L

*,** Significant at 5% and 1% probability levels, respectively

Table 8: Estimates of specific combining ability effects of significant crosses for grain yield and associated traits in rice under saline condition.

S.N.	Line	Panicle bearing tillers/plant	Panicle length (cm)	Spikelet/ panicle	Grains/ panicle	Spikelet fertility (%)	Biological yield / plant (g)	Harvest index (%)	Grains yield / plant (g)
1	NDRK 5071 × Narendra Usar Dhan 2009	-1.12*	0.35	-13.67**	-19.00**	-5.12**	16.90**	-1.78	6.23**
2	NDRK 5032 × Narendra Usar Dhan 3	-0.62	1.06	18.29**	17.08**	0.25	5.92**	7.86**	6.06**
3	NDRK 5030 × NarendraUsarDhan 2009	-0.04	-0.64	-14.19**	-19.61**	-6.04**	-1.68	6.23**	3.87**
4	NDRK 5071 × Narendra Usar Dhan 3	-1.91**	-0.39	-15.47**	-11.69**	1.8	-4.18**	6.75**	3.51**
5	NDRK 5071 × Narendra Usar Dhan 2	-0.58	0.72	11.90**	9.46**	-0.64	2.46	5.24**	3.20**
6	CSR 23 × Narendra Usar Dhan 3	-0.23	0.01	-0.88	-3.40*	-2.26	3.32*	4.33**	2.92**
7	NDRK 50001 × Narendra Usar Dhan 3	1.18**	0.47	27.01**	17.86**	-3.66**	3.44**	2.68*	2.90**
8	NDRK 5043 × NarendraUsarDhan 3	0.35	-0.02	-15.92**	-18.26**	-2.79**	3.93**	2.52*	2.22**
9	IR 27579-B-2R × Narendra Usar Dhan 2	-1.37**	-1.70**	3.11*	5.41**	1.89	1.57	2.48	1.96**
10	CSR 23 × Narendra Usar Dhan 2009	-1.22**	-0.93	31.61**	34.71**	5.74**	5.20**	-0.95	1.66*
11	HPU-CIJ × Narendra Usra Dhan 2009	-1.58**	3.06**	10.13**	10.40**	0.67	2.02	1.02	1.45*

*,** Significant at 5% and 1% probability levels, respectively

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