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Genetic Variability, Heritability and Divergence Studies in Rice (*Oryza sativa* L.) Under Sodic Soil

GYANENDRA PAL, O. P. VERMA, G. P. VERMA, NARENDRA PRATAP, MANOJ KUMAR
R. K. CHAUDHARY AND KARAN SINGH

Department of Genetics & Plant Breeding, Narendra Deva University of Agriculture & Technology Kumarganj, Faizabad 224229 (UP), India
E-mail : npratap82@gmail.com

Abstract

Genetic parameters of variability, heritability, genetic advance in per cent of mean and diversity for different characters were studied in 60 genotypes of rice during *kharif* of 2007-08 under sodic (pH 9.65, EC (dS/m) 2.21, OC 0.40%) situation. The maximum genotypic and phenotypic coefficients of variability were observed for spikelets per panicle followed by number of panicle bearing tillers per plant and grain yield per plant. The values of broad sense heritability (>75%) were observed for all the characters except panicle length (73.60%). High heritability and low genetic advance were recorded for harvest index followed by spikelet fertility, test weight, plant height, days to maturity and L : B ratio of the grains suggesting predominance of non-additive gene action in the inheritance of these traits. High heritability (h^2_b) coupled with high genetic advance was recorded for grain yield/plant followed by spikelets per panicle, panicle bearing tillers per plant, flag leaf area and days to 50% flowering hence, these traits were predominantly under the control of additive gene action. Diversity study revealed that the maximum cluster mean was found for grain yield per plant in cluster III, which also exhibited highest cluster mean for harvest-index. It reflects that clustering pattern may be utilized in identifying the promising genotypes for the traits of interest as genetic donors for rice improvement in sodic soil.

Key words : Gene action, Genetic divergence, Coefficient of variation, Heritability, Rice.

Salts are not alien to the land but it has converted large areas once under cultivation into barren lands. It occupies 10% of the world's arable land and 33% of the irrigated land. Globally, 932 m ha are estimated to be under problem soils while 100 m ha are affected in South and South-East Asia because of salinity, alkalinity and strong acidity. Soil salinity and soil sodicity have affected more than 8.6 m ha severely in India which has its own significant role to play for sustaining the future national food security. Nature has gifted a wide range of inter and intra genetic variability in crop plants but we have limited choice of crops which differ among themselves for salt tolerance, even different varieties of the same crop differ considerably in their behavior to various levels of salinity and sodicity tolerance. The recent advances in plant breeding for enhanced salt tolerance have lead to the development and release of high yielding and salt tolerant varieties in rice. Rice becomes the most adopted mono crop in coastal saline soils while best adopted crop for sodic soil. The pioneer work lead to the release of first dwarf, high yielding salt tolerant variety CSR 10 which was widely used in biological amelioration of sodic soils termed as 'Low Cost Technology' for resource poor and marginal farmers. Again, the pioneer to develop and release first basmati type salt tolerant rice variety CSR 30 (Yamini) which has become popular in Haryana and western UP. Growing of salt tolerant rice variety has reduced the productivity loss significantly on long term basis. Therefore, the present study was undertaken to screen out diverse genotypes of rice adopted under sodic situation.

Methods

The experimental material used in the present study included 60 entries of rice. These entries were grown under sodicity (pH 9.65, EC (dS/m) 2.21, OC 0.40%) at Research Farm of Genetics and Plant Breeding, N. D. U. A. & T., Kumarganj, Faizabad in *kharif* of 2007-08. The experiment was laid out in randomized block design, consisting of three replications. The crop was spaced row to row 20 cm and plant to plant

Table 1. Mean, range, coefficient of variation, heritability and genetic advance for different characters in rice.

Characters	Mean	Range		Coefficient of variation (%)		Heritability in broad sense (%)	Genetic advance in per cent of mean
		Mini-mum	Maxi-mum	Geno-typic	Pheno-typic		
1. Days to 50% flowering	93.20	65.00	121.00	10.39	10.56	96.90	31.07
2. Days to maturity	122.87	96.00	151.66	7.59	7.91	92.20	15.02
3. Plant height (cm)	101.88	72.86	131.93	12.36	12.52	97.40	25.14
4. Panicle bearing tillers per plant	13.88	9.26	24.46	18.45	19.80	86.90	35.43
5. Panicle length (cm)	24.54	20.26	26.70	5.47	6.38	73.60	9.67
6. Flag leaf area (cm^2)	54.82	29.28	72.73	16.63	17.75	87.80	32.10
7. Spikelets per panicle	166.02	111.00	258.20	19.34	19.81	95.30	38.90
8. Spikelet fertility (%)	79.39	57.81	95.03	12.12	12.25	98.00	24.72
9. Test weight (g)	25.49	19.33	31.46	10.24	10.35	97.90	20.88
10. Harvest-index (%)	47.03	38.56	54.87	8.65	8.73	98.20	17.66
11. Grain yield per plant (g)	24.30	12.02	30.66	18.00	18.09	99.00	36.90
12. L/B : ratio of the grains	3.89	2.47	5.02	13.75	14.60	88.70	26.66

15 cm. Observations were recorded on 5 competitive plants for 12 quantitative traits viz., days to 50% flowering, days to maturity, plant height (cm), panicle bearing tillers per plant, panicle length (cm), flag leaf area (cm^2), spikelets per panicle, spikelet fertility (%), test weight (g), harvest-index (%), grain yield per plant (g) and L : B ratio of the grains. Analysis of variance for each character was done following Panse and Sukhatme (1). The coefficient of variation was estimated as suggested by Burton and de-vane (2). Heritability in broad sense (h^2_b) was calculated according to the formula suggested by Hanson et al. (3). Expected genetic advance in per cent of mean was calculated following Johanson et al. (4). Genetic divergence was estimated by standard methods (5, 6).

Results and Discussion

The analysis of variance revealed significant differences among the 60 rice genotypes for all the 12 characters. The mean, range, coefficient of variation, heritability in broad sense and genetic advance in per cent of mean are depicted in Table 1. Results revealed that out of 60 genotypes, maximum numbers of genotypes are low performing for number of panicle bearing tillers per plant (9.26) and spikelets per panicle (111.00) because its mean performance was oriented to these minimum figures due to high sodicity level. It indicates that only few genotypes were extremely of high performance for these traits and easily be selected. However, characters viz., flag leaf length (72.73 cm^2), grain yield per plant (30.66 g) and L : B ratio (5.02) having maximum number of genotypes for its high performance since its mean performance was oriented to these maximum figures. It indicates that ample scope for selection of maximum number of genotypes for better performance under sodic situation. Whereas, there was also equal number of genotypes having minimum and maximum performance for rest of the traits. In general, phenotypic coefficient of variation (PCV) were slightly higher than genotypic coefficient (GCV) indicating least influence of environment on these traits. In other words, the phenotypic expression was under the control of genotype/genetic components indicating selection could be effective. The maximum genotypic coefficient of variation were observed for spikelets per panicle followed by panicle bearing tillers per plant, grain yield per plant, flag leaf area and L : B ratio of the grains, indicating sufficient opportunity for selection as these are already detected through mean performance and range of respective traits (7—9). The values of broad sense heritability (>75%) were observed for all the studied characters except panicle length (73.60%). High heritability values indicates that the characters are least influenced by environmental factors, yet the selection for improvement of such characters may not be useful because broad sense heritability values are based on total genetic variance which indicates presence of both fixable (additive) and non-fixable (domi-

Table 2. Clustering pattern of 60 rice genotypes on the basis of non-hierarchical euclidean cluster analysis.

Number of clusters	Number of geno-types	Genotypes
I	13	NDRK5070, NDRK5000, CSR-13, CSRC (5) -52-1-1, NDRK-5056, 21-2-9-B-1-5, IR-26, IR-71866-3R-1-2-1-B, BW267-B, IR65847-3B-6-2, IR7657-5R-B-12P, IR69323-4R-2B-1-3-1-B, IR711A23-3R-73-1-2-B
II	12	NDRK50009, NDRK50008, CSR-02-228, CSR (S) 5-1-7, NDRK 5082, NDRK-5059, NDRK5054, IR70023-4B-R-12-3-1-1-B, NDR5095, IR50709-2B-5-2B-1-1, CN1914, IR47547-3B-26-2B-1
III	9	IR72593-B-3-2-2-2-B NDRK5097, NDRK 5091, CSR- 27, CSR30 (Yamini), Sarjoo-52, NDRK5086, IR71991-3R-2-1-B, IR71-8963R-8-3-B
IV	12	NDRK5088, NDRK50007 Vikas, NDRK50-003, jaya, NDRK 5018, NDR509, NDRK-5011, CR2577, NDRK 5026,NDRK5090, Usar 1
V	14	CSR92063, NDRK5089, NDRK5022, IR718-95-3R-26-2-1-B, Narendra Usar Dhan-2, CST-7-1, CSR(S)5-22-5,NDRK5035, IR6592-4B-8-1, Geetu, Kalmuhi, CSR10, IR69920-3B-22-2-1, IR70023-4B-R-12-3-1-B

nance and epistasis) variance (8, 9). High heritability and low genetic advance was recorded for harvest index followed by spikelet fertility, test weight, plant height, days to maturity and L : B ratio of the grains suggesting predominance of non-additive gene action in the inheritance of these traits. Panicle length had low heritability and low genetic advance suggesting character is highly influence by environmental effects and selection would be ineffective (9, 10).

Table 3. Estimate of average intra and inter cluster distance for five clusters in rice germplasm. Bold figures represent intra cluster distance.

Number of clusters	I	II	III	IV	V
I	**2.961**	3.164	3.191	3.508	3.793
II		**2.507**	3.114	3.137	2.973
III			**3.036**	3.079	3.177
IV				**2.944**	3.045
V					**2.897**

High heritability (h^2_b) coupled with high genetic advance was recorded for grain yield per plant followed by spikelets per panicle, panicle bearing tillers per plant, flag leaf area and days to 50% flowering. Hence, these traits were predominantly under the control of additive gene action.

Sixty genotypes were placed were in five different clusters (Table 2). The distribution of different genotypes exhibited that cluster V was the largest possessing 14 genotypes followed by cluster I (13), cluster II and cluster IV each with 12 genotypes while cluster III has only 9 genotypes.

The intra-cluster distance, based on Euclidean cluster analysis, was maximum in cluster III (3.036) and minimum in cluster II (2.507) indicating thereby, that nine genotypes in this cluster are most divergent (Table 3). As regards inter-cluster distance, the maximum distance was observed between cluster V and cluster I (3.793) followed by cluster IV and I (3.508), suggesting the maximum diversity between them (cluster V, I and IV).

The average cluster mean of 12 characters (Table 4) revealed that cluster III comprising of nine genotypes recorded highest grain yield per plant (26.59 g), harvest-index (48.53%) and medium flowering (69.00).

Table 4. Cluster mean of different characters for five clusters in rice germplasm.

Cluster no	Days to 50% flowering	Days to maturity	Plant height	Panicle bearing tillers per plant	Panicle length	Flag leaf area	Spikelets per panicle	Spikelets fertility	Test weight	Harvest index	Grain yield per plant	L/B : ratio
i	91.23	125.46	80.99	11.63	21.85	42.08	129.96	78.63	23.50	44.87	22.25	3.69
ii	93.00	128.58	94.50	9.40	25.26	41.34	148.70	84.53	21.34	43.70	23.28	4.31
iii	69.00	129.44	81.50	10.31	21.99	33.93	113.93	83.89	24.97	48.53	26.56	4.36
iv	101.42	132.92	95.56	10.50	24.29	44.24	167.59	81.20	23.26	47.21	25.83	3.81
v	91.29	125.14	97.87	10.61	24.39	41.08	161.26	87.72	26.88	45.63	24.43	3.73

Cluster IV had high mean value for days to 50% flowering (101.42), days to maturity (132.92), flag leaf area (44.24 cm^2) and spikelets per panicle (167.59). The genotypes with medium maturity (125.14), maximum spikelet fertility (87.72%) and high test weight (26.88 g), were found in cluster V. In the same way, high value of panicle length (25.26 cm) was observed in cluster II while cluster I possessed genotypes with high estimates of panicle bearing tillers per plant (11.63) and short plant stature (80.99 cm) (5, 6, 11).

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