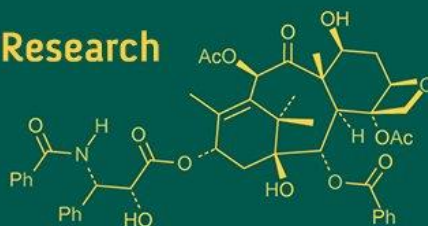


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Assessment of genetic variability for yield and yield contributing traits in rice (*Oryza sativa* L.) using Mahalanobis D² analysis

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Abstract

The present study aimed to investigate genetic divergence and variability of yield and its contributing traits involved in rice (*Oryza sativa* L.). A total of 52 genotypes were evaluated in a Randomized Complete Block Design (RCBD) for the genetic variability present in the material for yield and yield contributing traits. The phenotypic coefficient of variation was slightly higher than the genotypic coefficient of variation for all the characters. The high heritability estimate coupled with high genetic advance as% of mean were observed for days to 50% flowering (80.03), plant height (cm) (97.25), number of tillers/plant (81.732), grain L/B ratio (82.73), biological yield/plant (77.09), harvest index (%) (77.03) and grain yield per plant (74.35). This indicates that genotypes with high genetic advance are governed by additive genes and selection for these traits will be useful in improving grain yield. Mahalanobis D² statistics were utilized to investigate the presence of genetic divergence between the 52 rice genotypes that were grouped into eight clusters. There were 38 genotypes in cluster I, which was the largest cluster. There were 5 genotypes in cluster II, 2 genotypes in cluster III, IV, and V, and 1 genotype each in cluster VI, VII, and VIII. Inter-cluster distance were calculated among the eight clusters of each yield characters. Among the yield traits maximum inter-cluster distance was present between cluster IV and VI (863.27) followed by between cluster IV and VIII (811.98) followed by between cluster III and VII (506.69) followed by VII and VIII (351.70). Minimum inter cluster distance was present between cluster I and II (105.32) followed by cluster I and IV (1.8.39).

Keywords: Rice, heritability, genetic variability, genetic diversity and clusters

Introduction

Rice is the most important grain crop in the world. The world wide diffusion has established this crop as the most important human food. Farmers have fed rice more than any other important cereal crop like wheat, barley and maize. Near about 40% world's human population rice is the most important staple food, especially in East Asia, South East Asia, South Asia, the Middle East and the West Indies.

In Chhattisgarh rice occupies average of 3.6 million hectare with the productivity of the state ranging between 1.2 to 1.6 tonnes/hectares depending upon the rainfall. National wise Chhattisgarh stood 7th rank in production. The unabated growth of rice consumers, breeders have manipulated the rice phenotype for higher grain yield by accessing the rich diversity. Yield apart, the diversity has also assured the climate resiliency of the crop in the years to come. There is a need to changes to be made in phenotype for its progression with the intent for revision of genetic yield ceiling is evident in compare assessment of rice cultivars used by the farmers such as traditional, semi dwarf, hybrid, new plant type and super-rice.

Genetic Divergence Analysis

Analysis of genetic diversity existing within and between groups of germplasm is important and useful in making proper choice of parents for higher heterosis and useful recombinants. The quantitative assessment of genetic divergence was made by adopting Mahalanobis D² statistics for yield and its contributing characters. D² statistics, a concept developed by Mahalanobis (1936), is an important tool for plant breeders to classify the genotypes into different groups based on genetic divergence between them.

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Materials and Methods

The experimental materials comprised 50 rice genotypes including two checks namely Purnima and Danteshwari. The experimental materials were received from germplasm section, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalay, Raipur (C.G). These genotypes were evaluated in Randomized Block Design with 2 replications during *Kharif* 2023. Observations were recorded on 3 plants from each replication.

Results and Discussion

The highest mean performance was observed for plant height 157.44 cm, while high PCV% and GCV% were observed for harvest index (%) and grain yield per plant whereas biological yield per plant, grain length breadth ratio, number of tillers per plant and plant height (cm) expressed moderate type PCV% and GCV% (Table 1). High heritability were observed for all the characters under study except panicle length (cm), 100 grain weight(g) and

grain length (mm). The high heritability estimate shows that all the traits under study except (panicle length, 100 grain weight and grain length) reflects that all these traits are governed by additive gene action and hence the phenotypic selection would be effective for improving the overall mean for these characters

The character which have high genetic advance as% of mean coupled with high heritability estimates such as days to 50% flowering, plant height (cm), number of tillers per plant, grain length breadth ratio, biological yield per plant harvest index (%) and grain yield per plant suggested that genotypic variation in the present material for these character may possibly due to high additive genetic variance and hence selection for these characters must be effective for bringing improvement.

Similar results were reported by Kujur *et al.* (2023) for grain yield per plant, biological yield per plant and number of tillers per plant. Sao *et al.* (2024) for grain yield per plant, 1000 grain weight (g), plant height (cm) and days to 50% flowering.

Table 1: Genetic variability parameters of variation for yield and its contributing traits

S. No.	Characters	Mean	Range		GCV (%)	PCV (%)	H ² (bs) (%)	GA% as of mean
			Min	Max				
1	Days to 50% flowering (days)	67.396	43.5	82.165	11.002	12.298	80.031	20.275
2	Plant height (cm)	157.44	83.14	169.69	10.24	10.383	97.259	20.803
3	Panicle length (cm)	25.505	23.17	30.235	5.05	6.582	58.861	7.981
4	Number of tillers/plant	4.445	3.15	7.65	17.04	18.848	81.732	31.735
5	100 grain weight (g)	2.786	2.165	3.65	6.213	15.327	16.434	5.189
6	Grain length (mm)	8.371	7.2	9.85	5.231	6.745	60.142	8.357
7	Grain width (mm)	2.671	2.15	3.15	7.916	8.699	82.805	14.838
8	Grain L/B ratio	3.088	2.35	4.05	10.741	11.809	82.736	20.126
9	Biological yield/Plant (g)	35.796	29.165	50.5	13.837	15.759	77.098	25.029
10	Harvest index (%)	41.021	18.83	71.8	25.134	28.636	77.037	45.444
11	Grain yield/plant (g)	13.216	5.5	24.5	24.389	28.284	74.355	43.322

GCV% = Genotypic coefficient of variation, PCV% = Phenotypic coefficient of variation, h² (bs) = Heritability in broad sense, GA as% of mean = Genetic advance as% of mean, Min. = Minimum, Max. = Maximum.

For genetic divergence cluster analysis was performed by D² clustering analysis method using Euclidean distance as dissimilarity measure which divided 52 genotypes into eight clusters in table 2. respectively. The cluster I constituted of 38 genotypes, forming the largest cluster followed by cluster

II (5 genotypes), cluster III IV and V (2 genotypes) and cluster VI VII and VIII (1 genotypes). The pattern of group constellation proved the existence of significant amount of genetic divergence and variability among the genotypes.

Table 2: Clustering pattern of 52 rice germplasm genotypes

Cluster	Number of genotypes	Name of genotypes
I	38	(CGR:2046) Barangi, (CGR:2047) Barangi, (CGR:2045) Barangi, (CGR:2023) Barang, (CGR:2015) Banspor (A), (CGR:2043) Barangi, (CGR:2037) Barangi, (CGR:2039) Barangi, Banskotiya, Barang, Banskupi, Barangi, Banspor (A), (CGR:2023) Barangi, Banspor (I) Badekarigoti, Barang (II), Barangi(II), Barang (II), Banspor, (CGR:2028) Barangi, Barang (I), Barang Dhan, Barangi(I), Barang, Basanpati, Barang (III), Barangi, Banspor (II), Banspor (A), (CGR:2030) Barangi, (CGR:2041) Barangi, (CGR:2006) Banskupi, (CGR:2009) Banskupi, Banskupi(II), Barang, Bhado Chinga, Banspor (II)
II	5	Banskotiya, (CGR:2050) Barangi, (CGR:2049) Barangi, Banskupi, Banspor (I)
III	2	Banskotiya (I), Banskotiya
IV	2	Purnima, Danteshwari
V	2	Banskotiya, Barangi (IC-132995)
VI	1	Barangi (IC-132980)
VII	1	Barangi (IC-132985)
VIII	1	Barangi (IC-132990)

Inter-cluster distance were calculated among the eight clusters of each yield characters and presented in table 3. presented below respectively. Among the yield traits maximum inter-cluster distance was present between cluster IV and VI (863.27) followed by between cluster IV and VIII

(811.98) followed by between cluster III and VII (506.69) followed by VII and VIII (351.70).Minimum inter cluster distance was present between cluster I and II (105.32) followed by cluster I and IV (1.8.39).

Table 3: Average inter-cluster mean values for eleven and fifty-two genotypes for yield and yield attributing traits in rice

Cluster Number	I	II	III	IV	V	VI	VII	VIII
I	61.31	105.32	303.46	108.39	142.58	109.66	109.51	157.55
II		47.82	327.48	135.49	126.22	203.38	144.66	245.50
III			29.57	612.25	251.37	320.57	506.69	219.51
IV				29.84	120.60	863.27	129.75	811.98
V					88.26	240.42	209.07	184.59
VI						0.00	222.06	119.98
VII							0.00	351.70
VIII								0.00

The genotypes were grouped into different clusters based on their genetic distance in table 4. respectively. Cluster I exhibited largest mean value for grain width (2.844). Cluster II exhibited largest mean value for harvest index (56.916). Cluster III exhibited largest mean value for plant height (165.184) followed by grain length (8.411). Cluster IV exhibited largest mean value for panicle length (26.277)

followed by hundred grain weight (2.914). Cluster V exhibited largest mean value for grain length breadth ratio (4.025). Cluster VII exhibited largest mean value for days to 50% flowering (74.610). Cluster VIII exhibited largest mean value for biological yield (43.325) followed by grain length (20.392).

Table 4: Mean performance of genotypes in individual clusters for yield traits

Cluster/Character	PDF	PH	PL	NOT	HGW	GL	GW	LBR	BY	HI	GY
I I	54.554	164.20	25.389	4.875	2.844	8.104	2.833	2.916	41.735	43.247	15.031
II II	76.399	160.41	25.182	4.36	2.668	8.313	2.77	2.96	34.434	56.916	14.943
III III	68.31	165.18	25.550	4.05	2.761	8.411	2.568	3.181	33.937	24.914	9.341
IV IV	61.497	154.56	26.277	4.4	2.914	8.664	2.85	2.925	33.883	52.117	17.5
V V	65.245	86.645	23.832	3.975	2.85	8.875	2.175	4.025	30.915	43	12.385
VI VI	66.650	163.13	26.192	4.036	2.691	8.380	2.604	3.154	31.906	42.425	11.985
VII VII	74.610	159.54	24.875	4.533	2.872	8.189	2.658	2.975	38.711	36.108	12.099
VIII VIII	60.412	134.28	25.832	7.275	2.625	8.8	2.75	3.425	43.325	45.512	20.392

1. PDF-Days to 50% flowering
2. HGW-Hundred grain weight
3. BY-Biological yield
4. PH-Plant height
5. GL-Grain length
6. HI-Harvest index
7. PL-Panicle length
8. GW-Grain width
9. GY-Grain yield
10. NOT-Number of tillers
11. LBR-Grain length breadth ratio

Conclusion

- Results indicated that high PCV and GCV was recorded for harvest index and grain yield/plant, biological yield/plant, grain L:B ratio, number of tillers/plant and plant height showed moderate value, while grain length, grain width and panicle length exhibited low value.
- High heritability observed for all traits except panicle length, 100 grain weight and grain length is an indication that all traits possessed high heritability are governed by additive gene action and hence phenotypic selection is effective in improvement of characters.
- High heritability coupled with high genetic advance as% of mean were traits days to 50% flowering, plant height, number of tillers per plant, grain L:B ratio, biological yield, harvest index% and grain yield/plant an indication of predominance of additive gene action

in governing expression of these traits. Selection for further improvement these traits would be rewarding.

- Cluster I constituted of 38 genotypes, forming the largest cluster followed by cluster II (5 genotypes), cluster III IV V (2 genotypes) and cluster VI VII VIII (1 genotypes). The pattern of group constellation proved the existence of significant amount of variability.
- Cluster IV and VI had a largest inter-cluster distance among yield attributing characters respectively, which indicates that they were highly divergent populations. Hence, crossing between genotypes belonging to these clusters may result in high heterosis, which could be exploited in crop improvement.

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