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Combining ability analysis for yield and its quality traits in rice (*Oryza sativa* L.) over environment

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Abstract

Line \times tester experiment was conducted to evaluate the performance of 54 F_1 hybrids along with 18 parents in rice. Analysis of variance revealed highly significant differences in treatment for 1000 grain weight, kernel length, kernel breadth, L:B ratio and grain yield per plant under both normal and saline conditions except kernel breadth which found significant for normal condition. Analysis of variance revealed highly significant differences among crosses and lines \times testers for 1000 grain weight, kernel length, kernel breadth, L:B ratio and grain yield per plant under both normal and saline conditions. Parents *vs.* crosses were for kernel length and grain yield per plant for normal condition while in case of saline condition kernel breadth was found highly significant. Lines were highly significant and significant for 1000 grain weight and grain yield per plant in normal and saline condition, respectively. Testers were non-significant for all the traits in both conditions except kernel length in normal condition which was found significant. 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 quality traits were more than testers and line \times tester interaction under both conditions.

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

1. 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-alkaline 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 million tonnes and 140 million tonnes, respectively. This increased productivity and quality rice 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 alkaline soils are wide spread in inland areas as that in U.P.

Line \times 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 quality hybrid variety or quality cultivar development programme.

Information on general and specific combining ability for quality components will prove very useful in selection of appropriate parents for the development of superior quality hybrids. The knowledge of heritability and genetic advance of quality 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 objectives to assess combining ability based on mean performance, genetic components and heterosis controlling some quality traits in rice. The information obtained thus will be used in selection of suitable parents and choice of appropriate breeding methods to develop high quality and 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 quality traits like 1000 grain weight (g), kernel length (mm), kernel breadth (mm), L:B ratio (%) and grains yield per plant (g). In this paper above these characters are discussed. 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) [11]. 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). 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

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

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

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

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

$$\text{Heterosis over standard variety (Standard heterosis)} = \frac{\bar{F}_1 - \bar{SV}}{\bar{SV}} \times 100$$

Where,

$$\bar{F}_1 = \text{Mean of } F_1$$

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

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

$$t' (\text{Standard heterosis}) = \frac{\bar{F}_1 - \bar{SV}}{\text{S.E.}}$$

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

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 in treatments for 1000 grain weight, kernel length, kernel breadth, L:B ratio and grain yield per plant under both normal and saline conditions except kernel breadth which found significant only in normal condition. Analysis of variance revealed highly significant differences among crosses and lines × testers for 1000 grain weight, kernel length, kernel breadth, L:B ratio and grain yield per plant under both normal and saline conditions. Parents vs. crosses were highly significant for kernel length and grain yield per plant for normal condition while in case of saline condition kernel breadth was found highly significant. Lines were highly significant and significant for 1000 grain weight and grain yield per plant in normal and saline condition, respectively. Testers were non-significant for all the traits in both conditions except kernel length in normal condition which was found significant. The success of selection in improving quality 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 quality 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 action. The above results suggested importance of both additive and non-additive gene effects for quality and yield 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 five characters of 54 crosses and their parents (Table 1 and 2 for normal and saline conditions, respectively).

In normal condition, none of the character having high estimates for genotypic and phenotypic coefficient of variation, heritability in broad sense along with genetic advance in per cent of mean. 1000 grains weight recorded high heritability estimates, while, moderate for GCV, PCV and genetic advance in per cent of mean. Kernel length showed moderate estimates for heritability and genetic advance in per cent of mean, while, low estimates for PCV, GCV. Kernel breadth showed low estimates for PCV, GCV, heritability in broad sense and genetic advance in per cent of mean. L:B ratio showed moderate PCV, GCV, heritability in broad sense and genetic advance in per cent of mean. Grain yield per plant were recorded with high estimates of heritability and genetic advance in per cent of mean and moderate for PCV and GCV.

Under saline condition, 1000 grain weight recorded high heritability and genetic advance in per cent of mean, while, moderate for PCV and GCV. Kernel length and kernel breadth showed low estimates for PCV, GCV, heritability and genetic advance in per cent of mean. L:B ratio showed moderate for PCV and genetic advance in per cent of mean, while, low estimates for GCV and heritability in broad sense. Grain yield per plant were recorded high estimates for heritability and genetic advance in per cent of mean and moderate for PCV and GCV. The low to high estimates of direct selection parameters for above mentioned characters indicated that ideal traits with high estimates are ideal 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. Traits with low estimates of selection parameters indicated that improving through selection in context of present material would be difficult due to lack of genetic variability for these traits. The high estimates of direct selection parameters observed for the above characters are broadly in agreement with earlier reports in rice (Basavaraja *et al.* 2013 and Sathya and Jebaraj, 2013) [2, 11].

Proportional contribution of lines, testers and lines \times testers interaction for 5 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 1000 grain weight (62.57%) followed by grain yield per plant (56.12%), L:B ratio (26.35%), kernel breadth (24.24%), and kernel length (24.23%) for normal condition. Under saline condition the maximum contribution of females (lines) was recorded for grain yield per plant (59.48) followed 1000 grain weight (45.06), kernel length (25.99), L:B ratio (23.35) and kernel breadth (15.60).

Maximum contribution of male (testers) in normal condition was recorded for kernel length (12.73%) followed by L:B ratio (10.93), kernel breadth (4.7%), 1000 grain weight (2.79%), and grain yield per plant (1.42%), while in saline condition maximum contribution of male lines (testers) was recorded for L:B ratio (6.82%), followed by kernel length (6.57), kernel breadth (2.27%), 1000 grain weight (1.28%) and grain yield per plant (2.2%).

Proportional contribution of lines \times testers was found maximum for the kernel breadth (71.05%) followed by L:B ratio (62.41), grain yield per plant (42.45%), kernel length (36.03%) and 1000 grain weight under normal condition.

Proportional contribution of lines \times testers was found maximum for the character kernel breadth (82.12%) followed by L:B ratio (69.83%), kernel length (67.44%), 1000 grain weight (53.66%) 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, NDRK 50001, CSR – 28, IR 74095AC -64, IR 72579-2-2R, HPU-CIJ and LD 183-4 among line and by Narendra Usar Dhan-2 among testers. The parent NDRK 5014, with highest GCA effects for grain yield per plant also showed significant and desirable GCA effects for 1000 grain weight, kernel length and L:B ratio. Line NDRK 5071, NDRK 50001, IR 74095 AC 64 and HPU-CIJ emerged as good general combiner for 1000 grain weight. LD 183-4 emerged as good general combiner for 1000 grain weight and kernel breadth while in case of tester Narendra Usar Dhan-2 was showed highly significant and positive GCA effects for grain yield per plant also showed significant and desirable GCA effects for kernel length 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 1000 grain weight, kernel length and L:B ratio. Line NDRK 50001, CSR 28 and HPU-CIJ emerged as good general combiner for 1000 grain weight while in case of tester Narendra Usar Dhan 3 was showed highly significant and positive GCA effects for grain yield per plant also showed significant and desirable GCA effects for 1000 grain weight 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 quality traits as mentioned above may serve as valuable parents for hybridization programme or multiple crossing programme for obtaining high yielding quality 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 usefulness of a particular cross combination in the exploitation of hybrids.

Fifteen crosses, IR SST N 27 \times Narendra Usar Dhan 2009, IR 27579-B-2R \times Narendra Usar Dhan 3, IR 74095 AC 64 \times Narendra Usar Dhan 3, NDRK 5071 \times Narendra Usar Dhan 2, CSR 23 \times Narendra Usar Dhan 2009, NDRK 50001 \times Narendra Usar Dhan 3, NDRK 5071 \times Narendra Usar Dhan 3, LD 183-4 \times Narendra Usar Dhan 3, NDRK 5032 \times Narendra Usar Dhan 3, NDRK 5071 \times Narendra Usar Dhan 2009, NDRK 5014 \times Narendra Usar Dhan 2, HPU-CIJ \times NarendraUsraDhan 2009, NDRK 5014 \times Narendra Usar Dhan 2009, CSR 23 \times Narendra Usar Dhan 2 and NDRK 5030 \times Narendra Usar Dhan 3 exhibited significant and positive SCA

effects for grain yield per plant, as well as for some quality 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 \times high (IR 27579-B-2R \times Narendra Usar Dhan 3, IR 74095 AC 64 \times Narendra Usar Dhan 3, NDRK 50001 \times Narendra Usar Dhan 3, NDRK 5071 \times Narendra Usar Dhan 3 and LD 183-4 \times Narendra Usar Dhan 3), high \times average (NDRK 5071 \times Narendra Usar Dhan 2 and NDRK 5014 \times Narendra Usar Dhan 2), high \times low (NDRK 5071 \times Narendra Usar Dhan 2009, HPU-CIJ \times Narendra Usra Dhan 2009 and NDRK 5014 \times Narendra Usar Dhan 2009), average \times high (NDRK 5032 \times Narendra Usar Dhan 3), low \times high (NDRK 5030 \times Narendra Usar Dhan 3), low \times average (CSR 23 \times Narendra Usar Dhan 2), low \times low (IR SST N 27 \times Narendra Usar Dhan 2009) general combining parents. These results are in agreement with the findings of Ram *et al.* (1994)^[10], Dwivedi *et al.*, (1999)^[4, 5]. However, in self-pollinated crops, the additive \times 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 \times 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 \times high GCA combiners would be involved in high heterosis, it would be due to interaction between positive \times 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 \times high general combiner 9.25% and high \times low with 5.55% 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 \times additive interaction. Young (1987) 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 27579-B-2R \times Narendra Usar Dhan 3, IR 74095 AC 64 \times Narendra Usar Dhan 3, NDRK 50001 \times Narendra Usar Dhan 3, NDRK 5071 \times Narendra Usar Dhan 3, LD 183-4 \times Narendra Usar Dhan 3, NDRK 5071 \times Narendra Usar Dhan 2 and NDRK 5014 \times Narendra Usar Dhan 2 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 performance 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, NDRK 5071 \times Narendra Usar Dhan 2009, HPU-CIJ \times Narendra Usra Dhan 2009, NDRK 5014 \times Narendra Usar Dhan 2009 and NDRK 5030 \times Narendra Usar Dhan 3 resulted from high \times low or average \times high and in crosses IR SST N 27 \times Narendra Usar Dhan 2009 resulted from low \times 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 quality contributing characters such as 1000 grain weight, kernel length, kernel breadth and L:B ratio. In general, the reports in the literature (Ram *et al.*, 1994)^[10] also supported the present findings. Some crosses, specifically NDRK 50001 \times Narendra Usar Dhan 3, CSR 23 \times Narendra Usar Dhan 2, NDRK 5032 \times Narendra Usar Dhan 3, NDRK 5014 \times Narendra Usar Dhan 2 and HPU-CIJ \times Narendra Usra Dhan 2009 exhibited high SCA, mean performance and standard heterosis were suggested for exploitation in the breeding program to create high-yielding quality pure lines by pedigree selection and/or directly for quality 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 three characters.

Eleven crosses, NDRK 5071 \times Narendra Usar Dhan 2009, NDRK 5032 \times Narendra Usar Dhan 3, NDRK 5030 \times Narendra Usar Dhan 2009, NDRK 5071 \times Narendra Usar Dhan 3, NDRK 5071 \times Narendra Usar Dhan 2, CSR 23 \times Narendra Usar Dhan 3, NDRK 50001 \times Narendra Usar Dhan 3, NDRK 5043 \times Narendra Usar Dhan 3 and IR 27579-B-2R \times Narendra Usar Dhan 2 showed highly significant and positive SCA effects for grains yield per plant while two crosses CSR 23 \times Narendra Usar Dhan-2009 and HPU-CIJ \times Narendra Usra Dhan 2009 exhibited significant and positive SCA effects for yield and some quality 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 \times high (NDRK 50001 \times Narendra Usar Dhan 3), high \times low (HPU-CIJ \times Narendra Usar Dhan 2009 and NDRK 5043 \times Narendra Usar Dhan 3), and low \times low (NDRK 5071 \times Narendra Usar Dhan 2, NDRK 5030 \times Narendra Usar Dhan 2009, NDRK 5071 \times Narendra Usar Dhan 3 and IR 27579-B-2R \times 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 \times additive type of interaction component is fixable if the crosses showing high SCA effects involved parents with high general combiners. If high \times high GCA combiners would be involved in high heterosis, it would be due to interaction between positive \times 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 \times low or low \times low parents (Table 7), the high yield with high quality would be non-fixable in subsequent generations. It is evident from the SCA effects of crosses for grain yield per plant and quality traits were attributed almost equally due to dominance and epistasis gene interaction or due to additive \times additive interaction. Young (1987) indicated that, in majority of the crosses, the high SCA effects of grain yield were attributed to dominance and epistasis effects.

The estimates of standard heterosis ranged between -52.52 to 48.64%. The hybrids NDRK 50001 \times Narendra Usar Dhan 3, IR 27579-B-2R \times Narendra Usar Dhan 2, NDRK 5043 \times

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 (NDRK 5071 × Narendra Usar Dhan 2, NDRK 5030 × Narendra Usar Dhan 2009, NDRK 5071 × Narendra Usar Dhan 3 and IR 27579-B-2R × Narendra Usar Dhan 2). The cross having both high general combiner parents

can be exploited to isolate high-yielding pure lines with high quality and crosses involving high × low and low × low general combining parents can be exploited directly for breeding quality hybrid.

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 quality contributing characters such as 1000 grain weight, kernel length, kernel breadth and L:B ratio. In general, the reports in the literature (Dwivedi *et al.*, 1999)^[4, 5] also supported the present findings.

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

Source	d.f.	1000- grains weight (g)	Kernel length (mm)	Kernel breadth (mm)	L:B ratio	Grains yield per plant(g)
Replication	2	2.22	0.07	0.08	0.09	0.5
Treatment	74	18.23**	0.65**	0.10*	0.35**	36.48**
Parents	20	19.13**	0.41**	0.09**	0.29**	18.92**
Parent vs crosses	1	0.61	0.49**	0.00	0.17	11.62**
Crosses	53	18.23**	0.74**	0.10**	0.38**	43.57**
Line	17	35.56**	0.56	0.08	0.31	76.24**
Tester	2	13.49	2.51*	0.13	1.09	16.43
L×T	34	9.84**	0.73**	0.11**	0.37**	28.83**
Error	148	1.36	0.07	0.02	0.07	1.47
σ^2 GCA		0.09	0.00	0.00	0.00	0.16
σ^2 SCA		5.75	0.40	0.03	0.17	12.42
σ^2 GCA/ σ^2 SCA		0.02	0.00	0.00	0.00	0.01
σ^2 A		0.179	0	0	0	0.315
σ^2 D		5.754	0.4	0.027	0.172	12.418
$(\sigma^2$ A/ σ^2 D) ^{1/2}		0.0156	0.0000	0.0000	0.0000	0.0127
PCV		11.64	8.17	9.73	14.44	14.74
GCV		10.45	7.02	6.88	10.81	13.89
h^2 (b.s.) & ±SE		80.54±0.95	73.71±0.21	49.98±0.13	56.01±0.22	88.78±0.99
GA		19.34	12.41	9.84	16.59	26.95
Contribution % of Lines		62.57	24.23	24.24	26.35	56.12
Testes		2.79	12.73	4.7	10.93	1.42
Line×Tester		34.62	36.03	71.05	62.41	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 × tester to the total variance in rice genotypes under saline condition

Source	d.f.	1000- grains weight (g)	Kernel length (mm)	Kernel breadth (mm)	L:B ratio	Grains yield per plant (g)
Replication	2	0.53	0.01	0.13**	0.24*	2.48
Treatment	74	21.96**	0.45**	0.05**	0.21**	50.56**
Parents	20	32.74**	0.23	0.03*	0.11*	46.36**
Parent vs crosses	1	4.54	0.06	0.57**	0.73**	0.65
Crosses	53	18.22**	0.55**	0.05**	0.24**	53.09**
Line	17	25.60*	0.44	0.03	0.17	98.45*
Tester	2	6.2	0.95	0.03	0.43	31
L×T	34	15.24**	0.57**	0.07**	0.26**	31.71**
Error	148	1.45	0.17	0.02	0.07	1.36
σ^2 GCA		0.032	0.000	0.000	0.000	0.229
σ^2 SCA		4.626	0.162	0.009	0.075	16.597
σ^2 GCA/ σ^2 SCA		0.007	0.000	0.000	0.000	0.014
σ^2 A		0.064	-0.001	0.000	0.000	0.457
σ^2 D		4.626	0.162	0.009	0.075	16.597
$(\sigma^2$ A/ σ^2 D) ^{1/2}		0.007	-0.003	0.000	0.000	0.014
PCV		13.78	8.32	7.53	12.11	19.65
GCV		12.52	4.90	4.92	7.92	18.88
h^2 (b.s.) & ±SE		82.53±0.98	34.7±0.34	42.61±0.10	42.77±0.21	92.34±0.95
GA		23.40	5.90	6.79	10.79	37.32
Contribution % of Lines		45.06	25.99	15.6	23.35	59.48
Testes		1.28	6.57	2.27	6.82	2.2
Line×Tester		53.66	67.44	82.12	69.83	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 quality and yield in rice under normal condition

S. No.	Line	1000- grains weight (g)		Kernel length (mm)		Kernel breadth (mm)		L:B ratio		Grains yield / plant (g)	
		MEAN	GCA	MEAN	GCA	MEAN	GCA	MEAN	GCA	MEAN	GCA
1	NDRK-5014	23.09	2.48**	5.67	0.27**	2.1	-0.07	2.7	0.22*	25.29	2.16**
2	NDRK-5016	21.66	-0.48	7.33	0.11	2	-0.13*	3.68	0.21*	21.57	-0.97*
3	NDRK-5030	21.88	0.61	6.27	-0.30**	2.3	0.12*	2.74	-0.29**	24.47	-5.99**
4	NDRK-5032	23.43	0.81*	6	0.17	2.37	0.04	2.54	0.02	14.23	0.55
5	NDRK-5035	22.36	-2.39**	6.13	-0.03	2.3	0.04	2.67	-0.09	23.2	1.37**
6	NDRK-5043	24.89	-3.04**	5.9	-0.29**	2.47	0.08	2.39	-0.14	18.8	-2.51**
7	NDRK-5062	22.75	-4.67**	5.73	0.23**	2.44	0.03	2.35	0.08	23.71	-3.91**
8	NDRK-5071	24.62	2.44**	7.43	-0.18*	2.09	0.05	3.55	-0.15	26	2.73**
9	NDRK-5081	23.04	-1.65**	6.27	0.15	2.37	0.03	2.65	0.01	26.16	-1.34**
10	NDRK-5092	16.36	-1.89**	6.23	0.29**	2.4	-0.06	2.6	0.20	24.17	-1.32**
11	NDRK-50001	22.35	1.69**	6.33	0.01	2.33	-0.03	2.72	0.04	27.37	2.97**
12	CSR – 23	21.74	-0.28	6.27	-0.21*	2.17	0.07	2.9	-0.20*	26.78	-4.81**
13	CSR – 28	21.14	1.70**	6.05	0.57**	2.67	-0.02	2.27	0.27**	23.36	1.72**
14	IR SST-N 27	18.22	0.89*	6.47	-0.06	2.53	-0.03	2.56	0.03	22	-0.45
15	IR 74095 AC 64	19.14	1.29**	5.53	-0.14	1.82	-0.06	3.22	-0.03	21.33	4.80**
16	IR 72579-B-2R	18.26	0.41	6.14	-0.01	2.41	-0.10	2.55	0.10	20.43	0.85*
17	HPU-CIJ	17.67	0.82*	6.14	-0.17*	2.4	-0.17**	2.57	0.14	20.36	2.50**
18	LD 183-4	17.83	1.26**	7.33	-0.41**	2.05	0.20**	3.58	-0.42**	21.7	1.63**
	GM	21.14	0.39	6.29	0.09	2.29	0.05	2.79	0.09	22.83	0.40
	SE (gi) line		1.87		0.42		0.25		0.43		1.94
	Tester										
1	Narendra Usar Dhan 2	26.12	0.06	7.09	0.21**	2.0	-0.05*	3.57	0.16**	29.14	0.44**
2	Narendra Usar Dhan 3	23.53	-0.53**	6.62	0.00	2.28	0.05*	2.91	-0.05	25.3	-0.62**
3	Narendra Usar Dhan 2009	25.27	0.16	6.04	0.04	2.29	0.02	2.65	0.04	26.24	0.17
	GM	24.97	0.22	6.58	0.05	2.19	0.03	3.04	0.05	26.89	0.23
	SE(gi) tester		0.22		0.05		0.03		0.05		0.23

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

Table 4: Mean performance and general combining ability (GCA) effects of parents (lines and testers) for quality and yield in rice under salinity condition

S.N.	Line	1000- grains weight (g)		Kernel length (mm)		Kernel breadth (mm)		L:B ratio		Grains yield /plant(g)	
		Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
1	NDRK-5014	17.49	2.23**	5.53	0.49**	2.07	0.00	2.69	0.25**	24.42	3.60**
2	NDRK-5016	21.62	0.42	6.27	0.05	2.13	-0.05	2.95	0.07	22.31	2.34**
3	NDRK-5030	25.08	0.07	6.97	-0.12	2.3	-0.06	3.03	0.02	24.73	-7.28**
4	NDRK-5032	20.49	0.23	5.9	0.18	2.23	0.02	2.65	0.05	13.05	0.09
5	NDRK-5035	20.77	-1.62**	5.83	-0.07	2.2	-0.03	2.65	-0.01	18.26	3.16**
6	NDRK-5043	21.91	-1.65**	6.53	-0.38**	2.04	0.09	3.24	-0.28**	11.28	-0.44
7	NDRK-5062	20.28	-3.34**	5.8	-0.15	2.27	0.02	2.55	-0.06	22	-1.77**
8	NDRK-5071	22.59	1.64**	7.07	0.31*	2.1	0.04	3.37	0.10	23.47	-2.97**
9	NDRK-5081	20.77	-2.57**	6.3	-0.13	2.33	0.03	2.71	-0.09	19.24	-2.81**
10	NDRK-5092	15.62	-0.82*	5.87	0.27	2.17	-0.06	2.71	0.20*	22.23	-1.77**
11	NDRK-50001	21.76	2.58**	6.13	-0.01	2.29	-0.06	2.67	0.06	26.73	3.99**
12	CSR – 23	20.72	0.78	6.39	-0.27	2.1	0.10*	3.05	-0.25**	24.95	0.67
13	CSR – 28	20.92	2.18**	5.63	-0.13	2.15	-0.01	2.62	-0.06	22.44	2.99**
14	IR SST-N 27	18.37	-1.71**	5.99	-0.07	2.51	-0.01	2.38	-0.03	20.01	-6.11**
15	IR 74095 AC 64	18.72	0.68	5.87	-0.03	2.23	0.07	2.63	-0.10	20.68	3.45**
16	IR 72579-B-2R	18.22	0.38	5.6	-0.07	2.27	-0.09*	2.5	0.09	18.5	-0.67
17	HPU-CIJ	17.48	0.95*	5.43	0.26	2.4	-0.02	2.26	0.15	20.33	1.92**
18	LD 183-4	17.22	-0.45	7.13	-0.14	2.03	0.01	3.52	-0.09	20.3	1.63**
	GM	20		6.12		2.21		2.79		20.83	
	SE (gi) line		0.40		0.14		0.04		0.09		0.39
1	Narendra Usar Dhan 2	23.51	-0.06	7.13	-0.15**	2.23	0.02	3.2	-0.10**	25.1	-0.57**
2	Narendra Usar Dhan 3	22.97	0.36*	7.07	0.05	1.97	-0.03	3.6	0.06	25.19	0.86**
3	Narendra Usar Dhan 2009	23.15	-0.31	5.9	0.10	2.44	0.00	2.42	0.04	24.95	-0.29
	GM	23.21		6.7		2.21		3.07		25.08	
	SE(gi) tester		0.16		0.06		0.02		0.03		0.16

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

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. No.	Line	SCA	Mean	Standard heterosis	GCA
1	IR SST N 27 × Narendra Usar Dhan 2009	5.73**	24.83	21.91**	L×L
2	IR 27579-B-2R × Narendra Usar Dhan 3	4.32**	21.58	5.92	H×H
3	IR 74095 AC 64 × Narendra Usar Dhan 3	4.04**	24.75	21.50**	H×H
4	NDRK 5071 × Narendra Usar Dhan 2	4.01**	27.3	34.04**	H×A
5	CSR 23 × Narendra Usar Dhan 2009	3.67**	23.13	13.55**	L×A
6	NDRK 50001 × Narendra Usar Dhan 3	3.44**	33.42	64.05**	H×H
7	NDRK 5071 × Narendra Usar Dhan 3	3.41**	24.29	19.23**	H×H
8	LD 183-4 × Narendra Usar Dhan 3	2.69**	23.42	14.96**	H×H
9	NDRK 5032 × Narendra Usar Dhan 3	2.54**	30.43	49.40**	A×H
10	NDRK 5071 × Narendra Usar Dhan 2009	2.11**	19.07	-6.4	H×L
11	NDRK 5014 × Narendra Usar Dhan 2	2.07**	30.19	48.21**	H×A
12	HPU-CIJ × NarendraUsraDhan 2009	1.66*	28.55	40.16**	H×L
13	NDRK 5014 × Narendra Usar Dhan 2009	1.53*	23.47	15.22**	H×L
14	CSR 23 × Narendra Usar Dhan 2	1.49*	31.13	52.84**	L×A
15	NDRK 5030 × Narendra Usar Dhan 3	1.49*	23.67	16.18**	L×H

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

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

S. No.	Line	1000- grains weight (g)	Kernel length (mm)	Kernel breadth (mm)	L:B ratio	Grains yield per plant(g)
1	IR SST N 27 × Narendra Usar Dhan 2009	1.67*	-0.07	-0.13	0.18	5.73**
2	IR 27579-B-2R × Narendra Usar Dhan 3	-1.54*	0.57**	-0.12	0.40*	4.32**
3	IR 74095 AC 64 × Narendra Usar Dhan 3	0.47	-0.45**	-0.04	-0.17	4.04**
4	NDRK 5071 × Narendra Usar Dhan 2	-0.93	-0.09	-0.03	-0.03	4.01**
5	CSR 23 × Narendra Usar Dhan 2009	0.7	0.36*	0	0.16	3.67**
6	NDRK 50001 × Narendra Usar Dhan 3	1.3	0.43**	-0.07	0.31*	3.44**
7	NDRK 5071 × Narendra Usar Dhan 3	2.19**	-0.19	-0.11	0.05	3.41**
8	LD 183-4 × Narendra Usar Dhan 3	0.2	0.1	0.08	-0.05	2.69**
9	NDRK 5032 × Narendra Usar Dhan 3	0.2	0.1	0.08	-0.05	2.69**
10	NDRK 5071 × Narendra Usar Dhan 2009	0.24	0.02	0.05	-0.06	2.11**
11	NDRK 5014 × Narendra Usar Dhan 2	1.2	0.04	-0.09	0.13	1.53*
12	HPU-CIJ × NarendraUsraDhan 2009	0.26	0.56**	-0.1	0.34*	1.66*
13	NDRK 5014 × Narendra Usar Dhan 2009	1.2	0.04	-0.09	0.13	1.53*
14	CSR 23 × Narendra Usar Dhan 2	0.7	0.36*	0	0.16	3.67**
15	NDRK 5030 × Narendra Usar Dhan 3	0.71	0.79**	-0.28**	0.74**	1.49*

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

Table 7: 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 salinity condition

S. No.	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 × Narendra Usar Dhan 3	3.51**	20.3	-5.76	L×L
5	NDRK 5071 × Narendra Usar Dhan 2	3.20**	23.47	8.94*	A×H
6	CSR 23 × Narendra Usar Dhan 3	2.92**	22.67	5.23	A×H
7	NDRK 50001 × Narendra Usar Dhan 3	2.90**	24.36	13.11**	H×H
8	NDRK 5043 × Narendra Usar Dhan 3	2.22**	24	11.42**	L×H
9	IR 27579-B-2R × Narendra Usar Dhan 2	1.96**	25	16.06**	L×L
10	CSR 23 × Narendra Usar Dhan 2009	1.67*	21.7	0.74	A×L
11	HPU-CIJ × NarendraUsraDhan 2009	1.46*	23.67	9.87*	H×L

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

Table 8: Estimation of specific combining ability effects of significant crosses for grain yield and quality traits in rice under salinity condition

S. No.	Line	1000- grains weight (g)	Kernel length (mm)	Kernel breadth (mm)	L:B ratio	Grains yield per plant (g)
1	NDRK 5071 × Narendra Usar Dhan 2009	2.36**	0.42	0.17*	-0.02	6.23**
2	NDRK 5032 × Narendra Usar Dhan 3	-0.1	0.02	-0.08	0.11	6.06**
3	NDRK 5030 × Narendra Usar Dhan 2009	-2.51**	-0.33	-0.04	-0.11	3.87**
4	NDRK 5071 × Narendra Usar Dhan 3	-0.26	0.05	-0.02	0.02	3.51**
5	NDRK 5071 × Narendra Usar Dhan 2	-0.65	-0.31	0.07	-0.26	3.20**
6	NDRK 50001 × Narendra Usar Dhan 3	1.19	-0.46	-0.11	-0.04	2.90**
7	CSR 23 × Narendra Usar Dhan 3	-2.66**	-0.2	0.06	-0.18	2.92**
8	NDRK 5043 × Narendra Usar Dhan 3	-0.31	-0.02	0.24**	-0.32*	2.22**
9	IR 27579-B-2R × Narendra Usar Dhan 2	1.64*	-0.04	-0.17*	0.18	1.96**
10	CSR 23 × Narendra Usar Dhan 2009	-0.64	-0.37	0.04	-0.24	1.67*
11	HPU-CIJ × Narendra Usra Dhan 2009	2.62**	-0.02	-0.02	0.04	1.46*

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

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