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UNIVARIATE AND MULTIVARIATE ANALYSES IN RICE (*Oryza sativa* L.) OVER SEASONS UNDER COASTAL ECO-SYSTEM

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Abstract

Fifty genotypes of rice were evaluated for 13 seed yield and its component traits over two seasons under the coastal – eco system. The analysis of variance revealed the presence of significant variability among the genotypes for all the 13 traits of interest in S1, S2 and pooled analysis. The GCV was higher for days to 50 per cent flowering, total number of tillers per plant, number of productive tillers per plant, number of grains per panicle, weight of 100 seeds, total dry matter production per plant and harvest index, in all the analyses. The GCV was closer to PCV for all these traits, implying the less influence of environment. High heritability estimates coupled with high genetic advance as percentage over mean was observed for all the traits, except, length of primary panicle and length of seeds. Those traits may be under the control of additive gene action. Hence, simple selection would be rewarding. Genetic diversity among the fifty genotypes of rice for thirteen grain yield and its component traits under two seasons was also investigated. Both individual as well as pooled analysis were performed. The data were analyzed by adopting Mahalanobis' D^2 statistic. In D^2 analysis, the 50 rice genotypes were grouped into eight different clusters in S1; four different clusters in S2 and nine different clusters in pooled analysis. Based on *per se* performance, two genotypes *viz.,* CO 19 and CO 32 were adjudged as best, owing to their superior *per se* performance in S1, S2 and pooled analysis. D^2 analysis of 50 genotypes based on thirteen traits confirmed the presence of high genetic diversity among the genotypes studied. The pattern of clustering demonstrated that genetic diversity was not to fully related to geographical diversity. Days to 50 per cent flowering contributed maximum towards genetic divergence. Selection of parents has been suggested based on the consistency in genetic divergence. Accordingly, the genotypes *viz.,* CO 47 and PTB 15 were found as consistently divergent from the remaining 48 genotypes of interest. The maximum intra-cluster distance was observed with cluster III in S1; cluster IV in S2 and cluster V in pooled analysis. The maximum inter-cluster distance was observed between clusters VII and VIII in S1; Cluster I and III in S2 and cluster IV and VI in pooled analysis. Parents selected from these clusters could produce superior hybrids and segregants

Keywords: Rice; Genetic parameters; Mahalanobi's D^2 statistic.

Introduction

Rice is the stable food crop in India. It is cultivated in diverse ecological conditions, with varied phenology and seed yield. History showed that technological advancement and its applications in agricultural crop plants brought great respite at times, when burgeoning population desperately needed security in food fronts (Shetty *et al.,* 2014). Before exploiting a population for trait improvement it is necessary to understand the magnitude of variability in the population which is fundamental for genetic improvement in all the crop species. Genetic variability represents the heritable variation within and between populations of rice plants. The success of any plant breeding programme depends on the availability of genetic variation, knowledge about desired traits and efficient selection strategies that make it possible to exploit the existing genetic resource. The pool of genetic variation with in an inter-mating population is the basis for selection as well as crop improvement. Univariate analyses excavates the necessary genetic information on the choice of traits.

Genetic diversity among the rice genotypes form the basis for selecting parental combinations which would throw useful heterotic hybrids as well as superior progenies in the segregating generations. Multivariate analysis is used to estimate the genetic diversity among the rice genotypes. Genetic statistical method of classification is usually done by multivariate analysis. It has extensive use in summarizing and describing the inherent variation among rice genotypes. The present study is aimed to determine the level of germplasm variation in *Oryza sativa* (L.) to identify and classify variation for grouping the accessions by taking into account several traits and relationship between them, using Mahalanobi's D^2 statistic.

Materials and Methods

The germplasm collection consisting 50 rice accessions was used in the present study. The accessions were collected from different rice growing states of India. For easy identification and retrieval, each accession was named as G_1 to G_{50}. A set of 50 genotypes were grown in the Plant Breeding Experimental Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India (MSL 5.86 m) during Kuruvai and Samba 2018. The genotypes were transplanted 25 days after sowing as single seedling per hill in Randomized Block Design, replicated thrice, with a spacing of 20 × 15 cm. Each plot per genotype consisted of two rows of 3.0 m length. Recommended agronomic practices and need based plant protection measures were judiciously followed. Thirteen quantitative traits were measured according to the *O. sativa* (IRRI, 1980). Variables considered in the descriptive and multivariate analyses were phonological (days to 50% flowering), morphological (plant height at maturity, total number of tiller per plant, number of productive tillers per plant, length of primary panicle, number of filled grains per panicle, seed traits (length of seeds, width of seeds; length: breadth ratio of seeds, 100 seed weight and seed yield per plant) as well as traits related to partitioning efficiency (total dry matter production per plant and harvest index). The observations recorded on 13 traits were statistically analyzed in Indo-state, licensed at NRRI, Cuttack, Odisa.

Results and Discussion

The ANOVA indicated that all the traits differed significantly from each other in the two seasons as well as pooled analysis (Table 1). Hence, further analysis is appropriate.

In S_1, the GCV was higher for X1, X3, X4, X6, X10, X11, X12 and X13. The PCV was also higher for these traits. There was a close agreement between GCV and PCV. It indicated the less influence of environment. The heritability estimates were always high. The GA as percentage over mean were higher for all the traits except X5, X7 and X8. High heritability estimates coupled with high genetic advance as a percentage over mean were recorded for X1, X2, X3, X4, X6, X9, X10, X11, X12 and X 13. These traits may be under the control of additive gene action. Hence, simple selection would be rewarding. The traits *viz.,* X5, X7 and X8. Showed high heritability coupled with low genetic advance indicating that these traits were under the control of non-additive gene action (Table 3).

In S2, the GCV was higher for X1, X3, X4, X6, X10, X12, X12 and X13. The PCV was also higher for these traits. There was a close agreement between GCV and PCV. The heritability estimates were always high. The GA as percentage over mean was higher for all the traits except X5 and X7. High heritability estimates coupled with high genetic advance as percentage over mean was higher for X1, X2, X3, X4, X6, X8, X9, X10, X11, X12 and X13. These traits may be under the control of additive gene action. Hence, simple selection would be rewarding. The traits *viz.,* X5 and X7 exhibited high heritability coupled with low genetic advance indicating that these traits were under the control of non-additive gene action (Table 4).

In the pooled analysis, GCV was higher for X1, X3, X4, X6, X10, X11, X12 and X13. The PCV was also higher for these traits. There was a close agreement between GCV and PCV. The heritability estimates were always high. The GA as percentage over mean was higher for all the traits except X5 and X7. High heritability estimates coupled with high mean was recorded for all the traits except X5 and X7. Those traits may be under the control of additive gene action, whereas X5 and X7 were under the control of non-additive gene action (Table 5).

It is quiet interesting to conceive that the traits *viz.,* X1, X2, X3, X4, X6, X8, X9, X10, X11, X12 and X13 had high heritability estimates coupled with high genetic advance over percentage of mean, consistently, over seasons. They may be under the control of additive gene action. Similar results were earlier reported by Kirubhakaran *et al.* (2019). Hence, simple selection for any one of the aforementioned traits is likely to improve the productivity of rice in east-coast eco-system. It is also envisaged that gene action as influenced by season.

D^2 analysis of 50 genotypes confirmed the presence of high genetic diversity among the genotypes of their resolution into eight clusters in S1; four clusters in S2 and nine clusters in pooled analysis. Genotypes of different eco-geographic regions were grouped in different clusters.

The genotypes originating from Coimbatore and Aduthurai origin were found scattered in different clusters in the different season and pooled analysis. This indicated that the presence of wide range of genetic diversity among the genotype of the present study. These genotype could well be exploited in recombination breeding.

Crosses among the divergent parents are likely to be yield desirable combinants. Therefore a crossing programme should be initiated between the genotypes belonging to different clusters. In this context, two important point to be considered are (i) choice of the particular cluster from which genotypes are to be used as parent in crossing programme and (ii) selection of particular genotypes from selected groups.

The greater the distance between two clusters, the wider the genetic diversity among the parents to be included in hybridization programme. Parents combining high yield potential with wider genetic diversity are likely to yield superior segregants with in a shorter period.

The tendency of genotypes from diverse geographical regions to group together in one cluster or scattered distribution of genotypes of same origin in different cluster or scattered distribution of genotypes of same origin in different clusters has been observed in the present study. The studies of several workers confirmed this tendency, that the geographical diversity could not be directly related in any of the crops: Linseed, Wheat, Sorghum (Murthy and Arunachalam, 1966); Sesame (Thirugnanakumar, 1991); Venkatesan (2004); Sree Krishna (2005); Sangeetha Banu (2015), Anbarasu (2017).

Genetic drift and selection in different environment could cause greater diversity than geographical distance (Murthy, 1965). Clusters II and VIII in S1; cluster III in S2 and Cluster VI in pooled analysis recorded the lower intra-cluster distance value. This may indicate the closeness of the genotypes. This may be explained on the basis that yield being a complex character of polygenic inheritance, similar genotypes could be produced by many different combination of genes and such combinations may have similar selective advantage (Singh and Gupta, 1968). Further, under constant selection on the segregating population such similar types are expected to be established.

The intra-cluster distance maximum in cluster V in S1. It included at many as five genotypes. Intra-cluster distance was maximum in cluster II in S2. It included three genotypes. Intra-cluster distance was maximum in cluster V in pooled analysis. It included five genotypes. This may indicate that these genotypes were dissimilar. The limited gene exchange between the type of selection of diverse characters could be responsible for such intra-cluster divergence.

In S1, inter cluster distance was maximum between the cluster VII and VII. Cluster VIII had lowest means for days to 50 per cent flowering and plant height at maturity and higher mean for all the other traits of interest. The genotypes originate from these clusters may be recombined to evolve yielding lines. In S2, inter cluster distance was maximum between the clusters II and IV. Cluster II had lower mean for days to 50% flowering and highest mean for filled seeds per panicle, weight of 100 seeds, total dry matter production and seed yield per plant. The genotypes originate from these clusters may be recombined to evolve high yielding lines. In pooled analysis, inter-cluster distance was maximum between the clusters IV and VIII. Cluster IV recorded higher mean for primary panicle length and harvest index. Cluster VIII had higher mean number of filled seeds per panicle,

weight of 100 seeds, total dry matter production and harvest index. The genotypes of these clusters may be crossed to develop high yielding lines.

As pointed out by Sokal (1965), the choice of character is important in multivariate analysis and the choice made in the present study appears to be appropriate. Cyclic breeding and crossing may be helpful in brining new genes into a population of rice and thus expanding the range of adaption, polygenic variability, which is necessary for prospective, adoptive and evolutionary change need not exists as true phenotypic variation which effect fitness. Therefore, phenotypic uniformity with genetic diversity within the population appears to be very useful in rice. In fact, this is possible with a proper use of the suggested parents in the formation of gene complexes to replace the existing varieties.

It can be concluded that there is no relationship between genetic and geographical diversity in the material under investigation. Inter and intra-cluster distances were also not related. The grouping pattern was not consistent across seasons indicating that genetic diversity do depend on the season and that genotype × season effect genetic diversity.

It is highly desirable that the extent of genetic between the population reflected through any analysis comparatively stable over seasons and environment to be utility of plant breeders. The differential grouping of different genotypes of varying origin in different environment mean that a breeder should study the divergence in varying seasons as well as environments.

The approach suggested by Thirugnanakumar (1991) is followed in the present study to suggest the parents based on the divergence pattern in varying environments.

a. One may select the parents on the basis of divergence exhibited in the richest and most productive environment, because it provides opportunity for the fullest expression of genetic potential of a genotype. Seed yield was higher in S1. Using this criterion divergent genotypes in S1 may be selected from different clusters having high inter cluster distance (between clusters VII and VIII). Cluster VII composed of two genotypes and cluster VIII composed of only one genotype. Cluster VII recorded higher mean for number of filled seeds per panicle, length of panicle, breadth of seeds, weight of 100 seeds, total dry matter production, seed yield and harvest index. Cluster VIII had lower mean for days to 50 per cent flowering and higher mean for the remaining traits. Hence, by effecting crosses among he genotypes gathered in these clusters, one may expect higher seed yield per plant, coupled with earliness.

b. Selection of parents can also be made on the basis of divergence which is consistent over two seasons. This can be taken as reliable indication of genetic divergence. Utilizing this criterion among the genotypes studied, the genotype namely CO 47 and PTB 15 were gathered in cluster III in all the two seasons. Hence, it may be suggested that one may effect crosses between these two genotypes and the remaining 48 genotypes studied. It may be result in high heterosis as well as high yielding segregants.

c. Once may argue that the divergence expressed in pooled analysis may be reliable estimate and therefore should be used for selecting the parents. If this criterion is followed, the genotypes that were grouped in nine clusters may be crossed to evolve heterotic lines and superior segregants.

Out of three approaches one may prefer approach 'b' as it suggested that genotypes based on consistency in the diverse patterns. The approach 'a' suffers from environmental influence and approach 'c' suffers from the under estimation of genetic divergence because of measures of divergence estimated in different seasons may cancel each other in pooled analysis.

Table 1 : List of genotypes of interest and their geographic origin

S. No.	Name of the Genotype	Origin	Genotype code
1.	CO 41	Coimbatore, Tamil Nadu	G_1
2.	CO 47	Coimbatore, Tamil Nadu	G_2
3.	CO 32	Coimbatore, Tamil Nadu	G_3
4.	CO 43	Coimbatore, Tamil Nadu	G_4
5.	CO (R) 50	Coimbatore, Tamil Nadu	G_5
6.	CO 19	Coimbatore, Tamil Nadu	G_6
7.	PTB 15	Pattambi, Kerala	G_7
8.	CO 39	Coimbatore, Tamil Nadu	G_8
9.	JGL 1798	Jagathial, Andhra Pradesh	G_9
10	CO 49 (R)	Coimbatore, Tamil Nadu	G_{10}
11.	CSR 23	Karnal, Haryana	G_{11}
12.	ADT 49	Aduthurai, Tamil Nadu	G_{12}
13.	ADT 46	Coimbatore, Tamil Nadu	G_{13}
14.	ADT 43	Coimbatore, Tamil Nadu	G_{14}
15.	MTU 1121	Marteru. Andhra Pradesh	G_{15}
16.	MTU 1157	Marteru, Andhra Pradesh	G_{16}
17.	MTU 1158	Marteru, Andhra Pradesh	G_{17}
18.	OR 1895-2	Cuttack, Odissa	G_{18}
19.	OR 2163-14	Cuttack, Odissa	G_{19}
20.	OR 2325-25	Cuttack, Odissa	G_{20}
21.	OR 2324-14	Cuttack, Odissa	G_{21}
22.	OR 2329-38	Cuttack, Odissa	G_{22}
23.	CR 2641-42-8-4-2	Cuttack, Odissa	G_{23}
24.	CR 2643-1-4-3-1	Cuttack, Odissa	G_{24}

25.	CR 3299-11-1-1-1	Cuttack, Odissa	G_{25}
26.	CR 3420-7-1	Cuttack, Odissa	G_{26}
27.	CR 3421-1	Cuttack, Odissa	G_{27}
28.	NDR 359	Faizabad, Uttar Pradesh	G_{28}
29.	NDR 3325	Faizabad, Uttar Pradesh	G_{29}
30.	NDR 8002	Faizabad, Uttar Pradesh	G_{30}
31.	AD 06207	Aduthurai, Tamil Nadu	G_{31}
32.	AD 07312	Aduthurai, Tamil Nadu	G_{32}
33.	AD 08-142	Aduthurai, Tamil Nadu	G_{33}
34.	CN 1744-313-19-8-8	Aduthurai, Tamil Nadu	G_{34}
35.	CN 1755-9-7-5 MLD20	Aduthurai, Tamil Nadu	G_{35}
36.	UPR 3330-9-12	Pant Nagar, Uttar Pradesh	G_{36}
37.	UPR 3443-7-2-1	Pant Nagar, Uttar Pradesh	G_{37}
38.	WGL 536	Warangal, Andhra Pradesh	G_{38}
39.	WGL633	Warangal, Andhra Pradesh	G_{39}
40.	JGL 15230	Jagathial, Andhra Pradesh	G_{40}
41.	JGL 17574	Jagathial, Andhra Pradesh	G_{41}
42.	RNR 2448	Rajendra Nagar, Telangana	G_{42}
43.	RNR 2836	Rajendra Nagar, Telangana	G_{43}
44.	HUR 1204	Varanasi, Uttar Pradesh	G_{44}
45.	HKR 08-1	Kaul, Haryana	G_{45}
46.	PAU 3835-62-5-1	Ludhiana, Punjab	G_{46}
47.	TM 07278	Aduthurai, Tamil Nadu	G_{47}
48.	KJT 15-1-36-5-23-16	Karjat, Maharashtra	G_{48}
49.	CB 1777-5	Coimbatore, Tamil Nadu	G_{49}
50.	CB 05-031	Coimbatore, Tamil Nadu	G_{50}

Table 2 : Analysis of variance for thirteen yield and yield contributing traits in 50 genotypes of rice

Traits	Mean squares								
	Replication df=2			Genotypes df=49			Error df=98		
	S1	S2	Pooled analysis	S1	S2	Pooled analysis	S1	S2	Pooled analysis
X1) Days to 50% flowering	01.36	2.5466	1.02	1422.49**	1581.01**	1720.05**	0.78	1.1779	0.8721
X2) Plant height (cm)	34.99	57.41*	41.60	1035.72**	957.78**	990.81*	19.55	16.08	14.08
X3) Total number of tillers per plant	34.07	17.76	24.66	168.92**	129.36**	142.71**	16.45	19.96	17.19
X4) Number of productive tillers per plant	06.13	01.67	02.86	88.04**	65.84**	70.34**	04.89	3.24	3.13
X5) Length of panicle (cm)	07.06	01.86	0.44	34.50**	27.83**	29.10**	04.08	3.54	2.82
X6) Number of filled seeds/panicle	69.85	06.66	11.11	6695.24**	5974.82**	6267.47**	92.56	244.42	125.75
X7) Length of seeds (mm)	00.03	00.02	0.02	1.90**	2.0112**	1.68**	00.01	0.01	0.01
X8) Breadth of seeds (mm)	0.00009	00.004	0.004	0.2553**	0.4411**	0.33**	0.0059	0.003	0.002
X9) Length/breadth ratio of seeds	0.0096	00.02	0.002	1.1649**	1.2266**	1.19**	0.0146	0.01	0.01
X10) 100 Seed weight (g)	0.0552	0.01	0.09**	0.9458**	0.9772**	0.91**	0.0229	0.01	0.009
X11) Total dry matter production/plant (g)	3.5698	13.77	1.52	1713.30**	1041.11**	1312.13**	37.30	14.48	18.77
X12) Seed yield/plant (g)	2.0934	03.43	0.20	725.86	1028.17**	704.56**	8.2583	4.87	4.25
X13) Harvest index (%)	4.0667	16.32	1.03	629.58	522.90**	532.79**	13.2426	10.05	7.59

Table 3 : Genetic parameters for seed yield and its component traits in rice genotypes – S1

Traits	GCV	PCV	Heritability	GA (%) of mean
X1	23.14	23.16	99.84	47.64
X2	18.52	19.04	94.54	37.09
X3	38.66	44.50	75.46	69.18
X4	45.59	49.46	85.00	86.59
X5	13.56	16.01	71.72	23.65
X6	36.33	37.08	95.96	73.31
X7	10.22	10.36	97.40	20.78
X8	12.66	13.09	93.36	25.19
X9	17.89	18.22	96.33	36.17
X10	73.62	76.04	93.74	146.83
X11	25.43	26.36	93.07	50.53
X12	42.07	43.41	93.94	84.00
X13	27.33	27.80	96.66	55.35

Table 4 : Genetic parameters for seed yield and its component traits in rice genotypes – S2

Traits	GCV	PCV	Heritability	GA (%) of mean
X1	40.42	41.59	94.45	80.92
X2	34.93	35.18	98.59	71.46
X3	24.21	24.24	99.78	49.83
X4	18.59	19.07	95.12	37.37
X5	35.53	44.19	64.63	58.85
X6	37.68	40.50	86.56	72.21
X7	12.71	15.24	69.59	21.84
X8	33.96	36.07	88.66	65.87
X9	10.31	10.38	98.69	21.11
X10	17.03	17.20	98.12	34.76
X11	17.63	17.76	68.54	36.04
X12	29.43	29.89	96.96	59.09
X13	67.43	68.84	95.94	136.07

Table 5 : Genetic parameters for seed yield and its component traits in rice genotypes – Pooled analysis

Traits	GCV	PCV	Heritability	GA (%) of mean
X1	23.68	23.70	99.83	48.73
X2	18.54	18.93	95.85	37.39
X3	36.55	43.42	70.87	63.39
X4	39.99	42.70	87.73	77.17
X5	12.89	14.83	75.66	23.11
X6	35.09	36.16	94.21	70.18
X7	9.51	9.57	98.82	19.48
X8	14.62	14.79	97.79	29.79
X9	17.72	17.85	98.55	36.24
X10	26.66	27.08	96.89	54.06
X11	69.75	71.25	95.83	140.65
X12	39.84	40.70	95.84	80.35
X13	27.92	28.17	98.21	56.99

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