

Studies on Choice of Parents and Characters for Breeding for Higher Grain Yield in Rice (*Oryza Sativa L.*) Genotypes

M.Venkatesan* and S.Suganthi

Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai nagar-608002,Tamilnadu, India

ABSTRACT

Genetic divergence was assessed among 50 genotypes of rice using Mahalanobis D^2 analysis. The 50 rice genotypes were grouped into 9 clusters. Cluster I and VIII was found to be largest comprising of 13 genotypes in each cluster followed by cluster VIII having VIII genotypes. The pattern of distribution of genotypes from different ecogeographical regions into various cluster was at random indicating that geographical diversity and genetic diversity were not related. The analysis of variance showed significant difference for all nine character under study, suggesting that the genotypes selected for the present study were genetically divergent. Hence, further analysis is appropriate. The maximum intra-cluster distance was registered in cluster IX, hence genotypes from this cluster could be exploited as a potential line or variety in hybrid or recombination breeding programme. Maximum inter cluster distance was estimated between cluster II and VIII followed by cluster VII and VIII and cluster IV and VII. Genotypes selected from the above clusters could be used in heterosis breeding as the progenies from the genotypes could confine a greater magnitude of heterosis within. Genotypes from cluster IX, VII and III could be used as parents for combining characters for yield and its component characters for further improvement through hybridization and selection. Cluster III chronicled earliness in flowering and might be utilized as a suitable source for incorporation of earliness in other genotypes. Cluster III registered minimum cluster mean for plant height. Hence, genotypes from the cluster could be made use in development of dwarf and semi dwarf line or the traits could be transferred into other desirable genotypes. Cluster IX had the maximum cluster mean value for grain yield per plant. Hence, the genotypes could be utilized in yield improvement breeding programme. On the basis cluster mean, inter and intra cluster distance and IX, VII and III may be used for their desirable in breeding programme of rice.

Keyword : Clustering pattern, Inter-intra cluster distance, Rice.

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INTRODUCTION

Rice (*Oryza sativa L.*) is one of the staple cereal crop of the world and it is one of the main sources of carbohydrates for nearly one half of the world population. Genetic variability is the basic requirement for making progress in crop breeding. Inclusion of genetically divergent parents in any breeding programme is essential to create new genetic Stocks. Genetic diversity is the most important tool in the hands of the plant breeder in choosing the right type of parents for hybridization programme. The divergence can be studied by techniques using D^2 statistics developed by Mahalanobis [6]. It is based on multivariate analysis and grouped into various cluster as given by Spark [11]. This is considered as the most effective method for qualifying the degree of genetic diversity among the genotypes included in the study. The present investigation aimed to estimate the magnitude of genetic

divergence present in the 50 rice genotypes and to identify the diverse genotypes for future breeding programme. The observations were recorded on Days to 50 % flowering, Plant height, Number of tillers per plant, Number of panicles per plant, Panicle length, number of grains per panicle, Grain L/B ratio, Hundred grain weight and Grain yield per plant.

MATERIALS AND METHODS

The present investigation was conducted at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar, Tamil Nadu, India during the year 2017 – 2019.

The experimental materials for this genetic divergence study comprised of 50 rice genotypes collected from various places. The details of the materials are presented in Table 1.

Seeds of the 50 genotypes were sown in raised nursery beds during February, 2018. In each genotype, one seedling per hill was transplanted in the main field after 25 days with spacing of 20 cm × 20 cm. These genotypes were grown in saline soil with electrical conductivity (EC) of 3.83 dSm⁻¹. The experiments were conducted at the Experimental Farm of Plant Breeding (11°24' N latitude and 79° 44' E longitude, + 5.79 MSL), Annamalai University, Tamil Nadu, India. The experiment was carried out in a Randomized Block Design with three replications. As recommended, agronomic and plant protection measures were followed during the crop period. A uniform population of 12 plants in a row was maintained.

Eleven productive and quality characters were recorded on single plant basis in ten randomly selected plants of each genotype per replication. The mean data were utilized for the statistical studies. The following were the agronomic and quality characters studied for D2 analysis. The observations were recorded for days to 50% flowering, Plant height, Number of tillers per plant, Number of panicles per plant, Panicle length, Number of grains per panicle, Grain L/B ratio, Hundred grain weight and Grain yield per plant. Mean data were used for statistical analysis. Intra and Inter cluster distance and mean performance of the clusters for the characters were also computed.

RESULT AND DISCUSSION

Analysis of variance for different characters is presented in Table 1. The treatment i.e mean sum of square due to genotypes showed significant differences for all nine characters under study, suggesting that the genotypes selected for the present study were genetically divergent. Hence, further analysis is appropriate.

Using Mahalanobis D² analysis, the fifty genotypes taken for divergence studies were grouped into nine clusters. Clusters were grouped utilizing clustering technique based on the relative magnitude of D² values.

Cluster I and VII, the largest cluster, comprised of 13 genotypes, whereas clusters II, III, IV, V and VI comprised of minimum number of genotypes i.e., two genotypes in each. Cluster VIII composed 8 genotypes and cluster IX composed 6 genotypes. The nine clusters with the corresponding genotypes are tabulated in Table 2.

The intra and inter-cluster distances among the nine clusters for D² are provided in Table 3.

The cluster mean values for nine characters were studied and tabulated in Table 4. Among the nine clusters, cluster III showed early flowering (58.66 days) which was followed by cluster VI (61.60 days), cluster V (63.00 days) and cluster IV (74.16 days) recorded the maximum number of days to 50% flowering followed by cluster IV (74.16), cluster VIII (68.04 days) and cluster VII (65.20 days). Clusters I, II, III, V, VI and IX showed minimum values than general mean values for days to 50% flowering. Out of nine clusters, cluster III showed the minimum plant height of 62.19 cm followed by cluster I (70.78 cm), cluster VII (71.09 cm) and cluster IX (73.28 cm). The cluster which showed maximum plant height is cluster V (91.29 cm). The clusters which showed minimum values compared to general mean were Clusters I, III, VII and IX.

From nine clusters, only cluster VIII (15.67) showed maximum number of tillers per plant. The other clusters which had maximum number of tillers per plant were cluster V (15.10), cluster IX (14.58), cluster IV (13.60) and cluster VII (12.60). The minimum number of tillers per plant was found in cluster II (8.00). About four cluster namely cluster IV, V, VIII and IX valued higher than general mean value. Among the nine clusters, cluster V (13.30) showed

maximum number of panicles per plant. The other clusters which had maximum number of panicles per plant were cluster VIII, cluster IX, cluster IV and cluster VII. The minimum number of panicles per plant was found with cluster III (5.70). Five clusters *viz.*, cluster IV, V, VII, VIII and IX valued higher than general mean.

Cluster IV (21.29 cm) recorded the maximum cluster mean value for panicle length followed by cluster II (20.25 cm), cluster VIII (19.99 cm), cluster VI (19.02 cm) and cluster V (18.87 cm). The smallest panicle length was observed in cluster III (14.91 cm). Cluster II, IV, V, VI, VIII and IX obtained highest cluster mean values than general mean value. The highest mean for number of grains per panicle was recorded with cluster VII (128.74). The clusters which encompassed higher number of grains per panicle other than cluster VII, were cluster IX (104.11), cluster I (102.76), cluster III (95.00) and cluster V (90.50). The cluster with minimum number of grains per panicle was cluster II (68.50). Among the nine clusters, cluster I, cluster IX and cluster VII were found to have higher values than general mean value for number of grains per panicle.

Maximum cluster mean value for grain L/B ratio was revealed in cluster IX (2.36), cluster VI (2.31), cluster I (2.31) and cluster VII (2.28). The minimum cluster value was unveiled in cluster V (2.15). Only clusters I, II, III, IV, V, VI, VII, VIII and IX divulged to have higher values than general mean value. The cluster mean ranged from 1.51 g (cluster II) to 2.48 g (cluster VI). Cluster VI was followed by cluster IV (2.13 g), cluster V (2.02 g), cluster IX (1.94 g) and cluster VII (1.92 g). Out of nine clusters, clusters VI (2.48 g) exhibited higher values than general mean. The cluster IX recorded maximum cluster mean of 26.48 g among the nine clusters. It was followed by cluster III (24.80 g), cluster VII (24.29 g) and cluster VIII (23.69 g). The minimum cluster mean value for grain yield per plant was made down as cluster VI (20.68 g), cluster VII, cluster III and cluster IX exhibited higher than general mean value for grain yield per plant.

The relative contribution of individual character towards the expression of genetic diversity estimated over character wise D^2 value is furnished Table 5. The contribution of characters toward genetic divergence is an important criterion for selection of characters in hybridization programmes. Grain yield per plant (37.63 per cent), plant height (22.77 per cent) and number of grains per panicle (12.61 per cent) were the top most contributors towards total genetic divergence among the genotypes. Characters like number of grain per panicle (12.61 per cent), number of panicles per plant (11.34 per cent), hundred grain weight (7.26 per cent) had aided next to the above mentioned contributors towards the expression of genetic diversity. The least contributors among the selected genotypes were panicle length (1.14 per cent), days to 50 % flowering (1.38 per cent), and number of tillers per plant (2.12 per cent) and grain L/B ratio (3.75 per cent).

The intra cluster distance ranged from 5.71 to 43.01. The maximum intra cluster distance was exhibited by cluster IX (43.01) followed by cluster VII (40.66), cluster I (34.25) and cluster VIII (25.77) and the minimum intra cluster distance was found in cluster II (5.71).

The inter-cluster distance ranged from 11.89 to 57.49. The maximum inter cluster distance was found between Cluster II and Cluster VII (57.49) followed by Cluster VII and VIII (56.12), cluster IV and VII (55.99), cluster V and VII (48.72) and cluster VI and VII (46.55). The minimum inter-cluster distance was exhibited between Cluster II and Cluster IV (11.89).

Analysis of variance revealed significant differences for all the characters in respect of the genotypes under present study indicating the presence of considerable amount of variability among the genotypes. Similar findings were reported by Chandramohan *et al.* (2016) and Toshimenla *et al.* (2016).

Genetic diversity is one of the key factors in tailoring the effective breeding programme in any crop. Success of hybridization followed by selection depends largely on the selection of parent with high genetic variability for different characters. The genetically diverse parents are likely to produce heterotic effects and desirable segregants.

Genetic divergence studies revealed that 50 genotypes were grouped into nine clusters based on their D^2 values. Among the nine clusters, cluster I and VII accommodated maximum of 13 genotypes for each cluster followed by cluster VIII of 8 genotypes and cluster IX of 6 genotypes. The remaining clusters *ie.* II, III, IV, V and VI were accommodated with two genotypes each cluster.

The genotypes included in cluster I originated from different origins indicating that there was no parallelism between clustering pattern and geographic distribution of genotypes [7]. Therefore, the kinds of genetic diversity found among the genotypes belonging to same geographic origin might be due to differences in adoption, selection criteria, and selection pressure in environmental conditions [5].

The grouping of genotypes into so many clusters suggested the presence of high degree of diversity in the material evaluated. Earlier workers have also reported presence of substantial genetic diversity in rice (Kumar *et al.*, 2014, Ahmed *et al.*, 2014, and Sandhya *et al.*, 2015).

The highest intra-cluster distance was registered in cluster IX (43.01) followed by cluster VII (40.66), cluster I (34.25) and cluster VIII (25.77). Thus the genotypes from those clusters had high degree of divergence that would produce more desirable segregants for achieving greater genetic advance. The least intra-cluster distance was revealed in cluster II (5.71), followed by cluster III (6.68), cluster IV (6.77) and cluster V (7.59) indicating homogenous nature of the genotypes with less deviation between the genotypes. Parallel findings were found by Nirosha *et al.* [8].

Highest inter cluster distance (57.49) was found between cluster II and VII followed by cluster VII and VIII (56.12), cluster IV and VII (55.99), cluster V and VII (48.72) and cluster VI and VII (46.55) indicating the wider genetic diversity among the genotypes between these clusters. This indicated that the genotypes in these clusters are having broad spectrum of genetic diversity and could very well be used in hybridization programme. Similar results were reported by Yadav *et al.* [14] and Sandhya *et al.* [9].

The minimum inter cluster distance was found between cluster II and IV (11.89). The inter cluster distances were greater than intra cluster indicating wide genetic diversity among genotypes. Similar results were reported by Chamundeshwari [3] and Nirosha *et al.* [8].

The overall clustering pattern indicated that genotypes developed in same geographical region were distributed in different cluster. Shanmugam and Rangasamy (1982) reported that grouping of material of same geographical origin into different clusters was an indication of the broad genetic base of genotypes belonging to the origin. Similar results of non association of geographical region with the genetic diversity was reported by Chandramohan *et al.* [2] and Thippeswamy *et al.* [12].

Cluster mean analysis revealed a wide range of variation for all the traits under study. Cluster III had lowest cluster mean value for day to 50% flowering indicating that the genotypes in the cluster had earliness in flowering while in cluster IV, late flowering was observed. Cluster III exhibited lowest cluster mean value for plant height whereas cluster V had highest value. Hence genotypes from cluster II could be used in breeding for obtaining semi-dwarf segregants. Cluster VIII had maximum number of tillers per plant however cluster II had minimum number of tillers.

Number of panicle per plant was found maximum in cluster V but in cluster III had the minimum values for number of panicles per plant. Thus genotypes from cluster V could be utilized with breeding programme for developing semidwarf segregants but with more number of panicles. Cluster IV had the longest panicle but cluster III had the shortest panicle of all clusters. Cluster VII registered maximum number of grains per panicle yet cluster II had the least number of grains.

Obtaining bold grain type segregates would also be possible by using genotypes from cluster VI as it had maximum hundred grain weight. Minimum hundred grain weight was registered in cluster II from which genotypes could be used in developing fine grain type. Cluster IX had the highest cluster mean value of grain L/B ratio compared with cluster V which had the least value. Grain yield per plant was observed maximum in cluster IX while cluster VI was characterized with minimum grain yield.

This indicated that none of the clusters had all the desirable characters. Almost the minimum and maximum cluster mean values were distributed in relatively distant cluster.

The findings of the present study suggested that inter crossing of genotypes from different clusters exhibiting good mean performance may be helpful for obtaining higher yield and thus, selection of more diverse parent for hybridization is believed to provide the chances of getting better heterosis and give broad spectrum of variability in segregating generation.

The relative contribution of each characters towards D^2 depend upon the inter cluster distances in all combinations (Table 5). The selection and choice of parents mainly depends

upon contribution of characters towards divergence. In this present investigation, the highest contribution in manifestation of genetic divergence was exhibited by grain yield per plant (37.63 per cent) followed by plant height (22.77 per cent) and number of panicles per plant (11.34 per cent). Similar results were reported by Toshimenla *et al.* [12] for grain yield per plant. Toshimenla *et al.* [12] and Kumar *et al.* [4] for plant height.

Next to the above characters hundred grain weight (7.26 per cent) and grain L/B ratio (3.75 per cent) had moderately contributed towards the genetic divergence. Other characters like number of tillers per plant (2.12 per cent) and days to 50% flowering (1.38 per cent) and panicle length (1.14 per cent) were also contributed in differentiating genotypes morphologically.

The major traits contributing to the total divergence may be utilized as parents in selecting genetically diverse parents. Singh *et al.* [10] reported that while considering the genetic diversity among the parents to be included in hybridization programme, this potential should not be ignored.

It is necessary to carefully analyse the selection of a particular cluster from which genotypes are to be chosen in crossing programme as well as selection of a particular genotype from the selected cluster while selecting genotypes from distinct clusters for hybridization programme, their *per se* performance of different traits should also be given due importance depending upon the traits to be combined.

The present study revealed that considerable diversity existed both within and between the clusters, viz., cluster II and VII. Thus genotypes from cluster II could be selected for earliness and hundred grain weight and cluster II for grain yield per plant in hybridization programme since hybridization between divergent parents would likely produce wide variability and transgressive segregants crosses between unrelated line or varieties tend to exhibit heterosis. Thus, diverse line from different clusters should be chosen for crossing in a hybrid rice breeding programme.

Table 1: Analysis of variance for nine characters in rice genotypes

	Grain yield per plant	100 seed weight	Grain L/B ratio	No. of grains per panicle	Panicle length	Number of panicles per plant	Number of tillers per plant	Plant height	Days to 50% flowering	Df	Source	S. No.
	15.08	0.04	0.77	19.82	2.37	0.31	0.03	1.62	79.43	2	Replication	1
	38.08**	36.18**	40.80**	3047.23**	30.60**	43.79**	42.45**	495.14**	114.65**	49	Genotype	2
	1.06	0.09	0.10	2.08	0.89	0.89	0.75	0.88	18.46	98	Error	3

*Significant at 1 per cent level

Table 2. Distribution of rice genotype in different clusters based on D² analysis

Cluster No	Number of genotypes	List of the genotypes
I	13	AURC1, AURC2, AURC3, AURC4, AURC5, AURC6, AURC7, AURC8, AURC9, AURC10, AURC11, AURC12, AURC13
II	2	AURC25, AURC44
III	2	AURC27, AURC47
IV	2	AURC31, AURC34
V	2	AURC32, AURC35
VI	2	AURC18, AURC24
VII	13	AURC14, AURC15, AURC16, AURC17, AURC19, AURC20, AURC21, AURC22, AURC23, AURC26, AURC28, AURC45, AURC46
VIII	8	AURC29, AURC30, AURC33, AURC36, AURC37, AURC38, AURC39, AURC40
IX	6	AURC41, AURC42, AURC43, AURC48, AURC49, AURC50

Table 3. Average intra (bold) and inter cluster (unbold) D values in rice

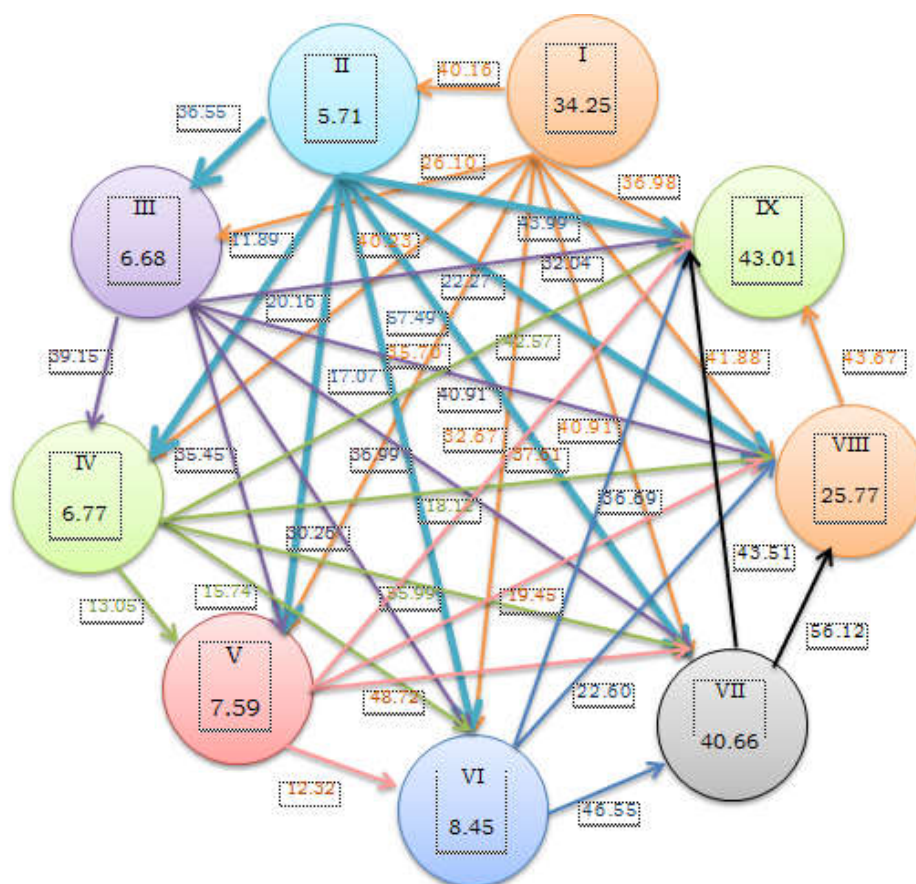
Cluster no	I	II	III	IV	V	VI	VII	VIII	IX
I	34.25	40.16	26.10	40.23	35.70	32.67	40.91	41.88	36.98
II		5.71	36.55	11.89	20.16	17.07	57.49	22.27	43.99
III			6.68	39.15	35.45	30.26	36.99	40.91	32.04
IV				6.77	13.05	15.74	55.99	18.12	42.57
V					7.59	12.32	48.72	19.45	37.61
VI						8.45	46.55	22.60	36.69
VII							40.66	56.12	43.51
VIII								25.77	43.67
IX									43.01

Table 4. Cluster means of rice genotypes for different traits

Clusters	Days to 50% flowering	Plant height	Number of tillers per plant	Number of panicles per plant	Panicle length	Number of grains per panicle	Grain L/B ratio	Hundred grain weight	Grain yield per plant
Cluster I	63.89	70.78	11.84	9.59	17.28	102.76	2.31	1.74	22.06
Cluster II	64.83	84.05	8.00	7.30	20.25	68.50	2.20	1.51	21.28
Cluster III	58.66	62.19	8.78	5.70	14.91	95.00	2.21	1.74	24.80
Cluster IV	74.16	89.39	13.60	11.80	21.29	76.00	2.22	2.13	21.92
Cluster V	63.00	91.29	15.10	13.30	18.87	90.50	2.15	2.02	23.34
Cluster VI	61.00	86.67	9.40	7.80	19.02	90.50	2.31	2.48	20.68
Cluster VII	65.20	71.09	12.60	10.78	17.80	128.74	2.28	1.92	24.29
Cluster VIII	68.04	89.07	15.67	12.67	19.99	79.50	2.26	1.69	23.69
Cluster IX	63.83	73.28	14.58	12.01	18.61	104.11	2.36	1.94	26.48
General Mean	64.98	79.48	12.81	10.60	18.33	102.22	1.85	2.28	23.50

Table 5. Relative contribution of different characters to genetic divergence

S. No	Character	Per cent contribution
1	Days to 50% flowering (days)	1.38
2	Plant height (cm)	22.77
3	Number of tillers per plant	2.12
4	Number of panicles per plant	11.34
5	Panicle length (cm)	1.14
6	Number of grains per panicle	12.61
7	Grain L/B ratio	3.75
8	Hundred grain weight (g)	7.26
9	Grain yield per plant (g)	37.63



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