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Studies on genetic divergence in rice germplasm lines.

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Abstract: Fifty four elite rice germplasm lines being maintained at Agricultural Research Station. Nellore were evaluated for their genetic diversity with regard to yield, yield components and quality trails. The genotypes were grouped into nine clusters, based on Mahalanobis D^2 statistics. Geographical and genetic diversity were observed to be unrelated, as genotypes from diverse geographical regions were placed in the same cluster, while genotypes from the same centre were grouped into different clusters. Results on inter-cluster distances revealed maximum diversity between genotypes of clusters IV and VIII. Inlra-cluster distance was maximum for Cluster V, indicating the existence of variability with in the cluster. A perusal of the results on cluster means revealed high yield, number of grains per panicle, panicle length, plant height and days to 50 per cent (lowering for Cluster IV, indicating the desirability of genotypes from the cluster for improvement of grain yield and the above yield components. Further, plant height and days to 50 per cent flowering, together accounted for 82.04 per cent of the total genetic divergence, indicating their importance in the choice of parents for hybridization programmes.

Key words : D^2 analysis, Genetic divergence, germplasm, Rice.

Introduction

Information on the nature and degree of divergence is useful in selecting the desirable parents in breeding programmes, since it is known that exploitation of heterosis and success in obtaining desirable recombinants is dependent on the degree of divergence of the parents (Acharya and Gupta, 1993; Parameswarappa and Patil, 1994), Mahalonobis D^2 statistic is a valuable tool in quantifying the degree of divergence. It helps the breeder to estimate the genetic divergence in the base population. germplasm for use in plant breeding programmes. The present study was undertaken to ascertain the nature and magnitude of genetic diversity among the elite germplasm lines collected from different centres, within and outside the country, and being maintained at Agricultural Research Station. Nellore. Andhra Pradesh.

Materials and Methods

Experimental material for the present investigation comprised of 54 elite rice genotypes obtained from Agricultural Research Station, Nellore. Andhra Pradesh. These were sown during *Rabi* 2001-2002 at the wetland farm of Sri Venkateswara Agricultural College, Tirupati in a randomized block design with three replications. Thirty day old seedlings of each genotype were transplanted in three rows, each of 4.5 m length by adopting a spacing of 15 cm between rows and 15 cm between plants with in the rows. All recommended practices were followed to raise a healthy crop. Observations were recorded for 16 characters, including yield, yield components and quality parameters of the rice genotypes. The observations on plant height, number effective tillers per plant, panicle length, number of grains per panicle and fertility percentage were recorded from five randomly selected plants

Table 1. Cluster composition of 54 rice genotypes (Tocher's method)

Cluster	Number of Genotypes	Name of Genotypes
I	14	SC 216, NLR 33633, NLR 30491, NLR 33899, MTU 1010, SC 521, SC 847, NLR 33359, MTU 1001 BPT 1235, NLR 33358, SC 480, NLR 34242, JGL 1768
II	16	SC 507, NLR 33356, CO 43, SC 505, Vadasamba, SC 515, PR-106, SC 823, SC 518, Secamolo, SC 508-1, SC 555-2, Pottinella Vair, SC 474, NLR 145, SC 437-2
III	11	Kuruhonda Rawalu, SC 438-11, Dular, Sinne sivappu, INRC 2285, PTB 33, Isanakora, SC 547, RP 1574 1864-70-33-64, PLA 1100, MTU 4870
IV	3	SC 584, Hawarobato, SC 405-2
V	6	CR 294-29-1, BPT 5204, IR-26, RPW6-17, IRAT 104, SC 460
VI	1	VL 96-6821
VII	1	WGL 14377
VIII	1	Suweon 330
IX	1	SC 425

for each entry in each replication. However, for days to 50 per cent flowering, days to maturity, grain yield per plant and harvest index, observations were recorded on plot basis. In contrast, observations for the quality parameters, namely, hulling recovery, kernel length, kernel breadth, kernel L/B ratio, volume expansion ratio, kernel elongation ratio and 1000-grain weight were obtained from a random grain sample drawn from each plot, in each entry and replication. The data obtained was subjected to standard statistical procedures. Genetic diversity in the material was analysed using Mahalanobis D^2 statistic described by Rao (1952). The genotypes were grouped into different clusters according to Tocher's method (Rao, 1952).

Results and Discussion

Analysis of variance revealed highly significant differences for all the characters studied. Further, the 54 genotypes studied were grouped into nine clusters (Table 1), based on the relative magnitude of 1431 D^2 values. Among the nine clusters, Cluster II consisted of maximum genotypes (16), representing collections from different centres of the country, namely, Nellore, Hyderabad, Coimbatore, Cuttack and Punjab, while Cluster I had 14 genotypes, collected from different centres within Andhra Pradesh state, namely Maruteru, Bapatla, Nellore, Jagityal and Hyderabad. The Cluster III had 11 genotypes from Maruteru, Pulla, Nellore and Hyderabad within Andhra Pradesh; Kerala, Raipur and Manipur within the country; and Philippines and Thailand, outside the country. Similarly, cluster V had six genotypes from Bapatla within Andhra Pradesh; Cuttack and Raipur within the country; and Phillipines and Ivory

Table 2. Inter-cluster and Intra-cluster (diagonal) average of D^2 and of 54 Rice genotypes (Tocher's method)

Cluser Number		I	II	III	IV	V	VI	VII	VIII	IX
I	1078.46	2985.52	7288.89	12419.09	2769.18	4671.85	1649.57	1582.52	2362.25	
II		1299.60	2721.39	6458.85	3071.04	1885.64	4498.25	4428.37	2379.87	
III			1365.74	2889.92	5044.97	2393.557	10020.61	10520.60	5521.38	
IV				1914.67	7566.30	6025.48	16577.33	17570.56	10415.01	
V					1999.69	4369.07	4809.69	5166.59	3975.80	
VI						0.000	5021.13	6261.55	2988.69	
VII							0.000	1042.90	2411.98	
VIII								0.000	3176.11	
IX									0.000	

Table 3. Cluster means for sixteen characters in 54 genotypes of Rice (Tocher's method)

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of effective tillers per plant	Panicle length (cm)	Number of grains per panicle	Fertility percentage	Harvest index (%)	Hulling recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio	Volume expansion ratio	Kernel elongation ratio	1000-grain weight (g)	Grain yield per plant(g)
I	96.66	128.00	83.24	7.05	20.56	115.99	84.09	55.09	73.64	6.48	2.35	2.78	4.44	1.58	22.03	16.86
II	94.89	128.64	104.79	6.63	21.35	123.01	84.56	40.74	72.13	5.87	2.74	2.19	4.41	1.46	21.38	17.39
III	102.87	134.39	125.03	7.67	23.92	130.16	83.67	41.54	71.07	6.07	2.75	2.25	3.67	1.47	24.11	21.09
IV	121.11	150.11	138.94	6.29	28.12	245.35	85.98	48.34	69.10	6.40	2.15	3.00	4.03	1.54	23.66	25.03
V	117.55	144.77	98.61	6.35	21.92	133.26	81.98	52.24	71.45	6.91	2.26	3.16	3.98	1.62	22.73	18.08
VI	86.00	119.00	110.03	3.93	20.13	90.66	80.85	29.99	68.23	7.25	3.02	2.39	3.86	1.63	27.62	9.20
VII	80.33	115.66	75.26	6.53	16.63	83.23	73.41	36.33	67.86	7.03	2.05	3.52	4.76	1.65	19.50	8.45
VIII	83.00	120.33	71.13	5.53	15.46	112.73	86.31	41.18	70.00	4.93	3.00	1.63	4.60	1.52	20.30	10.84
IX	86.33	120.33	95.53	7.20	20.13	114.60	86.51	31.29	75.13	4.50	1.73	2.59	4.66	1.74	12.00	8.90

Table 4. Relative contribution of sixteen characters to genetic diversity in rice.

S.No	Character	Times Ranked First	Contribution (%)
1.	Days to 50% flowering	257	17.96
2.	Days to maturity	6	0.42
3.	Plant height	917	64.08
4.	Number of effective tillers per plant	2	0.14
5.	Panicle length	1	0.07
6.	Number of grains per panicle	0	0.00
7.	Fetility percentage	0	0.00
8.	Harvest index	10	0.70
9.	Hulling recovery	40	2.80
10.	Kernel length	13	0.91
11.	Kernel breadth	0	0.00
12.	Kernel L/B ratio	0	0.00
13.	Volume expansion ratio	52	3.63
14.	Kernal elongation ratio	97	6.78
15.	1000- grain weight	21	1.47
16.	Grain yield per plant	15	1.05

Coast, outside the country. The Cluster IV had three genotypes from Hyderabad, while clusters VI. VII, VIII and IX were monogenotypic with genotypes from Tamilnadu, Warangal, Korea and Hyderabad, respectively. The distribution pattern of genotypes into different clusters revealed no parallelism between genetic and geographic diversity as genotypes chosen from same eco-geographical region were found in different clusters as well as in the same cluster, while genotypes from diverse geographical regions were included in the same cluster. Similar results were reported in rice by earlier workers (Mehetre *et al.*, 1997). The production of greater diversity by genetic drift and selection, compared to that produced by geography was also observed in the present study. Genotypes from Hyderabad were observed to be distributed over five clusters (Cluster I, II, III, IV and IX), while genotypes from diverse geographical regions of different countries were placed in the same cluster (Clusters III and V). Similar results were reported earlier (Murty and Arunachalam, 1996).

An analysis of inter and intra cluster distances (Table 2) revealed maximum inter-cluster distance between Clusters IV and VIII (17570.56); followed by IV and VII (16577.33); and I and IV (12419.09), indicating that genotypes from these clusters were highly divergent meriting due consideration in selection of parents for hybridization. Kandhola and Panwar (1999) also reported greater diversity between genotypes from different clusters based on their inter-cluster distance. Minimum inter-cluster distance was observed between VII and VIII clusters (1042.90), indicating their close relationship and similarity with regards to the characters studied for most of the genotypes in the two clusters. Further, intra-cluster distance was observed to be minimum for Cluster I (1078.46) and maximum for cluster V (1999.69), while it was zero for the monogenotypic clusters, namely. Cluster VI, VII, VIII and IX as they included only single genotype. The genotypes included in Cluster V, exhibiting maximum intra-cluster distance, are inferred to be more divergent than those in other clusters.

A perusal of the results on cluster means for yield, yield components and quality characters (Table 3) revealed considerable differences between the clusters for all characters under study. High grain yield, number of days to 50 per cent flowering, days to maturity, plant height, panicle length and number of grains per panicle were noticed for Cluster IV; while high harvest index was observed for Cluster I; high number of effective tillers per plant for Cluster III; greater kernel length and 1000-grain weight for Cluster VI; greater kernel L/B ratio and volume expansion ratio for Cluster VII; and greater fertility percentage, hulling recovery, kernel elongation ratio and lower kernel breadth for Cluster IX, indicating the importance of selection of genotypes from the corresponding clusters in hybridization programmes for effecting improvement of the respective traits.

Information on the relative contribution of various plant characters towards divergence was reported to aid the breeder in choice of parents for hybridization and effective selections (De *et al.*,' 1988). In the present study, plant height contributed maximum (64.08%), followed by days to 50 per cent flowering (17.96%) and kernel elongation ratio (6.78%) towards the total divergence (Table 4). Contribution of the remaining characters to the total divergence was however, relatively low. Therefore, plant height and days to 50 per cent flowering, contributing to 82.04 per cent of the total divergence need to be stressed in selection of parents for hybridization, in this particular set of germplasm lines.

The study revealed existence of genetic diversity for the genotypes studied. However, no relation was observed between geographic and genetic diversity. Further, plant height and days to 50 per cent flowering were observed to contribute more than 80 per cent of the total genetic divergence, indicating their importance in the choice of parents.

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