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Assessment of genetic diversity for yield and its components traits in rice (*Oryza sativa* L.) landraces

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Abstract

The aim of this study was to determine the nature and extent of genetic variability and diversity among twenty rice genotypes consisting of fifteen landraces and five cultivated varieties. The Experiment was conducted in randomized block design replicated thrice, for the evaluation of thirteen quantitative traits. Significant difference for all the quantitative traits was observed among all the genotypes reflecting presence of variability and scope of selection. Based on Mahalanobis D^2 analysis using Tocher' method, five clusters were formed. Cluster V was monogenotypic and cluster I was largest having 8 genotypes. Cluster II and III consist of 5 genotypes and IVth cluster involved 3 genotypes respectively. The clustering pattern revealed that, geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different cluster and vice-versa. The highest intra-cluster distance was exhibited by cluster III indicating presence of high diversity within cluster, hence providing scope for exchange of genes among genotypes within these clusters. Maximum diversity based on inter-cluster distance was observed between Cluster III and IV followed by cluster II and III and cluster I and III which can be utilized by hybridization-selection breeding programme through involving genotypes in these clusters to obtain useful transgressive segregants. High cluster mean for Flag leaf length was exhibited by cluster II. Mean of cluster III was high for effective tillers per plant & chlorophyll content with early flowering, early maturity and reduced plant height. High mean of cluster for flag leaf width & panicle length with high 1000 seed weight & Harvest index was exhibited by cluster IV whereas, cluster V showed highest mean for fertile spikelet per plant and grain yield. Percent contribution towards divergence was observed maximum by plant height and appreciable by panicle length and biological yield per plant. Most of the land races were of photosensitive group and days to maturity along with harvest index did not reflect any contribution.

Keywords: Genetic variability, genetic diversity, D^2 analysis, land-races, rice

Introduction

Rice (*Oryza sativa* L.) is the most important cereal crop of the world and about 90 per cent of the people of south-East Asia consume rice as staple food. It is obvious to tap the diversified classes of rice harbouring crucial and desirable combinations of genes for its improvement. Genetic diversity of a population within any species or genus is the sum of genetic characteristics (Rao and Hodgkin 2002) [13]. It provides the information of genetic barriers like biotic and abiotic stresses and scope of crossing between diverse parents to get maximum heterosis. It differs from genetic variability, which describes the variation within these genetic characteristics. Landraces of a crop conserve great genetic potential for the improvement of desirable traits. Unlike high-yielding varieties (whose variability is limited due to

homozygosity), the landraces maintained by farmers are endowed with tremendous genetic variability, as they are not subjected to subtle selection over a long period of time. This aids in the adaptation of landraces to wide agro-ecological niches and they also have unmatched qualitative traits and medicinal properties. This rich variability of complex quantitative traits still remains unexploited. Landraces are also important genetic resources for resistance to pests and fungal diseases. India is a primary centre of origin of rice and has many local landraces, most of which are not cultivated today. While many are lost, a few are still cultivated by resource-poor traditional farmers in areas practicing subsistence farming. The exact genetic potential, differences from commercial varieties, and the magnitude of heterogeneity still present in local landraces are not well catalogued. So, we formulated our research by taking fifteen land-races and five cultivated varieties of rice to know the nature and extent of genetic variability and genetic divergence of traits with grain yield among these genotypes. Multivariate analysis based on Mahalanobis-D² statistics and canonical variant analysis has been considered as an important tool in quantifying the genetic divergence in different crops (Rao, 1952) [14]. A number of scientists (Arunachalam, 1981) [2] have emphasized the importance of genetic diversity in plant breeding for obtaining broad spectrum of desirable variability in segregating generations. Reports of many researchers has suggested that, the nature and magnitude of variation existing in available plant breeding materials is of obvious important for selection of desirable genotypes under planned breeding programme and yield improvement.

Materials and Methods

Twenty rice genotypes were evaluated for thirteen quantitative traits in three replicated Randomized Block Design (RBD) at the experimental farm of Dr. Rajendra Prasad Central Agricultural University, Pusa, Bihar. Recommended spacing, dose of fertilizers and plant protection measures were followed to raise a healthy crop. The data were recorded for days to 50% flowering (DFF), days to Maturity (DM), plant height (cm) (PH), effective tillers/ plant (ETP), flag leaf length cm (FLL), flag leaf width cm (FLW), chlorophyll content (CC), panicle Length cm (PL), fertile spikelets/panice (FSP), test weight (gm) (TW), biological yield/ plant (BYP), harvest index (HI) and grain yield per plant (GYP). Chlorophyll content was recorded by chlorophyll meter (SPAD). Test of significance for each character were analyzed as per methodology advocated by Panse and Sukhatme (1967) [12]. The genetic divergence was estimated by Mahalanobis (1936) D² statistics and the grouping of the genotypes into clusters were done using Tocher's method (c. f. Rao, 1952) [14].

Results and Discussion

A significant difference between multivariate traits is the pre-requisite for multivariate analysis and grouping of genotypes. It is further used in selection of the diverse parents for generation of desirable recombinants in segregating generation. In the present study, analysis of variance (ANOVA) (Table-1) revealed that, all the twenty rice genotypes significantly differed in respect of all quantitative traits. This shows the presence of considerable variability among the studied genotypes, suggesting the adequate scope for selection of superior genotypes aimed at enhancing yield potential of rice genotype.

On the basis of Mahalanobis D² following Tocher method for clustering, twenty genotypes were grouped into five clusters

with cluster-wise variable number of genotypes (Table 2) developed by various centres and located at different geographical locations suggesting considerable amount of genetic diversity in the material. Amongst five, a cluster V was mono-genotype cluster. Cluster I was the largest having 8 genotypes involving varieties/land races from various centres. Similarly, cluster II and III consisted of 5 genotypes and IV involved 3 genotypes, respectively. The pattern of distribution of genotypes in different clusters exhibited that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different cluster and vice-versa, as supported by earlier findings of Clustering based on D² distances was also performed by Chauhan *et al* (2003) [7], Bhutia *et al.*, (2005) [14].

The intra and inter cluster distances (Table 3) and the mean performance of the clusters (Table 4) were used to select genetically diverse genotypes. The highest intra -cluster distance was shown by cluster III indicated presence of high diversity within cluster, hence revealing scope for exchange of genes among genotypes within these clusters.

Maximum diversity based on inter-cluster distance was observed between Cluster III and IV followed by cluster II and III and cluster I and III which can be utilized by hybridization- selection breeding programme through involving genotypes in these clusters to obtain useful transgressive segregants.

High cluster mean for Flag leaf length was exhibited by cluster II. Mean of cluster III was high for effective tillers per plant & chlorophyll content with early flowering, early maturity and reduced plant height. High mean of cluster for flag leaf width & panicle length with high 1000 seed weight & Harvest index was exhibited by cluster IV whereas, cluster V showed highest mean for fertile spikelet per plant and grain yield. The result reflected probability of getting better segregants and primary recombinants expected to more, in case if the genotypes of these clusters will be used in hybridization programme, which was in accordance as earlier reported by Gahalain *et al.*, (2010) [9], Chaturvedi *et al.*, (2011) [6]. Plant height and panicle length pre-dominantly contributed maximum towards the genetic divergence and no contribution of Days to Maturity, Effective Tillers/ Plant, Fertile spikelets/ Panicles, Harvest Index (Table 4). These results are in accordance with the result of Chandra *et al.*, (2007) [5], Chaturvedi *et al.*, (2011) [6]. Noteworthy is that cluster II and IV reflected high cluster means for Flag leaf length and width, panicle length, 1000 seed weight and Harvest index; cluster III and V high for effective tillers per plant & chlorophyll content with early flowering, early maturity, grain yield additionally with lowest plant height and high fertile spilkelet/panicle might be utilized in hybridization selection breeding programme for rice improvement. Inter-mating of Sita from mono-genotype cluster V and Swarna, Rajendra Mahsuri & BPT-5204, from cluster IV showing maximum inter-cluster distance for getting better recombinants in segregating generations and enhancing the yield potential whereas crossing between mono-genotype cluster (cluster V) with 3 genotypes from cluster IV suggested for the development of increased flag leaf width, panicle length, test weight and harvest index and so that high yield/plant and chances of getting better recombinants in segregating generations and enhancing the yield. Crossing sita (cluster V) with Barogar, Singhra and Pakhar (cluster III) may enhance early flowering and maturity, reduced plant height, effective tillers/plant, and chlorophyll content with high fertile spikelets/panicles.

Table 1: Analysis of variance for thirteen quantitative characters in rice genotypes

S. No.	Characters	Sources of variation		
		Replication (df=2)	Treatment (df=19)	Error (df=38)
1	Days to 50% flowering	0.816	44.921**	1.658
2	Days to Maturity	4.550	53.876**	2.707
3	Plant Height	0.434	3009.047**	3.871
4	Effective Tillers/ Plant	1.600	85.762**	0.625
5	Flag Leaf Length	4.783	88.341**	2.668
6	Flag Leaf width	0.009	0.065**	0.007
7	Chlorophyll content	1.784	12.415**	1.405
8	Panicle Length	1.065	20.575**	0.265
9	Fertile spikelets/ Panicles	127.050	988.842**	292.681
10	Test weight	12.054	93.353**	5.332
11	Biological Yield/ Plant	11.886	254.178**	11.176
12	Harvest Index	9.857	51.027**	12.994
13	Grain Yield/ Plant	1.183	15.829**	2.834

Table 2: Distribution pattern of 20 genotypes of rice into five clusters based on D² statistics

Cluster No.	Name of genotypes	No. of genotypes
I	Bakol, dhumma bakol, dudhraj, karmi, dudhi bakol, silhat, dhusari, rajshree	8
II	Meghnad, jaswa, katahi, desaria, panjhali	5
III	Barogar, singhra, pakhar	3
IV	Swarna, rajendra mahsuri, bpt-5204	3
V	Sita	1

Table 3: Intra (diagonal) and inter cluster average distance (D²) in rice

Clusters	I	II	III	IV	V
I	40.201	76.399	772.742	132.332	142.708
II		81.705	826.488	146.981	154.458
III			89.375	1294.549	339.551
IV				0.000	406.606
V					0.000

Table 4: Mean values of five clusters for 13 quantitative characters in 20 rice genotype

S. No.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Contribution %
1	Days to 50% flowering	115.963	117.4	112.583	115.333	116	2.63
2	Days to Maturity	149	149	143.333	149.667	148	0
3	Plant Height	155.58	153.173	83.1	185.467	126.3	58.95
4	Effective Tillers/ Plant	6.622	7.187	19.233	5.4	14.267	0
5	Flag Leaf Length	26.868	34.182	23.646	25.837	30.667	7.37
6	Flag Leaf width	1.419	1.457	1.318	1.703	1.233	0.53
7	Chlorophyll content	38.859	37.153	41.25	39.333	39.033	8.42
8	Panicle Length	24.295	27.337	20.991	27.963	24.413	10.53
9	Fertile spikelets/ Panicles	102.704	105.267	111.25	130.667	133.667	0
10	Test weight	31.303	28.521	20.347	33.84	23.613	1.05
11	Biological Yield/ Plant	55.163	56.511	48.631	35.997	66.357	10
12	Harvest Index	25.32	25.395	22.467	33.61	24.833	0
13	Grain Yield/ Plant	13.396	14.163	10.804	13.2	24.833	0.53

Conclusion

All the twenty rice genotypes significantly differed in respect of all quantitative traits providing scope of selection for desirable traits. The intra -cluster distance was highest in cluster III indicated presence of high diversity within cluster, thus a breeder have scope for exchange of genes among genotypes within these clusters. Maximum diversity based on inter-cluster distance was observed between Cluster III and IV followed by cluster II and III and cluster I and III which can be utilized by hybridization-selection breeding programme through involving genotypes in these clusters to obtain useful transgressive segregants. High mean of cluster for flag leaf width & panicle length with high 1000 seed weight & Harvest index was exhibited by cluster IV whereas, cluster V showed highest mean for fertile spikelet per plant and grain yield. The result reflected probability of getting better segregants and primary recombinants expected to more, in case if the

genotypes of these clusters will be used in hybridization programme.

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