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GENETIC DIVERGENCE IN RICE (*Oryza sativa* L.)

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Abstract: *Nature and magnitude of genetic divergence was assessed among 54 genotypes of rice using Mahalnobis D²statistic for 12 quantitative characters on the pooled basis over E4, E5 and E6, the genotypes were grouped into eight clusters. The cluster III was the largest, involving 32 genotypes. The cluster II included 13 genotypes whereas cluster I included 4 genotypes. The remaining fiver clusters (IV, V, VI, VII and VIII) were solitary and included only one genotype. The average intra cluster variation was ranged from 0.00 to 1.05. The highest intra – cluster distance was in cluster III (D=1.05) followed by II (D=0.71). The intra cluster distance of solitary clusters was zero. The average inter-cluster distance was maximum between cluster IV and VI (D=4.01) followed by IV and VIII (D=3.62), while it was at a minimum between clusters V and VI (D=0.84). The intra- cluster means of various characters revealed that cluster VII ranked first in the performance of grain yield per plant (22.4), productive tillers per plant (12.2). The genotype No 38 was the only the member of this cluster. Further the cluster VIII was ranked first for early maturity (123 days) and the genotype No 53 was included in this cluster. The per cent contribution of different characters towards genetic divergence ranged from 0.56 to 37.88 per cent.*

Key words*: Rice genotypes, genetic divergence, cluster analysis.*

Introduction:

Rice, *Oryza sativa* (L.) is the most important cereal crop cultivated widely in many parts of the world. More than 90% world rice is grown and consumed in Asia (Tyagi *et al.*,2004). Total area under rice in India is 45.05 million hectares with annual production of 103.27 million tons, though production is large, the per hectare yield is very poor *i.e.* 2.29 tons per ha. The basic objective of crop improvement programmes is to realize marked characters in the germplasm collections of the plant species. Germplasm is important source for current and future crop improvement. A wide range of genetic variability is observed in rice germplasm for various quantitative and qualitative traits. Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for breeding programme. Therefore in the present study, 54 rice genotypes were evaluated to assess the genetic diversity among these genotypes.

Materials and Methods

The experimental material consisted of 54 genotypes from germplasm maintained at Regional Agriculture Research Station, Karjat. The experiment was conducted in randomized block design with three replications during *Rabi* 2013-14 at Regional Agriculture Research Station, Karjat(E4), Agriculture College, Dapoli(E5) and Agriculture Research Station Shirgaon(E6).The plot size was 3 rows of 1.5 m length with row to row spacing 20 cm and between plants in row 15 cm. Thirty days old one seedling per hill was transplanted in the field. Fertilizer dose of 100 kg N + 50 Kg P_2O_5 + 50 kg K_2Oper hectare and other cultural practices were carried out as per the recommendations to grow healthy rice crop. The data on the character days to initiation of flowering, days to 50 per cent flowering and days to maturity was recorded on the plot basis and on randomly selected five effective plants for the characters *viz.*, plant height (cm), total tillers per plant, productive tillers per plant, panicle length (cm), grains per panicle, spikelet fertility (%), 1000 grain weight (g), straw yield per plant (g) and grain yield per plant (g).

The mean performance of individual genotype over three environments was pooled and used for statistical analysis.The data were subjected to Mahalonobis (1936) D^2 analysis and the genotypes were grouped by Tochers methods as suggested by Rao (1952).

Result and Discussion

In the present investigation, a wide range of variation was observed for almost all characters. The analysis of variance showed that the differences among the genotypes were highly significant for all twelve characters under study.

The 54 genotypes were grouped into eight clusters. The cluster III was the largest, involving 32 genotypes. The cluster II included 13 genotypes whereas cluster I included 4 genotypes. The remaining five clusters (IV, V, VI, VII and VIII) were solitary and included only one genotype (Table1). The clustering pattern of genotypes revealed that the genotypes of native to different countries were clubbed together or genotypes of a states or region were distributed in different clusters. As observed from the clusters, the genotypes included in different clusters are originated from different regions indicating that there was no association between eco-geographical distributions of genotypes and clustering pattern. Similar findings were reported by Shiva Datta and Mani (2003), Nayak *et al.* (2004), Singh *et al.* (2006) and Subudhi *et al.* (2008).

Table 1: Composition of D^2 clusters in environment on pooled basis (*Rabi*) over E4, E5 and E6.

Cluster No.	No. of genotypes included	Genotypes
I	04	No 04, No 34, No 33, No 08
II	13	No 21, No 22, No 23, No 46, No 36, No 11, No 12, No 01, No 03, No 13, No 42, No 15, No 05
III	32	No 19, No 31, No 14, No 16, No17, No 54, No 20, No 35, No 09, No 52, No 47, No 07, No 40, No 43, No 30, No 51, No 50, No 48, No 10, No 25, No 26, No 29, No 37, No 49, No 27,No 28, No 45, No 41, No 32, No 39, No 18, No 06
IV	01	No 24
V	01	No 02
VI	01	No 44
VII	01	No 38
VIII	01	No 53

On the pooled basis *(Rabi)* over E4, E5 and E6 season, the total population could be divided into eight clusters. The cluster I had minimum (0.35) intra cluster distance and thus was found to be the most compact cluster. This indicated that genotypes of this cluster resemble with one another genetically. The cluster III was found to be least compact cluster as it had maximum (1.05) intra cluster distance. The inter cluster distance was maximum between clusters IV and VI (4.01). This revealed that genotypes of cluster IV were genetically most diverse from those of the cluster VI. Hybridization between parental lines selected from these clusters is likely to produce most variable progeny. The inter cluster distance recorded minimum between clusters V and VI (0.84), which showed that genotypes of these clusters were somewhat similar in genetic constitution and hybridization between these clusters may not result in sufficient variability. Similar findings were also reported by Hegade and Patil (2000), Shiva Datta and Mani (2003), Deepak *et al.* (2006) and Singh *et al.* (2006).

Table 4h.: Intra and inter cluster distance D^2 (above the diagonal) and D value (below the diagonal) on pooled basis (*Rabi*) over E4, E5 and E6

Clusters	I	II	III	IV	V	VI	VII	VIII	Intra cluster
I		0.92	1.21	3.20	1.48	1.48	3.24	3.53	**0.12**
II	0.96		1.72	2.19	2.46	3.53	1.46	6.40	**0.50**
III	1.1	1.31		3.80	3.61	5.06	3.92	5.48	**1.10**

IV	1.79	1.48	1.95		9.67	16.08	7.73	13.10	**0.00**
V	1.22	1.57	1.90	3.11		0.71	1.23	7.67	**0.00**
VI	1.22	1.88	2.25	4.01	0.84		4.28	11.42	**0.00**
VII	1.80	1.21	1.98	2.78	1.11	2.07		9.73	**0.00**
VIII	1.88	2.53	2.34	3.62	2.77	3.38	3.12		**0.00**
Intra cluster	**0.35**	**0.71**	**1.05**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	

The intra cluster means (Table 3), noticed that cluster VII exhibited highest grain yield per plant (22.4 g), productive tillers per plant (12.2). The genotype No 38 was the only member of this cluster. Further the cluster VIII was ranked first for early maturity (123 days). The genotype No 53 was included in this cluster.

Table 3: Intra cluster means for different characters of rice on pooled basis (*Rabi*) over E4, E5 and E6

Clusters	Days to initiation of flowering	Days to 50 % flowering	Days to maturity	Plant height (cm)	Total tillers/ plant	Productive tillers/ plant	Panicle length (cm)	Grains/ panicle	Spikelet fertility %	1000 grain weight (g)	Straw yield/ plant (g)	Grain yield plant (g)
I	106	109	137	75	11.3	9.6	21.8	124	82.9	23.8	19.4	17.3
II	110	114	142	73	12.2	10.0	21.8	100	80.1	25.6	18.4	17.2
III	104	107	136	75	11.9	9.7	22.1	105	84.4	24.3	16.9	17.2
IV	106	109	137	66	12.2	9.2	20.2	67	91.3	28.0	19.0	19.7
V	108	111	140	68	11.3	9.3	20.6	146	76.8	24.0	14.8	18.8
VI	119	122	151	78	14.4	12.0	22.8	170	82.0	24.2	18.4	16.7
VII	112	116	143	70	14.1	12.2	22.4	112	72.2	24.2	19.0	22.4
VIII	88	92	123	82	12.3	9.8	24.4	110	78.5	27.3	20.0	18.4

The contribution of various characters towards the expression of genetic divergence was ranged from 0.56 to 37.88 per cent (Table4). The days to initiation of flowering had maximum (37.88 %) contribution towards total diversity, followed by grains per panicle (13.77 %), spikelet fertility (12.37 %), straw yield per plant (11.04 %) and grain yield per plant (7.41 %), panicle length (5.59 %) and plant height (4.96 %) and minimum by productive tillers per plant (0.21 %). Similarly, Shiva Datta and Mani (2003) also reported that the greatest contributors to genetic diversity in rice crops were the 50 per cent flowering and plant height. Singh *et al.* (2006) also reported the plant height was the major contributors of the total divergence and productive tillers had the minimum contribution.

Table 4: Contribution of character towards genetic divergence over pooled environments

Sr. No.	Characters	Contribution (%)
1	Day to initiation of flowering	37.88
2	Days to 50 % flowering	0.56
3	Days to maturity	0.56
4	Plant height (cm)	4.96
5	Total tillers/plant	3.84
6	Productive tillers/plant	0.21
7	Panicle length (cm)	5.59
8	Grains/panicle	13.77
9	Spikelet fertility (%)	12.37
10	1000 grain weight (g)	1.82
11	Straw yield/plant (g)	11.04
12	Grain yield/plant (g)	7.41

References

Deepak, Naik, Abhinav Sao., A.K. Sarawgi, and Pushpendra Singh, (2006). Genetic divergence studies in some indigenous scented rice (*Oryza sativa* L.) accessions of central India. *AsianJ. of Pl. Sci.*, **5**: 197-200.

Hegde, S.G. and Patil, C.S. (2000).Genetic divergence in rainfed rice.*Karnataka J. Agril. Sci.*, **13**(3): 549-553.

Mahalanobis, .P.C. (1936).On the generalized distance in statistics.*Proc. Nat. Inst. Sci.* (India), **2**: 49-55.

Nayak, A.R., Chaudhury, D. and Reddy, J.N. (2004). Genetic divergence in scented rice.*Oryza*.,**41**(3 & 4): 79-82.

Rao, C.R. (1952). *Advanced Statistical Methods In Biometric Research*. John Wiley and Sons, Inc., New York.

Tyagi, A.K., Khuran,J.P., Raghubanshi,S., Gour,A and Sharma,S.A. (2004). Structural and functional analysis of rice genome.*J.Genet.*83(1):79-99

Shiv Datta and Mani, S.C. (2003). Genetic divergence in elite genotypes of basmati rice (*Oryza sativa* L.). *Indian J. Genet.***63**(1): 73-74.

Shobha Rani G., Radhika K., Ravindra Babu, V., Padma V. and Usharani G. (2012). Genetic diversity studies in popular rice (*Oryza sativa* L.) varieties of India. *Madras Agric. J.***99** (7-9):468-470.

Singh, R., Mehla, B.S., Kumar, Y. and Sangwan, O. (2006).Genetic divergence in rice under normal and late sown condition.*National J. of Pl. Improv.***8**(2): 166-168.

Subudhi, H.N., Prasad, D., Bose, L.K. and Swain, D. (2008). Genetic diversity studies in promising lowland rice varieties. *Oryza*.,**45**(4):273-276.