Genetic diversity analysis for yield traits in rainfed rice (*Oryza sativa* L.) under water stress condition

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Abstract

The present experiment comprised with thirty eight advanced rice cultures and conducted during *Rabi* 2017-18 under rainfed rice ecosystem. They were evaluated for ten yield and yield related traits *viz.,* days to 50% flowering, plant height, number of productive tillers per plant, number of panicles per square metre plot area, panicle length, number of filled grains per panicle, spikelet fertility, grain yield, straw yield and harvest index using D^2 analysis. Based on the analysis, the genotypes were grouped into nine clusters. Maximum number of genotypes (16 genotypes) was grouped in cluster I. Cluster II, III and VII consists of ten, four and three genotypes respectively. Remaining clusters were represented by a single genotype each. Maximum inter cluster distance was observed between cluster III and VI (17.48) followed by between cluster III and IV (17.05) indicating wider genetic diversity between genotypes. Hence these lines may be utilized in further breeding programme for the exploitation of hybrid vigour. The intra cluster distance was maximum in cluster III (7.96) followed by cluster VII (7.23) indicates hybridization involving genotypes within the same clusters may result in good cross combinations. Among the ten traits studied, grain yield contributed maximum divergence (36.13%) followed by days to 50% flowering (29.73%), filled grains per panicle (12.09%) and number of panicles per square metre (9.39%). Hence these altogether contribute more than eighty five per cent towards total divergence. Therefore these characters may be given importance during hybridization programme in rainfed rice ecosystem under water stress condition.

Key words: Genetic diversity, yield traits, rainfed rice, water stress.

Introduction

Rice is an important food crop for about half of the world's population and 90% of it is being produced and consumed in Asia (Rao *et al.,* 2016) and share maximum in grain production. It contributes about 43 per cent of caloric requirement and 20-25% of agricultural income. Rainfed rice accounts for around 45% of the world's rice area and around 40 million ha of rainfed area is concentrated in South and South East Asia alone (Maclean *et al*., 2002). Although more than 1200 rice varieties have been released in India, many of them becoming obsolete due to disparity in consumer preference and inconsistent performance in diverse environments and less than 40 varieties are found in large scale adoption in farmers field with stable performance continue under cultivation after 15 to 20 years of their release. The rice production area in the country are very diverse in hydrology and combined to other soil and climatic factors make a difference in rice yield (Singh *et al.,* 1997).Yield of rainfed lowland rice is drastically reduced by intermittent drought due to unpredictable, and uneven distribution of rainfall during the crop growing period. To reduce yield losses of rice crop in rainfed lowland areas and to increase overall rice production, new rice varieties with greater adaptation to drought are essential. Hence, the development of drought resistant cultivars with a higher yield potential is one of the main objectives of rainfed lowland rice breeding programmes.

The success of any breeding programme depends on the selection of parents for hybridization. The parents involved in the development of varieties should be divergent. The germplasm provides immense scope for wide variability. Genetic divergence is an efficient tool for an effective choice of parents for hybridization programme. Such study also selects the genetically divergent parents to obtain desirable combinations in the segregating generations. Information on nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding programme (Vivekanandan and Subramanian, 1993). An attempt was made in the present investigation to assess the genetic diversity of thirty eight advanced rice cultures for yield traits in rainfed rice ecosystem.

Materials and methods

The experimental material comprised with thirty eight advanced rice cultures which were evaluated in a randomized block design with three replications at Agricultural Research Station, Tamil Nadu Agricultural University, Paramakudi during *Rabi* 2017-18. The experimental site is located at 9" 21' N latitude, 78" 22' E longitudes and an altitude of 242 m above mean sea level with average annual rainfall of 840 mm. This site has clay loam soil texture with pH of 8.0. Each genotype was raised in 5x2 m plot keeping 15 x 10 cm spacing. The recommended agronomic practices were followed to raise good crop stand. The data were recorded on ten randomly selected plants from each replication for various quantitative traits studied were *viz,* days to 50% flowering, plant height (cm), number of productive tillers per plant, number of panicles per square metre plot area, panicle length, number of filled grains per panicle, spikelet fertility, grain yield (t/ha), straw yield (t/ha) and harvest index. The genetic distance between the genotypes was worked out using Mahalanobis D^2 analysis (1936) and grouping of varieties into clusters was done following the Tochers method as detailed by Rao, (1952).

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating existence of variability among the genotypes. Based on the relative magnitude of D^2 values, thirty eighty genotypes were grouped into nine clusters (Table 1).

Table 1: Clustering pattern of 38 genotypes

Cluster	No. of genotypes	Name of genotypes
I	16	PM 17003 (G3), CB 14530 (G32), CB 13805 (G38), IR64 dt QTL (G34), PM 17010 (G10), PM 17002 (G2), PM 17018 (G18), PM 17012 (G12), PM 17020 (G20), PM 17011 (G11), PM 17019 (G19), PM 17026 (G26), PM 17005 (G5), PM 17021 (G21), PM 17014 (G14), PM 17017 (G17).
II	10	TM 12039 (G35), CB 13084 (G36), PM 14042 (G28), Anna(R)4(G30), PM 17022 (G22), PM 17023 (G23), PM 17015 (G15), PM 17024 (G24), PM 17025 (G25) and PM 17006 (G6).
III	4	TM 13018 (G31), TM 12077 (G33), PM 17008 (G8) and CB 14756 (G29).
IV	1	PM 17007 (G7)
V	1	PM 17013 (G13)
VI	1	PM 17001 (G1)
VII	3	PM 17009 (G9), TKM 12 (G37) and PM 17016 (G16).
VIII	1	PM 17027 (G27)
IX	1	PM 17004 (G4)

Maximum number of genotypes (16 genotypes) was grouped in Cluster I. Cluster II, III and VII consists of ten, four and three genotypes respectively. Remaining clusters were represented by a single genotype each. The overall composition of the clustering pattern showed that genotypes collected from the same geographic origin were distributed in different clusters. Therefore, the selection of parental material for hybridization programme simply based on geographic diversity may not be rewarding exercise. The choice of suitable diverse parents based on genetic divergence analysis would be more fruitful than the choice made on the basis of geographical distances. Similar findings of non-correspondence of geographic origin with genetic diversity were also reported by Shanmugasundaram*et al.,* (2000), Nayak *et al.,*(2004) and Ranjith *et al.*, (2018).

The intra and inter cluster distance are presented in Table 2. Inter cluster distance was higher than intracluster distance indicating wider genetic diversity among the genotypes. The maximum inter cluster distance was observed between cluster III and VI (17.48) followed by between cluster III and IV (17.05) indicating wider genetic diversity among the genotypes between these groups. The hybrids developed from the selected members of these clusters would produce highly variable population in the segregating generations. The minimum inter cluster distance was found between cluster VI and VII (6.36) followed by between cluster V and IX (6.37). These genotypes in these clusters are genetically very close and hence, hybridization among the varieties will not give fruitful result.

Table 2: Intra (diagonal) and inter cluster average distance of yield traits in 38 genotypes

	I	II	III	IV	V	VI	VII	VIII	IX
I	6.74	9.72	13.12	8.37	8.41	9.29	9.90	9.00	9.62
II		6.42	13.94	14.45	11.95	12.65	13.34	11.86	15.10
III			7.96	17.05	12.51	17.48	16.79	10.39	12.96
IV				0.00	9.84	8.59	9.50	11.45	8.39
V					0.00	12.13	11.35	11.59	6.37
VI						0.00	6.36	11.60	14.04
VII							7.23	12.31	13.21
VIII								0.00	11.53
IX									0.00

The maximum intra cluster distance was observed in cluster III (7.96) followed by cluster VII (7.23). Hence, selection within these clusters may be exercised based on the highest areas for the desirable traits, which would be made use of in improvement through inter-varietal hybridization (Joshi *et al.,* 2008).A perusal of results of cluster means (Table 3) revealed that cluster I with 16 genotypes surprisingly exhibited no highest and lowest values for

all the traits studied. Cluster II with ten genotypes exhibited highest mean value for productive tillers per plant (7.10), straw yield (5.90) and grain yield (2.95). The genotypes in Cluster III had taken more number of days for fifty per cent flowering (96.75) and exhibited highest harvest index (0.39). Cluster IV was characterized by lowest panicle length (17.53) and short stature (59.07); likewise the cluster V had minimum number of productive tillers per plant (5.33), filled grains per panicle (74.33) and harvest index (0.25). The genotype PM 17001 with less number of days for fifty per cent flowering (75.00) and lowest spikelet fertility (78.33) was grouped in cluster VI. The Genotypes PM 17009, TKM 12 and PM 17016 (Cluster VII) had shown tall stature (87.76) and lesser number of panicles per square metre (122.22) but possess lengthy panicles (23.13). The genotype PM17027 showing highest mean values for number of panicles per square metre area (238.00), filled grains per panicle (150.33) and spikelet fertility (94.00) was grouped in cluster VIII.The genotype PM 17004 in Cluster IX exhibited lowest straw (3.30) and grain yield (1.40).

Table 3: Cluster mean of different yield characters in 38 rice genotypes

Cluster	Days to 50% flowering	Plant Height (cm)	Productive tillers per plant	No. of panicles per sq.metre	Panicle length (cm)	Filled grains / panicle	Spikelet fertility (%)	Straw yield (t/ha)	Grain yield (t/ha)	Harvest Index
I	81.25	64.36	6.56	179.54	18.89	97.35	91.85	5.28	2.17	0.30
II	79.80	67.28	7.10	205.33	18.60	79.93	93.42	5.90	2.95	0.34
III	96.75	64.72	6.42	148.08	19.30	134.17	93.94	4.40	2.63	0.39
IV	78.00	59.07	6.33	154.67	17.53	99.00	89.63	3.80	1.50	0.28
V	88.00	73.00	5.33	159.00	18.33	74.33	83.83	5.83	1.93	0.25
VI	75.00	74.33	6.00	164.00	21.93	110.00	78.33	5.40	2.30	0.30
VII	76.56	87.76	5.78	122.22	23.13	111.78	88.27	5.76	2.26	0.29
VIII	86.00	68.13	6.33	238.00	19.33	150.33	94.40	5.80	2.40	0.29
IX	90.00	59.20	6.33	153.33	18.30	95.00	93.33	3.30	1.40	0.30

None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. However the cluster II and VIII recorded desirable mean value for maximum number of productive traits *viz.*, productive tillers per plant, number of panicles per square metre area, filled grains per panicle, spikelet fertility, straw yield and grain yield. Similar results were also reported by Banumathy *et al.*(2010) and Rai *et al.* (2014), thereby underlining the fact that the hybridization between genotypes of different clusters is necessary for the development of desirable genotypes. The crossing between

the entries belonging to cluster pairs having large inter cluster distance and possessing high cluster means for one or other characters to be improved may be recommended for isolating desirable recombinants in the segregating generations in rice. However, caution should be exercised in selecting very diverse genotypes, because the frequency of heterotic crosses and magnitude of heterosis for yield and its components were found to be higher in crosses between parents with intermediate divergence than the extreme one (Arunachalam *et al*., 1984 and Datta *et al*., 2004) The selection on diverse parents for hybridization programme should be done after considering the inter-cluster distances and mean performance of genotypes for

different characters. The lines belonging to diverse clusters and showing high mean performance in desirable direction for different traits may be chosen as parents.

The contribution of each trait to total divergence is presented in table 4. Among the traits studied, grain yield contributed maximum divergence (36.13%) followed by days to 50% flowering (29.73%), filled grains per panicle (12.09%) and number of panicles per square metre (9.39%). The minimum percentage of contribution was observed in productive tillers per plant (0.28%) followed by harvest index (1.14%), straw yield (2.42%), plant height (2.70%), panicle length (2.84%) and spikelet fertility (3.27%). The traits *viz.,* grain yield, days to 50% flowering, filled grains per panicle and number of panicles per square metre contributed more than eighty five per cent towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population under water stress condition.

Table 4: Percentage of contribution of each character towards total divergence

Character	No. of Times Ranked First	Contribution (%)
Days to 50% flowering	209	29.73
Plant Height (cm)	19	2.70
Productive tillers per plant	2	0.28
No. of panicles per sq.metre	66	9.39
Panicle length (cm)	20	2.84
Filled grains / panicle	85	12.09
Spikelet Fertility	23	3.27
Straw yield (kg/ha)	17	2.42
Grain yield (kg/ha)	254	36.13
Harvest Index	8	1.14
Total	**703**	**100**

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