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UNVEILING GENETIC DIVERSITY AND CORRELATION OF ADVANCED BREEDING LINES IN PADDY (*ORYZA SATIVA* L.)

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ABSTRACT

The present investigation was conducted during Kharif 2022. Thirty-two advanced breeding lines of rice cross RNR-15048 × KPR-1 and five checks were studied under randomised complete block design for genetic variability, character association and genetic diversity under non- submergence condition at AHRS, Kathalagere. Correlation study revealed significant positive association with grain yield for number of tillers per plant, number of productive tillers, number of spikelets per panicle, number of filled grains per panicle, panicle length, spikelet fertility, test weight and length breadth ratio. Mahalanobis D^2 statistics grouped 32 advanced breeding lines with five checks into six clusters. Maximum inter-cluster distance was observed between cluster IV and VI. Among advanced breeding lines screened under submerged condition, highest survival percentage was observed for R×K-1-4-5 and R×K-1-4-17. Advanced breeding lines R×K-1-4-5 and R×K-1-4-17 could be proposed for further screening in different locations of hill zone of Karnataka.

***Keywords*: Mahalanobis $D^{2,}$ Diversity, Cluster

Introduction

Rice scientifically known as *Oryza sativa* L. having chromosome number 2n=24. It is the most important cereal crop cultivated widely in many parts of the world. Genus *Oryza* belongs to the tribe Oryzeae in the family Poaceae. Out of 24 species of rice, 22 species are wild and only two species are cultivated, *i.e., Oryza sativa* and *Oryza glaberima*. It is a staple food for more than half of the world's population and is a major source of income in many Asian countries. It is grown in more than 100 countries in 154 million hectares with 90 per cent of the total global production from Asia (Bista, 2018).

Rice provides 21 per cent of global human per capita energy and 15 per cent of per capita protein. It is the primary source of food and protein (30%) providing 50-60 per cent of the total calories for about half of the mankind with an enormous nutritional and economic impact. The protein quality is around 0.55 which is also higher compared to other cereals. Apart from carbohydrates and proteins rice also provides essential amino acids, minerals (P, Mg, Ca), vitamins (Folic acid) and fibre. It is the crucial dietary and food security source of many Asian countries like China, India, Indonesia, Bangladesh and Vietnam. China and India are the largest producers and consumers of rice. India ranks the highest area of cultivation of rice in the world, next being China. In India, West Bengal has highest total rice production followed by Uttar Pradesh. The other major rice producing states in India are Punjab, Andhra Pradesh, Tamil Nadu, Bihar, Chhattisgarh, Odisha (Ashraf *et al.,* 2016). In 2021-22, the rice area, production and productivity in India was 46.38 Mha, 130.29 mt and 2.81 t/ha respectively. In Karnataka, rice occupies 1.39 million hectares with 4.29 million tonnes of production and 3.72 t/ha productivity (Anonymous, 2022).

Assessing genetic diversity is a fundamental aspect for the development of new genotypes with a desired combination of traits. Moreover, it hastens the revelation of promising genotypes without the need to evaluate all possible cross combinations in breeding programs. Multivariate analysis tool like Mahalanobis D^2 statistic is functional for measuring genetic diversity by considering morphological and quantitative characteristics in a given population. It is utilized in detecting clustering patterns, to establish a link between genetic and environmental divergence, to study quantitative traits which determines maximum divergence and also to identify the characters which significantly contribute to divergence among the genotypes (Jangala *et al.,* 2022).

Correlation is a very important factor for any selection program. Success in selection depends on the knowledge of the association of component traits with grain yield hence indirect selection for yield component traits are more reliable than selection for yield (Nath and Kole, 2021). Therefore, character association studies help to understand the nature of physical linkage and also provide information on the nature and direction of correlation which exists between the variables.

Materials and Methods

The experimental material consisted of 32 rice germplasm (Table 1) and present investigation was carried out at the Agricultural and Horticultural Research Station, Kathalagere, Chennagiri(T), Davanagere (D), Karnataka. Twenty-one days old seedlings were transplanted in 2 × 1 m2 plot in randomized block design with three replications. Distance between plant to plant and row to row were 20 cm and 15cm respectively. Standard agronomic practices were followed throughout the crop growth period to obtain good harvest. Observations were recorded on five randomly selected plant from each progeny row for 13 biometrical characters viz, days to 50% flowering, plant height, flag leaf length, flag leaf width, tillers per hill, panicles per hill, panicle length, spikelet per panicle, days to maturity, biological yield, harvest index, test weight and grain yield per hill. The Analysis of variance was estimated as per procedure suggested by Panse and Sukhatme (1961) , coefficient of variation (GCV and PCV) by Burton (1952) . Heritability for the grain yield and yield components in rice were worked out in broad sense by adopting formula suggested by Burton and Devane (1953). Genetic advance was calculated by the method suggested by Johnson *et al.* (1955). Correlation coefficient and path coefficient was worked out as method suggested by Al Jibouri et al. (1958) , Dewey and Lu (1959) . Genetic divergence was calculated based on Mahalanobis (1936) D2 statistics respectively.

Results and Discussion

For assessing the genetic diversity in a large number of genotypes, D^2 statistics is useful which detects genetically divergent parents so they can be effectively utilized in hybridization programmes. Thirty-two advanced breeding lines of rice and five checks were subjected to the Mahalanobis' D^2 analysis in the current investigation.

Grouping of Genotypes into Various Clusters

On the basis of Mahalanobis D^2 statistics, 37 genotypes were grouped into six clusters (Table no. 3). The clustering pattern obtained revealed that the biggest cluster formed was cluster I, which had fifteen lines within it. This was followed by cluster II with eleven lines present in the cluster; cluster III and cluster V was found to have three lines in it and cluster IV had four lines. Cluster VI is the smallest one with one advanced breeding line. Thirty-seven genotypes including 32 advanced breeding lines and five checks were grouped into six clusters based on D^2 statistics. The groups formed were of such a way that within each cluster, genotypes had smaller value of D^2 statistics compared to those existing between the clusters. Clustering pattern obtained revealed that the biggest cluster formed was cluster I which had 15 genotypes carrying within it followed by cluster II with 11 genotypes, cluster IV had four lines, cluster III and cluster V had three lines. Cluster VI was the smallest with one genotype in the cluster. The results were in accordance with Khalequzzaman *et al.* (2008), Kodihalli and Dushyanthakumar (2014), Rashid *et al.* (2014) and Mith *et al.* (2018).

Average Intra and Inter Cluster Distances

Cluster IV exhibited the maximum intra cluster distance (45.67) followed by cluster V (37.92). Because of the greater amount of diversity existing among themselves the advanced breeding lines present within these two groups could be utilized better for hybridization program. Hence, hybridization is effectively utilized by selecting the genotypes of cluster IV and cluster V followed by cluster II and cluster VI. Cluster IV with four genotypes (R×K-4-4-11, R×K-6-2-15, R×K-1-4-18 and KHP 11) and cluster VI with 1 genotype (KPR-1) were found to be the most divergent because of maximum inter cluster distance existing between them followed by cluster II (R×K-1-4-8, R×K-12-2-6, R×K-1-4-9, R×K-7-2-7, R×K-1-6-10, R×K-7-2-9, R×K- 8-2-10, R×K-1-4-13, R×K-1-4-15, R×K-1-4-16 and R×K-7-2-16) with cluster VI (KPR-1). Clusters with the highest inter cluster distance are having more genetic diversity and such genotypes belonging to the clusters will be utilized for hybridization program. Meanwhile, those clusters with minimum inter cluster distance are found to have narrow genetic diversity and hybridization between them will not be exhibiting better heterosis. Therefore, it is better to select those advanced lines having clusters with more inter cluster distance than with low inter cluster distance. Cluster I (R×K-1- 4-3, R×K-1-4-4, R×K-7-2-2, R×K-1-4-5, R×K-5-2-4, R×K-1-4-7, R×K-7-2-5, R×K-14-2-8, R×K-1-4-12, R×K-7-2-11, R×K-2-2-14, R×K-7-2-12, R×K-4-2-13, R×K-3-2-14 and R×K-1-4-17) and cluster V (R×K-7-2-1, R×K-8-2-3 and R×K-1-4-6) recorded the minimum inter cluster distance between them followed by cluster I (R×K-1-4-3, R×K-1-4-4, R×K-7-2-2, R×K-1-4-5, R×K-5-2-4, R×K-1-4-7, R×K-7-2-5, R×K-14-2-8, R×K-1-4-12, R×K-7-2-11, R×K-2-2-14, R×K-7-2-12, R×K-4-2-13, R×K-3-2-14 and R×K-1-4-17) and cluster III (RNR-15048, BPT-5204 and JGL-1798)(Table 3). Existence of higher genetic diversity between the clusters with more inter cluster distance could be better utilised for developing the high yielding varieties or hybrids than selecting genotypes with minimum inter cluster distance for hybrid development. Pradhan and Roy, (1990), Mishra *et al.* (2003) and Chaturvedi and Maurya (2005) recommended that parents should be selected from two clusters having wider inter-cluster distance. Selection of genotype from cluster IV and cluster VII has recorded high mean value for grain yield and its components traits were suggested for utilization in hybridization programme and aimed at improvement of these traits. Therefore, hybridization between selected genotypes from divergent clusters is essential to judicially combined all the target traits.

Cluster Means of the Character

The genotypes with high mean values may be directly used for adaptation or may be used as parents in the future breeding programme. In the present study, cluster I have low mean vales for plant height, flag leaf length, flag leaf width, number of tillers per hill and grain yield per hill. Cluster II shows low mean values for Panicle Length, biological yield per hill. Cluster III shows high mean values for days to maturity and low mean value for number of panicles per hill. Cluster IV shows high mean value for Flag leaf length, flag leaf width, panicle length, spikelets per panicle, harvest index and grain yield per hill and low mean value for Days to 50% flowering and days to maturity. Cluster V shows high mean value for days to 50% Flowering and test weight and low mean value for spikelets per panicle and harvest index. Cluster VI shows high mean values for number of tillers per hill, number of panicles per hill and biological yield per hill. Cluster VII shows high mean value for plant height (Table 4).

Relative Contribution of Characters towards Genetic Divergence

The selection and choice of parents mainly depend upon the contribution of characters towards divergence. Among 13 characters studied panicle length followed by plant height, spikelets per panicle, harvest index and flag leaf length contributed maximum to the total genetic divergence. The present investigation revealed that grain yield per hill and test weight were the major contributors towards divergence and accounted for about 78.77% of contribution towards total divergence (Table.5). Number of panicles per hill and harvest index had zero contribution towards divergence. Ovung *et al.* (2012) also reported a maximum contribution of plant height and spikelets per panicle. Singh and Singh (2008) reported the minimum contribution of days to 50% flowering, tillers per plant and grain yield among all characters.

Genotypic and phenotypic correlation coefficients (Table 6) indicate the genotypic and phenotypic correlation coefficients were of higher in magnitude than the phenotypic correlation coefficient which might be due to the modified effect of environment at the genetic level. Grain yield per plant showed the high significant positive correlation with plant height, flag leaf width, number of tillers, number of panicles, biological yield per plant and spikeslets per panicle showed positive significant correlation at phenotype and genotypic levels. The positive correlation of grain yield with various traits was supported by the Abdul *et al.* (2011), Rashmi *et al.* (2017), Aditya *et al.* (2013), Shiva *et al.* (2018). In the present study path coefficient analysis has been conducted taking grain yield per hill as the depended variable and the other characters as independent is presented in (Table 6). The path analysis at phenotypic level of the characters like plant height, flag leaf width, number of panicles, panicle length, days to maturity, biological yield per hill and harvest index had positive direct effect on grain yield per hill. whereas, days to 50% flowering, flag leaf length, number of tillers, spikes per panicle and test weight showed negative direct effect on grain yield per hill Similar results were reported earlier by Abdul *et al.* (2011) for spikelets per panicle, biological yield per hill, harvest index, test weight; Rashmi *et al.* (2017) for days to maturity, plant height, panicle length, Days to maturity; Aditya *et al.* (2013) for Day to 50% flowering, Plant height, flag leaf width, panicle length, Days to maturity, test weight and Kishore *et al.* (2015) for Plant height, flag leaf length. The path analysis at genotypic level of the characters like plant height, flag leaf length, number of panicles, spikes per panicle, harvest index and biological yield per hill had positive direct effect on grain yield per hill whereas, days to 50% flowering, flag leaf width, number of tillers, panicle length days to maturity and test weight showed negative direct effect on grain yield per hill. Similar results were reported earlier by Abdul *et al.* (2011) for Plant height, number of tillers per hill, panicle length, biological yield per hill, harvest index, test weight; Kishore *et al.* (2015) for Plant height, panicle length and Bhandari *et al.* (2019) for Day to 50% flowering.

Conclusion

The 37 advanced breeding lines were grouped into six different clusters based on D^2 values and reported the presence of significant amount of genetic diversity among the genotypes. Cluster I comprising of 15 genotypes the largest followed by cluster II, III, IV and V and VI. The maximum inter-cluster distance was noticed between cluster III and cluster V (6243.98) followed by cluster II and cluster III (6166.44) and between cluster II and cluster IV (6022.47). Maximum intra cluster differences among the genotypes were observed in cluster IV followed by cluster I,III,II, and V. grain yield per plant, days to 50% flowering, days to maturity, panicle length, number of filled grains per panicle, number of panicles per plant, grain yield per plant and 1000 grain weight contributed maximum towards genetic divergence, which can be used in future hybridization programme to obtain transgressive segregents among the six clusters.

Table 1 : List of rice genotypes used in the present experiment

Line no.	Genotype	Line no.	Genotype
1	R×K-1-4-3	22	R×K-7-2-11
2	R×K-7-2-1	23	R×K-2-2-14
3	R×K-1-4-4	24	R×K-7-2-12
4	R×K-7-2-2	25	R×K-1-4-15
5	R×K-1-4-5	26	R×K-4-2-13
6	R×K-8-2-3	27	R×K-1-4-16
7	R×K-1-4-6	28	R×K-3-2-14
8	R×K-5-2-4	29	R×K-1-4-17
9	R×K-1-4-7	30	R×K-6-2-15
10	R×K-7-2-5	31	R×K-1-4-18
11	R×K-1-4-8	32	R×K-7-2-16
12	R×K-12-2-6	33	RNR-15048 (Check I)
13	R×K-1-4-9	34	KPR-1 (Check I)
14	R×K-7-2-7	35	BPT-5204 (Check I)
15	R×K-1-6-10	36	JGL-1798 (Check I)
16	R×K-14-2-8	37	KHP 11 (Check I)
17	R×K-4-4-11	38	FR13A (Check II)
18	R×K-7-2-9	39	Swarna sub-1(Check II)
19	R×K-1-4-12	40	Jyothi (Check II)
20	R×K-8-2-10	41	BPT-5204 (Check II)
21	R×K-1-4-13		

Table 2 : Clustering pattern advanced breeding lines based on D^2Values

Cluster No.	No. of genotypes	Genotypes
I	15	RxK-1-4-3, RxK-1-4-4, RxK-7-2-2, RxK-1-4-5, RxK-5-2-4, RxK-1-4-7, RxK-7-2-5,RxK-14-2-8, RxK-1-4-12, RxK-7-2-11,RxK-2-2-14, RxK-7-2-12, RxK-4-2-13, RxK-3-2-14, RxK-1-4-17
II	11	RxK-1-4-8, RxK-12-2-6, RxK-1-4-9, RxK-7-2-7, RxK-1-6-10, RxK-7-2-9, RxK-8-2-10, RxK-1-4-13, RxK-1-4-15, RxK-1-4-16, RxK-7-2-16
III	3	RNR-15048 (Check), BPT-5204 (Check), JGL-1798 (Check)
IV	4	RxK-4-4-11, RxK-6-2-15, RxK-1-4-18, KHP-11 (Check)
V	3	RxK-7-2-1, RxK-8-2-3, RxK-1-4-6
VI	1	KPR-1 (Check)

Table 3 : Inter and intra cluster distance for yield and component characters in advanced breeding lines

Cluster	**I**	**II**	**III**	**IV**	**V**	**VI**
I	13.35	45.65	42.40	121.35	22.60	85.15
II		**15.96**	78.34	46.76	48.12	181.43
III			**24.13**	148.62	58.25	46.42
IV				**45.67**	123.79	295.41
V					**37.92**	109.12
VI						**0.00**

- Diagonal values indicate intra cluster distances
- Above diagonal values indicate inter cluster distances

Table 4 : Cluster means for yield and its components characters in advanced breeding lines

Cluster / Characters	**X_1**	**X_2**	**X_3**	**X_4**	**X_5**	**X_6**	**X_7**	**X_8**	**X_9**	**X_{10}**	**X_{11}**	**X_{12}**
I	112.07	143.00	139.62	15.63	15.25	18.84	227.27	214.59	86.40	20.56	3.18	31.16
II	120.18	150.14	137.80	16.56	16.50	21.62	236.98	223.86	89.53	21.03	3.46	34.09
III	110.17	141.00	131.30	20.77	20.77	22.30	339.83	312.17	94.77	23.05	3.79	40.77
IV	124.88	154.63	141.13	17.17	17.04	21.40	292.69	254.33	89.16	22.64	3.42	34.28
V	112.17	145.00	129.67	15.83	15.68	22.11	213.47	207.33	85.50	20.60	3.19	31.70
VI	103.00	133.00	139.00	19.90	19.90	22.65	336.00	316.50	94.56	18.50	2.99	41.00

Where,

X_1- Days to 50% Flowering
X_2- Days to maturity
X_3- Plant height (cm)
X_4- Number of tillers per plant
X_5- Number of productive tillers per plant
X_6- Panicle length (cm)
X_7- Number of spikelets per panicle
X_8- Number of filled grains per panicle
X_9- Spikelet fertility (%)
X_{10}- Test weight (g)
X_{11}- Length breadth ratio
X_{12}- Grain yield per plant (g)

Table 5 ; Contribution of different traits towards total divergence

Sl No.	**Character**	**Contribution%**
1	Daysto50 percent flowering	41.8
2	Number of filled grains per panicle	11.7
3	Days to maturity	10.3
4	Number of productive tillers per plant	8.4
5	Number of spikelets per panicle	5.9
6	Grain yield per plant(g)	5.6
7	Spikelet fertility (%)	4.3
8	Length breadth ratio	4.1
9	Others	8

Table 6 : Phenotypic correlation for grain yield and yields contributing traits in advances breeding lines of rice under non submergence.

	X_1	**X_2**	**X_3**		**X_5**	**X_6**	**X_7**	**X_8**	**X_9**	**X_{10}**	**X_{11}**	**X_{12}**
X_1	1	0.82**	-0.16	-0.19	-0.17	0.19	-0.15	-0.14	0.14	0.18	0.26*	-0.10
X_2		1	-0.08	-0.33**	-0.26	0.09	-0.28*	-0.25*	-0.06	0.07	0.11	-0.18
X_3			1	-0.48**	-0.55**	-0.57*	-0.23*	-0.30**	-0.24*	-0.35**	-0.14	-0.12
X_4				1	0.93**	0.57**	0.67**	0.76**	0.45**	0.54**	0.30*	0.60**
X_5					1	0.62**	0.62**	0.70**	0.49**	0.56**	0.35**	0.63**
X_6						1	0.54**	0.58**	0.69**	0.59**	0.39**	0.66**
X_7							1	0.81**	0.66**	0.42**	0.31**	0.70**
X_8								1	0.52**	0.47**	0.25*	0.72**
X_9									1	0.48**	0.42*	0.67**
X_{10}										1	0.37**	0.45**
X_{11}											1	0.36**
X_{12}												1

X_1- Days to 50% Flowering
X_2- Days to maturity
X_3- Plant height (cm)
X_4- Number of tillers per plant
X_5- Number of productive tillers per plant
X_6- Panicle length (cm)
X_7- Number of spikelets per panicle
X_8- Number of filled grains per panicle
X_9- Spikelet fertility (%)
X_{10}- Test weight (g)
X_{11}- Length breadth ratio
X_{12}- Grain yield per plant (g)

Competing interests

Authors have declared that no competing interests exist

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