STUDIES ON GENETIC DIVERSITY AND VARIABILITYIN RICE(*Oryzasativa*L.) GENOTYPES

Abstract

The present investigation was carried out to assess the genetic diversity and variability among twenty-two fine grainrice genotypes for eight biometrical traits. Genetic diversity analysis revealed that based on D^2 values, 22 genotypes were grouped into eight clusters with variable number of genotypes.Cluster I was the biggest consisting of eight genotypes followed by cluster II and III with 5 and 3 genotypes respectively. Intra cluster distance was maximum in cluster V followed by cluster II, cluster III and cluster I.Cluster III showed highest inter-cluster distance with cluster VII and cluster VIII. The traits yield / plot, grains per panicle, plant height and spikelet fertility contributed 94.8 per cent towards total divergence. Hence, these characters should be given due importance during hybridization and selection in the segregating population.Presence of high and moderate magnitude of PCV and GCV for the traits single plant yield,productive tillers per plant, filled grains per panicle and hundred grain weight suggested the possibility of improving these characters through selection. Presence of highheritability along with high genetic advance as percent of mean for the traits single plant yield followed by filled grain per panicle and hundred seed weight indicated that these charactersattributable to additive gene effects which are fixable revealing that improvement in thesecharacterswould be possible through direct selection.

Keywords: Genetic Diversity, Phenotypic Coefficient of Variation, Genotypic Coefficient of Variation, Heritability, Genetic Advance.

Introduction

Rice plays a fundamental role in Indian agriculture as it is the staple food for more than 70 per cent of the population and provides 43% of calorie requirement. It accounts for 43 per cent of food grain production and 55 per cent of the cereal production in the country. However, the average productivity of China (6.72 t/ha) is much higher than that of India (3.61 t/ha).Since grain yield in rice is a complex trait, breeding of high-yielding rice varieties is crucial for meeting the food demand of the increasing world population and to achieve

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food security in the country. In order to meet the food requirement of growing population, development of high yielding varieties is essential [1].

In recent years,rice production has reached a plateau. In general, the narrow genetic base of semi-dwarf varieties is likely to make them vulnerable to different biotic and abiotic stresses. Therefore, to meet the ever-increasing demand of food grains, for higher production emphasis should be given to the genetic improvement of existing varieties of rice.The major thrust area for such genetic improvement has been known to lay importance on selecting efficient breeding system and identifying desirable parent in hybridization programme. This would depend to large extent on the knowledge of genetic variation and genetic system controlling the yield and yield traits.

In rice breeding,the most important qualities sought by the breeders are high yield potential and improved grain quality. Development of new high yielding, quality rice varieties superior to the existing varieties mostly depends upon the amount of genetic diversity and variability present in the population. Further,assessing thegeneticdiversityand variability presentingermplasmcollectionisthebasicforany crop improvementprogrammeandforadopting of appropriate selection techniques. Information on germplasmdiversity creates chance for plant breeders to develop better cultivars with desirablecharacteristics,whichincludeboth farmer-preferredandbreeder-preferred traits. Genetic parameters like GCV and PCV are useful in detecting the amount of variability present in the germplasm. Heritability coupled with high genetic advance would be more useful tool in predicting the resultant effect in selection of the best genotypes for quality, yield and its attributing traits and it also helps in determining the influence of environment on the expression of genotypic and reliability of characters. Recognizing the importance of genetic diversity and variability in plant breeding experiments, the present study was undertaken to study the mean performance, genetic diversity and variability in the fine grain rice genotypes

Materials and Methods

The present study was carried out at the research farm of Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai during Summer, 2021. The experimental material consisted of 22 fine grain rice varieties and advanced cultures.All the twenty-two genotypes were sown in raised bed nursery during Summer, 2021. Seedlings were transplanted in the main field on 26thday after sowing in a plot size of 3 x 3 m in a Randomized Block Design, replicated thrice adopting a spacing of

20cm between rows and 10cm between plants within a row. The recommended package of practices and plant protection measures were adopted. Biometrical measurements were recorded on ten randomly selected plants in each genotype and in each replication for the traitsdays to fifty per cent flowering, plant height, productive tillers/plant, panicle length, filled grains/panicle, spikelet fertility, 100 grain weight and plot yield. The mean data of the above observations were utilized for statistical analysissuch as ANOVA, Mean performance, Genetic Diversity [2] and variability. The genotypic and phenotypic variances were calculated as per formulae proposed by Burton, 1952. Heritability in broad sense was calculated by the formulae given by Lush, 1940. From the heritability estimates the genetic advance (GA) was calculated by the formula given by Johnson *et al.*, 1955.

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Results and Discussion

BasedontheD^{2}values,22genotypesweregroupedinto eight clusters (Table 1)with variable number of genotypes. Maximum number of genotypes was grouped in cluster I(8)followedbyclusterII(5). TheclustersIII and V possessed 3 and 2 genotypes respectively. The remaining clusters (IV, VI, VII and VIII) had single genotype each.The clustering pattern revealed that grouping of genotypes into so many clusters suggested the presence of high degree of genetic diversity in the material studied. Presence of substantial genetic diversity among the genotypes studied indicated that this material may serve as good source for selecting the diverse parents for hybridization programmes.

The intra and inter cluster distances among 22 genotypes were computed and presented in Table 2. The more inter and intra cluster distances, the more variability among the genotypes between and within the cluster, respectively and vice versa. Maximum intra cluster distance *i.e.*, distance between the genotypes within the same cluster was observed in Cluster V (62.07) which has only two genotypes followedby cluster II (52.38),ClusterIII(48.51) andClusterI(47.72).Genotypes belonging to clusters V, II, III and I were having high degree of divergence would produce more desirable segregants for achieving greater genetic advance. Intra cluster distance was zero in clusters IV, VI, VII and VIII since they had single genotypes each.

Inter cluster distance recorded in the present study varied from 86.53 to 417.58. Cluster III showed highest inter-cluster distance with cluster VII (417.58) and cluster VIII(414.96). Similarly, Cluster IV showed next highest inter cluster distance with cluster VI(404.19). Greater the distance between two clusters wider the genetic diversity among the genotypes of these clusters and such highly divergent genotypes would be of greater use in recombination breeding program. Maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. Hybridization between the superior genotypes of above diverse cluster pairs such as the genotypes ACM 20013, ACM 20017, ACM16004 of cluster III with ACM 20003 (Cluster VII) or with ADT 53 (Cluster VIII) as well as ACM 20022 (Cluster IV) with TM 12077 (cluster VI) may provide desirable transgressive segregants for developing high yielding fine grain rice varieties. There was wider genetic diversity among the genotypes of different cluster as inter cluster distances were larger than intra cluster distances.

The information on cluster mean values for different characters can be used to assess the superiority of clusters which in turn could be considered for the improvement of particular trait. Genotypes with more number of desirable traits based on cluster mean values but belonging to different clusters is always preferable. Cluster mean values for the traits studiedwere given in Table 3. The contrasting genotypes for days to 50% flowering were present in cluster VI and cluster VII;cluster IV and VIII for plant height and productive tillers per plant; cluster IV and V for panicle length, cluster VI and cluster VII for filled grains per panicle, cluster V and cluster VIII for spikelet fertility, cluster VI and cluster VII for single plant yield. The genotype TM 12077 of cluster VI possess early maturity, more number of filled grains per panicle with fine grain. Cluster IV with single genotype ACM 20022 exhibited more number of productive tillers per plant, lengthy panicle with fine grain. The rice variety ADT 53 in Cluster VIII exhibited maximum spikelet fertility. For developing fine grain varieties, genotypes ACM 20022, TM 12077 and ADT-53 from cluster IV, VI and VII respectively may be utilized. None of the clusters contained genotypes with all the desirable traits for selecting and utilizing directly in the crossing programme suggesting that the genotypes grouped in the above clusters of superior mean values could be involved in a multiple crossing programme to obtain transgressive segregants with high genetic yield potential. Similar results were opined by [6].

The contribution of each trait to total divergence in presented in Figure 1. Among the traits studied, single plant yield contributed maximum divergence (43.29 %) followed by plant height (22.94 %), filled grains per panicle (17.75 %) and days to fifty per cent flowering (10.82 %). The contribution of productive tillers per plant, panicle length was nil and spikelet fertility (0.43) was minimum to the total divergence. The traits yield / plot, grains per panicle, plant height and panicle harvest index contributed 94.8 per cent towards the total divergence. Hence, these characters should be given due importance during hybridization and selection in the segregating population.

Genetic variability

Plant breeding mainly relies on the extent of genetic variation present in a breeding population. The success of breeding program depends upon the quantum of genetic variability available for exploitation and the extent to which the desirable characters are heritable [7].The effectiveness of selection depends on the magnitude of heritability which enables the breeder to predict the genetic gain under selection. Both heritability and genetic advance are two selection parameters which were estimated during the course of present investigation.

Components of genetic parameters for yield and yield attributing traits are presented in Table 5. The PCV was higher than the corresponding GCV which could be attributed to the role of environment. This was in conformity with the earlier findings of[8,9,10 and 11]. GCV provides a mean to study the genetic variability generated in quantitative traits. Higher magnitude of both PCV and GCV was recorded by plot yield indicated the presence of high degree of variation for this traits among the genotypes. This finding was reported by [11].Moderate magnitude of PCV and GCV was recorded by the traits productive tillers per plant, filled grains per panicle and hundred grain weight indicated the considerable level of variability in these traits. These results are in conformity with the findings of [12]for effective bearing tillers per plant. Presence of high and moderate magnitude of PCV and GCV for the traits single plant yield,productive tillers per plant, filled grains per panicle and hundred grain weight suggested the possibility of improving these characters through selection.

Genotypic coefficient of variation measures the extent of genetic variability percent for a trait but it is not sufficient for determination of the amount of heritable variability. In addition, estimation of heritability and Genetic Advance as % of mean is also needed to assess the heritable portion of total variation and extent of genetic gain expected for effective selection. According to Johnson et al., 1955,broad sense heritability was classified as low (<30%), medium (30% to 60%) and high (>60%). In the present study, the high heritability was recorded by the characters days to 50 % flowering, plant height, filled grains per panicle, hundred seed weight and single plant yield. The presence of high heritability indicates that these characters are least influenced by the environment. This serves as an index of transmissibility of traits from parents to their offspring. However, character exhibiting high heritability may not necessarily give high genetic advance [14] because of involvement of non-additive gene action. Thus, selection for the characters should be based on high heritability as well as high genetic advance (Johnson *et al.*, 1955). Therangeofgeneticadvanceaspercentofmeanwasclassifiedas low(0-10%),moderate(10-20%)andhigh (>20%) suggestedbyJohnson*et al.* (1955). The genetic advance was high for single plant yield followed by filled grain per panicle and hundred seed weight whereas moderate genetic advance as percent of mean was registered by plant height and productive tillers per plant. while low genetic advance was observed for days to 50 % flowering, panicle length and spikelet fertility. Highheritability along with high genetic advance as percent of mean for the traits single plant yield followed by filled grain per panicle and hundred seed weight (Table 5). Highheritability along with high genetic advance as percent of mean for the traits single plant yield was also reported by [15]. Presence of high heritability and genetic advance for the traits single plant yield, filled grain per panicle and hundred seed weightindicating the presence of additive gene action [16,17]and improvement in thesecharacterswould bepossiblethrough direct selection.

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Conclusion

Clustering of genotypes into eight clusters suggested the presence of substantial genetic diversity among the genotypes studied indicated that the experimental material may serve as good source for selecting the diverse parents for hybridization programmes.Hybridization between the superior genotypes of diverse cluster pairs such as the genotypes ACM 20013, ACM 20017, ACM16004 of cluster III with ACM 20003 (Cluster VII) or with ADT 53 (Cluster VIII) as well as ACM 20022 (Cluster IV) with TM 12077 (cluster VI) may provide desirable transgressive segregants for developing high yielding fine grain rice varieties.The traits yield / plot, grains per panicle, plant height and panicle harvest index contributed 94.8 per cent towards the total divergence. Hence, these characters should be given due importance during hybridization and selection in the segregating population.Presence of high heritability and genetic advance for the traits single plant yield, filled grain per panicle and hundred seed weight indicating the presence of additive gene action and improvement in thesecharacterswould bepossiblethrough direct selection.

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S.NO	**Source of variation**	**d.f**	**DFF**	**PH**	**PT**	**PL**	**NGP**	**HSW**	**PHI**	**PY**
1.	Replication	2	4.74	23.22	3.45	0.4715	368.81	7.33	0.013	35.67
2.	Treatment	21	65.49*	303.29*	7.25*	10.14*	2975.69*	52.21*	0.097*	293.83*
3.	Error	42	2.93	7.48	3.03	3.94	121.50	20.51	0.008	11.63

Table 1. Analysis of variance of yield and yield components in rice

Clusters	I	II	III	IV	V	VI	VII	VIII
I	47.72	86.53	155.71	115.36	162.97	112.22	149.25	128.69
II		52.38	94.85	91.58	135.39	116.52	240.07	256.65
III			48.51	115.54	182.31	144.08	417.58	414.96
IV				0.00	312.23	237.39	222.55	326.85
V					62.07	94.86	370.06	232.20

VI						0.00	404.19	261.48
VII							0.00	95.65
VIIII								0.00

Cluster	DFF	PH (cm)	PT	PL (cm)	NGP	SF (%)	HSW	SPY (g)

Table 2. Intra and inter cluster distance

Table 3. Cluster mean values for 8 quantitative traits in rice

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I	95.88	103.33	11.17	20.25	248.96	89.68	1.23	42.60
II	96.33	105.40	11.47	21.06	206.73	89.47	1.21	31.36
III	95.22	113.89	13.11	22.81	234.33	87.33	1.61	31.20
IV	102.00	119.67	14.00	23.93	228.00	86.37	1.10	34.80
V	95.00	84.33	10.33	16.85	226.00	84.12	1.50	26.22
VI	86.67	99.67	12.00	19.97	278.00	85.27	1.10	27.60
VII	104.33	97.67	13.33	19.53	205.00	89.53	1.20	60.23
VIII	101.33	81.00	11.00	19.33	271.67	95.00	1.27	49.77

Table 4. Grouping of rice genotypes based D^2 value

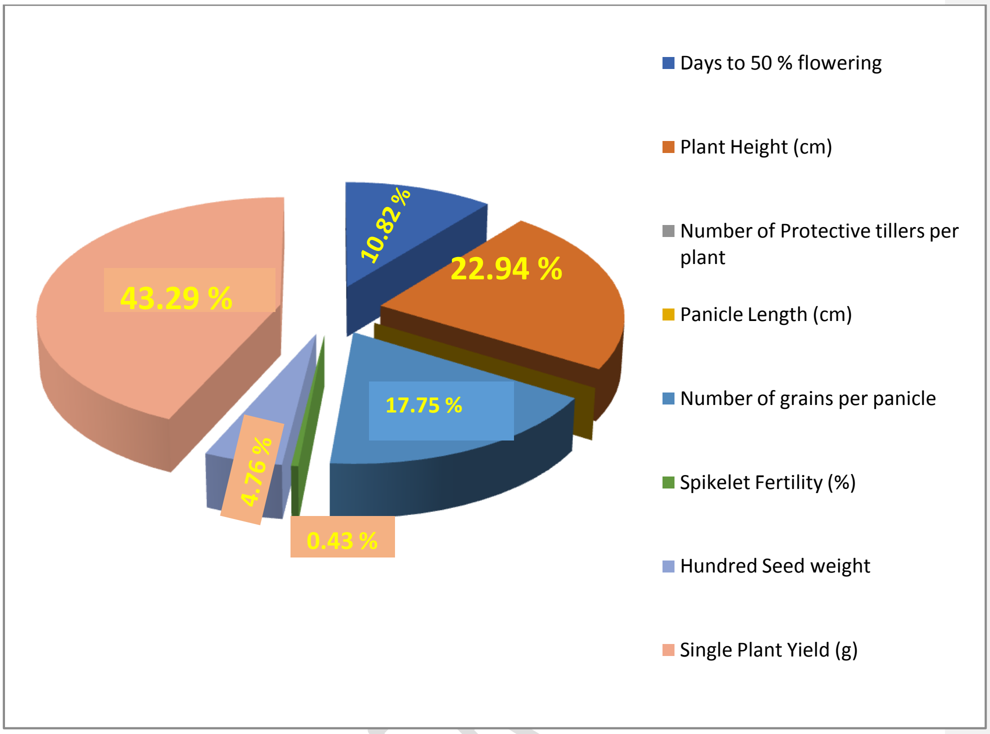
Cluster	**No of accessions**	**Genotypes**

I	8	ASD-20, ACM 16006, ADT 54, ACM 20023,MDU-6,ACM 20021, ACM 20020, ACM 20015
II	5	ACM 20011, ACM 20012, ACM 20018, MDU-5, ACM 20016
III	3	ACM 20013, ACM 20017, ACM16004
IV	1	ACM 20022
V	2	ACM 20014, ACM 20019
VI	1	TM 12077
VII	1	ACM 20003
VIII	1	ADT-53

Table 5. Components of genetic parameters for yield and yield attributing traits in rice

Characters	**PCV**	**GCV**	**Heritability in broad sense (%)**	**Genetic advance as percent of mean**
Days to 50 % flowering	5.06	4.74	87.67	9.15
Plant Height (cm)	10.02	9.66	92.95	19.18
Protective tillers per plant	18.03	10.16	31.77	11.80
Panicle Length (cm)	11.92	6.99	34.43	8.45
Filled grains per panicle	13.96	13.14	88.68	25.50
Spikelet Fertility (%)	6.29	3.66	33.99	4.40
Hundred Seed weight	15.10	13.39	78.65	24.47
Single Plant Yield (g)	27.72	26.15	89.00	50.82

Fig 1. **Relative contributions of yield and yield components to genetic diversity**


10.82 %
22.94 %
43.29 %
17.75 %
4.76 %
0.43 %
Days to 50 % flowering
Plant Height (cm)
Number of Protective tillers per plant
Panicle Length (cm)
Number of grains per panicle
Spikelet Fertility (%)
Hundred Seed weight
Single Plant Yield (g)