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Study of genetic diversity in rice (*Oryza sativa* L.) genotypes for grain yield under humid south eastern plain of Rajasthan

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Abstract

Rice (*Oryza sativa* L.) is the most important food source for more than half of the world's population, so determining the best genotypes for proper crossing is important to produce high yielding varieties with good cooking quality. Diversity helps the plant breeder in choosing the right parents for breeding programmes. The genotypes were grouped into six clusters based on Mahalanobis's D² statistics. Cluster II consisted with the highest number of (8) genotypes from different origin, whereas cluster VI consisted with the lowest number of (1) genotypes. Cluster I consisted of 7 cultivars showed maximum mean grain yield. Maximum inter cluster distance was recorded between cluster III and VI. Cluster I had the highest mean values for grain yield and Number of productive tillers per plant and Cluster VI had the highest mean values for 1000-grain weight. The cultivars from these clusters with desirable characters may be used as potential donor for future hybridization program to develop high yielders.

Keywords: Rice (*Oryza sativa* L.), genetic diversity, grain yield

Introduction

Rice (*Oryza sativa* L.) is the most important food source for more than half of the world's population (Violita 2019) ^[17]. Approximately 90 per cent of the world's rice is grown in the Asian continent. India ranks first in area 43.79 million hectare and second in the production 116.42 million tonnes with a productivity of 2650 kg/ ha. (Anonymous, 2018-19) ^[1, 2]. Major Rice producing states are West Bengal, Uttar Pradesh, Andhra Pradesh, Chhattisgarh, Telangana, Punjab, Tamil Nadu and Haryana. Rajasthan occupies an area of 0.199 million hectares with the production of 0.46 million tones and productivity of 2310 kg/ha. (Anonymous, 2018-2019) ^[1, 2]. Kota region (humid south eastern plain zone) occupies an area of 0.099 million hectare with a production of 0.35 million tones and productivity of 3530 kg/ha (Anonymous, 2018-2019) ^[1, 2]. Due to the growing population and the need for more rice production in the world, the use of hybrid varieties should be considered (Tait and Barker 2011) ^[15]. In this regard, identification of suitable cultivars for use in hybrid production programs is essential, so that the cultivars used as parents of hybrid varieties must also have high acceptability among the farmers as well as the high specific combining ability for seed yield (Okada and Whitford 2019) ^[11]. In rice breeding, general objectives are to increase yield potential by enhancing the primary and secondary yield components, yield stability and grain quality, which are of high importance (Heinemann *et al.* 2019) ^[3]. In the breeding programs, determination of the level of genetic diversity in plant species is of great importance for the selection of suitable parents in breeding programs and maximum utilization of heterosis (Luo *et al.* 2019) ^[8]. Genetic variation among parental genotypes is usually evaluated by morphological and physiological differences of important economic and quantitative traits (Ibraheem and El-Ghareeb 2019) ^[4]. Moreover, evaluation of genetic diversity is important for the source genes of particular traits within the available germplasm (Roy and Panwar, 1993). Genetic diversity assessment between and within groups or clusters is very important for the proper selection of parents for the better search of heterosis (Murty and Arunachalam, 1966) ^[10]. Since variety is the raw material of plant breeding and this plant has a wide genetic diversity and high adaptation range, rice requires proper methods for breeding and introducing high-yielding quality cultivars, which requires proper understanding of its diversity and nature.

Therefore, this study was undertaken to determine the genetic diversity in rice for the maximum utilization of the genetic resources and proper selection of donor parents.

Material and Method

The experiment was conducted at the experimental field of Agricultural Research Station Ummadganj Kot in irrigated condition during *Kharif* 2019. The experimental materials comprised of 25 rice genotypes. (Table 1). The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Row and plant spacing were maintained 20×15 cm and two seedlings per hill were transplanted. Normal package of practices were applied to the experimental plots. Data were collected on 10 agronomic characters *viz.* days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, panicle length (cm), number of grains per panicle, 1000-grain weight (g), amylose content (%), protein content (%) and grain yield per plant (g). Data were taken from 10 randomly selected plants of each genotype. All the analyses in respect of ten different morphological traits of 25 rice genotypes were analyzed by indostat software program. The genotypes were grouped into clusters based on Mahalanobis's D^2 statistics analysis.

Table 1: List of twenty five rice genotypes along with their sources

Sr. No.	Name of the genotypes	Source
1	RSK-1155-2-4-1	ARS, KOTA
2	RSK-1155-3-3-1	ARS, KOTA
3	RSK-1157-4-5-1	ARS, KOTA
4	RSK-1157-6-3-1	ARS, KOTA
5	RSK-1157-9-2-2	ARS, KOTA
6	RSK-1161-1-1	ARS, KOTA
7	RSK-1163-8-1	ARS, KOTA
8	RSK-1165-4-2	ARS, KOTA
9	RSK-1165-4-3	ARS, KOTA
10	RNSK-1167-11-1	ARS, KOTA
11	RNSK-1168-2-1	ARS, KOTA
12	RSK-1164-1-1	ARS, KOTA
13	RSK-1172-1-1	ARS, KOTA
14	RSK-1221-1-1	ARS, KOTA
15	RSK-1162-8-1	ARS, KOTA
16	RSK-1164-6-1	ARS, KOTA
17	RSK-1164-6-2	ARS, KOTA
18	RSK-1165-3-1	ARS, KOTA
19	RSK-1165-3-2	ARS, KOTA
20	RNSK-1167-5-1	ARS, KOTA
21	RSK-1155-6-1-2	ARS, KOTA
22	RSK-1155-6-3-1	ARS, KOTA
23	P-1121	IARI NEW DELHI
24	P-2511	IARI NEW DELHI
25	P-1460	IARI NEW DELHI

Result and Discussion

The result of the genotypes grouping into clusters is presented in Table 2. As per the D^2 values, the 25 genotypes of rice were grouped into six clusters. Cluster II had maximum number of genotypes (8) followed by cluster I with (7), cluster III with (4) genotypes, Cluster IV had (3) and Cluster V had (2) genotypes in each cluster. Cluster VI is mono-genotypic. Inter and intra cluster distance among six clusters were presented in the Table 3. The intra cluster distance ranged from 0.00 (cluster VI) to 29.17 (cluster IV). Cluster IV had the highest intra cluster distance (29.17) followed by cluster II (23.01), cluster I (16.16), cluster V (13.30) and cluster III (12.56). The highest inter-cluster distance (495.10)

was found between cluster III and VI followed by cluster I and III (391.90), cluster III and V (369.88), cluster IV and V (225.64) and cluster II and cluster III (211.67). The smallest inter-cluster distance (50.17) was observed between II and V followed by cluster I and VI (55.23) and cluster I and V (64.17). The intra-cluster distance for clusters VI was observed to be zero since these contains only one genotype in cluster. Cluster IV had the highest intra cluster distance followed by cluster II, cluster I, cluster V and cluster III. The highest inter-cluster distance was found between cluster III and V followed by cluster I and III and cluster III and V. The greater the distance between two clusters, wider is the expected genetic diversity between them similar result were also reported by Kulsum *et al.* (2013)^[6], Khare *et al.* (2015)^[5], Kumar *et al.* (2015)^[7], Umesh *et al.* (2016)^[16], Rukmini *et al.* (2020)^[12], Sadia *et al.* (2020)^[13]. Cluster I had genotypes having higher mean values for characters like grain yield per plant, number of productive tillers per plant. Whereas, clusters like IV had high values for grain yield per plant, protein content, amylose content per cent and also desirable for early flowering and maturity. Cluster VI for plant height, panicle length, number of grains per panicle, 1000-grain weight. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

The cluster mean of different quantitative characters for different clusters have been presented in Table 4. The days to 50 per cent flowering was earliest in cluster III (79.08) followed by cluster IV (86.22), and cluster II (97.38) whereas, highest values for days to 50 per cent flowering was observed in cluster V (102.67) followed by cluster VI (101.00) and cluster I (98.86). Early maturity was observed in cluster III (113.00 days) followed by cluster IV (121.78 days), Whereas late maturity was recorded in cluster V (137.83 days) followed by cluster VI (137.33 days). The cluster V have the highest plant height (116.33cm), followed by the cluster V (116.33). Lowest plant height (99.33cm) was observed for cluster III. Maximum number of productive tillers per plant was observed in cluster I (10.00) followed by cluster IV (9.00) and cluster V (8.50). Whereas, minimum number of productive tillers per plant was observed in cluster III (6.42) followed by cluster II (6.92). The cluster VI have the highest panicle length (28.77) followed by cluster I (28.53) whereas, the cluster III have the shortest panicle length (25.47) followed by cluster II (27.57). Maximum number of grains per panicle was observed in cluster V (189.67) followed by cluster VI (178.00) and cluster II (170.71) whereas the lowest number of grains per panicle was reported in cluster III (134.50). The highest 1000-grain weight (g) was recorded in cluster VI (30.33), followed by cluster I (28.20) and cluster IV (27.54) whereas, the minimum 1000-grain weight was reported in cluster III (22.52). The maximum value for grain yield per plant (g) was recorded in cluster I (17.97) followed by cluster IV (15.61) and cluster V (14.90), whereas the minimum was in cluster VI (9.47 g). The maximum per cent of amylose content estimated in cluster IV (26.71) followed by cluster III (23.95) and minimum amylose content recorded in cluster V (23.00). Maximum protein content was recorded in cluster IV (9.17) and minimum protein content per cent found in cluster V (7.16). Cluster I had genotypes having higher mean values for characters like grain yield per plant, number of productive tillers per plant. Whereas, clusters like IV had high mean values for grain yield per plant, protein content, amylose content and also desirable for early flowering and maturity. Cluster VI for plant height, panicle

length, number of grains per panicle, 1000-grain weight. Therefore, hybridization between the selected genotypes from

divergent clusters is essential to judiciously combine all the targeted traits.

Table 2: Grouping of 25 genotypes of rice into six clusters (by Tocher's method)

Cluster No.	Name of genotypes	Number of genotype
I	RSK-1155-2-4-1, RSK-1155-3-3-1, RSK-1157-4-5-1, RSK-1157-6-3-1, RSK-1157-9-2-2, RSK-1155-6-1-2, RSK-1155-6-3-1	7
II	RSK-1164-1-1, RSK-1172-1-1, RSK-1221-1-1, RSK-1162-8-1, RSK-1164-6-1, RSK-1164-6-2, RSK-1163-8-1, P-1460	8
III	RSK-1165-4-2, RSK-1165-4-3, RSK-1165-3-1, RSK-1165-3-2	4
IV	RNSK-1167-11-1, RNSK-1168-2-1, RNSK-1167-5-1	3
V	P-1121, P-2511	2
VI	RSK-1161-1-1	1

Table 3: Average intra and inter-cluster distance based on corresponding D² values

Clusters	I	II	III	IV	V	VI
I	16.16	94.62	391.90	145.98	64.17	55.23
II		23.01	211.67	133.36	50.17	130.44
III			12.56	149.75	369.88	495.10
IV				29.17	225.64	210.40
V					13.30	109.74
VI						0.00

Table 4: Mean values of different characters for 25 genotypes of rice grouped in different clusters

Characters	Days to 50% flowering	Days to Maturity	Plant height (cm.)	Number of productive tillers per plant	Panicle length (cm.)	Number of grains per panicle	1000-grain weight (g)	Amylose content (%)	Protein content (%)	Grain yield per plant (g)
I	98.86	134.62	112.48	10.00	28.53	169.95	28.20	23.42	8.15	17.97
II	97.38	132.33	107.38	6.92	27.57	170.71	23.86	23.48	8.00	11.03
III	79.08	113.00	99.33	6.42	25.47	134.50	22.52	23.95	7.58	10.81
IV	86.22	121.78	102.78	9.00	27.81	151.89	27.54	26.71	9.17	15.61
V	102.67	137.83	116.33	8.50	27.73	189.67	24.43	23.00	7.16	14.90
VI	101.00	137.33	116.00	5.67	28.77	178.00	30.33	23.83	8.37	9.47

Fig 1: Relative disposition of clusters showing average intra and inter distance. Genetic Divergence

Conclusion

For a successful breeding programme, the diversity of parents is of utmost importance, since the crosses made between the parents with maximum genetic divergence would more likely to yield desirable recombinants in the progenies. However, it is desirable to select suitable genetically divergent parents, based on information about the genetic variability and genetic diversity present in the available germplasm (Singh and Chaudhary 1977)^[14]. The variability among different genotypes of a species often reflects the genetic diversity of different characters considered in totality. One of potent techniques of measuring genetic diversity is the D^2 statistic proposed by Mahalanobis in 1936^[9]. This technique measures the forces of differentiation at two levels, namely intra cluster and inter cluster level, thus help in selection of genetically divergent parents for their exploitation in hybridization. D^2 statistic measures the degree of diversification and determines the relative importance of each character to total divergence.

References

1. Anonymous. Agriculture Statistics at a Glance, Directorate of Economics & Statistics, Department of Agriculture & Cooperation, Ministry of Agriculture. Government of India 2018-19.
2. Anonymous. Rajasthan Agriculture statistics at a Glance, Commissionerate of Agriculture, Rajasthan, Jaipur 2018-19.
3. Heinemann AB, Ramirez-Villegas J, Rebolledo MC, Neto GMFC, Castro AP. Upland rice breeding led to increased drought sensitivity in Brazil. *Field Crops Res* 2019;231:57-67.
4. Ibraheem F, El-Ghareeb EM. Assessment of natural variability in leaf morphological and physiological traits in maize inbreds and their related hybrids during early vegetative growth. *Egypt J Basic Appl Sci* 2019;6:25-45.
5. Khare R, Singh AK, Singh PK. Genetic variability association and diversity analysis in upland rice (*Oryza sativa* L.). *SAARC Journal of Agriculture* 2015;12(2):40-51.
6. Kulsum MU, Hasan MJ, Siddique MA, Begum F, Akond Z. Genetic diversity in selected rice genotypes (*Oryza sativa* L.). *Bangladesh J Agric* 2013;38-40:63-72.
7. Kumar K, Shinde SR, Jagtap SM. Genetic studies in upland rice (*Oryza sativa* L.). *Internl. J of Plant Sci* 2015;10(1):60-63.
8. Luo X, Tan Y, Ma C, Tu J, Shen J, Yi B *et al.* High-throughput identification of SNPs reveals extensive heterosis with intra-group hybridization and genetic characteristics in a large rapeseed (*Brassica napus* L.) panel. *Euphytica* 2019;215:157.
9. Mahalanobis PC. On the generalized distance in statistics. *Proceedings of the National Institute of Sciences of India* 1936;2(1):49-55.
10. Murty BR, Arunachalam V. The nature of genetic diversity in relation to breeding system in crop plants. *Indian J Genet* 1966;26:188-198.
11. Okada T, Whitford R. Hybrid wheat and abiotic stress. In: Rajpal V, Sehgal D, Kumar A, Raina S (eds) *Genomics assisted breeding of crops for abiotic stress tolerance*, vol II. Springer 2019, 211-224.
12. Rukmini K, Rajendra PK, Venkanna VC, Satish V, Vankudoth YH, Lingaiah N *et al.* Studies on genetic diversity and variability for yield and quality traits in promising germplasm lines in rice (*Oryza sativa* L.). *The Pharma Innov J* 2020;9(1):391-399.
13. Sadia P, Anand K, Bishun DP, Mukesh C. Assessment of genetic diversity in rice (*Oryza sativa* L.) under irrigated and drought stress condition. *Curnt of Appl Sci and Tech* 2020;39(1):112-125.
14. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi 1977, 215-218.
15. Tait J, Barker G. Global food security and the governance of modern biotech nologies. *EMBO Rep* 2011;12:763-768.
16. Umesh JHK, Sravan T, Waza SA. Genetic divergence analysis for yield and quality traits in some indigenous genotypes of basmati rice (*Oryza sativa* L.). *Green Farm* 2016;7(2):345-348.
17. Violita V. Morphological indices of drought tolerant of some paddy varieties (*Oryza sativa* L.) in West Sumatera using standard evaluation system (SES) for rice. *Biosci* 2019;3:60-68.