RESEARCH ARTICLE

Genetic divergence in upland rice (*Oryza sativa* L.)

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SUMMARY

Genetic diversity was assessed in 40 genotypes of rice for 12 quantitative characters including grain yield using Mahalanobis D^2 statistics. The D^2 values between all possible pairs of 40 genotypes ranged from 26.32 to 404.814. The results revealed that 40 genotypes were grouped into 8 clusters with substantial divergence between them. Cluster I was very large comprising 24 genotypes followed by cluster II with 10 genotypes, while clusters III to VIII were solitary clusters. The maximum inter-cluster distance was obtained between cluster VI and VII (D = 20.12) followed by those between cluster VII and VIII (D = 18.56) which may serve as potential parents for hybridization, whereas, minimum between cluster III and IV (D = 5.13). The highest intra cluster distance was recorded for cluster II (D = 7.96) and lowest for cluster I (D = 6.62). The genotypes in the cluster VI had lowest mean value (89.67) for days to 50 per cent flowering indicating their use in breeding program for development of early maturing varieties. Cluster VIII recorded high grain yield per plant showing its potential for yield improvement. The characters number of spikelets per panicle and days to 50 per cent flowering contributed maximum in the manifestation of genetic divergence. RDN-20, RDN-11, Phule Radha, RDN-18 and RDN-5 may serve as potential donors for future hybridization programmes.

Key Words : *Oryza sativa*, Genetic diversity, Cluster analysis, D^2 analysis

The rice (*Oryza sativa* L.) is a member of Gramineae family. There are two cultivated and twenty-one wild species of genus *Oryza*. *Oryza sativa*, the Asian cultivated rice is grown all over the world. The African cultivated rice, *Oryza glaberrima* is grown on a small scale in West Africa. Rice has supported a greater number of people

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for a longer period of time than any other crop since it was domesticated between 8,000 to 10,000 years ago (Greenland, 1997). Total estimated area under rice production in the world is 156 million hectares with a production of 650 million tonnes and the average yield is 3689 kg per hectare (FAOSTAT, 2008). The D^2 statistics is a tool which helps in the identification of genetically diverse parents for their exploitation in hybridization programmes as hybrids between lines of diverse origin display a greater heterosis than those between closely related strains. Murthy and Arunachalam (1966) stated that multivariate analysis with "Mahalanobis D^2 statistics" is a powerful tool to know the clustering pattern to establish the relationship between genetic and geographic divergence and to determine the role of different quantitative characters towards the maximum divergence. The knowledge about the source of genetic diversity for the different characters is of considerable importance, since the prime aim of the plant breeder is to improve the yield and the quality by evolving superior

varieties. The degree of divergence is useful for understanding the course of evolution and for classifying population into different groups on the basis of diversity, particularly, when they are overlapping for one or more characters.

MATERIAL AND METHODS

The experimental material comprising 40 genotypes were raised in Randomized Block Design in three replications during *Kharif* 2012, at Post Graduate Research Farm, College of Agriculture, Kolhapur. Each entry was represented by a double row of 3 m length with a spacing of 20 cm between rows and 15 cm between plants within a row. Four grains were dibbled per hill to ensure better crop stand and a single seedling was kept per hill after thinning. Observations on following 12 quantitative

characters were recorded on five randomly selected plants from each plot in each replication. These plants were tagged before flowering. The data were recorded on days to 50 per cent flowering, days to maturity, plant height (cm), productive tillers per plant, panicles per running meter, panicle length (cm), spikelets per panicle, spikelet fertility (%), 1000 grain weight (g), grain yield per plant (g), straw yield per plant (g) and harvest index (%).The analysis for divergence was done by following Mahalanobis (1936) D^2 statistic. Tocher´s method as described by Rao (1952) was followed for cluster formation.

RESULTS AND DISCUSSION

The analysis of variance revealed the presence of significant variability among rice genotypes. On the basis of

Table 1: Distribution of 40 rice genotypes in different clusters on the basis of D^2 statistic

Clusters	Number of genotypes	Name of the genotypes
I	24	RDN-1, RDN-2, RDN-4, RDN-7, RDN-8, RDN-9, RDN-13, RDN-15, RDN-16, RDN-17, RDN-19, RDN-21, RDN-22, RDN-24, RDN-26, RDN-27, RDN-28, RDN-29, RDN-30, RDN-33, RDN-34, RDN-35, RDN-36, RDN-39.
II	10	RDN-5, RDN-6, RDN-10, RDN-12, RDN-18, RDN-23, RDN-25, RDN-31, RDN-32, Bhogavati.
III	1	RDN-3.
IV	1	RDN-38.
V	1	RDN-14.
VI	1	RDN-20.
VII	1	Phule Radha
VIII	1	RDN-11

Table 2 : Average intra and inter cluster distances (D^2) and D values for 40 genotypes of rice

Cluster	I	II	III	IV	V	VI	VII	VIII
I	43.824 (6.62)	70.392(8.39)	62.568(7.91)	99.201(9.96)	95.062(9.75)	168.740(12.99)	205.348(14.33)	189.062(13.75)
II		63.361(7.96)	129.504(11.38)	166.668(12.91)	132.710(11.52)	101.404(10.07)	225.000(15.00)	211.411(14.54)
III			0.000	26.316(5.13)	149.572(12.23)	266.016(16.31)	303.456(17.42)	204.204(14.29)
IV				0.000	186.322(13.65)	306.250(17.50)	304.153(17.44)	275.892(16.61)
V					0.000	297.907(17.26)	66.748(8.17)	130.644(11.43)
VI						0.000	404.814(20.12)	333.427(18.26)
VII							0.000	344.473(18.56)
VIII								0.000

Table 3 : Cluster means for 12 characters in rice

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Productive tillers / plant	Panicles / running meter	Panicle length (cm)	Spikelets / panicle	Spikelet fertility (%)	1000 grain weight (g)	Grain yield / plant (g)	Straw yield / plant (g)	Harvest index (%)
I	117.50	148.61	102.34	5.98	11.18	20.77	131.59	75.00	16.72	8.80	21.08	28.75
II	107.53	139.70	94.38	6.61	11.89	20.44	115.05	79.59	20.23	11.54	20.98	34.54
III	128.67	158.33	109.87	5.00	10.72	20.92	115.00	52.67	15.33	5.36	25.36	16.86
IV	128.67	158.67	89.33	6.23	15.66	18.12	105.87	47.66	13.60	3.35	36.25	8.36
V	109.33	140.33	102.47	6.37	12.50	21.79	204.80	60.35	14.53	10.92	24.87	30.31
VI	89.67	124.67	99.53	8.23	14.89	18.93	60.67	91.29	22.80	13.84	21.72	38.49
VII	100.33	130.33	62.87	6.33	12.11	18.80	208.27	55.32	9.60	5.44	9.99	33.34
VIII	109.67	138.67	145.33	7.40	12.00	26.19	187.87	57.39	23.27	24.59	54.84	30.07
Mean	114.04	145.36	100.23	6.22	11.65	20.68	129.77	74.01	17.56	9.75	22.21	29.81
S.E.±	1.26	1.28	2.04	0.46	0.86	0.73	3.56	2.22	0.58	0.83	1.72	2.17
% contribution	22.56	8.33	13.85	0.64	0.26	0.51	22.92	7.82	12.69	5.64	4.64	0.13

Mahalanobis D² statistics and Tocher method, the 40 rice genotypes were grouped into 8 clusters. Cluster I comprised 24 accessions, cluster II had 10 genotypes and remaining clusters were mono-genotypic (Table 1). The clustering pattern of the accessions showed that geographical diversity was not related with genetic diversity. Sharma (2000), Mundhe *et al.* (2006) and Rajesh *et al.* (2010) also reported that there is no association between genetic diversity and geographical diversity.

Intra cluster distance was highest in cluster II (63.361) and followed by cluster I (43.824). The intra cluster distance was not observed in cluster III, IV, V, VI, VII and VIII as these clusters had only one genotype each (Table 2). The high intra cluster distance values revealed the presence of genetic diversity between the genotypes which were grouped together in those clusters. Hence, there is a lot of scope for exchange of genes among genotypes within these clusters. With regard to inter cluster distance, the cluster VI and cluster VII were most diverse as distance between them was 404.81. It can be inferred that crossing between these genotypes may result in good recombinants for successful breeding programme. As indicated by inter cluster D² values the cluster III and cluster IV were closest (26.316) which revealed that those genotypes were not very distant but could not be grouped together. Several authors have suggested that the crossing between the genotypes of clusters with high inter cluster would yield good segregates for selection.

The cluster means (Table 3) for 12 characters are presented with their per cent contribution towards the total genetic divergence. The results revealed that spikelet's per panicle contributed maximum (22.92%) as a first ranker towards the total divergence with its average ranging from 60.67 for cluster VI to 208.27 for cluster VII. The next major contribution towards total divergence came from days to 50 per cent flowering (22.56%), plant height (13.85%) and 1000 grain weight (12.69%). Days to 50 per cent flowering ranged from ranged from 89.67 (cluster VI) to 128.67 (clusters III and IV), plant height ranged from 62.87 cm (cluster VI) to 145.33 cm (cluster VII) and 1000 grain weight ranged from 9.60 g (cluster VII) to 23.27 g (cluster VIII). On the other hand, rest of the traits had lower contribution towards the total genetic divergence. A considerable genetic diversity of 68.96 per cent was observed due to these four characters. Hence, selection for divergent parents based on these four characters would be useful for heterosis breeding in soybean.

The best combination of parents for improvement in various characters can be recommended on the basis of *per se* performance of the genotypes and inter cluster divergence. Based on mean performance of 12 characters, Cluster VIII exhibited higher grain yield per plant (24.59 g). It contained one genotype, *viz.,* RDN-11 having medium maturity, higher plant height, highest panicle length and 1000 grain weight. Cluster IV was found to be the least yielder. It comprised of

single genotype, *viz.,* RDN-38 having late maturing, medium plant height, high straw yield per plant and low harvest index. Low yield of RDN-38 can be attributed to lesser panicle length (18.12 cm), lower spikelets per panicle (105.87), less spikelet fertility (47.66 %) and low harvest index (8.36%). Per cent contribution of characters towards divergence was analysed and it was found that spikelets per panicle contributed highest (22.92%) for divergence, followed by days to 50 per cent flowering (22.56%) (Table 3). Hence, these characters should be given importance during hybridization and selection in the segregating population. Similar results were reported by Chauhan and Chauhan (1994) and Roy *et al.* (2002) for days to 50 per cent flowering, Singh *et al.* (2006) for productive tillers per plant and panicle length, Banumathy *et al.* (2010) for plant height and spikelet fertility, Dushyantha and Anand (2010) for straw yield per plant, Rajesh *et al*. (2010) for 1000 grain weight, Vennila *et al*. (2011) for grain yield per plant and Chanbeni *et al.* (2012) for panicle length, spikelets per panicles and harvest index. Thus, some discrepancies in the characters contributing to divergence were observed in the present investigation and results of previous workers. Such discrepancies in the results might be due to the different sets of material and also due to the role of environmental variability as suggested by Bhaskar *et al.* (2007) and Karthikeyan and Anubuselvam (2008).

Thus, D² analysis proved to be a very useful technique in isolating diverse groups from the germplasm under study. On the basis of inter cluster distances, cluster means, *per se* performance observed in the present study the five genotypes *viz.,* RDN-20, RDN-11, Phule Radha, RDN-18 and RDN-5 were found to be superior and can be used as potential parents for improvement of rice.

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