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Genotypic Diversity in Rice (*Oryza sativa* L.) Based on Morphological Characters

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ABSTRACT

Genotypic diversity among forty five rice genotypes grown during warm wet season was worked out on the basis of ten morphological characters. Wilk's Lambda criterion (λ~0 and V= 2983.22 with 440 df) revealed highly significant differences among the genotypes for the pooled effect of all the characters. The genotypes were grouped into seven clusters. Cluster-I comprised the maximum number of 23 genotypes, cluster-II contained 5 genotypes, cluster-III consisted of 10 genotypes and cluster-IV with 4 genotypes. The remaining cluster-V, VI and VII were the solitary clusters. The average intra cluster distance ($\sqrt{D^2}$) varied from 0 to 11.92. The maximum inter-cluster distance was 41.44 found between cluster-II and cluster-III. The relative contribution of different plant characters to the total genetic divergence estimated by D^2 analysis indicated that test weight (37.98%) followed by days to 50% flowering (32.22%) and plant height (18.79%) and grain yield per plant (8.18%) were the important traits contributing maximum towards divergence in this rice population under study. Selection of parents from within and between clusters for initiating crossing program has been suggested.

Keywords Rice, Diversity, Multivariate analysis, Morphological traits.

INTRODUCTION

Rice (*Oryza sativa* L. 2n=2x=24) is one of the most important staple food throughout the world. In Asia and Africa it is consumed daily. That is why the slogan "rice is life" was given in international year of rice (2004). Nowadays population is increasing exponentially in developing country like China, India, Bangladesh, Pakistan. Rice is the major sources of energy in these countries. The excess use of ground water has come to an alarming state. The capricious behavior of climate leads to evolution of new pathotypes and insect-pest activities and changing physiological rhythm of the crop plants. These reduce the economic yields.

Use of few selective high yielding varieties has already reduced the genetic variability and continuous cultivation of these high yielding varieties already replaced many well established local varieties. Due

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to changing environment the importance of genetic diversity and local landraces is very important. Many desirable genes related to stress tolerance are mainly present in many land races and local varieties. Selection of parents is very critical for realizing success in cross-breeding program. Mahalanobis D^2 statistics is an important tool for study of genotypic divergence. Clustering of genotypes helps in selection of parents for initiating hybridization program. Keeping this in view, the present study was conducted to assess the genetic diversity of 45 rice genotypes using Mahalanobis D^2 statistics.

MATERIALS AND METHODS

The present investigation was carried out at the Agriculture Farm of Palli-Siksha Bhavana (Institute of Agriculture), Visva-Bharati, Sriniketan (23°19´N, 87°42´E, 58.9 m above msl), under sub-humid, subtropical, red and lateritic belt of West Bengal. Forty-five diverse genotypes collected from different rice growing zones comprising mostly aromatic and non aromatic landrace and some established varieties were the experimental materials. The genotypes were grown in a randomized complete block design (RCBD) with 3 replications during *kharif* (warm wet) season of 2020. Twenty seven days old seedlings were transplanted under puddled field condition, with fertilizer dose @ N: P: K = 60:30:30 kg ha^{-1}. Each plot consisted of five rows of five meter long with inter and intra row spacing of 20 cm and 15 cm, respectively. Standard cultural practices were followed for raising a healthy crop. Data were recorded on 10 quantitative characters from five plant randomly selected from the middle rows of each replication. Mahalanobis's D^2 statistic (Rao 1952) was used for estimation of genetic divergence among 45 genotypes for 10 traits and Grouping of genotypes into different clusters was done by using Tocher's method.

RESULTS AND DISCUSSION

The analysis of variance showed significant difference among genotypes for all the ten characters. Wilks Lambda criterion ($\lambda \sim 0$ and V= 2983.22 with 440 df) revealed highly significant differences among the genotypes for the pooled effect of all the characters. The D^2 value ranged from 11.87 (between Nilanjana and Rajendra Mashuri) to 3434.54 (between Annada and Sitabhog). Mahalanobis's D^2 statistic based on multiple characters for estimating diversity among genotpyes has been suggested by Anand and Murty (1968), Arunachalam (1981) and Anand and Rawat (1984). The amount of diversity between the cross-parents, within certain limits, increases the chances of getting a greater amount of heterosis in F_1 and wide array of recombinants in segregating generations (Anand and Murty 1968).

This work aims to group the 45 genotypes into different clusters according to the genetic divergence and such grouping would help to initiate crossing program by selecting parents from within and between clusters. Based on the relative magnitude of D^2 values, 45 genotypes are grouped into seven clusters (Table 1).Cluster-I comprised the maximum number of 23 genotypes, Cluster-III consisted of 10 genotypes, Cluster-IV had 4 genotypes. Remaining cluster-V, VI and VII were the solitary clusters.

Genotypes viz., Green Rice, Chinakamini, RH-1442, RH-15, Sitabhog, Danaguri and Kartikkhas having characters of tall *indica* short grain type were grouped in a same cluster, i.e., Cluster-III. Varieties like Falguni, MTU-1010, Lalat, Annada and Gotra

Table 1. Distribution of 45 genotypes into various clusters.

Cluster	Number of genotypes	Genotype
I	23	MTU-7029, Bango Bandho II, MTU-1075, Nilanjana, Rajendra Masuri, Protiksha, Shilkhi, Bahadur, Gotra Bidhan-1, Lalmarich, Super Shamali, Ranjeet, Kerela Sundari, Latisal, Baskamini, Kajoli, Khajurkata, Simulphool, Black Rice, Gangajali, Malsiraj, Gheush, Manipur Rice
II	5	Falguni, MTU-1010, Lalat, Annada, Gotra Bidhan-3
III	10	Kartikkhas, RH-1442, Danaguri, Tulaipanji, RH-15, Chinakamini, Joha, Kalonunia, Green Rice, Sitabhog
IV	4	Benajhuri, Santibhog, Biharisal, MBR
V	1	Dangapatnai
VI	1	Red Husk Rice
VII	1	Dudheshwar

Table 2. Average intra- and inter-cluster values of D^2 in the seven clusters. Figures within the parenthesis are D values.

Cluster	I	II	III	IV	V	VI	VII
I	141.98 (11.92)	889.28 (29.82)	469.81 (21.68)	231.73 (15.22)	323.03 (17.97)	335.91 (18.33)	676.01 (26.00)
II		114.52 (10.70)	1716.93 (41.44)	1459.57 (38.20)	941.43 (30.68)	749.48 (27.38)	1629.70 (40.37)
III			117.57 (10.84)	473.33 (21.76)	1085.90 (32.95)	371.33 (19.27)	405.43 (20.14)
IV				85.72 (9.26)	279.01 (16.70)	690.52 (26.28)	891.98 (29.87)
V					0.00	928.16 (30.47)	1422.58 (37.72)
VI						0.00	347.29 (18.64)
VII							0.00

Bidhan-3 are early maturing high yielding variety were grouped in Cluster-II. Similarly, genotypes like Kerela Sundari, Latisal, Baskamini, Kajoli, Khajurkata, Simulphool, Black Rice, Gangajali, Malsiraj, Gheush and Manipur Rice are all landraces which belonged to the cluster-I.

The distribution pattern of genotypes in different clusters stipulated that genetic divergence was not related to geographical differentiation. Many genotypes of close geographic proximity fell into the different clusters and vice-versa. Tendency to form such type of clustering ignoring the geographical boundaries showed the regional isolation was not the only factor conferring to diversity in the natural population (Rao *et al*. 1980) or unidirectional selection practiced by breeder to acclimatize the promising cultivars for different regions.

Clustering of genotypes from different eco-geographic locations into one cluster could be attributed to the possibility of free exchange of breeding materials. However unidirectional selection, practiced for a particular trait or a group of linked traits in several places may produce a similar phenotype, which can aggregate into one cluster irrespective of their geographic region (Singh and Gupta 1968). The formation of different clusters among the genotypes of the common geographic regions may be due to their parentage, developmental traits, past history of selection and different out crossing rates (Arnold *et al*. 1996).

This statistical distance represents the index of genetic diversity among the clusters. This study reveals (Table 2) that the average intra cluster distance ($\sqrt{D^2}$) varies from 0 to 11.92. The maximum inter-cluster distance was 41.44 found between cluster-II and cluster-III, followed by cluster-II and cluster-VII and (40.37), cluster-II and cluster-IV (38.20), cluster-V and cluster-VII (37.72) and so on. This indicates the considerable amount of divergence within and between the clusters. Genotypes selected from these clusters could be used in a hybridization program since hybridization between divergent parents is likely to produce wide variability and transgressive segregations with high heterotic effects (Rama 1992).

The cluster means (Table 3) varied for days to 50% flowering from 91.40 (Cluster-II) to 122.58 (Cluster-IV), plant height from 99.47 (Cluster-VII) to 161.79 (Cluster-IV), flag leaf area from 19.72 (Cluster-VII) to 59.64 (Cluster-IV), tiller number from 7.57 (Cluster-V) to 20.91 (Cluster-VII), panicle length from 23.70 (Cluster-VII) to 31.74 (Cluster-III), primary branches from 8.39 (Cluster-VII) to 12.62 (Cluster-V), filled grain per panicle from 51.83 (Cluster-VII) to 137.39 (Cluster-III), test weight from 10.58 (Cluster-VI) to 28.52 (Cluster-V), straw yield from 18.70 (Cluster-VI) to 58.29 (Cluster-IV), and grain yield per plant from 8.95 (Cluster-VII) to 28.24 (Cluster-IV).

Cluster-I is characterized by a moderate mean of

Table 3. Cluster means of ten quantitative characters of rice. DFF- days to 50% flowering, PH- plant height, FLA- flag leaf area, TN-tiller number per plant, PL- panicle length, PB- primary branches per panicle, FG- filled grain per panicle, TW-test weight, SY- straw yield per plant, GY/P- Grain yield per plant.

Cluster	DFF	PH	FLA	TN	PL	PB	FG	TW	SY	GY/P
I	115.94	132.05	51.10	10.05	28.95	11.85	131.95	19.22	38.67	22.86
II	91.40	108.90	39.07	9.07	26.50	9.69	86.22	19.41	37.22	19.21
III	118.03	157.79	39.90	11.42	31.74	11.53	137.39	10.75	40.86	17.91
IV	122.58	161.79	59.64	10.01	31.45	11.69	120.25	21.91	58.29	28.24
V	115.00	161.72	56.78	7.57	26.22	12.62	130.50	28.52	52.00	25.04
VI	108.00	112.73	42.23	10.43	24.20	8.80	98.78	10.58	18.70	12.23
VII	116.33	99.47	19.72	20.91	23.70	8.39	51.83	10.89	38.02	8.95
%Contribution	32.22	18.79	0.00	0.20	0.71	0.20	1.21	37.98	0.51	8.18

days to 50% flowering, plant height, flag leaf area, tiller number, filled grain and grain yield per plant. Plant height, test weight and grain yield is moderate in cluster-II with lowest days to 50% flowering. Cluster-III had maximum number of filled grain per panicle and panicle length. Cluster-IV represented maximum flag leaf area, straw yield and yield along with highest days to 50% flowering and plant height which could be taken into consideration during selection. The solitary cluster-V had highest primary branch and test weight along with high number of filled grain. The mono-genotypic cluster-VI was characterized by lowest test weight and straw yield, with second lowest days to 50% flowering. The solitary cluster-VII showed minimum cluster means for plant height, flag leaf area, panicle length, primary branch per panicle, filled grain per panicle and yield per plant but with maximum tiller number per plant.

The relative contribution of different plant characters to the total genetic divergence estimated by D^2 analysis indicated that test weight (37.98%) followed by days to 50% flowering (32.22%) and plant height (18.79%) and grain yield per plant (8.18%) were the important traits contributing maximum towards divergence in this rice population under study. Similar results were reported for test weight by Mohan 2015 and for days to 50% flowering by Banumathy *et al*. (2010), Chandramohan *et al*. (2016) and Rukmini Devi *et al*. (2020). Traits contributing maximum to genetic divergence help selection of genetically diverse parents for hybridization program. Other characters viz. filled grain, panicle length, straw yield, tiller number and primary branch per panicle contributed very little amount to genetic divergence.

Considering complementarity of traits among parents, genotypic divergence and cluster means, for intra cluster hybridization program in cluster I, crossing between Gotra Bidhan-1 × Kerala Sundori, Gotra Bidhan-1 × Ranjeet for high yield with early maturity; Super Shamali × Protiksha, Super Shamali × Shilkhi for increasing the test weight; Super Shamali × Khajurkata, Super Shamali × Ranjeet may improve yield by complementing themselves for filled grain and test weight. In cluster II, Gotra Bidhan-3 × Annada may produce dwarf stature with improved yield. For improvement in yield, in cluster III, Joha × Chinakamini and in cluster IV, Benajhuri × Biharisal may be attempted.

Inter-cluster hybridization program between Gotra Bidhan-3 × RH-15 (Cluster-II × Cluster-III) for high yield with early maturity; Ranjeet × Gotra Bidhan-3, Kajoli × Annada (Cluster-I × Cluster-II) for increasing yield with early maturity and short stature; RH-15 × MBR (Cluster-III × Cluster-IV) may improved in yield by complementing themselves for filled grain and test weight. Crossing between Bango Bandho II × Green rice (Cluster-I × Cluster-III) may increase yield by complementing themselves for high fertility %, filled grain per panicle and test weight; Joha×Benajhuri (Cluster-III × Cluster-IV) for increasing filled grain per panicle and test weight; Ranjeet × Dudheshwar (Cluster-I × Cluster-VII) and Benajhuri × Dudheshwar (Cluster-IV × Cluster-VII) for transferring high tillering and dwarf stature genes by MABC. These crosses may produce a considerable amount of heterosis in F_1 generation and to provide an array of recombinants in segregating generations, in which promising segregates may be recovered.

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