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GENETIC DIVERGENCE IN RICE

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Thirty-eight genotypes of rice were grouped into five clusters following non-hierarchical Euclidean cluster analysis utilizing data on a set of eleven characters related to yield and its contributing characters. The genetic diversity observed was not related to geographic diversity. Grain yield/plant, total spikelets and seeds per panicle and panicle grain weight were mainly responsible for the genetic divergence. Based on statistical distance and cluster mean values, five genotypes, namely Pusa Basmati-1, Bengawan (from cluster II), J-56, IR- 56762-B and Cemposelak (from cluster V) were found to be most promising and hence, these genotypes may be used in future hybridization programmes to evolve desirable segregants.

Key words : Rice, germplasm, divergence, cluster analysis

Genetic diversity is an essential requirement for any crop improvement programme, because genetically diverse parents when crossed, can bring together diversity of gene combinations either to exploit heterosis or to obtain superior recombinants. The genetic diversity or genetic divergence between populations can be quantified by using several available statistical methods, of which multivariate analysis has been found to be most appropriate (Murty, 1965; Joshi and Dhawan, 1966; Maurya and Singh, 1977). Non-hierarchical Euclidean cluster analysis (Beale, 1969) has great utility in choosing parents for generating good segregates as it permits precise comparison among all possible pairs of genotypes in any given group before effecting actual crosses. In this investigation, the magnitude of genetic diversity was evaluated among 38 rice genotypes that include types from all the three races (indica, japonica and javanica) of *Oryza sativa* L.

MATERIALS AND METHODS

The experimental material consisted of 38 rice genotypes (mostly cultivars and few breeding lines) developed at different national (CRRI, Cuttack; GBPUA & T, Pantnagar; IARI, New Delhi) and international (IRRI, Philippines) research centres. These materials include few japonica (J-34, J-56 and J-85) and javanica (Bengawan and Cemposelak) genotypes alongwith indica types. All the 38 genotypes were grown in a randomized block design with two replications at the Department of Agricultural Botany Research Farm, Ch. Charan Singh University, Meerut during Kharif 1996. Thirty days old seedlings were transplanted to a well prepared field at the rate of one seedling per hill with a spacing of 20 cm × 15 cm. Fertilizer at the rate of 120 Kg N : 60 KgP_2O_5 : 60 Kg K_2O/ha was applied. Each genotype was evaluated in a plot of 4 rows. The row length was 10 m. Data were recorded on five random plants per genotype per replication for 11 quantitative characters. The data were subjected to non- hierarchical Euclidean cluster analysis to measure genetic divergence following Beale (1969) and Spark (1973).

RESULTS AND DISCUSSION

The analysis of variance showed highly significant differences between genotypes for each of the eleven metric characters studied. All the 38 genotypes were grouped into five clusters (Table 1). Maximum number of genotypes were included in cluster III (13 genotypes) whereas cluster II contained only two genotypes. Cluster III included genotypes from almost all sources. Similarly, the three genotypes that were grouped under cluster V belong to the three different races i.e. indica (IR- 56762-B), japonica (J-56) and javanica (Cemposelak). This suggests that there is no association between clustering pattern and eco-geographical distribution of the genotypes. Earlier, Roy and Panwar (1993) also arrived at a similar conclusion while studying the divergence in rice.

Table 1. Distribution of 38 rice genotypes in different clusters

Cluster No.	No. of genotypes	Names of genotypes
I	9	CR-564-35, Kalyani-2, Kalinga-3, Basmati-370, Pusa Basmati, Ratna, Haryana Basmati, T-3, Sita
II	2	Pusa Basmati-1, Bengawan
III	13	J-34, J-85,Saket-4, Pant Dhan-10, Pusa 2-21, Pusa-33, Pusa-169, Pusa-834, IR-8, IR-36, $T(N)_1$, Pant Dhan-6, Raasi
IV	11	CR-564-12, Annada, Govind, Pant Dhan-4, IR-24, Jaya, Pant Dhan- 12, PRH-1, ND-80, Sarju-52, Manhar
V	3	J-56, IR-56762-B, Cemposelak

All the genotypes included in the present study were of Asiatic origin and belong to India, Philippines, Japan and China. *Oryza sativa,* the Asian cultivated rice (with Asian origin), has been domesticated in many Asian countries for centuries because of which it is likely that the genotypes of different countries have some common genes. Therefore, genotypes from Japan, Indonesia and Philippines fall in one cluster (cluster V). There has also been considerable exchange of material from one place to another and hence, geographical classification may not offer a clear system of clustering (Van der Masson, 1972). Morphological grouping is helpful for broad classification. However, it may not be possible to differentiate between genotypes with poor and better performance belonging to a particular morphological group.

The genetic affinity or similarity between genotypes in the present study is due to the application of directional selection pressure for realising high yield. Further, the genetic drift and selection in different environments have caused greater genetic diversity than geographical distance, as suggested by Murty and Arunachalam (1966) and Singh *et al.* (1979).

The intra and inter cluster distances among five clusters were variable (Table 2). The intra cluster genetic distance value ranged from 2.123 (cluster III) to 2.411 (cluster I). The maximum inter cluster distance was observed between cluster I and II (6.594) followed by cluster II and III (6.045) while minimum inter cluster distance D^2 (2.575) was between cluster I and III, suggesting relatively close relationship between these two clusters. Mean values for different characters in various clusters (Table 3) provide an interesting picture of the nature of diversity. Considerable differences in cluster mean values are evident for all the characters. Genotypes of cluster II showing maximum inter cluster distances with cluster I and III exhibited higher mean performance for most of the characters studied. Infact, cluster II had the highest mean values for total spikelets/panicle, seeds/panicle, secondary branches/panicle, panicle grain weight, grain yield per plant and also higher mean values for plant height, primary branches/panicle and productive tillers. Cluster V was also more divergent and it showed maximum inter cluster distance with cluster II (Table 2).

Table 2. Estimates of average intra- and inter-cluster D^2 for five clusters constructed from 38 genotypes in rice

Clusters	I	II	III	IV	V
I	**2.411**[a]	6.594	2.515	3.741	4.193
II		**2.371**	6.045	4.299	5.136
III			**2.123**	3.212	4.570
IV				**2.323**	3.663
V					**2.240**

[a] Figures in bold print indicate intra-cluster D^2 values.

Crosses among genetically diverse genotypes are likely to yield desirable recombinants. Therefore, a crossing programme should be initiated between the genotypes belonging to divergent clusters. Following is worthwhile to consider while selecting genotypes: (a) choice of clusters which are separated by maximum inter-cluster distance and (b) selection of particular genotypes that showed highest mean performance for various characters in the selected clusters. The greater the distance between two clusters, the wider the genetic diversity between their genotypes. However, while considering genetic diversity among the parents to be included in hybridization programme parents combining high yielding potential with wide genetic diversity are likely to yield superior segregates within a short period. Based on these facts, genotypes Pusa Basmati-1 and Bengawan from cluster II and J-56, IR-56762-B, Cemposelak from cluster V are expected to give promising segregants.

Table 3. Mean values of different characters in various clusters

	Characters	clusters				
		I	II	III	IV	V
1	Plant height (cm)	123.63	133.81	97.13	100.87	143.63
2	Panicle length (cm)	26.41	35.09	25.33	26.04	31.06
3	Productive tillers	12.33	13.80	16.26	11.99	10.87
4	Flag leaf area (cm)^2	29.74	30.23	32.89	36.19	48.17
5	No. of primary branches/panicle	10.68	12.90	10.97	11.73	12.67
6	No. of Secondary branches/panicle	26.71	36.35	28.12	34.81	28.67
7	Total spikelets/ panicle	139.86	215.05	143.78	182.16	155.87
8	Seeds/panicle	125.26	175.65	129.06	158.82	145.57
9	Seed set(%)	89.75	79.02	88.07	87.06	93.38
10	Panicle grain weight (g)	2.84	4.46	3.09	3.85	4.03
11	Grain yield/ plant (g)	34.45	62.72	50.03	45.78	45.24

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