Genetic divergence in rice

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Abstract

Mahalanobis D^2 statistics revealed considerable genetic diversity among the forty three genotype of rice. The genotypes were grouped into 7 clusters namely cluster I (8 genotypes), cluster II (9 genotypes), cluster III (5 genotypes), cluster IV (10 genotypes), cluster V (5 genotypes) and cluster VI (3 genotypes) and cluster VII (3 genotypes). This indicates that the genotypes grouped within a particular cluster are more or less genetically similar to each other and apparent wide diversity is mainly due to the remaining genotype distributed over rest of the other clusters. The maximum intra cluster distance exhibited for cluster V (315.260) and lowest for cluster II (154.493). The maximum inter cluster distance was showed between cluster VII and III (989.482) whereas, minimum between clusters II and I (412.977). The hybridization between the genotypes Sathi Safed, PR 113 and Punjab Basmati 2 with Vallabh Basmati 21, PR 114 and Pusa Basmati 1509 would produce heterotic hybrids and wide spectrum of variability in subsequent generations. The grain yield per plant followed by number of grains per panicle, biological yield per plant, harvest index, plant height, panicle length, test weight and days to 50% flowering contributed most towards genetic divergence.

Key Words: *Oryza sativa*, genetic divergence

Introduction

Rice grown in the state of Punjab, Haryana, Western Uttar Pradesh and Uttrakhand will have to find place in the international market as the major rice growing states have become self sufficient in rice production. To remain competitive in the international market, the choice lies with the basmati rice. This region is also gifted with agronomic conditions most conducive for the production of best quality basmati rice. Basmati rice is known and preferred for its unique cooking and eating quality. India is second leading producer of rice in the world India's annual rice production is around 85 to 90 million tones and annual consumption is around 85 million tones. The total area, production and productivity of rice are 163.20 million hectare, 719.73 million tones and 4.41 tones per hectare of rough rice in world. In India total area, production and productivity of rice are 42.75 million hectare, 105.24 million tones and 2.46 tones per hectare. In Uttar Pradesh the total area, production and productivity of rice are 5.86 million hectare, 14.41 million tones and 2.46 tones per hectare, respectively. However the productivity of the crop is less and if varies from year to year. This low productivity is accounted for various factors. Rice is grown as a irrigated crop, but availability of irrigation facilities is limited and lack of rainfall during crop growth period. Farmers either do not have enough resources or otherwise hesitate to put costly input under unassured conditions. Production of rice is also limited owing to non adoption of recommended practices and high yielding varieties. This reduces the yield to a greater extent. An understanding about the magnitude of genetic diversity with respect to various yield and yield attributes traits. For increasing the productivity of rice, plant breeding programmes play an important role. Further, for exploitation of heterosis and for enlarging the variability in the subsequent segregating generations, understanding the genetic divergence among the parents is essential. The present investigation is therefore, carried out with the objective of studying the genetic diversity to enhance rice breeding programme.

Materials and methods

Forty three diverse genotypes of rice were grown in randomized block design with three replications during the *kharif* 2014 at Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U.P.). Each plot comprised of four rows of 5 m length, with row to row and plant to plant spacing of 20 cm and 15 cm, respectively. Observations on eleven quantitative characters namely days to 50% panicle emergence, days to 50% flowering, days to maturity, plant height,

number of reproductive tillers per plant, panicle length, biological yield per plant, harvest index, test weight, number of grain per panicle and grain yield per plant were recorded from five plants in each replication. The mean values were transformed in to uncorrelated linear function for Mahalanobis D^2 analysis. The genotypes were grouped in to different clusters per Tocher's method (Rao, 1952), whereas intra and inter cluster distances were computed.

Results and discussion

In the present study thirty one genotypes of rice were subjected to D^2 analysis using eleven component characters. Out of the 7 clusters, cluster I, II, III, IV, V, VI and VII had 8, 9, 5, 10, 5, 3 and 3 genotypes, respectively (Table 2). It was concluded that in general, there was parallelism between genetic and geographic diversity. This view point has been supported by Singh *et al.,* 2012 and Sharma *et al.,* 2014. The intra cluster distance among various clusters exhibited maximum intra cluster distance for cluster V (315.260) and lowest for cluster II (154.493). The maximum intra cluster distance was because of wide genetic diversity among its genotypes. The chance of developing good segregates by crossing the genotypes of the same cluster showing low value for intra cluster distance. Therefore, it would be logical to attempt crosses

between the genotypes of clusters separated by larger inter cluster distances. The little diversity and selection of parents within the cluster having higher mean for a particular character may also be useful for further developing high yielding rice varieties. The maximum inter cluster distance was revealed between cluster VII and III (989.482) followed by cluster VII and V (980.856) cluster VI and V (959.560), cluster III and II (910.305), cluster VI and III (896.688), cluster V and II (849.322) and cluster V and cluster III (813.935) Table 1. The clearly indicates that the genotypes included in this clusters are having broad spectrum of genetic diversity and could very well be used in hybridization programme of rice for improving grain yield. The least inter cluster distance was between clusters VII and VI (450.702) followed by cluster V and IV (447.346) and cluster II and I (412.977). The lowest inter cluster distances indicate that the genotype of these clusters had close relationship and hence, may not be emphasized upon to be used in hybridization programme. Crosses involving parents belonging to most divergent clusters would be expected to manifest maximum heterosis and also wide variability of genetic architecture Sarkar et al., 2006 and Singh *et al.,* 2014. Thus the crosses between the genetically diverse genotypes of cluster VI characterized by days to 50%

Table 1: Average intra and inter cluster (D^2 value) distance in forty three of rice

Cluster	I	II	III	IV	V	VI	VII
I	**196.721**	412.977	550.777	454.604	621.020	475.263	584.497
II		**154.493**	910.305	622.846	849.322	670.695	693.769
III			**314.041**	735.968	813.935	896.688	989.482
IV				**235.977**	447.346	679.218	716.129
V					**315.260**	959.560	980.856
VI						**279.922**	450.702
VII							**311.877**

Bold values are intra cluster distances

Table 2: Distribution of forty three genotypes of rice

Clusters number	No. of genotypes	Genotypes
I	8	Vallabh Basmati-22 , Pusa-677, CSR-27, Vallabh Basmati-23 , Super Basmati ,CSR-30, Pusa-1121, Pusa Basmati-1 ,
II	9	Nagina-22 , MAUB-57, Sharbati, Pusa -1612, Pant Sugandh Dhan-15, IET-2165, Centuri Patna, PR-10
III	5	Pusa Basmati-2, Pusa -2511, I.R-64, VLD-65 , Basmati-564,
IV	10	Vallabh Bangani, Type-3, MAUB-13, IET-8085, Dhan-12, Pusa Sugandha-3, VLD-61, MAUB-171, Govind, CSR-10
V	5	Ranvir Basmati, Tarori Basmati, Basmati-370, Basmati-386, Unnat Pusa Basmati-1,
VI	3	Sathi Safed, PR-113, Punjab Basmati-2
VII	3	Vallabh Basmati-21, PR-114, Pusa Basmati-1509

Table 3: Cluster means values for eleven characters in rice

Character / Cluster	Days to 50% panicle emergence	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of reproductive tillers/plant	Panicle length (cm)	Biological yield/ plant (g)	Harvest index	Test weight (g)	No.of grains/ panicle	Grain yield/ plant (g)
I	81.756	90.711	122.933	108.156	15.040	25.893	169.724	36.750	24.400	138.080	61.316
II	78.000	88.500	118.500	149.433**	18.067	27.233	167.033	32.870	23.500	112.467	54.633
III	71.500*	79.500*	117.833*	77.633*	19.900**	21.867**	155.567*	28.925	27.002	93.167*	43.833*
IV	88.750	97.250	123.750	120.083	17.450	27.017	169.283	37.646**	28.500	122.283	62.217**
V	83.667	91.267	120.533	115.493	13.653	28.013	173.760**	34.043	29.200**	197.173**	56.480
VI	95.500**	103.800**	124.600**	112.927	17.347	25.973	161.480	36.657	23.100	137.913	58.193
VII	89.400	96.800	123.867	129.573	13.040*	29.973**	169.240	31.775*	20.799*	188.840	52.267

*, ** represent minimum and maximum values, respectively.

*, ** Significant at 5% and 1% level, respectively

Table 4: Contribution of different characters in creating diversity in rice based on Mahalanobis's D^2 analysis.

S. No.	Character	Contribution (%)
1	Days to 50% panicle emergence	2.27
2	Days to 50% flowering	10.55
3	Days to maturity	3.44
4	Plant height (cm)	20.96
5	No. of reproductive tillers per plan	1.25
6	Panicle length (cm)	20.83
7	No. of grains per panicle	26.95
8	Biological yield per plant (g)	22.79
9	Harvest index	21.44
10	Test weight (g)	18.23
11	Grain yield per plant (g)	31.29

panicle emergence, days to 50% flowering and days to maturity with genotypes Sathi safed, PR 113 and Punjab Basmati 2 and cluster VII characterized by number of reproductive tillers per plant, panicle length, harvest index and test weight with these genotypes like Vallabh basmati 21, PR 114 and Pusa Basmati 1509 are expected to exhibit high heterosis and are also likely to produce new combinants with desired characters to get desirable segregates with higher yield for developing superior variety of rice. The percent contribution of number of grain yield per plant (31.29) followed by number of grains per panicle (26.95), biological yield per plant (22.79), harvest index (21.44), plant height (20.96), panicle length (20.83), test weight (18.23) and days to 50% flowering (10.55) contributed most towards genetic divergence (Table 4). Remaining characters contributed very little or did not contribute at all towards genetic divergence. These results are somewhat in accordance with the findings of Singh et al., 2012 and Sharma et al., 2014.

Referances

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