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Selection of Parents for developing high yielding rice hybrids through Diversity analysis in rice (*Oryza sativa* L.)

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Abstract

The investigation was carried out to explore and assess the genetic divergence in 85 genotypes of rice and two checks by employing D^2 statistic on the basis of grain yield and other important traits. The Mahalanobis' D^2 analysis grouped 87 genotypes into ten distinct clusters. Maximum numbers of 21 genotypes were present in cluster IV and least of 1 genotype with X cluster. The highest intra cluster distance was 1337.43 for cluster VII and maximum inter-cluster distance was recorded between cluster X and I (75658.09) followed by cluster X and II (63358.13). The genotypes from these distant clusters could be crossed to attain maximum heterosis with the selection of parents based on spikelet fertility % and panicle length which are highest contributors towards the diversity explored in current study.

Keywords: genetic divergence, D^2 statistics, rice, cluster distance

Introduction

Rice is grown worldwide over an area of 154 million hectares with total production of 672 million tonnes. India annually plants rice on a total area of 43 million hectares, which produces approximately of 130 million tons of rice. Notwithstanding past achievements in rice production, which made India self-sufficient, the future years warrant refined approaches to overcome the already attained yield plateau and stagnant genetic potential. Being one of the richest crop species in terms of genetic divergence with over 1 lakh landraces and improved cultivars rice can be exploited to the maximum extent to come out with ever needed yield gain by selecting the right parents in core breeding program. In the process of assessing the heterotic ability of different combinations of genotypes in crossing program, genetic diversity is a powerful tool to determine the genetic discrimination among the genotypes which can be used to select appropriate parental genotypes for hybridization to develop high yielding potential variety. Diversity not only results in inducing genetic variation but also provides new recombination of genes in gene pool. Using advanced biometric techniques such as multivariate analysis based on Mahalanobis D2 statistic (Mahalanobis, 1936) [4], it has now become possible to quantify the degree of genetic divergence amongst biological populations and assessing the relative contribution of various desirable attributes of breeding and agronomic value to the total divergence. Thus, the investigation was about assessment of genetic divergence among 87 rice genotypes and to identify diverse genotypes for the future hybridization program.

Materials and method

A total of 87 genotypes including 2 checks (IR58025 and BPT5204) were taken up sowings for the current study. These entries were evaluated in randomized complete block design with three replications during *Kharif*, 2014 at R & D farm, Rasi Seeds (P) Ltd, Hyderabad. The observations were recorded on five randomly selected competitive plants in a plot in each replication for eight quantitative characters *viz.*, days to 50% flowering, plant height (cm), number of panicles per plant, panicle length (cm), Number of grains per panicle, Spikelet fertility %, thousand grain weight and single plant yield. The data was subjected to Mahalanobis D^2 analysis (Rao 1952) [6] to assess genetic divergence in the above said germplasm collection. The genotypes were grouped into different clusters, inter and intra cluster distances, mean performances for characters and their contribution to the divergence were also computed.

Results and discussion

The D^2 analysis grouped 87 genotypes into ten distinct clusters (Table 1). The discrimination of 87 rice genotypes into ten discrete and different clusters indicated existence of substantial genetic diversity in the material to suggest that it would serve as good source for providing suitable diverse parents for hybridization programme aimed at isolating superior segregants of rice.

Maximum numbers of 21 genotypes were present in cluster IV, followed by cluster VII with 13, cluster I and V with 12, cluster III with 10, cluster IX with 6, cluster II and VIII with 5 and IX with 1 genotype, *i.e.*RP33R.

Table 1: Clustering pattern of rice genotypes based on D^2 statistic

Cluster	No. of genotypes	Genotypes											
Cluster No. 1	12	RP1B	RP43R	IR58025B	RP28R	RP12B	RP3B	RP31R	RP7B	RP23R	RP53R	RP13B	RP14B
Cluster No. 2	5	RP30R	RP37R	RP34R	RP42R	RP47R							
Cluster No. 3	10	RP8B	RP22R	RP15B	RP51R	RP17R	RP56R	RP20R	RP13R	RP26R	RP18R		
Cluster No. 4	21	RP16R	RP32R	RP2B	RP63R	RP64R	RP59R	RP65R	RP69R	RP27R	RP44R	RP19R	RP45R
		RP9B	RP60R	RP62R	RP61R	RP66R	RP68R	RP67R	RP70R	RP58R			
Cluster No. 5	12	RP4B	RP6R	RP52R	RP24R	RP25R	RP55R	RP10B	RP11B	RP5B	RP15R	RP36R	RP38R
Cluster No. 6	2	RP35R	RP41R										
Cluster No. 7	13	RP2R	RP54R	RP4R	RP5R	RP48R	RP3R	RP49R	RP50R	RP6B	RP29R	RP39R	RP40R RP1R
Cluster No. 8	5	RP7R	RP12R	RP10R	RP14R	BPT5204							
Cluster No. 9	6	RP8R	RP46R	RP9R	RP21R	RP11R	RP57R						
Cluster No. 10	1	RP33R											

The estimates of intra- and inter - cluster distances represented by D² values have been given in Table 2. The intra-cluster distance ranged from 0.00 for clusters X to 1337.43 for cluster VII. The maximum inter-cluster distance was recorded between cluster X and I (75658.09) followed by cluster X and II (63358.13), cluster X and III (53832.47), cluster X and IV (50550.63), cluster X and V (40178.60), cluster X and VI (34872.45), cluster X and VII (33760.22), cluster IX and I (26193.15) and cluster X and VIII (20972.63). The minimum estimate for the inter-cluster distance was recorded between cluster IV and III (1208.37) followed by cluster V and IV (1473.07), cluster V and III (2127.76), cluster VII and V (2144.45), cluster IV and V (2547.06) and cluster III and II (2670.82).

Table 2: Estimates of average intra-(diagonal and bold) and inter-cluster distances for ten clusters in rice

Cluster number	I	II	III	IV	V	VI	VII	VIII	IX	X
I	1173.571	3164.823	3113.749	3295.022	6665.928	10268.560	10815.710	20426.470	26193.150	75658.090
II		1737.884	2670.821	3045.474	4679.759	7442.727	7154.372	13389.170	19879.340	63358.130
III			784.957	1208.374	2127.76	4553.708	3687.139	10742.980	13895.670	53832.470
IV				412.828	1473.067	3094.814	4041.457	9386.422	12951.360	50550.630
V					1010.031	2547.060	2144.448	5656.881	8225.992	40178.600
VI						1292.671	3362.065	4804.230	6729.453	34872.450
VII							1337.436	4413.441	5402.705	33760.220
VIII								1706.128	3255.165	20972.630
IX									1544.182	14753.410
X										0.000

The intra-cluster group means for eight characters (Table 3) revealed marked differences between the clusters in respects of cluster means for different characters. The genotypes having early maturity were grouped in cluster VI along with high cluster mean for number of grains per panicle. The cluster II and cluster VIII were constituted by the genotypes having late maturity with cluster mean 108.40 and 102.60 days along with lowest panicle length (cm) with cluster mean of 23.14.

Table 3: Clusters means for eight characters of ten clusters in rice

Cluster number	Days to 50% flowering	Plant Height (cm)	Number of panicles per plant	Panicle length (cm)	Number of grains per panicle	Spikelet fertility %	Thousand grain weight (g)	Single plant yield (g)
I	96.333	81.688	9.900	25.704	188.388	83.129	15.983	21.409
II	108.400	88.520	13.460	23.820	264.990	79.960	14.260	24.383
III	92.400	93.170	10.560	25.960	175.170	75.010	14.920	21.741
IV	99.138	99.071	8.795	26.919	213.969	85.607	14.643	22.870
V	101.792	103.088	9.267	25.029	183.492	81.563	14.946	20.810
VI	90.000	106.000	7.150	27.650	350.675	78.250	14.675	23.097
VII	97.662	110.935	11.835	26.419	179.638	73.808	15.485	23.025
VIII	102.600	119.200	11.240	23.140	289.890	81.660	15.070	23.726
IX	96.700	127.025	8.900	26.633	214.608	73.058	14.900	21.584
X	100.500	176.000	9.300	29.700	263.400	89.600	14.400	23.525

Table 3: Relative contribution of different characters to towards genetic divergence

Source	Contribution %
Days to 50% flowering	1.42
Plant Height (cm)	0.24
Number of panicles per plant	18.60
Panicle length (cm)	31.92
Number of grains per panicle	7.97
Spikelet fertility %	39.05
Thousand grain weight (g)	0.80
Single plant yield (g)	0.01

Cluster VI was responsible for resulting best desirable direction for days to 50% flowering with high number of grains per panicle and second best mean in panicle length. For the trait plant height, the desirable short stature genotypes were grouped in cluster I along with high cluster mean for thousand grain weight. The cluster X having only one genotypes shown tall stature with high cluster mean. The cluster X exhibited highest cluster mean for panicle length along with high spikelet fertility (%). Cluster II showed highest cluster means for single plant yield (g) along with high number of panicles per plant and second desirable short stature plant height besides having late flowering.

Based on inter-cluster distances, cluster means and mean performance of genotypes, the crossing of cluster II with promising genotypes of clusters exhibiting very high inter-cluster distances and contrasting high means for different traits with it such as cluster VI for high number of grain and desirable days to maturity isolating desirable recombinants for developing high yielding rice varieties suitable for irrigated conditions. Similar results were reported by Nayak *et al.* (2004) [5], Singh *et al.* (2010) [9], Gangapur *et al.* (2014) [3], Aishwarya *et al.* (2014) [8], Sandhya *et al.* (2015) [7] and have also advocated hybridization of genetically diverse parents for isolating transgressive segregates in rice.

The selection and choice of parents mainly depends upon contribution of characters towards divergence (Nayak et al., 2004 [5] and De and Suriya Rao, 1987) [1]. Contribution towards genetic divergence is depicted in Tab. 3. The highest contribution in manifestation of genetic divergence was exhibited by spikelets fertility (39.05%), panicle Length (31.92%), number of panicle per plant (18.60%) and number of grains per panicle (7.97%). The contribution of number of spikelets per panicle and yield in divergence has been also observed by (Nayak *et al*., 2004 and Eswaran R., 2012) [5, 2]. The contribution of various characters towards the expression of genetic divergence should be considered as criterion for choosing parents for crossing programme for the improvement in such characters (Nayak *et al*., 2004, Tripathi *et al*., 2013 [12] Aishwarya *et al.* 2014 [5, 8], Sandhya *et al.* (2015) [7].

Based on the above results, the genotypes viz., RP7B, RP13B, RP14B as females and RP8R, RP11R, RP21R as males for hybridization program can be selected from the clusters I and IX with a highest inter cluster distance where the cluster X is not considered because it had one genotype which is very tall. These clusters are suggested to provide a broad spectrum of variability in segregating generations. Also, the selection of the genotypes viz., RP2B, RP9B, RP16R, RP44R, RP58R, RP59R, RP60R, RP61R and RP68R within the cluster might be based on the traits *viz.*, spikelet fertility % in cluster IV, panicle length in cluster IV and VI, number of panicles per plant in II and VII and number of grains per panicle in cluster VI and VIII which have contributed more than 97 % to the divergence and the rest of the traits are negligible. Thus, the crossing of genotypes belonging to cluster separated by high inter cluster distances and differing markedly for characters having high contribution towards total genetic divergence would be more fruitful for isolating superior segregates in segregating generations.

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