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RESEARCH ARTICLE

VARIABILITY, HERITABILITY AND GENETIC DIVERGENCE IN RICE GENOTYPES UNDER SALINE CONDITION

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ABSTRACT

Rice is staple food for Asian people and there is urgent need to produce more rice per unit area, which can be enhanced by possibly utilizing the unexplored germplasm for adverse climatic and soil conditions. Among the stress, salinity is profound and gaining prime importance in upcoming years; only possible way is breeding for salt tolerance by utilizing available genetic resources. Sixty genotypes of rice were evaluated under natural saline conditions during 2013-2014 for eleven characters viz., days to first flower, plant height, number of tillers plant⁻¹, number of panicles plant⁻¹, panicle length, number of grains panicle⁻¹, thousand grain weight, grain length, grain breadth, grain L/B ratio and grain yield plant⁻¹. The analysis of variance revealed the presence of significant differences among all the genotypes studied. Heritability in broad sense was observed high for all the characters studied except number of tillers per plant. Except number of tillers per plant, panicle length and grain breadth, for all other traits were having high genetic advance as per cent of mean coupled with high heritability. The genetic divergence among the genotypes was estimated through Mahalanobis D^2 statistics. The sixty genotypes were grouped into 6 clusters. Grain yield plant⁻¹ (22.14 %) contributed maximum towards total genetic divergence followed by number of grains panicle⁻¹ (17.34%) and plant height (16.44 %).

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INTRODUCTION

Since rice (*Oryza sativa* L.) is the most staple food, the food production has to be increased substantially and this could be achieved either through increased productivity or increased crop area. The increase in area to meet the demand of rice will have to come from stress inducing marginal lands and problem soils like saline, sodic, saline-sodic, acidic soils etc. The adoption of varieties tolerant to saline conditions is likely to augment the productivity of crop and help the farmers to raise crops in saline soils as reclamation of the saline soil is cost prohibitive.

Genetic diversity in crop species is the gift of nature. The increase in productivity is mainly depending on exploitation of genetic resources already present in the ecosystem. It is estimated that, not even 15% of the genetic diversity has been utilized, it may be underutilized or overexploited for a particular trait. With the advent of scientific principles over the past decades, the plant breeders have been increasingly cognizant of the importance of genetic diversity in crop plants. An insight into the extent and magnitude of variability present in the crop species is of utmost importance as it forms the basis of selection and thus, enables execution of any effective crop improvement programme. Besides, its quantitative estimation would indicate the potentiality of the germplasm from where the selection of desirable types with desirable traits can be done for maximizing the yield level.

The yield and yield components of a breeding population are highly influenced by the environment, which renders it difficult to conclude whether the observed variability is heritable or not. It is therefore essential to partition the observed variability into heritable and non-heritable components, by looking at the genotypic as well as phenotypic variations existing among the germplasm. Sixty rice genotypes including improved varieties of rice were evaluated under natural saline condition during 2013-2014. The genetic divergence among these rice genotypes were assessed in this report along with the relative importance of different traits in the total divergence through Mahalanobis D^2 statistics.

MATERIALS AND METHODS

The material for the present investigation consisted of sixty rice genotypes comprises land races, local cultivars, advanced lines, improved and released varieties. The experiment was conducted at the Plant Breeding Farm (11°24' N latitude and 79° 44' E longitude, + 5.79MSL), Faculty of Agriculture, Annamalai University, Annamalainagar, Tamil Nadu, India during the year 2013-14. The experiment was laid out in a Randomized Block Design with three replications, using 20 x 20 cm spacing. These genotypes were grown in natural saline soil with electrical conductivity (EC) of 2.83 dsm⁻¹. All the recommended agronomical practices and plant protection measures were followed to ensure normal crop. Observations

were recorded on ten randomly selected plants for grain yield plant⁻¹ and other traits viz., days to first flower, plant height, number of tillers plant⁻¹, number of panicles plant⁻¹, panicle length, number of grains panicle⁻¹, thousand grain weight, grain length, grain breadth, grain L/B ratio. The analysis of variance was performed as per the standard statistical procedures (Singh and Chaudhary, 1985). Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was estimated as per the procedure given by Johnson *et al.* (1955), broad sense heritability (h²) by Burton and De-Vane (1953) and genetic advance as per cent of mean by Singh and Chaudhary (1985). The Mahalanobis D² distance was calculated to estimate the genetic divergence (Mahalanobis, 1936). The genotypes were grouped into different clusters on the basis of D² values, as suggested by Tocher (Rao, 1952). The intra and inter cluster distance was calculated as per Singh and Chaudhary (1985). Statistical software NPRC stat was used for analysis.

RESULTS AND DISCUSSION

The analysis of variance revealed the presence of significant differences among the genotypes for all the eleven traits under study (Table 1). The characters which contributed maximum towards diversity were grain yield per plant (22.14 %), number of grains per panicle (17.34%) and plant height (16.44 %).

The days to first flower showed lowest significant mean value as 59th day in the genotype ANR 37 whereas, the flowering was delayed till 99th day in genotype Burmadhan Black. The height of the plant varied from 65.67cm in Jaya to 172 in C 14-8. The mean height of sixty genotypes was 105.70. Genotype STBN 4 and Supermoti registered the maximum and minimum number of panicles per plant respectively. Number of grains per panicle varied from 41.67 in Basmati SPS to 196.33 in Co 43. Grain yield per plant was highest in Co 43 (29.93 g) followed by followed by CARI 1 (29.83 g) and Pokkali (29.50 g).

the characters viz., number of panicles per plant, number of grains per panicle and grain yield per plant indicating their greater role of contribution to the variability among the genotypes. The narrow differences between PCV and GCV values is suggestive of the fact that phenotypic variation was determined by and large by genotype with negligible influence of extraneous factors and therefore, selection for such traits will be rewarding. High heritability was recorded for all the characters except number of tillers per plant. Characters such as days to first flower, plant height, number of panicles per plant, number of grains per panicle, thousand grain weight, grain length, grain L/B ratio and grain yield per plant expressed both high heritability and high genetic advance as per cent of mean. Panicle length and grain breadth was accompanied by moderate estimate of genetic advance as per of mean and high estimate of heritability. Therefore, direct selection based on phenotypic observations may be effective for improvement of these traits.

All the 60 rice genotypes were grouped into 6 clusters, in such a way that the genotypes within cluster had smaller D² values among themselves than those belonging to different clusters. Out of the 6 clusters, Cluster I encompasses the largest number of 50 genotypes followed by Cluster II with four genotypes, Clusters IV and V had two genotypes each and the Clusters III and VI are solitary in nature. The mean of each character in each cluster are presented in Table 3. Murthy and Arunachalam (1966) have opined that hybridization programmes should be formulated in such a way that the parents belonging to different clusters with maximum divergence could be utilized so as to get desirable segregants. The maximum inter-cluster distance (89.02) was observed between cluster III and VI followed by clusters I and VI (76.57) and clusters II and VI (73.71) (Table 4). The genotypes grouped in a same cluster would display the lowest degree of divergence from one another, and therefore, crosses made between genotypes belonging to a same cluster may not give heterotic progenies as also reported by earlier workers (Mishra *et al.*, 2003; Chaturvedi and Maurya, 2005).

Table 1 Analysis of variance for eleven characters in 60 rice genotypes

Source of variation	df	Days to first flower (days)	Plant height (cm)	No. of tillers plant ⁻¹	No. of panicles plant ⁻¹	Panicle length (cm)	No. of grains panicle ⁻¹	Thousand grain weight (g)	Grain Length (mm)	Grain breadth (mm)	Grain L/B ratio	Grain yield plant ⁻¹ (g)
MSS												
Replication	2	17.67	16.21	20.68	1.72	12.05	216.72	6.34	0.02	0.02	0.00	1.64
Genotype	59	634.83**	967.18**	32.53**	13.17**	24.11**	4252.59**	36.95**	3.80**	0.33**	0.48**	169.14**
Error	118	7.65	21.13	6.78	1.23	3.96	118.78	2.08	0.03	0.01	0.01	2.41

**Significant at 1 per cent level

Table 2 Variability parameters for eleven traits in 60 rice genotypes

Parameters	Days to first flower (days)	Plant height (cm)	No. of tillers plant ⁻¹	No. of panicles plant ⁻¹	Panicle length (cm)	No. of grains panicle ⁻¹	Thousand grain weight (g)	Grain Length (mm)	Grain breadth (mm)	Grain L/B ratio	Grain yield plant ⁻¹ (g)
Range: Min	59.33	65.67	13.00	4.67	18.33	41.67	12.30	5.87	2.00	1.83	3.85
Max	99.33	172.00	26.00	14.00	29.67	196.33	28.07	9.45	3.85	3.60	29.93
PCV	17.89	16.79	15.96	20.96	10.36	32.48	19.67	13.29	10.12	15.01	39.98
GCV	18.22	17.35	21.35	23.97	13.07	33.85	21.35	13.44	10.68	15.44	40.84
Heritability (%) bs	96.47	93.72	55.86	76.47	62.91	92.06	84.83	97.78	89.86	94.49	95.84
Genetic advance (% of mean)	36.21	33.50	24.57	37.76	16.94	64.20	37.32	27.08	19.78	30.06	80.64
CD(P=0.05)	4.42	7.35	4.16	1.77	3.18	17.44	2.30	0.27	0.17	0.15	2.48

The estimates of variability parameters for 11 yield related characters of 60 rice genotypes under saline condition is presented in Table 2. High GCV estimates were recorded for

As evidenced from the clustering pattern, cluster III and VI are most diverse for the eleven morphological traits studied in rice genotypes.

Table 3 Cluster mean values for eleven traits of 60 rice genotypes

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Days to first flower	81.35	74.17	65.67	70.00	98.33	80.33
Plant height (cm)	103.73	107.00	100.67	112.17	154.17	94.33
Days to first flower	81.35	74.17	65.67	70.00	98.33	80.33
Plant height (cm)	103.73	107.00	100.67	112.17	154.17	94.33
Number of tillers plant ⁻¹	18.42	18.92	24.00	19.00	13.84	15.00
Number of panicles plant ⁻¹	9.99	7.25	11.00	7.00	6.00	5.67
Panicle length (cm)	25.41	24.34	20.33	20.17	24.50	22.00
Number of grains panicle ⁻¹	122.28	66.92	153.67	63.84	70.00	54.00
Thousand grain weight (g)	16.93	14.99	14.30	25.14	25.29	12.47
Grain length (mm)	8.39	7.15	5.87	10.57	8.89	9.45
Grain breadth (mm)	3.16	3.17	3.20	3.43	3.70	2.67
Grain L/B ratio	2.67	2.29	1.83	3.15	2.00	3.53
Grain yield per plant (g)	20.28	7.59	24.15	11.82	10.40	5.49

Table 4 Inter and Intra-cluster D (bold) values among six clusters of 60 rice genotypes

Cluster No	I	II	III	IV	V	VI
I	14.64	18.82	43.11	37.77	47.27	76.57
II		15.84	20.52	29.78	43.11	73.71
III			0.00	34.69	50.68	89.02
IV				16.82	26.23	44.21
V					14.14	38.00
VI						0.00

Hybridization between them may be expected to produce desirable segregants. Apart from it genotypes of cluster I and VI i.e genotype Pusa Basmati 1121 and 50 genotypes of cluster I could be utilized in hybridization programme for getting desirable segregants and high heterotic response. The genetic distance between the parents largely govern the variability spectrum generated the segregating populations and also heterosis in the F₁s. Therefore, identification of genetically diverse genotypes helps in selecting desirable parents for hybridization programmes. Based on the mean performance and their inter-cluster distances the promising genotypes identified were STBN 13, CSR 10, CARI 2 and STBN 11 might be utilized as potential donor parents. ANR 37 for earliness and Jaya for dwarfness. These genotypes can be used for improvement of the respective traits.

References

Burton GW and De Vane FH 1953. Estimating heritability in tall fescue (*Fasculata arundinaceae*) from replicated clonal material. Agron. J. 45:478-481.

Chaturvedi HP and Mauya DM 2005. Genetic divergence analysis in rice (*Oryza sativa* L.) genotypes in Kumaun Himalaya. Indian J. Genet. 66(1):37-38.

Johnson HW, Robinson HF and Comstock RE 1955. Estimation of genetic and environment variability in soybean. Agron. J. 47:314-318.

Mahalanobis PC 1936. On the generalized distance in statistics. Proc. Natl. Inst. Sci. (India), 12:49-55.

Mishra LK, Sarawgi AK and Mishra RK 2003. Genetic diversity for morphological and quality traits in rice (*Oryza sativa* L.) Adv. Plant Sci. 16(1):287-293.

Murthy BR and Arunachalam V 1966. The nature of genetic divergence in relation to breeding system in crop plants. Indian J. Genet. 26:188-198.

Rao CR 1952. Advanced Statistical Methods in Biometrical Research. John Wiley and Sons, Inc., New York.

Singh RK and Chaudhary BD 1985. Biometrical Methods in Quantitative Genetic Analysis (3rd Ed). Kalyani Publishers, New Delhi-Lu.
