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GENETIC DIVERGENCE IN INDIGENOUS UPLAND RICE VARIETIES

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ABSTRACT

Genetic divergence, using Mahalanobis D^2 statistic, was worked out in 30 traditional upland rice varieties from nine states of India including the Northeastern Region. Based on 10 agromorphological characters, these varieties were grouped into six clusters. Cluster I was the largest with 66.6% genotypes from different states except Punjab. Clusters IV, V and VI were monogenotypic. Varieties from the Northeastern Region exhibited the maximum diversity, and were represented in all the clusters except cluster V. However, no parallelism was observed between geographic diversity and genetic diversity. Characters like No. of secondary branches/panicle, yield/plant, and No. of fertile grains/panicle had sizeable contribution to total divergence. These characters could, therefore, form the basis for selection of parents from distantly placed clusters to obtain high heterotic combinations.

Key words: Upland rice, genetic diversity.

Upland rice is grown under diverse agroclimatic conditions. Most of the Indian farmers usually grow local varieties in these regions. These rice varieties have good adaptation but are poor yielders. Success of varietal improvement programme for such land situations depends on the knowledge of available diversity in upland traditional varieties for their utilization in a crossing programme. The importance of genetic diversity in selection of parents for hybridization has long been recognised by several workers [1-4]. The present investigation has been carried out to ascertain the nature and magnitude of genetic diversity present in the traditional upland varieties.

MATERIALS AND METHODS

Thirty popular geographically diverse upland varieties of rice from nine states of India, including the Northeastern Region were taken for the present study. These varieties were grown in red lateritic soil during kharif (July-December) 1987 at the Experimental Farm of the Central Rainfed Upland Rice Research Station, Hazaribag (Bihar), in randomized block design with three replications, at the spacing of 15 x 10 cm, keeping row length 4 m in a three-row plot. The recommended agronomical practices and plant protection measures were followed to ensure a normal crop. Observations were recorded on five random plants in each replication from the central row on days to 50% flowering, plant height, panicles/plant, panicle length, primary and secondary branches/panicle, fertile and sterile grains/panicle, 1000-grain weight, and yield/plant. Multivariate analysis of Mahalanobis [5] was conducted as per the procedure given by Rao [6]. Grouping of varieties was done following Tocher's method [7].

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences for all the characters. On the basis of degree of divergence, thirty varieties could be grouped into six clusters (Table 1). Cluster I comprised the maximum number of genotypes (19), representing Bihar, West Bengal, Orissa, Uttar Pradesh, Madhya Pradesh, Maharashtra, Gujarat and states of North eastern region. Cluster II included six genotypes from five states. Cluster III was represented by two genotypes from the Northeastern states. Clusters IV, V and VI were monogenotypic.

Table 1. Distribution of 30 upland rice varieties into various clusters

Cluster	Number of genotypes	Varieties/strains	Area of cultivation
Cluster I	19	N-22, Chipti and Bagari Black	Uttar Pradesh
		Brown gora (HRC 14), Brown gora (HRC 116) Black gora (HRC 118), Black gora (HRC 360) White gora (HRC 318), Charaka gora, Karhani and White gora (HRC 309)	Bihar
		Kalakari and Bhattadhan	Orissa
		Dumai and ARC 7098	Northeastern Region
		Dehule	Madhya Pradesh
		Dular	West Bengal
		Sathi 34-36	Gujarat
		Nagpur 14	Maharashtra
Cluster II	6	Lalnakanda-41	Punjab
		Delhi Sathi	Uttar Pradesh
		ARC 10372	Northeastern Region
		Nagpur 22	Maharashtra
		Panke	West Bengal
		Parimal 2-4-6	
Cluster III	2	ARC 7046 and ARC 7102	Northeastern Region
Cluster IV	1	ARC 7059	-Do-
Cluster V	1	Laloo 14	Madhya Pradesh
Cluster VI	1	ARC 11775	Northeastern Region

Clusters IV and VI include varieties only from the Northeastern states, while cluster V included varieties only from M.P. The distribution pattern of genotypes into different clusters revealed that upland varieties of Bihar and Orissa had the minimum diversity. This is probably due to the fact these varieties were of short duration, drought escaping type, and grown under similar edaphic and climatic conditions. The varieties from the Northeastern Region showed maximum diversity, as they were represented in all the clusters except cluster V. This may be due to the distinct agroclimatic conditions under which these varieties are grown with very little gene flow. Thus, varieties originating from states like West Bengal, Bihar, Orissa, U.P., M.P., Gujarat, Maharashtra and the Northeastern Region have been included in the same cluster while the varieties from a single region are distributed over different clusters. This indicates that there is no correspondence between genetic diversity and geographical diversity. Similar findings have been reported in rice by other workers as well [8,9].

It was found that the No. of secondary branches/panicle had the maximum (46.2%) and plant height and panicles/plant had the minimum contribution (0.69%) to the total divergence. Yield/plant was the second most important character, which contributed 14.7% to the total divergence. Sterile grains/panicle and 1000-grain weight had moderate and equal contribution of 9.7%. Days to 50% flowering, primary branches/panicle, panicle length and fertile grains/panicle contributed 1.8%, 3.7%, 4.4% and 8.3%, respectively. Thus, it appears that similar selection criteria seem to have been used for plant height, panicle number and duration in upland rice in different regions.

The intracluster distances varied from 0.0 (cluster IV, V and VI) to 9.83 (cluster I). The minimum intercluster distance (12.58) was observed between clusters I and IV, both of which taken together accounted for 66.6% genotypes of diverse origin. The maximum distance (25.08) was recorded between clusters I and VI, the former included the maximum number of genotypes and was characterized by heavy grains with fewer secondary branches

Table 2. Cluster means of ten characters in upland rice varieties

Character	Character means in different clusters					
	I	II	III	IV	V	VI
Days to 50% flowering	68.0	74.3	73.8	74.0	81.0	80.0
Plant height (cm)	93.5	89.9	110.4	97.4	109.3	125.0
Panicles/plant	2.7	2.5	2.3	2.8	2.6	2.4
Panicle length	16.7	16.3	19.2	14.8	20.2	22.3
Primary branches per panicle	6.4	5.7	7.4	7.4	8.8	7.2
Secondary branches per panicle	7.2	11.2	18.2	11.2	9.5	21.8
Fertile grains per panicle	46.0	50.0	94.2	67.8	52.5	81.7
Sterile grains per panicle	9.4	13.9	21.0	19.5	27.1	37.4
1000-grain weight (g)	25.6	20.5	23.5	21.4	22.0	22.0
Yield/plant (g)	3.5	2.8	5.1	3.7	3.0	4.2

and grains/panicle, while the latter included only one variety (ARC 11775) having long panicles with high number of secondary branches and fertile grains/panicle. Since the genotypes belonging to clusters I and VI are genetically most diverse, these may be used as parents in hybridization to obtain high heterotic combinations.

Cluster means (Table 2) showed large differences for various traits, particularly panicle length, secondary branches/panicle, fertile and sterile grains/panicle, and yield/plant. Cluster I exhibited a low mean for days to 50% flowering, secondary branches/panicle, fertile and sterile grains/panicle, while cluster II for plant height, primary branches/panicle, 1000-grain weight, and yield/plant. High mean for plant height, panicle length, secondary branches/panicle and fertile grains/panicle were recorded in cluster VI, and for yield/plant and fertile grains/panicle in cluster III. Cluster I had high mean for 1000- grain weight, which is one of the important yield characters in upland rice. Thus, characters like secondary branches/panicle, number of fertile grains and grain yield, which have contributed maximum to divergence, should form the basis of selection in the distantly placed clusters like I and VI.

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