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Divergence studies in rice genotypes and identification of suitable genotypes for Bastar region

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Abstract

Sixty-four rice genotypes were evaluated to estimate the magnitude of diversity associated with them using D^2 analysis to discover the diversity of genotypes. The analysis of 11 quantitative and 6 quality traits resulted in 7 different clusters from 64 rice genotypes, in which the maximum intra-cluster distance was recorded for cluster II (3.175) and maximum inter-cluster distance was found between cluster IV and cluster VII (6.332). The cluster V constituted 18 genotypes forming the largest cluster. Cluster VII with 9 genotypes exhibits the highest mean performance for the characters like the number of effective tillers, flag leaf length, grain length, grain L: B ratio, kernel length, kernel L: B ratio, biological yield and grain yield. Grain L: B ratio with 7.56% had the highest contribution towards genetic diversity. Grain yield ranged from 24.43 q/ha to 48.18 q/ha with a mean of 35.55 q/ha. Genotype RNR 35989 (48.18 q/ha), HKR 18-63 (48.15 q/ha), JGL 41255 (47.09 q/ha), BKR 421 (46.87 q/ha) and CSR 2021-E-294-153 (43.57 q/ha) were found to be high yielding. High heritability coupled with high genetic advance was reported for characters like flag leaf length, number of filled grains per panicle, test weight, biological yield, and grain yield. PCV values were found to be slightly higher than GCV values showing the influence of environment on character expression. A correlation study revealed that selection based on biological yield, harvest index, number of effective tillers per plant, flag leaf length and number of filled grains per panicle would be effective for increasing the grain yield of rice.

Keywords: Rice, divergence studies, heritability, genetic advance, correlation analysis

Introduction

The cultivated rice plant, *Oryza sativa* L., is an annual self-pollinated short-day monocotyledonous grass of the family Poaceae (Graminae) with chromosome number $2n=2x=24$. It is a warm-season crop originating from Southeast Asia, grown extensively in the world's humid tropical and sub-tropical regions. In India, rice was grown in an area of 47.83 million hectares, with a production level of 137.75 million tonnes and a productivity of 2838 kg ha⁻¹ during 2022-23 (Anonymous, 2023) [2]. The growing population in the country is intensifying the need for national food security, leading to a heightened demand for enhanced rice varieties in both quality and quantity. Therefore, improving rice production and productivity is crucial. Understanding the nature and extent of genetic variation that influences quantitative traits in rice is essential for plant breeders. Estimating genetic diversity among different genotypes is a crucial initial step in any plant breeding program. However, there has been limited emphasis on assessing the genetic diversity of rice. It is essential to identify genetically diverse accessions with desirable genes for effective use in crop breeding programs. Therefore, this study was conducted to evaluate 64 rice genotypes for their genetic divergence.

Materials and Methods

The present investigation was carried out during *khariif*, 2023 at the Instructional cum Research Farm of S. G. College of Agriculture and Research Station, Jagdalpur. The experimental material consisted of 64 genotypes of rice, which were sown in nursery beds and transplanted into the main field in Randomized Block Design in two replications with a spacing of 20 x 15 cm. Standard agronomic practices and plant protection measures were taken as per schedule. Observations were recorded on five randomly selected plants per replication for plant height (cm), number of tillers per plant, number of filled grains per

panicle, panicle length (cm), flag leaf length (cm), flag leaf width (cm), biological yield (g), harvest index (%), test weight (g), grain yield (q/ha) and observations on days to 50% flowering and days to maturity were recorded on plot basis. All grain quality parameters viz., grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, and kernel L/B ratio were done as per the DRR laboratory manual on rice grain quality procedures. The data was recorded for all the characters whose mean values were subjected to analysis of variance to test the significance for each character as per the methodology proposed by Patterson and Williams (1976) [20]. The genotypic and phenotypic variances, as well as the genotypic and phenotypic coefficient of variations (GCV and PCV), were calculated using the formulae given by Burton (1952) [4]. Heritability in a broad sense was calculated using the formula given by Allard (1960) [21] and genetic advance (GA) as percent mean was estimated by the formula given by Johnson *et al.* (1955) [9]. Genetic divergence among the genotypes was estimated using Mahalanobis' D^2 statistics (1936) and the genotypes were grouped into several clusters by Tocher's method as described by Rao (1952) [16].

Results and Discussion

A wide range of variation was observed among 64 rice genotypes for seventeen quantitative characters. The perusal of data revealed that variance due to treatment was highly significant for all the characters exhibited by the genotypes. Significant genetic variation in various component

characters might be effective. The phenotypic variance was higher than the genotypic variance for all the characters thus indicating the influence of environmental factors on these traits. Heritability and genetic advance were determined to study the scope of improvement in various characters through selection. Heritability and genetic advance are important selection parameters. High heritability estimates along with high genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johanson *et al.*, 1955) [9]. Heritability is a good index of the transmission of characters from parents to their progeny. The estimates of heritability help the plant breeder in the selection of elite genotypes from diverse genetic populations.

High heritability coupled with high genetic advance was reported for characters like flag leaf length, number of filled grains per panicle, test weight, biological yield, and grain yield. Similar findings were reported by Hasan *et al.* (2022) [8], Lakshmi *et al.* (2021) [10], Gupta *et al.* (2021) [7], Chamar *et al.* (2021) [5] and Nanda *et al.* (2021) [12]. PCV values were found to be slightly higher than GCV values showing the influence of environment on character expression. Moderate GCV and PCV values were observed for the character number of effective tillers per plant, flag leaf length, number of filled grains per panicle, test weight, kernel L; B ratio, biological yield, harvest index, and grain yield.

Table 1: Genetic parameters of variation for yield and yield attributing characters

Characters	Heritability (%)	GA%M	GCV	PCV
DF	93.97	15.69	7.86	8.10
PH	75.00	13.34	7.48	8.64
NET	63.25	18.47	11.27	14.17
PL	47.00	7.27	5.15	7.51
FLL	76.55	20.34	11.29	12.90
FLB	61.68	12.85	7.95	10.12
NFGP	80.38	28.88	15.64	17.44
TW	91.51	24.19	12.27	12.83
GL	89.35	13.05	6.70	7.09
GB	76.51	10.85	6.02	6.89
GL/GB	82.90	17.74	9.46	10.39
KL	88.92	14.07	7.25	7.68
KB	81.50	11.54	6.21	6.88
KL/KB	91.12	19.88	10.11	10.59
BY	87.15	26.24	13.65	14.62
HI	77.03	19.21	10.63	12.11
GY	90.98	30.30	15.42	16.16

Key words: DF=Days to 50% flowering; PH=Plant height; NET= Number of effective tillers; PL=Panicle length; FLL=Flag leaf length; FLB=Flag leaf breadth; NFGP=Number of filled grains per panicle; BY=Biological yield; TW=Test weight; HI=Harvest index; GL=Grain length; GB=Grain breadth; GL/GB= Grain L/B ratio; KL=Kernel length; KB=Kernel breadth; KL/KB= Kernel L/B ratio; GY=Grain yield.

The 64 genotypes which were grouped into 7 clusters were presented in Table 3.2. Cluster V was the largest with 18 genotypes followed by Cluster III and Cluster VII with 9 genotypes each, cluster I, cluster VI with 8 genotypes each, and cluster II and Cluster IV with 6 genotypes each, which represents a high level of genetic diversity in the experimented material and serves as a valuable source of genotype for economically important traits and can be used in a hybridization program. Tripathi *et al.*, (2017) [22] also reported the formation of 7 clusters of rice genotypes based

on D^2 and he said that the clustering pattern demonstrated that geographical diversity was not always related to genetic diversity and genotypes, while Mandal *et al.* (2022) [11] stated that to obtain higher heterotic responses, genotypes with distant clusters could be hybridized. Due to the maximum inter-cluster distance between the genotypes, exhibited a high degree of genetic diversity and thus may be utilized in the future for a heterosis breeding program for getting high-yielding recombinants.

Table 2: Distribution of the 64 rice genotypes into different clusters

Clusters	No. of genotypes	Genotypes
I	8	Pusa 5567-21-1, NVSR-931, NVSR-931, KMP-244, TRC 295-1-3-2, UPR 4592-3-1-1-1, Sahbhagidhan, Sanchuriya Mutant 12
II	6	Jhilli Dhan Mutant 19, NWGR-18202, TM 13327, CR 4418-4-1-2-1-2-1, KPS- 10631, KJT 23-MG-32
III	9	ODR-1-2-18-1, CB 17502, RP 6420-C10-183, TRC 2023-41, NWGR-19200, TRC 124-2-2-3, R 1672-126-1-24-1, Pusa 2095-23, Samleshwari
IV	6	MTU 1409, NLR 4020, CR 4469-RGA-126-27, CR 4606-14155-1-3-7-6-2-1, CR 2906-353-11-13, CR 4469-RGA-9
V	18	RP 6744-19023-1-1, KNM 14376, RP 6720-LVS2-CN-2094-16-7-1, PAU 10093-1R 129477-1629-14-1-4-1, WGL-1537, PAU 7682-1-3-1-1, KNM 15360, Pusa 2096-26, AD 21208, BRR-2107, ORR 1813, Shuts Dhan 11-IR18A1076, CR 4452, HURS-23-16-IR 143511-78-2-2-963-50-18, Tilkormel Mutant-12, CR 4379-4-1-1-1, RP 6680-RMS-3-5-9-16, AD 21209
VI	8	NVSR-908, CO 51, KJT-23-MG-13, CR 4396-97-2-4, CR 4472-1-1-2-1-1-1, BKR 421, TRC 2023-22, CB 18577
VII	9	JGL 41255, HKR 18-63, RNR 37913, RCPR 101-IR107891-B-B-1432-2-1, CSR 2021-E-294-153, CR 4400-1-5-IR18L1130, RNR 35989, BRR 0288, HURS-23-12-IR18A2005

The formation of clusters and estimation of intra and inter-cluster divergence lays the foundation for identifying genetically diverse parents from different clusters. The statistical distance (D) is supposed to be an assessment of genetic diversity. D² values from divergence analysis were used to calculate intra- and inter cluster D² and D values. The maximum intra-cluster distance was recorded for cluster II (3.175) followed by cluster I (3.014), cluster V (2.971), cluster VII (2.827), cluster VI (2.784) cluster IV

(2.610) and cluster III (2.576). The cluster which had low intra-cluster distance indicates limited genetic diversity among the genotypes. Highest inter cluster distance was found between cluster IV and cluster VII (6.332) followed by cluster I and II (6.264), which indicates that genotypes present in that cluster had considerable genetic distance among themselves and indicates the greater divergence between these clusters. Thus, divergent genotypes from these clusters could be used in the hybridization programme.

Table 3: Estimation of intra and inter-cluster distances among 7 clusters using Mahalanobis D² analysis

Clusters	I	II	III	IV	V	VI	VII
I	3.014						
II	6.264	3.175					
III	3.193	5.274	2.576				
IV	5.341	4.740	4.541	2.610			
V	3.963	4.743	3.819	5.661	2.971		
VI	3.654	4.261	3.527	4.153	4.107	2.784	
VII	5.809	5.270	4.776	6.332	2.974	4.802	2.827

Cluster means

Analysis of cluster means values indicated that the existence of considerable differences in the mean values of different traits (Table 4). Cluster VII with 9 genotypes, exhibits highest mean performance for the characters like number of effective tillers (9.76), flag leaf length (28.27), grain length (9.59), grain L: B ratio (3.66), kernel length (7.33), kernel L: B ratio (3.33), biological yield (85.42) and grain yield (37.46) Whereas, cluster IV with 6 genotypes, exhibited highest mean performance for the characters like days to 50% flowering (95.50), panicle length (24.08), plant height (96.39), flag leaf breadth (1.68) and number of filled grains per panicle (184.81). Cluster I with 8 genotypes, exhibited the highest mean performance for the characters like test weight (26.65), grain breadth (3.01), and kernel breadth (2.52). cluster VI with 8 genotypes, exhibited the highest mean performance for the character harvest index (49.81). The findings demonstrate that genotypes with high values for a specific trait can be selected from clusters VII and IV.

But primarily from cluster VII, which had the highest mean values for most of the traits. Furthermore, if used as a criterion for hybridization in genotypes of that cluster, characters with high cluster means will lead to better outcomes, while improving those traits. The mean performance of the cluster for yield and attributing characters is presented in Table 4.

From the cluster analysis, we can determine the contribution of each character towards genetic diversity. Grain L: B ratio (7.56) had highest contribution towards genetic diversity followed by panicle length (7.36), grain breadth (7.09), flag leaf length (8.87), number of effective tillers (6.70), kernel L: B ratio (6.67), plant height (6.60), number of filled grains per panicle (6.30), kernel breadth (6.15), flag leaf breadth (5.91), kernel length (5.53), grain length (5.18), grain yield (4.96), harvest index (4.47), biological yield (4.40) and test weight (4.15), while days to 50% flowering (4.11) showed low contribution towards genetic diversity.

Table 4: Cluster mean performance for yield and yield contributing characters

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
DF	80.81	86.75	78.67	95.5	86.08	82.5	78.56
PH	83.34	87.78	94	96.39	87.52	92.76	87.39
NET	8.2	8.08	8.5	6.88	8.36	9.01	9.76
PL	21.01	22.92	23.54	24.08	22.19	22.17	22.85
FLL	22.29	23.54	27.46	27.01	22.97	23.9	28.27
FLB	1.44	1.6	1.45	1.68	1.42	1.34	1.36
NFGP	121.04	178.57	127.19	184.81	121.73	137.29	134.67
TW	26.65	17.71	24.8	21.83	26.58	21.3	26.22
GL	8.66	8.27	8.56	8.06	9.5	7.97	9.59
GB	3.01	2.38	2.89	2.81	2.69	2.73	2.63
GL/GB	2.88	3.51	2.97	2.87	3.54	2.94	3.66
KL	6.56	6.14	6.56	6.17	7.27	6.16	7.33
KB	2.52	2	2.44	2.42	2.26	2.26	2.21
KL/KB	2.62	3.09	2.69	2.55	3.22	2.73	3.33
BY	55.89	73.72	68.24	74.1	68.83	66.84	85.42
HI	46.11	41.15	37.25	47.69	43.32	49.81	44.09
GY	25.49	30.27	25.28	35.31	29.61	33.15	37.46

Key words: DF=Days to 50% flowering; PH=Plant height; NET= Number of effective tillers; PL=Panicle length; FLL=Flag leaf length; FLB=Flag leaf breadth; NFGP=Number of filled grains per panicle; BY=Biological yield; TW=Test weight; HI=Harvest index; GL=Grain length; GB=Grain breadth; GL/GB= Grain L/B ratio; KL=Kernel length; KB=Kernel breadth; KL/KB= Kernel L/B ratio; GY=Grain yield.

Table 5: Contribution of yield and yield attributing characters toward Genetic diversity

Characters	% contribution
Days to 50% flowering	4.11
Plant height	6.60
Number of effective tillers	6.70
Panicle length	7.36
Flag leaf length	6.87
Flag leaf breadth	5.91
Number of filled grains per panicle	6.30
Test weight	4.15
Grain length	5.18
Grain breadth	7.09
Grain L:B ratio	7.56
Kernel length	5.53
Kernel breadth	6.15
Kernel L:B ratio	6.67
Biological yield	4.40
Harvest index	4.47
Grain yield	4.96

Correlation coefficient analysis

Correlation analysis reveals the interrelationships between various independent qualities and dependent traits such as grain yield/plant. In the current study, genotypic correlation coefficients were higher in magnitude in the same direction than phenotypic correlation coefficients, indicating that there is a strong inherent association between each pair of characters, which could be due to the environment's masking or modifying effect.

Grain yield showed a high positive significant association with biological yield (0.607**) followed by harvest index (0.455**). The number of effective tillers per plant (0.190*), number of filled grains per panicle (0.204*), and flag leaf length (0.181*) showed a positive significant association. A

positive non-significant correlation was recorded for days to 50% flowering (0.081), plant height (0.105), panicle length (0.157), flag leaf breadth (0.083), test weight (0.065), grain length (0.004), grain L: B ratio (0.055), kernel length (0.090) and kernel L: B ratio (0.116). A negative non-significant correlation was associated with grain breadth (-0.100) and kernel breadth (-0.088).

Similar findings were reported by Allam *et al.* (2015) ^[1] (number of effective tillers), Puttoju *et al.* (2022) ^[15] and Perween *et al.* (2020) ^[14] (biological yield, harvest index), Bhargava (2021) ^[3] (Number of effective tillers per panicle, panicle length, number of filled grains per panicle), Fentie *et al.* (2021) ^[16] (harvest index), Selvarani *et al.* (2022) ^[17] (harvest index) and Sinha *et al.* (2023) ^[19] (biological yield).

Table 6: Estimation of phenotypic correlation coefficient between yield and yield traits

Characters	DF	PH	NET	PL	FLL	FLB	NFGP	TW	GL	GB	GL/GB	KL	KB	KL/KB	BY	HI	GY
DF	1																
PH	0.037																
NET	-0.430**	-0.125															
PL	0.130	0.558**	-0.082														
FLL	-0.142	0.597**	-0.003	0.555**													
FLB	0.325**	0.222*	-0.344**	0.295**	0.081												
NFGP	0.374**	0.291**	-0.236**	0.353**	0.299**	0.539**											
TW	-0.279**	-0.127	0.192*	-0.125	-0.063	-0.280**	-0.583**										
GL	-0.128	-0.202*	0.206*	-0.047	-0.012	-0.335**	-0.450**	0.672**									
GB	-0.191*	0.133	-0.112	-0.081	-0.009	-0.001	-0.301**	0.505**	-0.107								
GL/GB	0.039	-0.220*	0.215*	0.033	0.003	-0.225*	-0.087	0.106	0.739**	-0.742**							
KL	-0.144	-0.162	0.228**	-0.052	-0.015	-0.356**	-0.461**	0.719**	0.937**	-0.050	0.653**						
KB	-0.152	0.102	-0.120	-0.128	-0.023	0.058	-0.261**	0.475**	-0.161	0.905**	-0.715**	-0.079					
KL/KB	-0.009	-0.179*	0.243**	0.057	0.009	-0.294**	-0.152	0.199*	0.765**	-0.615**	0.926**	0.758**	-0.703**				
BY	0.054	0.158	0.270**	0.244**	0.261**	0.190*	0.247**	0.003	0.122	-0.216*	0.214*	0.150	-0.185*	0.217*			
HI	0.030	-0.097	-0.060	-0.038	-0.102	-0.126	-0.026	0.050	-0.124	0.095	-0.148	-0.068	0.076	-0.092	-0.354**		
GY	0.081	0.105	0.190*	0.157	0.181*	0.083	0.204*	0.065	0.004	-0.100	0.055	0.090	-0.088	0.116	0.607**	0.455**	1

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

Key words: DF=Days to 50% flowering; PH=Plant height; NET= Number of effective tillers; PL=Panicle length; FLL=Flag leaf length; FLB=Flag leaf breadth; NFGP=Number of filled grains per panicle; BY=Biological yield; TW=Test weight; HI=Harvest index; GL=Grain length; GB=Grain breadth; GL/GB= Grain L/B ratio; KL=Kernel length; KB=Kernel breadth; KL/KB= Kernel L/B ratio; GY=Grain yield.

Conclusion

The results concluded that genotypes RNR 35989 (48.18 q/ha), HKR 18-63 (48.15 q/ha), JGL 41255 (47.09 q/ha), BKR 421 (46.87 q/ha) and CSR 2021-E-294-153 (43.57 q/ha) were found to be suitable for Bastar region. Characters like flag leaf length, number of filled grains per panicle, test weight, biological yield, and grain yield show high heritability coupled with genetic advance as percent of mean therefore should be given top priority during selection. Further cluster IV (MTU 1409, NLR 4020, CR 4469-RGA-126-27, CR 4606-14155-1-3-7-6-2-1, CR 2906-353-11-13, CR 4469-RGA-9) and cluster VII (JGL 41255, HKR 18-63, RNR 37913, RCPR 101-IR107891-B-B-1432-2-1, CSR 2021-E-294-153, CR 4400-1-5-IR18L1130, RNR 35989, BRR 0288, HURS-23-12-IR18A2005) were most diverse to each other. These clusters are suggested to provide a broad spectrum of variability in segregating generations and the genotypes present in them may be used as parents for future hybridization programs to develop desirable types.

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