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Genetic variation and heritability for quantitative traits in rice (*Oryza sativa*) under sodic soil

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ABSTRACT

The present investigation was carried out during 2016–17 at NDUA&T, Ayodhya to assess the genetic variation and heritability for quantitative traits in rice (*Oryza sativa* L.) under sodic soil. The experimental materials of rice comprised of 10 genotypes as lines (females) and three testers (males), viz. Pusa Basmati-1, CSR-10 and N.Usar-2009. Each of three testers was crossed with 10 lines during *kharif* 2016. The genotypes were grown during *kharif* 2017 and evaluated along with their parents and one check varieties (Narendra Usar-3) in randomized complete block design with three replications. The experiment was conducted at soil having *p*H 9.2, EC-2.21 dS/m and ESP 43%. The analysis of variance revealed that all the treatments, viz. parents, parent vs crosses, crosses, lines and testers were highly significant for majority of the yield and its contributing traits. The estimates of phenotypic coefficient of variation were higher than genotypic coefficient of variation for all the traits. Estimate of high heritability (broad sense) coupled with high genetic advance in percent of mean were observed for the characters like grain yield/plant, biological yield/plant, grains/panicle, panicle bearing tillers/plant, spikelet's/panicle, chlorophyll content and flag leaf area indicating the involvement additive gene action. The moderate narrow sense heritability with low genetic advance in percent of mean were observed for panicle length and harvest index indicating presence of non-additive gene action suggesting heterosis breeding may be useful for rice improvement in sodic soil.

Key words: Genetic advance, Genetic variability, Heritability, Rice

Rice (*Oryza sativa* L.) is the world's leading cereal crop as more than half of the world's population is dependent on rice as their staple food. The major intention of plant breeder is to create maximum extent of genetic variability in the existing genetic stock. Variation is the basis of plant breeding. Thus the success of any improvement programme will largely depend on the magnitude and range of variability in the available genetic stocks (Basavaraja *et al.* 2013). Rice is the life and the prince among cereals as this unique grain helps to sustain two thirds of the world's population. Uttar Pradesh is an important rice growing state in the country. The area and production of rice in this state is about 6.45 million ha and 18.25 millon tonnes, respectively, with the productivity of 4.95 tonnes/ha (Uttar Pradesh Directorate of Agricultural statistics 2017–18). Agriculture is the most important in the state, because, about 80% of its population resides in rural areas and 75% of the total workers are involved directly or indirectly in cultivation/farming which accounts for 27% of state's GDP. Agriculture is the main source of income for families in the state. It has 6.45 m ha of cultivated area, constituting 70% of the total geographical area. The irrigated area is over 13.43 m ha. Rice area with salt problem in state is estimated to be ≤2%. In land salinity areas are mainly concentrated in Raibareilly, Azamgarh, Sultanpur, Ayodhya, Lucknow, Unnao and Pratapgarh district. It is a backbone to the Indian agriculture. Rice production (USDA 2017–18) is forecast higher at 111.50 m tonnes from 43.39 m ha compared to 2016–17 production of 105 m tonnes. Heritability and genetic advance are important selection parameters which help in predicting the gain under selection. Hence, the present study was undertaken to determine the extent of variability and heritability for yield contributing characters with involvement of different genotypes.

MATERIALS AND METHODS

The experiment was laid out during two consecutive wet season of 2016–17 at the GPB farm of N.D. University of Agriculture and Technology, Ayodhya. The experimental materials of rice for this investigation comprised of 10 genotypes as lines (females) and three testers (males) Pusa Basmati-1, CSR-10 and Narendra Usar-2009. Each of three testers was crossed with ten lines during *kharif* 2016. Thus, total numbers of 30 hybrids (F1) were obtained. The total

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genotypes were grown during *kharif* in 2016 and evaluated along with their parents and one check varieties (Narendra Usar-3) in randomized complete block design with three replications crosses obtained through crossing in a line × tester mating design. Besides these checks, viz. Narendra Usar-3 a rice hybrid was also included for standard heterosis. The experiment was conducted in a soil having *p*H = 9.2, EC =2.21 dS/m and ESP 45%. The fertilizers were applied @120 kg nitrogen, 60 kg phosphorus and 60 kg potash per ha through urea, DAP and muriate 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, viz. days to 50% flowering, plant height (cm), flag leaf area (cm^2), panicle bearing tillers per plant, panicle length (cm), grains, grains per panicle, spikelet fertility (%), chlorophyll content (SPAD Value), 1000-grain weight (g), biological yield per plant (g), harvest-index (%), grain yield per plant (g), blast, BLB, brown spot, leaf folder, stem borer were recorded on the basis of five randomly selected competitive plants in each plot. The mean data of different traits were subjected to analysis by standard statistical and biometrical method for Line × Tester analysis following Kempthorne (1957). For genetic analysis of these traits for randomized block design (Panse and Sukhstme 1967 and Falconer 1981), estimates of coefficients of variation (Burton and de Vane 1953), heritability in narrow sense (Kempthorne 1957) and broad sense ((Hanson *et al*. 1956) and genetic advance in percent of mean (Johnson *et al*. 1955).

RESULTS AND DISCUSSION

The analysis of variance for line × tester set comprising of 30 crosses and 10 parents is presented in Table 1 and Table 2 under sodic soil. The analysis of variance revealed that mean sum of squares due to treatments, viz. parents, parents vs. crosses; crosses, lines and line × tester were highly significant for all the characters indicating the existence of sufficient variability in the materials. These findings are in conformity with Panwar *et al.* (2007) and Konate *et al.* (2016). The variances due to testers were non-significant for all the characters except days to 50% flowering (100.64) showed highly significant estimates (Kumar and Verma 2016). The mean sums of squares due to lines were highly significant for all the characters. The mean squares due to replications were non-significant for all the characters while grains per panicle (11.14) and spikelet fertility exhibited significant variances due to replications. Paikhomba *et al.* (2014) reported that the estimate of heritability is more advantageous when expressed in terms of genetic gain.

Phenotypic coefficients of variation (PCV) were higher than the genotypic coefficients of variation (GCV) for all the characters (Table 2). PCV was highest for grains/panicle (339.32%) followed by biological yield (81.52%), days to 50% flowering (35.84), spikelet's fertility (33.04%), plant height (22.64%), grain yield/plant (18.40%), harvest index (15.26%), but it was lowest for panicle bearing tillers/plant (9.66%), 1000-grain weight (4.05%), chlorophyll content (3.80), flag leaf area (4.02) and panicle length (2.94%). The highest GCV was recorded for grains/panicle (335.01%) followed by biological yield (78.00%) to 50% flowering (31.23), spikelet's fertility (30.76%), plant height (18.87%), grain yield/plant (17.43%), but it was lowest for harvest index (9.98), panicle bearing tillers per plant (8.93%), 1000-grain weight (3.30%), chlorophyll content (3.20), flag leaf area (2.86) and panicle length (2.01%). Percentage of PCV and GCV were of the similar magnitude for all the traits and as such the order is same except panicle bearing tillers/plant (having high environmental fluctuation) indicating least effect of environmental factors. The highest GCV was

Table 1 Analysis of variance including parents and crosses for 12 traits in rice under sodic soil

Character	Sources of variation					
	Replication	Treatment	Parent	Cross	Parent vs Cross	Error
d.f.	2	42	12	29	1	84
Days to 50% flowering	5.51	100.64**	231.13**	47.62**	72.36**	4.70
Plant height (cm)	2.91	59.75**	118.23**	23.85**	399.03**	3.82
Flag leaf area (cm^2)	1.91	9.37**	6.21**	10.69**	8.86**	1.15
Panicle bearing tillers per plant	1.12	28.15**	2.34**	35.48**	125.34**	0.74
Panicle length (cm)	0.40	7.11**	3.65**	8.46**	9.61**	0.94
Grains per panicle	11.14	1028.42**	45.46**	1457.24**	388.12**	4.86
Spikelet fertility (%)	5.38	96.62**	14.64**	133.83**	1.20	2.31
Chlorophyll content (SPAD Value)	0.49	10.08**	4.36**	11.83**	28.21**	0.61
1000 grain weight	0.22	10.53**	11.56**	8.20**	65.96**	0.73
Biological yield per plant (g)	0.79	240.49**	27.49**	268.97**	1970.71**	3.52
Harvest-index (%)	1.09	35.70**	27.82**	32.72**	216.39**	5.26
Grain yield per plant(g)	0.05	53.77**	8.72**	53.83**	592.88**	0.99

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

Table 2 Parent including crosses with genetic variability for 12 quantitative traits in rice under sodic soil

Character	Parent including crosses		Coefficient of variation (%)		Heritability (%)		Genetic components		Degree of dominance	Genetic advance	Genetic advance in % of mean
	Mean	Range	Genotypic	Phenotypic	Broad sense	Narrow sense	Additive variance	Dominance variance			
Days to 50% flowering	97.90 ± 0.18	75-108.33	31.23	35.84	87.21	15.52	2.21	12.13	1.19	13.77	14.07
Plant height (cm)	95.87 ± 0.17	81.28-105.05	18.87	22.64	83.23	7.87	3.2	12.95	4.09	10.47	10.92
Flag leaf area (cm^2)	22.43 ± 0.04	18.80-28.41	2.86	4.02	71.34	2.90	0.38	7.5	9.72	3.76	16.78
Panicle bearing tillers/plant	9.90 ± 0.07	6.50 - 17.60	8.93	9.66	92.31	4.04	0.24	33.4	6.79	7.58	83.37
Panicle length (cm)	20.80 ± 0.12	18.50 – 26.60	2.01	2.94	68.35	1.31	0.05	8.8	11.47	3.09	14.16
Grains per panicle	115.25 ± 0.20	83.33 -141.46	335.01	339.83	99.42	22.84	131.84	527.38	2.58	47.98	41.63
Spikelet fertility (%)	81.09 ± 0.13	69.26-91.83	30.76	33.04	93.30	8.63	0.76	93.83	4.52	14.13	17.42
Chlorophyll content (SPAD Value)	9.17 ± 0.06	6.57 – 15.60	3.20	3.80	84.46	2.25	0.20	11.96	8.444	4.33	47.22
1000 grain weight (g)	21.68 ± 0.17	18.13 – 24.86	3.34	4.05	82.50	4.23	0.24	6.8	6.22	4.38	20.21
Biological yield/ plant (g)	42.93 ± 0.12	30.4 – 57.50	78.00	81.52	96.21	21.54	1.17	99.31	2.63	22.81	53.13
Harvest-index (%)	36.82 ± 0.09	29.40 – 42.74	9.98	15.26	65.31	6.42	1.75	20.04	4.64	6.74	18.31
Grain yield /plant (g)	15.94 ± 0.32	10.40 – 23.13	17.43	18.40	95.40	9.84	0.33	8.76	4.20	10.72	67.28

recorded for grain per panicle (335.01%) and the lowest for panicle length (2.01%) indicating that the maximum variability of genotypes observed for the trait, grains per panicle and thus indicating that selection would be more effective for grain per panicle than panicle length. High coefficient of variability indicated a scope of selection and improvement of these traits (Paikhomba *et al*. 2014) while low values indicated the need for creation of variability by hybridization. These findings are similar to Chaudhary and Motiramani (2003).

Heritability values in broad sense and genetic advance are presented in Table 2. The highest values of broad sense heritability (>80%) were observed for all the characters except panicle length (68.20%) and harvest index (65.31) having moderate heritability (50–75%). Similar results were also reported by Saleem *et al*. (2008). The highest heritability was recorded for grains per panicle (99.42%), whereas harvest index showed the lowest heritability (65.31%). High heritability values indicate though the character is least influenced by environmental factors yet the selection for improvement of such characters may not be useful (Singh *et al.* 2018).

The broad sense heritability values are based total genetic variance which indicates presence of both fixable (additive) and non-fixable (dominance) variance. These results are similar to those of Bihari *et al.* (2004) and Basavaraja *et al.* (2013). The highest genetic advance as percent of mean was recorded for panicle bearing tillers per plant (83.37%) followed by grain yield/plant (67.28%), biological yield/plant (53.13%), chlorophyll content (47.22%), grains/panicle (41.63), 1000-grain weight (20.21%), harvest index (18.31%), spikelet fertility (17.42%), flag leaf area (16.78%), panicle length (14.16%) and days to 50% flowering (14.07%) but it was lowest for plant height (9.26%). Panicle bearing tillers/plant followed by grain yield per plant, biological yield/plant (53.13%), and chlorophyll content, grains/panicle, 1000-grain weight, harvest index, spikelet fertility, and flag leaf area exhibited high heritability coupled with high genetic advance suggesting preponderance of additive gene action and indicated that selection may be more effective. Similar results were also reported by Sathya and Jebaraj (2013). Days to 50% flowering and plant height had high heritability value but exhibited less genetic advance suggesting preponderance of non-additive gene action influencing the inheritance of these traits. Panicle bearing tillers/plant and panicle length had low heritability and low genetic advance suggesting these characters are highly influence by environmental effects and selection would be ineffective. These findings supported the results of Shaikh *et al*. (2017).

The estimates of narrow sense heritability are presented in Table 2. The narrow sense heritability was classified into three groups by Robinson (1966) as low (less than 10%), medium (10–30%) and high (more than 30%). The estimate of heritability ranged from -7.87% (plant height) to 15.52% (days to 50% flowering) showing low heritability values for all the characters under study and indicating preponderance of non-additive gene action. Similar observations have been reported by Shaikh *et al*. (2017) and Singh *et al.* (2018). In case of additive gene action the selection of traits are fixable means that no segregation occurs and those traits are directly useful in hybrid breeding but in dominance or non-additive gene action the selection of traits are non-fixable means that there segregation occurs so that they are preferred to heterosis breeding.

Based on the above result it may be concluded that the estimates of phenotypic coefficient of variation were higher than genotypic coefficient of variation for all the traits indicating that they all interacted with the environment to some extent. High heritability (broad sense) coupled with high genetic advance in percent were observed for the characters like grain yield per plant, biological yield per plant, grains per panicle, panicle bearing tillers per plant, spikelet per panicle, chlorophyll content and flag leaf area indicating the involvement additive gene action. The heritability in narrow sense (h^2_n) for majority of the traits further reflected the preponderance of non-additive gene action supporting heterosis breeding of rice improvement under less touched salt affected soil.

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