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Combining ability and gene action analysis for certain quantitative traits in rice (*Oryza sativa* L.) under sodic soil condition

Soni Singh, PK Singh, Kanhaiya Lal, Sarvesh Kumar Maurya and Harikant Yadav

Abstract

Twenty-one hybrids generated from crossing between seven lines and three testers were studied along with their parents and one check variety for combining ability and gene action involved in the expression of various characters in rice. The gca and sca effects were significant for majority of the traits. The magnitude of sca variance was higher than the gca variance for all the characters revealed the predominance of non-additive gene action in the inheritance of the characters under study. Among parents IR 870, NDRK 5001, IR11T205, IR14T104, IR11T189 and IR11T197 were the average general combiners for grain yield and the contributing traits. Three crosses, IR12T193 x Narendra Usar 2009, IR11T205 x CSR 10 and NDRK 5001 x CSR 10 showed significant and positive sca effects for grain yield per plant as well as some other yield components. The cross, IR12T193 x Narendra Usar 2009 having highest positive and significant sca effects for grain yield per plant also recorded significant sca effects in desirable direction for days to 50% flowering, flag leaf area, grain per panicle and biological yield per plant. The second ranking cross, IR11T205 x CSR 10 for higher positive and significant sca effect for grain yield per plant showed significant and desirable sca effects for days to 50% flowering, plant height, grains per panicle and 1000-grain weight. The third ranking cross for significant and positive sca effects for grain yield per plant was NDRK 5001 x CSR 10 which exhibited significant and positive sca effects for flag leaf area.

Keywords: Rice (*Oryza sativa* L.), combining ability, gene action and quantitative traits

Introduction

Rice (*Oryza sativa* L.) is the premier food crop in the world. It is a member of grass family, gramineae. It has $2n=2x=24$ chromosomes. It is one of the three major food crops of the world and forms the staple diet of about half of the world's population. Asia is the leader in rice production accounting for about 90% of the world's production. Over 75% of the world supply is consumed by people in Asian countries and thus rice is of immense importance to food security of Asia. The demand for rice is expected to increase with continuous increase in the global population.

India has the largest area 43.39 million hectare constituting 28.01% of the land under rice in the world and rank second in total production 111.50 million tonnes next to china (187.490 million tonnes) with an average productivity of 2804 Kg/hectare (Anonymous 2017-18) [1-2]. Asia has an area of only 140.036 million hectare and productivity as 5.32 tonnes/ hectare (Anonymous 2017-18) [1-2]. More than 80% of our countrymen depend fully or partially on rice as their main were at food and staple diet. Uttar Pradesh is important rice growing state of country. The area and production of rice in this state is about 6.45 million hectare and 18.251 million tons respectively with the productivity of 4.95 tonnes/ hectare (Uttar Pradesh directorate of agricultural ministry, 2017-18) [2].

Nearly 6.73 mha soils in India are salt affected and categorized into two broad groups alkali and saline soils. Recent estimates indicate that more than 1.5 mha salt affected area has been reclaimed which is contributing about 10 million tones additional food grains to the central pool. At present, in Indogangetic plains in India total 2.348 mha area is salt affected in which U.P. share 1.37 mha. (CSSRI Annual report, 2007-08).

With the help of combining ability analysis we can identify parents with high general combining ability (gca) effects and cross combinations with high – specific combining ability effects (sca) for commercial exploitation of heterosis and isolation of pure lines among the

progenies of the heterotic hybrids for sodic soil condition. Thus, keeping the above facts in view the present investigation was carried out to work out combining ability and gene action for certain quantitative traits in rice (*Oryza sativa* L.) under sodic soil.

Materials and Methods

The present investigation was carried out at the Main Experiment Station of N.D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya. Three testers (males) viz., CSR 10, Jaya, Narendra Usar-2009 were crossed with 7 lines (females) viz., IR11T197, IR870, IR11R189, IR12T193, IR11T205, IR14T104, NDRK 5001, comprising genotypes / varieties of rice in a line \times tester mating design. A total of 21 F₁s were produced during Kharif, 2015. The resulting set of 21 F₁s along with their 10 parents and 1 check variety (Narendra Usar Dhan 3) were evaluated in Randomized Complete Block Design with three replications during Kharif, 2016. The seeds of each entry were sown on 28st June, 2016 in separate plots and 22 days (19th July 2016) old seedlings were transplanted single seedling per hill in single row plots of 3 m length with inter- and intra- row spacing of 20 cm and 15 cm, respectively. All the recommended cultural practices were followed to raise a good crop. The fertilizers were applied @ 120 kg nitrogen, 60 kg phosphorus and 60 kg potash per hectare through urea, DAP and mutate of potash, respectively. The full dose of phosphorus and potash and half dose of nitrogen were applied as basal and rest of nitrogen was applied in two split doses as top dressing at tillering and panicle initiation stage of crop growth. The observations were recorded on randomly selected five competitive plants from each genotype for nine characters viz., Plant height (cm), Flag leaf area (cm²), Panicle bearing tillers per plant, Panicle length (cm), Grains per panicle, 1000 grain weight (g), Biological yield per plant (g), Harvest-index (%), Grain yield per plant (g), while for one character viz., days to 50 percent flowering data were recorded on the plot basis. The experimental data collected on all the ten characters in respect of experiment of the present study were compiled and subjected to various statistical and genetical analyses such as, analysis of variance for Randomized Complete Block Design (Panse and Sukhatme, 1967), Line \times Tester analysis for combining ability and gene action (Kempthorne, 1957)^[6].

Result and Discussion

The analysis of variance for combining ability for ten characters and estimates of components of genetic variance and other genetic parameters are given in Table 1. In the present study, the analysis of variance for combining ability revealed highly significant mean squares due to lines \times tester interactions for all the characters under study except panicle bearing tillers per plant and panicle length, representing importance of specific combining ability and non-additive gene effects. The above discussion suggests occurrence of non-additive gene effects for majority of characters. The estimates of sca variance were higher than the corresponding estimates of gca variance for all the characters. The values of average degree of dominance were more than unity (>1) revealing over dominance for majority of the characters. studied except the predictability ratio not calculated for biological yield per plant and grain yield per plant due to negative estimates of gca variance. The result indicated importance of non-additive gene action in the inheritance of these characters. The predictability ratio less

than one also suggested predominance of non-additive gene effects for all the characters. The importance of additive as well as non-additive gene effects with predominance of non-additive gene effects in inheritance of grain yield and yield components of rice has also been reported earlier (Pradhan *et al.*, 2006; Rashid *et al.*, 2008; Saleem *et al.*, 2010; Saidaiah *et al.*, 2010)^[8,9,14,11].

The predominance of non-additive gene effects representing non-fixable dominance and epistatic components of genetic variance indicated that maintenance of heterozygosity would be highly fruitful for improving the characters. Hence, the suitable breeding strategy for attaining high yield would be the full or partial exploitation of heterosis through development of hybrid cultivars for sodic soil. Since, the technology for development of hybrid rice varieties for commercial purposes is being widely and successfully used in different countries including India, it is recommended to explore possibility of isolating high yielding commercial hybrids utilizing the materials of the present investigation. The non-additive gene effects may also be exploited to some extent for improving the characters by resorting to breeding methods such as biparental mating followed by recurrent selection and population improvement methods as suggested by Jensen (1970)^[5] and Redden and Jensen (1974)^[10].

For illustrating genetic worth of parents for hybridization programme, the general combining ability (gca) effects of 10 parents (7 lines + 3 testers) for ten characters are listed in Table 2.

None of the seven lines and three tester exhibited desirable positive and significant general combining ability effect for grain yield per plant while the line IR12T193 recorded negative and significant gca effects for grain yield per plant only. The non-significant gca effects for grain yield per plant were exhibited by the all lines emerged as average combiners, namely, IR 870, NDRK5001, IR11T205, IR14T104, IR11T189 and IR11T197 except female line, IR12T193 which possessed significant and negative gca effects while none of the testers was found to be good general combiners for grain yield per plant.

The average general combiner parent with high value for grain yield per plant, IR870 also emerged as average general combiner for harvest index, biological yield per plant, panicle bearing tillers per plant, flag leaf area and days to 50% flowering but it was poor general combiner for grains per panicle, 1000-grain weight and panicle length. The second ranged general combiner for grain yield per plant, NDRK5001 was found to be good general combiner for grains per panicle, and panicle length while average combiner for harvest index, biological yield per plant, flag leaf area, 1000- grain weight, panicle bearing tillers per plant and plant height but it was poor general combiner for early flowering. The third ranking parent, IR11T205 possessed significant gca effects for grains per panicle, flag leaf area, 1000- grain weight and panicle length in desirable direction and for biological yield per plant, harvest index, panicle bearing tillers per plant and plant height showed average general combining ability.

The parent, IR14T104 appeared as good general combiner for grains per panicle, panicle length and short stature whereas poor general combiner for early flowering, flag leaf area and panicle bearing tillers per plant. The fifth ranked general combiner for grain yield per plant, IR11T189 was good general combiner for all characters except grains per panicle, panicle length, flag leaf area and 1000-grain weight for which it was identified as poor general combiners. The parents

showing positive and negative, non-significant 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 pure line or hybrid varieties for salt affected or sodic soils.

These parents may also be recommended for exploitation in hybridization programme as donor of component characters for which they emerged as good general combiner in spite of being average or poor general combiner for grain yield. It is evident from Table 2, that most of the lines showing average combiners for grain yield per plant also exhibited positive and significant gca effects for some of the important yield components such as grains per panicle, 1000- grain weight and panicle length. This indicated that the non-significant gca effects for grain yield in desirable direction resulted from similar gca effects of some other yield components suggesting that the combining ability for grain yield was influenced by the combining ability of its component traits. Therefore, simultaneous improvement in important yield components and other associated traits along with grain yield may be better approach for raising yield potential in rice. Similar results have also been reported by Saidaiah *et al.*, (2009) ^[12]; Saleem *et al.*, (2010) ^[14]; Bagheri and Jelodar (2010) ^[3] and Saidaiah *et al.*, (2011) ^[13].

The specific combining ability (sca) effects, which are supposed to be manifestation of non-additive components of genetic variance, are highly valuable for discrimination of crosses for their genetic worth as breeding materials. The estimates of sca effects of 21 crosses for 10 characters are given in Table 3.

In present study, none of the crosses showed significant sca effects in desirable direction for all the characters. 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 nine characters. Three crosses, IR12T193 x Narendra Usar 2009, IR11T205 x CSR 10 and NDRK 5001 x CSR 10 showed significant and positive sca effects for grain yield per plant as well as some other yield components. The cross, IR12T193 x Narendra Usar 2009 having highest positive and significant sca effects for grain yield per plant also recorded significant sca effects in desirable direction for days to 50% flowering, flag leaf area, grain per panicle and biological yield per plant. The second ranking cross, IR11T205 x CSR 10 for higher positive and significant sca effect for grain yield per plant showed

significant and desirable sca effects for days to 50% flowering, plant height, grains per panicle and 1000-grain weight. The third ranking cross for significant and positive sca effects for grain yield per plant was NDRK 5001 x CSR 10 which exhibited significant and positive sca effects for flag leaf area.

The three crosses having significant and positive sca effects for grain yield per plant also showed positive and desirable significant sca effects for some other characters, most commonly flag leaf area. This suggested that manifestation of sca effects for grain yield is related with higher sca effects for important yield components. In general, the crosses showing significant and desirable sca effects were associated with better *per se* performance for respective traits. However, the crosses having high sca effects in desirable direction did not always have high mean performance for the character in question. Thus, the sca effect of the crosses may not be directly related to their *per se* performance. This may be attributed to the fact that *per se* performance is a realized value, whereas, sca effect is an estimate of F₁ performance over parental one. Therefore, both *per se* performance along with sca effects should be considered for evaluating the superiority of a cross although the former may be more important if development of F₁ hybrids is the ultimate objective.

The critical examination of Table 4 revealed that the crosses exhibiting high order significant or non-significant sca effects undesirable direction for different characters involved parents having all types of combinations of gca effects such as high × high (H × H), high × average (H × A), high × low (H × L), average × average (A × A), average × low (A × L) and low × low (L × L) general combiner parents. The foregoing observation clearly indicated that there was no particular relationship between positive and significant sca effects of crosses with gca effects of their parents for the characters under study. Saidaiah *et al.*, (2009) ^[12]; Saleem *et al.* (2010) ^[14] and Dwivedi and Pandey (2012) ^[4] have also reported similar findings. High × high, high × average and average × average crosses give transgressive segregants and selection in early generation would be advantageous for development of pure lines as there are involvement of additive gene action, whereas, crosses having high × low, average × low and low × low general combining parents are suggested for heterosis breeding as their inheritance are controlled by non-additive and epistatic gene action.

Table 1: Analysis of variance for combining ability and genetic components of variance for 10 traits in rice under salt affected soil

Source of variation	df	D50F	PH	FL	PBTP	PL	GP	TW	BYP	HI	GYP
Lines	6	91.34	28.40	24.21	4.56	25.87	180.15	26.87	8.27	31.25	14.10
Testers	2	24.06	23.41	10.63	4.38	1.23	164.90	10.27	85.82	90.93	4.38
Lines × Testers	12	55.82	26.03	8.13	3.12	2.42	107.76	5.94	58.44	13.16	13.83
Error	60	3.90	3.77	1.65	1.45	1.64	7.00	1.63	7.56	3.81	2.17
Variance GCA		0.19	0.01	0.13	0.01	0.18	0.71	0.17	-0.3	0.34	-0.02
Variance SCA		17.30	7.41	2.15	0.55	0.25	33.58	1.43	17.53	2.89	3.88
Degree of Dominance		9.31	25.96	4.04	4.38	1.20	6.85	2.86	7.39	2.90	13.14
Predictability Ratio		0.02	0.00	0.10	0.04	0.58	0.04	0.19	@	0.19	@
Additive variance		0.7	0.04	0.52	0.05	0.72	2.85	0.69	-1.2	1.37	-0.09
Dominance variance		69.23	29.67	8.63	2.23	1.03	134.34	5.73	70.14	11.59	15.54
Heritability in Narrow sense		2.09	0.25	8.88	2.71	30.79	3.82	15.00	@	13.55	@

Traits: D50F=Days to 50% flowering, FL=Flag leaf area (cm²), PH=Plant height (cm), PBTP=Panicle bearing tillers per plant, PL=Panicle length (cm) GP=Grains per panicle, TW=1000 grain weight (g), BYP= Biological yield per plant (g), HI=Harvest index (%) and GYP= Grain yield per plant (g)

@= Negative value

*,**. Significant at 5% and 1% probability level, respectively.

Table 2: Estimates of general combining ability (gca) effects of parents for 10

Parent	D50F	PH	FL	PBTP	PL	GP	TW	BYP	HI	GYP
TESTER										
CSR 10	-1.13*	-1.17**	0.31	0.24	-0.20	-2.90	0.57*	1.29*	-1.68**	-0.42
Jaya	0.12	0.85	0.51	0.29	0.27	0.20	0.21	-2.33**	2.33**	0.49
NU-2009	1.00*	0.33	-0.81**	-0.53	-0.07	2.70	-0.78**	1.04	-0.65	-0.06
SE(g) tester	0.43	0.42	0.28	0.26	0.28	0.57	0.27	0.52	0.46	0.32
SE (gi-gi) tester	0.60	0.59	0.39	0.37	0.39	0.81	0.39	0.74	0.65	0.45
CD5%	1.23	1.21	0.80	0.75	0.80	1.65	0.79	1.50	1.31	0.91
CD1%	1.64	1.62	1.07	1.00	1.07	2.20	1.06	2.01	1.76	1.23
LINE										
IR11T197	0.40	2.95**	-1.00*	0.29	-1.66**	-1.07	-1.68**	-1.05	0.10	-0.67
IR 870	-0.97	2.12**	0.03	0.70	-1.53**	-2.21*	-1.64**	-0.31	1.40	0.96
IR11T189	-0.92	-1.29	-1.25**	-0.25	-1.73**	-3.00**	-0.92*	1.20	-0.22	0.36
IR12T193	-5.16**	-1.14	-0.01	-0.25	-0.20	-6.65**	0.54	-0.93	-4.03**	-2.56**
IR11T205	-1.23	-0.70	3.34**	0.72	2.20**	5.78**	3.34**	0.85	0.80	0.63
IR14T104	3.91**	-1.38*	-1.51**	-1.34**	1.41**	4.53**	0.02	-0.68	0.97	0.38
NDRK 5001	3.98**	-0.56	0.39	0.12	1.52**	2.62**	0.34	0.91	0.98	0.90
SE(g,l)	0.65	0.64	0.42	0.40	0.42	0.88	0.42	0.80	0.70	0.49
SE (gi-gj,l)	0.93	0.91	0.60	0.56	0.60	1.24	0.60	1.13	0.99	0.69
CD5%	1.88	1.85	1.22	1.14	1.22	2.52	1.21	2.30	2.01	1.40
CD1%	2.51	2.47	1.63	1.53	1.63	3.37	1.61	2.01	2.69	1.88

*, **. Significant at 5% and 1% probability level, respectively.

Table 3: Estimates of specific combining ability (sca) effects of crosses for 10 traits in rice under salt affected soil

Cross	D50F	PH	FL	PBTP	PL	GP	TW	BYP	HI	GYP
IR11T197*CSR 10	0.90	0.36	0.05	-1.07	0.63	3.44*	-0.54	0.65	-0.53	0.29
IR11T197*JAYA	2.22	2.32*	0.83*	-0.03	-0.08	-5.55**	-0.24	-6.33**	1.26	-1.97*
IR11T197*NU 2009	-3.12**	-2.68*	-0.77	1.09	-0.55	2.11	0.79	5.68**	-0.74	1.68
IR870*CSR 10	4.91**	2.70*	-0.99	0.28	0.03	-4.20**	0.95	1.72	-0.35	-0.32
IR870*JAYA	-3.18**	-0.62	0.76	0.27	-0.17	0.17	-1.35	1.99	-1.10	1.32
IR870*NU 2009	-1.73	-2.08	0.23	-0.55	0.14	4.03*	0.40	-3.72*	1.45	-1.00
IR11T189*CSR 10	3.34**	2.59*	1.23	0.52	0.42	4.83**	-0.50	-0.57	1.39	0.82
IR11T189*JAYA	-0.86	-1.78	-1.85*	-0.99	0.08	0.16	-0.17	-0.83	-0.75	-0.97
IR11T189*NU 2009	-2.47*	-0.81	0.62	0.47	-0.49	-4.98**	0.67	1.40	-0.64	0.15
IR12T193*CSR 10	1.23	-3.28**	-3.00**	0.35	-1.96*	-8.61**	-0.61	-7.29**	-2.99*	-3.99**
IR12T193*JAYA	2.08	0.97	1.01	-1.26	0.88*	-1.92	1.30	1.64	1.79**	1.40
IR12T193*NU 2009	-3.31**	2.31*	1.99*	0.91**	1.08	10.53**	-0.69	5.65**	1.19**	2.59**
IR11T205*CSR 10	-8.18**	-5.29**	1.48	0.29	-0.10	4.01*	2.55**	2.45	2.26**	2.23*
IR11T205*JAYA	0.91	2.42*	0.20	1.35	0.44	-0.34	0.00	-0.42	0.37	-0.14
IR11T205*NU 2009	7.27**	2.87*	-1.68*	-1.64*	-0.34	-3.66*	-2.55**	-2.03	-2.63*	-2.09*
IR14T104*CSR 10	-1.17	1.64	-0.32	-0.32	-0.16	1.17	-0.54	1.08	-2.20	-1.06
IR14T104*JAYA	-1.81	-1.79	0.48	0.83**	-0.26	1.02	0.37	1.54	0.24	0.36
IR14T104*NU 2009	2.98*	0.16	-0.16	-0.51	0.42	-2.19	0.17	-2.62	1.96**	0.70
NDRK 5001*CSR 10	-1.02	1.28	1.67*	-0.05	1.14	-0.63	-1.31	1.95	2.41**	2.03*
NDRK 5001*JAYA	0.65	-1.51	-1.44	-0.17	-0.90*	6.47**	0.10	2.41	-1.82	0.00
NDRK 5001*NU 2009	0.37	0.23	-0.22	0.22	-0.24	-5.84**	1.21	-4.37**	-0.59	-2.04*
CD 95% SCA	2.30	2.27	1.50	1.41	1.50	3.09	1.49	2.82	2.47	1.72

*, **. Significant at 5% and 1% probability level, respectively.)

Table 4: Most promising cross combinations for different characters along with their per se performance, sca effects and gca effects of parents

Characters	Crosses with significant effects	Per se performance	sca effects	gca effects of parents
Days to 50% flowering	IR11T205*CSR 10	85.56	-8.18**	A X H
	IR12T193*NU 2009	88.63	-3.31**	H X L
	IR870*JAYA	92.06	-3.18**	A X A
	IR11T197*NU 2009	94.38	-3.12**	A X L
	IR11T189*NU 2009	93.70	-2.47*	A X L
Plant height	IR11T205*CSR 10	86.10	-5.29	A X H
	IR12T193*CSR 10	87.66	-3.28	A X H
	IR11T197*NU 2009	93.86	-2.68	L X A
	IR870*NU 2009	93.63	-2.08	L X A
	IR14T104*JAYA	90.93	-1.79	H X A
Flag leaf area	IR12T193*NU 2009	23.18	1.99*	A X L
	NDRK 5001*CSR 10	24.38	1.67*	A X A
	IR11T205*CSR 10	27.14	1.48	H X A
	IR11T189*CSR 10	22.30	1.23	L X A
	IR12T193*JAYA	23.52	1.01	A X A

Panicle bearing tillers per plant	IR11T205*JAYA	13.68	1.35	A X A
	IR11T197*NU 2009	18.58	1.09	A X A
	IR12T193*NU 2009	11.45	0.91	A X A
	IR14T104*JAYA	11.09	0.83	L X A
	IR11T189*CSR 10	11.83	0.52	A X A
Characters	Crosses with significant effects	Per se performance	sca effects	gca effects of parents
Panicle length (cm)	NDRK 5001*CSR 10	23.33	1.14	H x A
	IR12T193*NU 2009	21.67	1.08	A X A
	IR12T193*JAYA	21.82	0.88	A X A
	IR11T197*CSR 10	19.63	0.63	L X A
	IR11T205*JAYA	23.78	0.44	H X A
Grains per panicle	IR12T193*NU 2009	140.20	10.53**	L X H
	NDRK 5001*JAYA	142.60	6.47**	H X A
	IR11T189*CSR 10	132.24	4.83**	L X L
	IR870*NU 2009	137.83	4.03*	L X A
	IR11T205*CSR 10	140.20	4.01*	H X L
1000- grain weight (g)	IR11T205*CSR 10	28.78	2.55**	H X H
	IR12T193*JAYA	24.36	1.30	A X A
	NDRK 5001*NU 2009	23.07	1.21	A X L
	IR870*CSR 10	22.19	0.95	L X H
	IR870*jaya	19.53	0.79	L X A
Biological yield per plant(g)	IR870*CSR 10	54.69	5.68	A X H
	IR12T193*NU 2009	61.10	5.65**	A X A
	IR11T205*CSR 10	59.92	2.45	A X L
	NDRK 5001*JAYA	56.33	2.41	A X H
	IR870*JAYA	54.69	1.99	A X L
Harvest-index (%)	NDRK 5001*CSR 10	40.28	2.41	A X L
	IR11T205*CSR 10	39.97	2.26	A X L
	IR14T104*NU 2009	40.86	1.96	A X A
	IR12T193*JAYA	38.67	1.79	A X H
	IR870*NU 2009	40.77	1.45	A X A
Grain yield per plant(g)	IR12T193*NU 2009	21.42	2.59**	A X A
	IR11T205*CSR 10	23.89	2.23*	A X A
	NDRK 5001*CSR 10	23.96	2.03*	A X A
	IR870*CSR 10	21.67	1.68	A X A
	IR12T193*JAYA	20.78	1.40	L X A

H = High (significant and positive), L= Low (significant and negative) and A= Average (non- significant)

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