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Multivariate analysis in late rice genotypes (*Oryza sativa* L.) under transplanted condition

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Abstract
Rice is the most important food source of the world along with wheat and maize. The present investigation was carried out with an objective to assess genetic divergence among the genotypes to identify superior genotypes with higher yield and ancillary traits to be utilized in future breeding programme. The experiment was carried out on the research field of EB-I section of Department of Plant Breeding and Genetics, College of Agriculture, OUAT, during Kharif, 2019.Thirty-two rice genotypes including three check varieties were grown in transplanted condition in a Randomized Block Design with three replications. Observations were recorded on 12 yield attributing characters like days to 50% flowering, plant height, panicle length, panicle number, number of fertile grains per panicle, fertility percentage, hundred grain weight, flag leaf length, flag leaf area, biological yield, grain yield per plant and harvest index. Statistical analysis revealed significant difference among the genotypes with respect to all characters under study. Thirty-two rice genotypes were grouped into six clusters out of which Cluster I and Cluster II were largest clusters with 11 genotypes each, Cluster V and VI were two mono genotypic clusters. Grain yield per plant contributed highest to overall genetic diversity followed by harvest index. Inter cluster distance was maximum among Custer I and Cluster IV and least between Clusters I and V. Cluster VI was characterized by highest plant height, panicle length, panicle number, number of filled grains per panicle, flag leaf length, flag leaf area, biological yield and grain yield per plant.

Keywords: Multivariate analysis, genetic divergence, clustering, inter cluster distance, average D^2

Introduction
Rice (*Oryza sativa* L.) is the most important food source of the world along with wheat and maize. It is the staple food of more than half of the world population particularly in Asia. (Muthayya *et al*.2014) [7]. The estimated world rice production for the year 2019-20 was 496.67 million metric tons. World population is estimated to increase from 6.2 billion in the year 2000 to nearly 8.2 billion by the year 2030, whereas rice requirement may reach to about 765 million tons (FAO 2020). Yield of rice has increased with a growth rate of 2.5 per cent per year since the green revolution. In India, low-land rice area is about 14.4 million hectares, which accounts 32.4 per cent of the total area under rice crop in the country and its production is highly variable. They are usually transplanted in levelled and bonded fields that retain surface water but the depth and duration of the soil varies greatly from year-to-year within a growing season. Depending upon the depth of water it can further classified to shallow water (<50 cm), semideep water (50-100 cm.) and deep water (>100 cm). Present agricultural research programs focus on development of high yielding varieties and adoption of advanced production technologies to make the country self-sufficient with respect to yield requirement. Genetic improvement mostly depends upon the amount of variability present in the population. Nature and degree of genetic divergence for agronomic traits is an efficient tool for effective selection of parents for hybridization programme and also a key segment in broadening the genetic base of the crop plants (Banumathy *et al*., 2010) [1]. Rice crop exhibits greater genetic diversity in cultivar's field and land races through the world. The study of genetic diversity assumes a critical role in the selection of diverse parents having wider variability to different traits (Nayak *et a*l., 2004) [4]. With an aim to attain maximum heterosis and transgressive segregants in the successive generations from the crosses between diverged parents genetic diversity among genotypes can

be estimated through various multivariate statistical analyses. Mahalanobis D^2 statistics is a potent statistical tool to quantify the genetic distance between genotypes based on replicated data of multiple variables (Mahalanobis, 1936) [5].

Materials and Methods

The experimental materials consist of 32 late duration genotypes of rice including three check entries. The test genotypes were evaluated on research plot of EB-I section of the Department of Plant Breeding and Genetics of Odisha University of Agriculture and Technology, Bhubaneswar during Kharif, 2019. The trial was carried out in a Randomized Complete Block Design with three replications. Observations were recorded on five competitive plants which were randomly selected and tagged from each experimental unit in all the replications. The plant wise data on the 12 metric characters were recorded except for the traits like days to 50% flowering which was recorded on plot basis. The mean values were used for statistical analysis. After testing differences among the genotypes for each character, Mahalanobis' D^2 statistic was used for assessing the genetic divergence among all the genotypes by the inclusion of twelve characters. Rao (1952) [10] described the multivariate analysis of genetic divergence using D^2 statistics. Since, the formula for computation requires inversion of higher order determinant, transformation of the original correlated un-standardized character mean to standardized uncorrelated variable was done by pivotal condensation to simplify the computational procedure. All the possible pairs of D2 values were calculated from the 33 genotypes with respect to 12 different characters. The clustering of D^2 values was done using Tocher's method as described by Rao (1952) [10], while the intra and inter- cluster distances were calculated using the formula given by Singh and Choudhary (1985) [12]. The relative contribution (in per cent) of each character to total divergence was assessed from average D2 for individual character as suggested by Singh, 1981 [12].

Results and Discussion

Genetic variability with respect to all traits is the important component and the measure to determine the norm and direction of manipulation. Hence analysis of variance for the characters is essential to study the genetic variability. Analysis of variance showed significant variation among the genotypes under study for all 12 quantitative characters under study at 1% level of significance. Simultaneous variation between 32 rice genotypes with respect to 12 quantitative characters were tested following Mahalanobis' D^2 statistics for assessment of magnitude of genetic divergence among them. Considering the magnitudes of D^2 following the Torcher's method all genotypes were grouped into six clusters. Cluster composition of 32 genotypes was presented in Table 1. Cluster I & Cluster II were two largest clusters with eleven entries each. Cluster III and cluster IV included six and two genotypes respectively. Cluster V & Cluster VI were mono-genotypic clusters. The genotypes showing proximity in their character expression were grouped into one cluster and those showing diversity were placed in different clusters justifying their individual identity. In terms of distribution also, those genotypes belong to same geographical region may be placed in separate clusters and those belongs to different geographical regions may be placed in same cluster. Hence divergence among genotypes of same geographical region may be due to selection criteria, differences in adoption, selection pressure and environmental conditions (Nayak *et al*., 2004 and Mandal *et al*., 2022) [4, 6].

Table 1: Cluster composition of 32 rice genotypes based on D^2 value

Cluster	No. of genotypes	Genotypes included in the cluster
I	11	RP 6288-12-305-106, RP 6286-Bio Patho 5-156-24-7, Swarna, Samba Mahsuri, RP 6288-12-305-92, RP 6285-Bio Patho 2-8-24, RP 6113-Patho RR-9, Pusa 1853-12-288, R-RF-158, 120 – 79 – RM – Sub -1, CR 3525-24-6-1-1-1-1
II	11	120–11–RM–Sub-1, Rajendra Mahsuri, RP 5863-Patho-3-8-47-22, RP 6118-24-1-19-106-3, RP 5862-Patho-1-40-21-86, BRR 0098 (IR 127339 -10-1-1-1), Sonagathi Mutant -1, DLHR -4, RP 6280 Patho - 9 - 12 – 9, R-RF-135, RP 6279 Patho-6-1-13
III	6	Improved Samba Mahsuri, PA 6444, RP 6286-Bio Patho5-156-24-10, RP 6285-Bio Patho 2-8-12, RP 6287-188-45-12-88, Hasanta
IV	2	RP 6298-FG3G-12-3, NDR 8002
V	1	RP 6298-FG3G-12-5
VI	1	RRX 027

Intra-cluster and inter-cluster distance among 32 genotypes were presented in Table 2 (Fig 1).Highest intra-cluster distance was found among the genotypes of Cluster I (766.568) followed by Cluster II (519.532), Cluster III (421.321 and Cluster IV (364.966). Cluster III and VI were the most diverse clusters with an inter-cluster distance of 13921.73 followed by Cluster V and Cluster VI (11879.88) and Clusters I and VI (10961.34), Clusters I and V were the closest clusters with inter cluster distance of 1539.88 followed by Clusters II and Cluster IV (1867.36), Clusters I and II (2136.00), Clusters I and III (2570.79), Clusters III and Clusters IV (2639.28), Clusters II & V(3543.89), clusters II and IV (4041.02), Clusters II and Cluster III (4108.31), Clusters II and VI (4482.27), Clusters III and V (5069.18), Clusters IV and Cluster VI (5614.03), and Clusters IV and V (6801.03). In the present study it was indicated that parents selected from Cluster III and IV are recommended for the hybridization program. Parents may be selected from diverse clusters on the basis of performance or component traits which would complement each other while giving the final out put (Sandhya *et al.*, 2014; Bibi *et al.*, 2015 Beevi & Venkatesan, 2015; Tandekar & Koshta, 2014; Radha *et al.* 2018) [11, 3, 2, 14, 9].

Table 2: Average Intra-cluster (diagonal) and inter cluster distance (D^2 value)

Cluster	I	II	III	IV	V	VI
I	766.568	2136.00	2570.79	4041.02	1539.88	10961.34
II		519.532	4108.31	1867.36	3543.89	4482.27
III			412.321	2639.28	5069.18	13921.73
IV				364.966	6801.03	5614.03
V					0.000	11897.88
VI						0.000

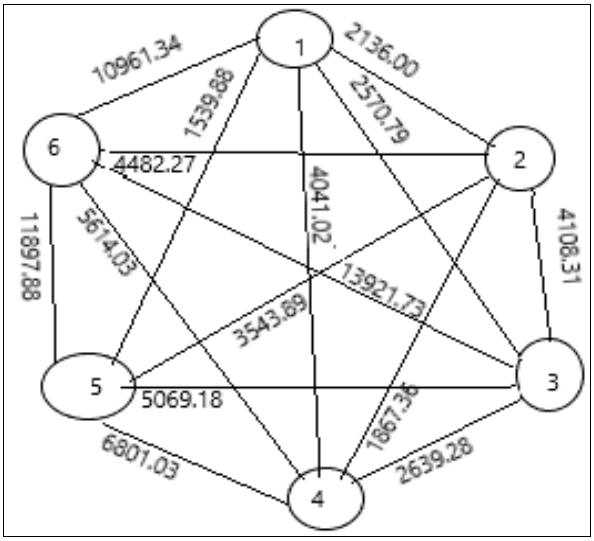

Fig 1:`Average Intra and inter cluster distances based on D^2values

Relative contribution of characters to genetic diversity

The contribution of various characters to genetic diversity was presented in Table 3.

Table 3: Relative contribution of different characters to genetic divergence

Sl. No.	Characters	Percentage of total D^2	Sl. No.	Characters	Percentage of total D^2
1	Days to 50% flowering	2.42 (8)	7	100-grain weight	7.8 (3)
2	Plant height	1.09 (12)	8	Flag leaf length	2.15 (10)
3	Panicle length	2.21 (9)	9	Flag leaf area	2.01 (11)
4	Panicle number	3.3 (7)	10	Biological yield	4.32 (5)
5	No. of fertile grains per panicle	4.01 (6)	11	Harvest index	1.05 (2)
6	Fertility percentage	4.32 (4)	12	Grain yield per plant	45.32 (1)

In D^2 analysis 12 characters were considered simultaneously for making clusters, usually the members having common features of growth and yield behaviour have clustered together. However, the contribution of different characters to genetic divergent was not same. Therefore, an understanding of relative contribution of different characters for diversity would be of great importance for scheduling future programme. In present study highest contribution towards genetic divergence was made by grain yield per plant (45.32%) followed by harvest index (21.05%). This result was in broad agreement with the findings of Tandekar and Koshta, 2014 [141] and Sandhya *et al.*, 2014 [11]. All other characters contributed very little towards genetic divergence. It was suggested that the genotypes selected from different clusters based on inter-cluster distance and mean performance can be utilized in further breeding programme as suggested by Sandhya *et al.*, 2014; [11]. Bibi *et al.*, 2015 [3]; Beevi & Venkatesan, 2015 [2]; Tandekar & Koshta [14], 2014 and Radha *et al.* 2018 [9]. So, mean performance of grain yield and harvest index should be given priority while selecting the parent for hybridization programme. All other characters contributed in a low proportion (7.8% to 1.1%) to total divergence.

Cluster mean for different characters was an important criterion for selection of parents for future hybridization programme. Cluster I was characterized by high plant height, panicle number, number of fertile grains per panicle and harvest index. Cluster II and Cluster IV showed highest harvest index and panicle number per plant. Cluster V, a mono-genotypic cluster exhibited highest mean value for days to 50% flowering, but lowest mean value for plant height, panicle length, flag leaf length, flag leaf area, biological yield and grain yield per plant. Cluster VI was clearly distinguished from other clusters by highest plant height, panicle length, number of fertile grains per panicle, though genotype present in Cluster VI (PRX 027) was superior with respect to many characters, but it was a hybrid. So, genotypes present in Cluster I, Cluster II and Cluster IV could be utilized in hybridization programme having high mean performance for many desirable traits which was attested by Chakravorty *et al.* 2013 [4] and Suresh *et al.*2014 [12].

Table 4: Cluster meanfor12 quantitative characters in rice

Sl. No.	Characters	I	II	III	IV	V	VI
1	Days to 50% flowering	104.878	100.242	100.000	112.833	125.000	102.333
2	Plant height	91.220	96.314	93.966	92.766	90.200	103.100
3	Panicle length	21.836	22.818	22.211	21.717	20.667	27.533
4	Panicle number	14.545	13.090	13.500	15.500	13.667	11.667
5	No. of fertile grains per panicle	192.272	184.908	162.666	144.833	188.000	202.667
6	Fertility percentage	87.959	88.831	84.818	83.100	88.140	90.433
7	100-grain weight	1.580	1.788	1.759	2.078	1.173	2.603
8	Flag leaf length	28.594.	27.093	28.185	22.916	24.033	31.233
9	Flag leaf area	30.027	27.838	28.395	26.216	24.000	34.267
10	Biological yield	44.872	50.860	40.333	54.600	28.200	78.067
11	Harvest index	0.446	0.462	0.395	0.374	0.392	0.415
12	Grain yield per plant	20.155	23.655	15.924	20.036	11.037	32.405

Over all observations revealed that the genotypes under study differ with respect to 12 quantitative characters providing ample scope for selection and utilization in further breeding programme.

Conclusion

Thirty-two genotypes were grouped into six clusters out of which two were mono-genotypic clusters. Grain yield per plant and harvest index contributed maximum towards genetic divergence. Based on maximum genetic distance and cluster mean genotypes present in Cluster I, Cluster II and Cluster IV can be utilized in hybridization programme.

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