

STUDIES ON GENETIC DIVERSITY AND VARIABILITY IN RICE (*Oryza sativa* L.) GENOTYPES

Abstract

The present investigation was carried out to evaluate the extent of genetic diversity and variability existing among the twenty two fine grain rice genotypes under study for eight significant yield attributes. Genetic diversity analysis based on D^2 values suggested the grouping of 22 genotypes into eight clusters with genotypes in varying numbers. The biggest cluster, Cluster I, consisted eight genotypes succeeded by cluster II with 5 and cluster III with 3 genotypes . Distance within cluster was maximum in cluster V followed by the clusters II, III and 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 warrants maximum attention in hybridization programme and also during selection in the segregating generations. Simple selection procedures may be employed for characters viz., single plant yield, productive tillers per plant, filled grains per panicle and hundred grain weight with high and moderate extent of PCV and GCV. . so also for the characters single plant yield, filled grain per panicle and hundred seed weight showing the prevalence of high heritability along with high genetic advance as per cent of mean which reveals the presence of additive genetic effect..

Key words: Genetic diversity, PCV, GCV, Heritability, Genetic Advance.

Introduction

Rice plays a pivotal role in Indian agriculture fulfilling the calorie requirement up to 43 % and is the staple food for as high as 70 per cent of the Indian population. It accounts for 43 per cent in production of food grains and 46 per cent in production of entire cereals in India [1]. However, in comparison, China (7.1 t/ha) stands way ahead of India (4.1 t/ha) in terms of average productivity [2]. In recent years, rice production has reached a plateau. In order to meet the food requirements of a ever increasing population worldwide and to increase the food grain production in India, varieties with high yield potential should replace the existing ones in a regular frequency [3].

In general, the narrow genetic base of semi-dwarf rice varieties makes them vulnerable to different biotic and abiotic stresses in the changing climatic conditions which ultimately will affect the grain yields. Therefore, to meet the ever-increasing demand for food grains, emphasis should be placed on the genetic improvement of existing varieties of rice. Identification of most suitable parents for hybridization and/or selection of efficient breeding systems plays a key role in genetic enhancement of rice. This depends to a greater extent on the knowledge of genetic variation and the genetic mechanism controlling yield and yield contributing traits.

In rice breeding, the essential attributes sought after by the breeders are high yield potential and improved grain quality. The synthesis of new varieties with high yield potential and grain quality superior over the ruling varieties mostly depends on the extent of diversity and variability parameters present in the population and is the basis for employing appropriate breeding methodology. Information on germplasm diversity creates the chance for breeders of the crop varieties to evolve better cultivars with characteristics preferable by both farmers and breeders. Genetic parameters like genotypic and phenotypic coefficients of variation are helpful in enumerating and exploiting the divergence in a germplasm. High heritability accompanied by genetic advance is a remarkable tool in anticipating the effect of the selection in grain quality, yield and their attributing characters in the best genotypes. It will also help ascertain the environmental influence over the genotypic expression and the extent to which the characters are reliable. Considering the worthiness of diversity and variability in formulating breeding procedures, the present investigation was performed in order to study the mean performance, genetic diversity and variability in rice genotypes with notable grain quality.

Materials and Methods

The current study was laid out at the research farm of Agricultural College and Research Institute, Madurai in the Department of Plant Breeding and Genetics, during Summer, 2021. The study material comprised of 22 fine grain varieties and advanced cultures of rice. All the 22 genotypes were sown in required rows raised bed nursery and the seedlings were transplanted on the 26th day of sowing in the main field in of 3 x 3 m plot size in Randomized Block Design with 3 replications allowing a spacing of 20cm between rows and 10cm between plants within a row. The package of practices and plant protection measures as recommended by the TNAU Crop Production Guide were adopted [4]. Biometrical measurements on ten randomly selected plants per genotype per replication

were recorded for the traits days to 50 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 was utilized for statistical analysis such as ANOVA, Mean performance, Genetic Diversity [5] and variability. The genotypic and phenotypic variances were calculated as proposed by [6]. Heritability in broad sense was worked out as suggested by [7]. From the heritability estimates, the genetic advance (GA) was calculated by the formula provided by [8].

Results and Discussion

Based on the D^2 values, 22 genotypes were aligned into eight clusters (Table 1) with variable number of genotypes. The cluster I (8) contained maximum number of genotypes followed by cluster II (5). The clusters III and V possessed 3 and 2 genotypes respectively. The remaining clusters (IV, VI, VII and VIII) had single genotype each. The clustering pattern indicated the prevalence of high order of genetic diversity in the experimental material studied. This suggested that the germplasm may serve as a potential source of diversified parents that could be employed in hybridization programmes.

The intra and inter cluster distances among 22 genotypes were computed and presented in Table 2. Greater the inter and intra cluster distances, more is the variability among the genotypes between and within the cluster respectively and so is the 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, followed by cluster II (52.38), Cluster III (48.51) and Cluster I (47.72). In order to realize greater genetic advance, selection of genotypes with a high degree of divergence belonging to clusters V, II, III and I would synthesize more desirable segregants in recombination breeding program. Within 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 was the farthest in distance with cluster VII (417.58) and cluster VIII (414.96), followed by Cluster IV and cluster VI (404.19). Highly divergent clusters would be of greater use in manifesting the higher magnitude of heterosis in cross combinations involving the parents with wider genetic diversity from farthest clusters. Hybridization between the superior genotypes of above diverse cluster pairs such as the genotypes ACM 20013, ACM 20017, ACM 16004 of cluster III with ACM 20003 of Cluster VII or with ADT 53 of Cluster

VIII as well as ACM 20022 of Cluster IV with TM 12077 of cluster VI may provide desirable transgressive segregants for synthesizing heavy yielding fine grain rice varieties. In the current investigation, wider genetic diversity among the genotypes belonging to different clusters could be elucidated as inter cluster distances were larger than intra cluster distances.

The information on cluster mean for various attributes can be used to analyse the supremacy of clusters in trait improvement. Genotypes with more number of desirable traits based on cluster mean values but belonging to varied clusters are always preferable. Table 3 depicts the Cluster mean values for the traits under evaluation. The genotypes in contrast for days to 50% flowering were found in cluster VI and cluster VII; plant height and productive tillers per plant in cluster IV and VIII; panicle length in cluster IV and V; filled grains per panicle in cluster VI and cluster VII; spikelet fertility in cluster V and cluster VIII; and single plant yield in cluster VI and cluster VII. The genotype TM 12077 of cluster VI possesses early maturity, more number of filled grains per panicle with fine grain. Cluster IV with the 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 that expressed all the noteworthy 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 series of more complex mating to obtain transgressive segregants for grain yield. Similar were the results devised by [9].

The contribution of individual trait to total divergence is presented in Figure 1. Single plant yield manifested the maximum divergence (43.29 %) trailed by plant height (22.94 %), filled grains per panicle (17.75 %) and days to 50 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 are the characters that need to be given weightage in hybridization and selection.

Genetic variability

Crop improvement relies mainly on the genetic variation present in a breeding population. A successful breeding program is determined by the quantum of genetic

variability accessible for exploitation and the extent to which the required characters are heritable [10]. The effectiveness of selection depends on the magnitude of heritability which enables the breeder to predict the genetic gain under selection. The two selection parameters *viz.*, heritability and genetic advance were estimated during the process of present investigation.

The components of genetic variability for yield and yield attributing traits are presented in Table 5. The possible role of environment in expression of the characters could be deciphered with PCV values higher than the corresponding GCV values.. This was in accordance with the earlier findings of [11, 12, 13 and 14]. GCV provides a mean to study the genetic variability generated in quantitative traits. Plot yield recorded the higher magnitude of PCV and GCV indicating the presence of high degree of variation for the trait among the genotypes. This was also reported in the findings of [15, 16, 17 and 18]. The moderate magnitudes of PCV and GCV was recorded for the traits productive tillers per plant, filled grains per panicle and hundred grain weight indicating a considerable level of variability in these traits. These results are in conformity to the findings of [19] for productive tillers per plant. Prevalence of high and moderate magnitudes of PCV and GCV for the traits single plant yield, productive tillers per plant, filled grains per panicle and hundred grain weight suggested that the improvement in these characters would be probable through selection.

Genotypic coefficient of variation measures the potent genetic variability present for a trait but it is insufficient for estimation of the amount of heritable variability and the extent of genetic gain expected from selection which necessitates the estimation of heritability and Genetic Advance as per cent of mean . Broad sense heritability could be categorized as low (<30%), medium (30% to 60%) and high (>60%) as suggested by [7]. In the present study, 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 in these characters suggests that they are least influenced by the environment and these characters are highly transmissible whereas the characters productive tillers per plant, panicle length and spikelet fertility recorded moderate heritability confirming the influence of environment in expression of these characters. from the parents to their offspring. However, high heritability in a character may not always entail high genetic advance [20] because of the predominance of dominance gene action. Thus, high heritability in combination with high genetic advance is more desirable for the characters to be involved in selection [8]. The range of genetic advance as per cent of mean was classified as low (0-10%), moderate (10-20%) and

high (>20%) as suggested by [8]. The genetic advance was high for single plant yield followed by filled grains per panicle and hundred seed weight whereas moderate genetic advance as per cent 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. The traits showing high heritability along with high genetic advance as per cent of mean were single plant yield, y filled grain per panicle and hundred seed weight (Table 5) which was in akin to the findings of [21]. The presence of high heritability and genetic advance for the traits single plant yield, filled grain per panicle and hundred seed weight indicates the involvement of additive gene action [22] and simple selection and hybridization followed by selection are enough to improve these traits. Whereas the traits viz., days to 50 per cent flowering and plant height with high heritability but with low and moderate GA as per cent of mean indicates the predominant role of dominance gene action and may be improved through heterosis breeding and recurrent selection procedures.

Conclusion

The study on genetic diversity resulted in clustering of genotypes into eight clusters which proposed the presence of substantial genetic diversity among the genotypes studied and indicated that the experimental material may serve as a potent source for selecting more diverse parents for hybridization programmes. Hybridization between the superior genotypes of distant 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 grain yield and fine grain. The traits yield / plot, grains per panicle, plant height and panicle harvest index contributed 94.8 per cent towards the total divergence and warrants due emphasis in hybridization and selection in the segregating generations. The presence of high heritability and genetic advance for the traits single plant yield, filled grain per panicle and hundred seed weight indicates the presence of additive gene action and these characters could be improved through simple selection and hybridization followed by selection.

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

S.NO	Source of variation	d.f	DF	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 2. Intra and inter cluster distance

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
VIII								0.00

Cluster	DFF	PH (cm)	PT	PL (cm)	NGP	SF (%)	HSW	SPY (g)
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 3. Cluster mean values for 8 quantitative traits in rice

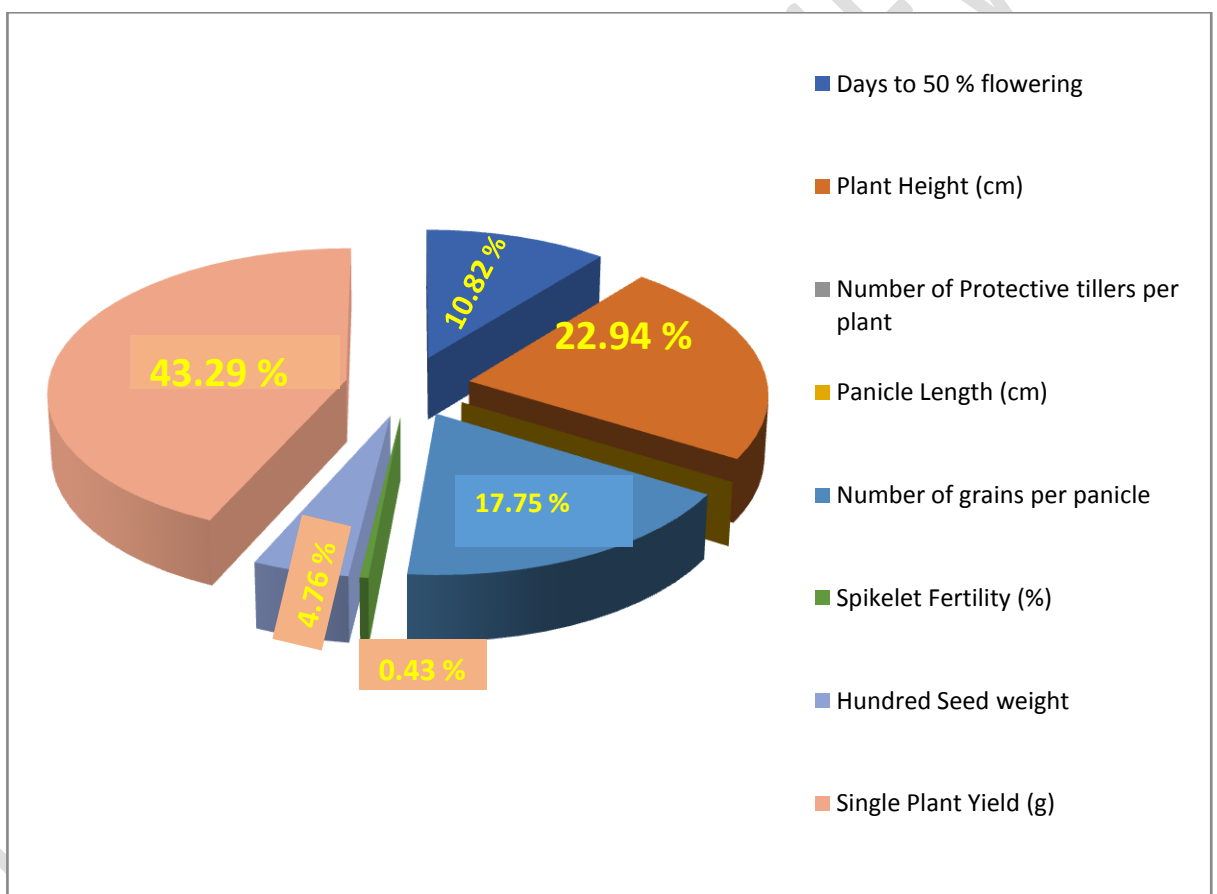
Table 4. Grouping of rice genotypes based D² value

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, ACM 16004
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



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