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Assessment of Genetic Diversity in Rice (*Oryza sativa* L.) Genotypes for Yield and Attributing Traits

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ABSTRACT: A set of 70 rice genotypes were assessed the genetic diversity using Mahalanobis D^2 statistics. The rice genotypes were grouped into eight clusters. Among these eight clusters, cluster V had maximum number of genotypes 17 followed by cluster VI with 15 genotypes, cluster VII with 12 genotypes, cluster III with 9 genotype, cluster VIII with 6 genotypes, cluster IV with 3 and the remaining clusters (I, II,) were in each cluster consisting of four genotypes. There were no distance (0) present between intra-clusters. The maximum inter-cluster distance was found between cluster IV and VIII followed by cluster II and IV. Cluster VIII showed the highest cluster mean for yield per plant (g), cluster I showed highest cluster mean for 1000-grain weight and cluster VII showed highest cluster mean for spikelet's per panicle. Hybridization between genotypes cluster IV and VIII followed by cluster II and IV could yield better segregants.

Keywords: Cluster, Genetic diversity, Rice, Hybridization.

INTRODUCTION

Rice (*Oryza sativa* L.) is by far the most important part of the diet for more than half of the worldwide people (Violita, 2019). The Asian continent supplies virtually 90% of the globe's rice. India is first in acreage 43.78 million hectare and second in terms of output 118.43million tonnes with an efficiency of 2705 kg/ ha. (Anonymous, 2018-19). The major rice farming jurisdictions are West Bengal, Utter Pradesh, Andhra Pradesh, Chhattisgarh, Telangana, Punjab, Tamil Nadu and Haryana. Because of the world's rising population and the need for expanded rice supply, hybrid cultivars should be researched (Tait and Barker 2011). In this aspect, determining suitable cultivars for use in hybrid production programmes is crucial, as the cultivars utilised as parents of hybrid varieties must also have high farmer acceptability and relatively high combining ability for grain yield per plant (Okada and Whitford 2019). Rice breeding strives to increase yield potential by strengthening general and specific yield components, yield stability, and grain quality that are all critical (Heinemann *et al.*, 2019). In fertilizing operations, assessing the extent of genetic variation in plant species is crucial for determining acceptable parents and achieving the most of hybrids (Luo *et al.*, 2019). The biological and behavioural discrepancies of significant economic and quantifiable attributes are generally used to assess genetic diversity across germplasm accessions (Ibraheem and El-Ghareeb 2019). Furthermore, assessing genetic diversity is critical for determining the source genes of specific features in accessible germplasm. The measurement of genetic diversity across and within groups or clusters is critical for the right selection of parents in the search for heterosis (Murty and Arunachalam, 1966). Genetic convergence analyses comparing cultivars or germplasm before any breeding programme would assist the geneticist to refocus emphasis on those combos that are far more expected to be extremely heterotic when several metric variables are accessible for a series of germplasm. Rice needs effective strategies for developing and releasing high-yielding qualitative varieties, which necessitates a strong grasp of its uniqueness and constitution, because variety is the major ingredient of breeding programmes and this crop has a huge genetic diversity and great adaptive range.

MATERIAL AND METHODS

The experimental material consisted of 70 rice genotypes representing diversity in adaptability and variability in characters. These materials were evaluated in randomized block design (RBD) with 3 replications at Research Farm of IAS, BHU, Varanasi, U.P. during *kharif* season to identify diversity among them. Each genotype was planted at rows spaced at 20 cm apart and plant to plant distance of 20 cm. All the recommended agronomic package of practices was followed for rising of healthy crop. Per replicates five plants were chosen at random for documenting observations on traits at varying stages of growth of the crop *viz.,* days to 50 per cent flowering, days to maturity, plant height, effective tillers per plant, panicle length, spikelets per panicle, grain weight per plant, 1000-grain weight, grain yield per plant and AUDPC. The data were analyzed according to Mahalanobis D^2 statistic (Mahalanobis, 1936); Rao (1952) proposed the framework for estimating genetic diversity in breeding program for the first time. Grouping of 70 genotypes of rice into eight different clusters were performed by Tocher's method (Rao, 1952). The intra and inter cluster distances were assessed following Singh and Chaudhary's (1985) methodology.

The sum of squares of differences in the values of the associated transformed variables was used to calculate the D^2 values between genotypes. The mean deviation, di = Y i1-Y i2, was determined for each pair of combinations, where Yi denotes the altered variables I = 1, 2, 3, 4, 5.......p), and the D^2 was calculated. Sum of the squares of those deviations, *i.e.*

$$D^2 = \sum(Y_i^1 - Y_i^2)^2$$

Where, p = Number of characters.

D^2 values were assessed for significance employing chi-square (2) at p degrees of freedom, where p is the number of characters analyzed.

RESULTS AND DISCUSSION

In the present investigation, 70 rice genotypes were grouped into 8 clusters by by using Tocher's method which indicates the presence of maximum divergence for further crop improvement programme (Table 1). Among these 8 clusters, cluster V had maximum number of genotypes 17 followed by cluster VI with 15 genotypes, cluster VII with 12 genotypes, cluster III with 9 genotypes, cluster VIII with 6 genotypes, cluster IV with 3 and the remaining clusters (I, II,) were in each cluster consisting of four genotypes. Similar finding were obtained by Kulsum *et al.* (2013); Khare *et al*. (2015); Kumar *et al.* (2015).

Table 1: Distribution of 70 rice genotypes into different clusters.

Cluster No.	Name of Genotypes	Number of Genotype
I	IC 256516, IC 256617IC 256629, IC 277248	4
II	IC 256528, IC 260937, IC 260961, IC 267428	4
III	IC 256521, IC 256523, IC 256530, IC 256616,IC 260891, IC 264136, IC 264148, IC 264725, IC 277291	9
IV	IC 256518, IC 260917, IC 277266	3
V	IC 256520, IC 256534, IC 256537, IC 256538, IC 256589, IC 256754, IC 260964, IC 267416, IC 274377, IC 275937,IC 277256, IC 277265,IC 277267,IC 277274, IC 277287, IC 277289, IC 277290	17
VI	IC 256535, IC 256621,IC 260924, IC 264143, IC 264149, IC 264151, IC 264229, IC 274397, IC 277193, IC 277252, IC 277253 , IC 277259, IC 277261,IC 277275, IC 277284	15
VII	IC 256527, IC 256613, IC 264141, IC 264691, IC 264727, IC 267444, IC 274408, IC 277234, IC 277237, IC 277261, IC 277277, IC 277281	12
VIII	IC 256514, IC 256515, IC 256525, IC 256807 , IC 273558, IC 277292	6

The intra and inter-cluster distance (Table 2) ranged from 0.00 (clusters I, II, III, IV, V, VI, VII, VIII) to 613.83 (clusters IV and VIII).There were no distance (0) present between intra-clusters. This indicates that genotypes present in these cluster had less variation among themselves. The maximum inter-cluster distance (613.83) was found between cluster IV and VIII followed by cluster II and IV (590.67), cluster I and IV (560.47) and III and IV (512.60) suggesting that the genotypes belonging to these clusters are diverse.

As a result of the hybridized between the genotypes of such clusters, the dispersing population may become more variegated. The smallest inter-cluster distance (52.40) was found between III and VII followed by clusters I and III (53.36), cluster II and VIII (82.42) and cluster I and II (88.32) indicating that the genotypes belonging them are less diverse and constitute similar genotypic makeup. Same results were obtained by Sadia *et al*. (2020).

Table 2: Average intra (bold) and inter-cluster D^2 values for eight clusters.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**0.00**	88.32	53.36	560.47	283.24	187.13	96.21	58.84
II		**0.00**	111.04	590.67	319.09	230.27	150.81	82.42
III			**0.00**	512.60	235.64	139.72	52.40	101.50
IV				**0.00**	277.28	373.82	466.33	613.83
V					**0.00**	96.73	189.39	336.82
VI						**0.00**	93.90	240.87
VII							**0.00**	150.10
VIII								**0.00**

Based on mean performance of different quantitative characters (Table 3) for various clusters revealed that genotypes present in cluster II (71.25 days) was early for days to 50% flowering followed by cluster IV (109.00 days). Genotypes in cluster II (99.75 days) was observed early maturity followed by cluster IV (138.66 days). Plant height had lowest cluster mean value of 103.37 was observed in cluster II followed by cluster IV (123.16). The cluster I have superior performance for effective tillers per plant (7.84) followed by cluster V (7.69). The maximum mean value for panicle length was recorded in cluster IV (26.78) followed by cluster II (25.21). Cluster VII possessed the maximum mean value for spikelet's per panicle (102.76) followed by cluster V (88.67). The maximum mean value of grain weight per plant was observed in cluster I (3.57) followed by cluster III (3.10). The clusters I showed highest mean value for 1000-grain weight (26.01) followed by cluster IV (24.64). The maximum mean value for grain yield per plant was recorded in cluster VIII (19.89) followed by cluster VII (19.19). Therefore crossovers between neighbour nodes with a high inter-cluster distance and a high mean value for crucial features are tends to be significantly lucrative (Rajalakshmi *et al.*, 2020). In conclusion, the extent of genetic divergence was observed among 70 genotypes of rice. Cluster VIII (IC 256514, IC 256515, IC 256525, IC 256807, IC 273558, IC 277292) can used to improve grain yield per plant. Genotypes IC 256518, IC 260917, IC 277266 are desirable parent with panicle length and 1000-grain weight. Genotypes in cluster IV (IC 256518, IC 260917, IC 277266) and VIII (IC 256514, IC 256515, IC 256525, IC 256807, IC 273558, IC 277292) had more genetic diversity followed by cluster II (IC 256528, IC 260937, IC 260961, IC 267428) and IV (IC 256518, IC 260917, IC 277266). Hence, crossing between these genotypes will be generate more variation in segregating population which can be help for improve the rice.

Table 3: Mean performance of characters in various clusters.

Cluster Number	Days to 50 per cent flowering	Days to maturity	Plant height	Effective tillers/ plant	Panicle length	Spikelet's/panicle	Grain weight/plant	1000-grain weight	Grain yield/ plant	AUDPC
I	120.50	151.75	146.60	7.84	24.55	87.74	3.57	26.01	18.72	476.81
II	71.25	99.75	103.37	7.50	25.21	85.45	2.97	24.54	17.13	448.65
III	126.11	155.77	124.00	6.73	24.59	85.51	3.10	22.92	18.46	524.49
IV	109.00	138.66	123.16	6.98	26.78	88.09	2.53	24.64	10.16	1,036.45
V	116.47	147.23	132.13	7.69	24.56	88.67	2.82	23.98	14.54	759.58
VI	123.66	154.13	136.84	7.73	24.39	85.83	2.66	21.58	16.33	663.56
VII	125.83	155.16	139.90	7.39	24.60	102.76	2.97	22.79	19.19	571.33
VIII	124.66	153.00	123.91	5.99	24.56	85.98	2.41	20.28	19.89	423.08

CONCLUSION AND FUTURE SCOPE

The allocation of genotypes from distinct environment into separate categories was random, demonstrating that topographical and genetic diversity were interdependent. Thus, for separating superior isolates in segregating generations, crossing genotypes pertaining to clusters dispersed by huge inter cluster distances and diverging dramatically for variables contributing significantly to total genetic differentiation would be more profitable. In the present investigation genotypes viz., IC 256514, IC 256515, IC 256525, IC 256807, IC 273558, IC 277292, IC 256528, IC 260937, IC 260961, IC 267428) and IV (IC 256518, IC 260917, IC 277266 were superior not only for grain yield per plant but also related traits. Hence, crossing of such genotypes will result in greater variation in the segregating population, which will be helpful to improve rice crop.

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Conflict of Interest. None.

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