Genetic variation in promising rice genotypes for sodicity tolerance

O.P. Verma^{*}, P.C. Ram, P.N. Singh, G.P. Verma, A. Ismail, R.K. Singh and Manoj Kumar

Department of Genetics and Plant Breeding, N.D.U.A.T., Kumarganj, Faizabad, U.P.

ABSTRACT

Twenty promising salt tolerant genotypes were evaluated in situ at Faizabad for estimation of the genetic variation of associated characters. The magnitude of difference between genotypic coefficient of variation and phenotypic coefficient of variation was relatively low for all the traits except sterile grains panicle⁻¹, biomass hill⁻¹ and panicle bearing tillers plant⁻¹. High broad sense heritability with high genetic advance in per cent of mean were recorded for single panicle weight hill⁻¹, panicle bearing tillers hill⁻¹ and plant height suggesting the preponderance of additive gene action in the inheritance. Grain yield showed significant positive correlation with biomass hill⁻¹, single panicle weight, fertile grains panicle⁻¹ and 100–grain weight. Hence, these traits should be given more emphasis while selecting genotype for yield improvement in rice for sodicity tolerance. On the basis of the above morpho-economic traits five genotypes which showed stable performance over two consecutive years were IR 65199-4B-10-1-2, CSR 23, IR 67519-3R-994-2B-2, IR 66946-3R178-1-1, and NDRK 50007 even though the rainfall varied from 536- 820 mm during the two years showing large variability in environmental stresses.

Key words: rice, sodicity tolerance, morphology, economic traits

Rice is an important staple food crop of the world which has adapted to diverse ecological niches. Soil sodicity is a complex trait which affects the plant at different growth stages viz., initial plant establishment to maturity. Low yield is a characteristic feature of sodic soil. In order to impart resistance to biotic and abiotic stresses, it is important to introduce desirable attributes in a rice variety of sodic soil of good agronomic base. For this, an inevitable requirement is to genetically characterize, identify and isolate the desirable and stable genotype from the existing germplasm. Genotypes having genetically diverse background may be helpful to obtain high heterotic response and transgressive segregants in future breeding programme. Studies on in situ selection of promising genotypes for sodicity tolerance based on physiological attributes are limited. In situ selection of promising rice genotypes for sodicity tolerance is of prime importance for resource poor farmers.

In view of the above, present study on the evaluation of twenty germplasm lines of rice including

relatively newer genotypes having exotic base, were undertaken to estimate genetic variance of the characters under consideration and interrelationship among them in order to identify the stable genotype for their better utilization in target rice improvement programme.

MATERIALS AND METHODS

In situ selection process was followed to identify salt tolerant rice genotypes and evaluate the efficacy of this process in breeding programme. Twenty promising genotypes of rice were grown at N.D. University of Agriculture & Technology, Faizabad in sodic soil (pH 9.7 EC (dSm^{-1}) = 2.21) during two consecutive wet seasons from 2006-2007 in randomized complete block design in micro plots with three replications.

Each genotype was shown in plot of eight rows of 4.0 m length. These genotypes comprised of a collection of local selection, advance breeding lines and commercial cultivars. Recommended cultural practices

* Present Address : Research Scholar, PG 0614, Deptt. of Genetics and Plant Breeding, Institute of Agricultural Sciences, BHU, Varanasi

and plant protection measures were followed to raise a good crop. The data were recorded on ten morphological characters *viz.*, days to 50 % flowering, plant height, panicle length, panicle bearing tillers hill⁻¹, biomass hill⁻¹, fertile grains panicle⁻¹, sterile grains panicle⁻¹, 100–grain weight, single panicle weight hill⁻¹ and grain yield hill⁻¹, were recorded on five randomly selected plants. Genetic parameters for variability and correlation were analyzed as proposed by Johnson *et al.* (1955) and Dewey and Lu (1959).

RESULTS AND DISCUSSION

The analysis of variance showed a wide range of variation and highly significant differences for all the characters studied except sterile grains panicle⁻¹ (Table 1). Coefficient of variation at phenotypic (PCV)

biomass hill⁻¹, sterile grains panicle⁻¹ and panicle length. Similar kind of result has been reported by Singh et al. (2007) and Manoj Kumar et al. (2008). Genetic advance expressed as per cent of mean was high for sterile grains panicle⁻¹, panicle bearing tillers hill⁻¹ and single panicle weight hill⁻¹; low for panicle length, days to 50 % flowering and 100-grain weight and moderate for remaining traits. The relationship between heritability and genetic advance for all the traits suggested that they were governed by both additive and dominance gene action. However, high heritability coupled with high genetic gain for single panicle weight hill⁻¹, panicle bearing tillers hill⁻¹ and plant height revealed that the preponderance of additive genetic variance employing the direct selection would be quite effective for these traits. Roy et al., (2001), Verma and Srivastava (2004)

Table 1. ANOVA for yield and its associated traits in rice during wet season 2006

Source of Variation	DF	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle bearing tillers plant ⁻¹	Biomass hill ⁻¹ (g)	Fertile grains panicle ⁻¹	Sterile grains panicle ⁻¹	Sterility (%)	100-grain weight (g)	Total panicle weight	Grain yield hill ⁻¹ (g) hill ⁻¹ (g)
						M	SS					
Replication	2	3.62	24.20	2.00	23.34	50.79	48.52	6.39	21.16	0.03	7.78	6.26
Treatment	19	116.99**	83.65	3.07	9.12	47.89	980.81*	*316.41*	*195.71	0.24**	16.43	12.99
Error	38	6.03	127.42	5.62	6.14	46.71	234.69	112.59	95.33	0.04	14.87	11.90
Total	59	41.23	108.8	4.65	7.87	47.27	463.63	172.61	123.9	0.1	15.04	11.99

*, ** Significant at 5 and 1 per cent probability levels, respectively

and genotypic (GCV) levels were relatively high for majority of the traits except days to 50 % flowering, panicle length, and 100-grain weight (Table 2). The magnitude of PCV was higher than GCV for all the characters indicating the influence of environment. High heritability was observed for all the traits except and Manoj Kumar (2008) have also observed the similar result. Correlation among different morpho-economic traits can be used to select a desirable plant type for the improvement of target ecosystem. Grain yield showed significant positive correlation with biomass hill⁻¹, single panicle weight hill⁻¹, fertile grains hill⁻¹ and

Table 1.	ANOVA for	yield and its	associated	traits in r	ice during	wet season 2007

Source of Variation	DF	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle bearing tillers plant ⁻¹	Biomass hill ⁻¹ (g)	Fertile grains panicle ⁻¹	Sterile grains panicle ⁻¹	100-grain weight ⁻¹ (g)	Single panicle weight hill ⁻¹ (g)	Grain yield hill ⁻¹ (g)
							MSS				
Replication	2	6.02	0.93	0.69	18.71	3.31	115.27	112.65	0.01	0.15	39.87
Treatment	19	91.07**	524.89*	*7.80**	23.49**	200.35**	1103.45**	249.10*	0.09**	0.93**	59.17**
Error	38	15.07	32.89	3.15	6.27	101.26	294.95	104.61	0.03	0.18	18.96
Total	59	39.24	190.25	4.56	12.24	129.85	549.22	151.42	0.05	0.42	32.62

*, ** Significant at 5 and 1 per cent probability levels, respectively

Character	Genotypic coefficient variation	Phenotypic coefficient variation	Heritability in broad sense (%)	Genetic advance	Genetic advance in per cent of mean (%)
Days to 50% flowering	7.40	7.98	85.99	11.62	14.14
Plant height (cm)	4.58	14.28	10.27	2.52	3.02
Panicle length (cm)	4.04	11.15	13.15	0.69	3.02
Panicle bearing tillers plant ⁻¹	8.28	22.19	13.91	0.77	6.36
Biomass hill-1 (g)	1.87	20.50	0.83	0.12	0.35
Fertile grains panicle-1	20.55	28.64	51.45	23.30	30.36
Sterile grains panicle ⁻¹	34.26	55.85	37.64	10.42	43.30
Sterility (%)	23.83	46.76	25.98	6.07	25.02
100-grain weight (g)	11.51	14.51	62.94	0.42	18.81
Total panicle weight hill-1 (g)	4.90	26.65	3.38	0.27	1.85
Grain yield hill-1 (g)	5.19	30.25	2.95	0.21	1.84

 Table 2. Estimates of genetic variability, heritability, genetic advance and genetic advance in per cent of mean in rice during wet season 2006

 Table 2. Estimates of genetic variability, heritability, genetic advance and genetic advance in per cent of mean in rice during wet season 2007

Character	Genotypic coefficient variation	Phenotypic coefficient variation	Heritability in broad sense (%)	Genetic advance	Genetic advance in per cent of mean (%)
Days to 50% flowering	4.79	6.04	62.70	8.21	7.81
Plant height (cm)	12.88	14.12	83.29	24.08	24.22
Panicle length (cm)	5.38	9.36	33.04	1.48	6.37
Panicle bearing tillers plant ⁻¹	22.18	32.07	47.80	3.41	31.58
Biomass hill ⁻¹ (g)	16.08	32.43	24.60	5.87	16.43
Fertile grains panicle ⁻¹	16.53	23.93	47.75	23.37	23.54
Sterile grains panicle ⁻¹	29.16	51.93	31.52	8.03	33.73
100-grain weight (g)	6.50	10.20	40.57	0.19	8.52
Single panicle weight hill-1 (g)	20.35	26.73	57.99	0.78	31.93
Grain yield hill-1 (g)	22.65	35.20	41.42	4.85	30.03

100-grain weight (Fig. 1). Surek and Beser (2003), Verma and Srivastava (2004), Chandra *et al.*, (2006) and Ramakrishnan (2006) have also reported similar association with grain yield. It reflected that due emphasis should be given to select these traits for rice improvement in sodic soil.

The study revealed that the stable promising genotypes IR 65199-4B-10-1-2, CSR 23, IR 67519-3R-994-2B-2, IR 66946-3R-178-1-1 and NDRK 5007 may be utilized as donors and yield better recombinants to enhance yield potential in risk–prone sodic soil, even though the rainfall varied from 536-820 mm during crop growth period. Most of these entries are of diverse exotic origin possessing moderate resistance to major rice (stem borer). These *in situ* selected lines could be utilized as donors in rice hybridization programme for developing salt tolerant varieties. Besides biomass hill⁻¹, single panicle weight hill⁻¹, fertile grains panicle⁻¹ and 100-grain weight were found important traits for selecting better yielding genotypes. Looking towards the improvement in grain yield, the traits *viz.*, single panicle weight hill⁻¹, panicle bearing tillers hill⁻¹ and plant height can be included in breeding programme as these traits have shown high heritability coupled with high genetic advance reflecting the preponderance of additive gene action for the inheritance. It is concluded that *in situ* selection process could be quite useful in

diseases like brown spot, sheath rot, leaf blast and pest



developing salt tolerant rice varieties which may insure reproducible stable performance and adaptability under sodic soil environments.

REFERENCES

- Chandra R, Pradhan SK, Singh S, Bose LK and Singh ON 2006. Agro-morphologic traits as selection parameters for improvement of upland rice. Indian J. Plant Genet. Resour., 19 (2): 184-187
- Dewey DR and Lu KH 1959. Correlation and path coefficient analysis of components on crested wheat grass and seed production. Agron. J., 51: 515-18
- Johnson HW, Robinson HR and Comstock RF 1955. Estimation of genetic and environmental variability in soybean. Agron. J., 47: 314-18
- Manoj Kumar, Verma OP and Verma GP 2008. Genetic variability and heritability estimates of rice hybrids under alkaline condition. Ad. Plant Sci., 20 (2): 169-170



- Ramakrishnan SH, Anandakumar CR, Saravanan S and Malini N 2006. Association analysis of some yield traits in rice (*Oryza sativa* L.). Journal of Applied Sciences Research, 2 (7): 402-404
- Roy B, Hossain N and Hossain F 2001. Genetic variability in yield components of rice (*O. sativa* L.). En. and Eco., 19(1): 186-189
- Singh M, Kumar K and Singh RP 2007. Study of coefficient of variation, heritability and genetic advance in hybrid rice. Oryza, 44 (1): 160-162
- Surek H and Beser N 2003. Correlation and path coefficient analysis for some yield-related traits in rice (*Oryza sativa* L.) under thrace conditions. Turk J Agric, 27: 77-83
- Verma, OP and Srivastava HK 2004. Productive association of quantitative traits in diverse ecotypes of rice (*Oryza sativa* L.). Jour. Sust. Agri. (USA), 25 (2): 75-91