Assessment of Genetic variability, Character Association of yield related traits and Genetic Divergence study in Rice (*Oryza sativa* L.)

ABSTRACT

The present study was carried out to assess the genetic diversity for various rice traits and their association with yield during *Kharif* 2023-24 at Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (Uttar Pradesh), India. 64 rice genotypes were evaluated on the basis of various morphological traits in a field experiment. Significant variation were observed among genotypes for all the traits studied. The results indicated that the highest genetic variability was observed in case of plant height, days to maturity, numbers of spikelets per panicle and biological yield per plant. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits studied. High GCV and PCV were observed for grain yield per plant. Broad sense heritability varied from 98.03% in case of days to maturity to 61.45% for harvest index. Significant positive correlation with grain yield was also noticed for harvest index (0.475), test weight (0.503), number of spikelet per panicle (0.827) and biological yield per plant (0.942). All the traits were also studied through path coefficient analysis and highest positive direct effect on grain yield per plant was recorded by biological yield per plant (0.942) followed by harvest index (0.267). The dendrogram of cluster analysis grouped 64 rice genotypes into seven clusters. Cluster II incorporated the highest number of genotypes. Data from this study exhibited the presence of sufficient genetic diversity among the genotypes which can be employed in future rice breeding programmes.

Key Words: Rice; Oryza sativa; Genetic diversity; Correlation; Cluster

1. INTRODUCTION

Rice (*Oryza sativa* L.) is the most important cereal consumed by more than 3.5 billion people comprises about half of the world's population [1]. It contains a significant number of calories and a wide variety of essential vitamins, minerals, and other nutritional value [2]. The total rice production is 135.76 million metric tons in India, with an area of 47.83 million hectare and the average yield of 4.26 metric tons per hectare after China

(USDA Global Analysis 2023). A phenomenal increase in productivity per hectare over the years has contributed to higher overall production. The reasons attributed for this higher productivity is the green revolution, in which the short and HYVs (high yielding varieties), fertilizer application and irrigation practices were introduced [3]. As we know that currently India is facing the issue of nutritional deficiencies; so it's crucial to diversify our agricultural focus towards cultivating millets, pulses, and oilseeds alongside rice production. The aim is to enhance agricultural output without compromising rice production. Rapidly increasing demand due to increasing population has forced us to search for another quantum jump in rice productivity. In the present scenario the rice productivity has reached a plateau. In order to achieve the expected targets, we have to develop the varieties with higher yield potential by breaking the existing yield plateau through utilizing more diversified parents in breeding programmes. The success of any plant breeding programme largely depends on the existence of diversity among the genotypes [4]. Genetic variability estimates are the basic parameters that a researcher should notice in order to plan a crop improvement programme. For this objective, the present experiment aims to assess the degree of genetic variability present in rice germplasm collections and the nature of traits in the evaluated genotypes in order to identify superior lines which can further be used as donor parents in breeding programmes. D^2 analysis was employed to assess the degree of genetic diversity among genotypes, which is based on multivariate analysis developed by Mahalanobis, 1936 [5]. This analysis provides a measurement of relative contribution of different components on diversity both at intra and intercluster level and genotypes drawn from widely divergent clusters are likely to produce heterotic combinations and wide variability in segregating generations.

2. MATERIALS AND METHODS

The present investigation was carried out during *Kharif* 2023-24 at Crop Research Station, Nawabganj of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (Uttar Pradesh). The geographical coordinates of the site were 26°29' 35" North latitude and 80°16'25" East Longitudes and is located on an elevation of about 125.9 m above mean sea level in Gangetic plain. The experimental material for the investigation comprised 64 strains/varieties of rice (*Oryza sativa* L.) which are presented in table 1. The design adopted was Randomized Block Design with three replications.

Table 1. Description of rice genotypes used in the study

S.No.	Designation	S.No.	Designation
1	KNM 13568	33	RP 6745-MSAC 23-49
2	NLR 3819	34	CR 4385-RGA-6-2
3	NWGR 17075	35	UPR 4611-1-1-1-1-1
4	KGT-23-3	36	JNPT 581-64
5	CB 17504	37	AD 21184
6	Nath 20 -20	38	HKR 18-33
7	RP 6475-CGR 16-CGIL 54-CGK 2- I-2131-S	39	KPS 10642
8	OR 2577-5	40	IR 19LJ054
9	RP 6746- IR 17A2831	41	RP 6459-C2-sel12
10	CR 4428-1-1-2-1-3-1	42	CR 4388-RGA-245
11	CR 4077-1357-5-4-2-1-1	43	CSR AP10
12	KMP 252	44	PR 113, Lalat, MTU 1020, Karjat-7 (ZC)
13	NDRK 11-27	45	RP 6744-19180-1-1
14	RP 6721-LVS 24-CN 2103-21-11-2	46	HURS-23-2-IR 18A1565
15	CR 3506-1-2-3-2-1	47	NVSR 941
16	CR 4396-291-2-6	48	Surya 27
17	MTU 1392	49	HURS-23-17-IR-143534-114-1-1-387-31-38
18	Pusa 2086-36-11-12-1	50	BNP-401
19	ORJ 1348	51	R 2341-329-2-169-1
20	RP5683-101-30-2	52	BRR-2134
21	SKL-8-33-1570-107-320-242-127	53	BRR 0287-IR 143532-95-1-1-177-44-4
22	CR 4388-RGA-60-53-1	54	CR 4396-1-13-11
23	NDR TFR-10	55	RP 6529-RMS-64-5-7-9
24	Pusa 2087-40-19-4-1	56	TRC 2023-51/ IR 126999-B-32-2-1-3
25	OROI-11-IR 88243-17-1-1-3	57	RP 6529-52-5-7-9
26	BRR 0053-IR 96321-10999-347-B-1-2	58	PAU 6707-22-1-2-2 (RYT 3889)
27	BKR 510	59	YNPK-7258
28	RNR 38125	60	RNR 38966
29	WGL 1740	61	GNV 2188-1
30	ORR 1815	62	CR 4415-3-1-3-1-3-1
31	NDR 8806-TFR-3	63	Gontra Bidhan-3 (NC)
32	CSR-30 (LC)	64	CR 4343-15-2-1-1

The observations were recorded on days to 50% flowering (DFF), days to maturity (DOM), plant height (PH), flag leaf length (FLL), flag leaf width (FLW), number of tillers per plant (NTPP), number of panicles per plant (NPPP), panicle length (PL), number of spikelets per panicle (NSPP), biological yield (BY), harvest index (HI), test weight (TW), and grain yield per plant (GY). The data were recorded on three randomly selected plants from each replication for all characters except days to 50% flowering and days to maturity. Plant height was measured in centimeters from the ground level to the top of the panicle (excluding awn) at the time of maturity. The total number of tillers and number of panicles in each of the three randomly selected plants were counted and averaged. Length of main panicle was recorded by measuring from the base of the panicle to the top most spikelet excluding awn in centimeters. The length of the flag leaf was measured in centimeters from the base to the tip of randomly selected flag leaves and flag leaf width was measured (cm) in the middle part of the leaf from one margin to another margin. Number of Spikelets per panicle was recorded by counting the total number of spikelets from the main panicle. Biological yield were recorded in gram separately and averaged for each replication before threshing. Grain yield (g) were recorded separately and averaged too. Harvest index is the ratio of economic yield to biological yield.

Harvest index (%) = Economic yield (Grain yield) / Biological yield (grain yield + straw) X100

The obtained data were analyzed using two-way analysis of variance (ANOVA) and Winostat 9.3 software was used. This analysis was aimed to get the information about genotypes and their interaction. The phenotypic and genotypic coefficient of variation, heritability in broad sense and genetic advance as percentage of mean were calculated by using the formula proposed by Burton and Devane in 1953 [6]. Simple correlation coefficients were computed at genotypic and phenotypic levels between pairs of characters adopting the following formula given by Johnson *et al.* (1955) [7]. Path analysis is worked out by using the estimates of simple correlation coefficients. To assess the genetic diversity, D^2 analysis was performed and a dendrogram was constructed.

3. RESULTS AND DISCUSSION

The genetic improvement in a crop species is inevitable and continuous process to meet the future challenges. Analysis of variance (ANOVA) revealed highly significant differences among all the traits, indicating a substantial amount of genetic variability and potential for selection in the desired direction which is presented through table 2.

Table 2. Analysis of variance of RBD for 13 characters in rice genotypes

S.No.	Characters	Mean Sum of Squares		
		Rep. d.f.(2)	Treat. d.f.(63)	Error d.f.(126)
1	DFF	45.19	166.13**	1.98
2	DOM	26.36	254.88**	1.69
3	PH	570.36	353.23**	18.88
4	FLL	2.01	62.55**	1.18
5	FLW	0.002	0.090**	0.001
6	NTPP	1.53	8.30**	0.14
7	NPPP	3.62	6.55**	0.17
8	PL	16.7	67.64**	0.85
9	NSPP	214.69	1771.69**	16.94
10	BY	16.6	720.34**	6.67
11	GY	2.29	118.49**	1.17
12	HI	24.03	42.40**	7.33
13	TW	12.81	46.19**	0.81

*,** significance at 5% and 1% level, respectively.

Coefficient of variation is preferred for comparison of variation between two characters. The estimates of GCV and PCV, heritability in broad sense (h^2_{bs} %) and genetic advance as percent of mean is given in table 3and depicted through graph in fig.2. The highest estimates of both GCV and PCV were recorded for Grain yield per plant, biological yield per plant, number of spikelets per panicle and number of tillers per plant. The PCV and GCV estimates indicating adequate scope for selection on the basis of these traits. The findings were in accordance to Zeleke *et al.*, (2021) [8] and Chaudhary *et al.*, (2023) [9]. Characters showing high heritability coupled with high genetic advance as percent of mean were GY, BY, NSPP and TW. These findings were in agreement with Nithya *et al.*, (2020) [10] and Sumanth *et al.*, (2017) [11]. It can be concluded that high GCV, PCV, heritability and GA as percent of mean were observed for grain yield, biological yield and number of spikelets per panicle indicating the preponderance of additive gene action, playing major role in expression of these characters. Similar findings were reported by Bhargawa *et al.*, (2021) [12] and Sudeepthi *et al.*, (2020) [13].

Table 3. Estimates of GCV and PCV, heritability in broad sense (h^2_{bs} %) and genetic advance as percent of mean (GA %) for different characters in Rice

genotypes

S.No.	Characters	GCV (%)	PCV (%)	h^2 (%)	GA as % of mean
1	DFF	8.52	8.67	96.52	17.23
2	DOM	7.34	7.41	98.03	14.97
3	PH	9.19	9.93	85.51	17.5
4	FLL	13.04	13.41	94.55	26.12
5	FLW	12.57	12.75	97.18	25.53
6	NTPP	21.11	21.66	94.98	42.38
7	NPPP	17	17.67	92.59	33.7
8	PL	19.54	19.91	96.34	39.52
9	NSPP	26.15	26.52	97.19	53.1
10	BY	27.33	27.71	97.27	55.52
11	HI	9.7	12.37	61.45	15.66
12	TW	20.42	20.96	94.94	40.98
13	GY	31.23	31.69	97.09	63.39

The most important economic character grain yield per plant exhibited highly significant positive correlation with number of spikelet per panicle, biological yield, harvest index and test weight at both genotypic and phenotypic level and the estimates are presented in table 4. This research aids breeders in upcoming breeding initiatives by identifying beneficial traits that are positively correlated with yield. Similar findings were recorded by Hossain *et al.*,(2020) [14] and Renuprasath *et al.*,(2023) [15]. The path coefficient analysis was worked out by using simple correlation among 13 characters to estimate the direct and indirect effect of different characters on grain yield per plant and are presented through table 5. The highest positive direct effect on grain yield per plant was exhibited by biological yield followed by harvest index, flag leaf width and number of panicles per plant. Whereas number of spikelet per panicle *via* biological yield and test weight *via* biological yield exhibited highest positive indirect effect on grain yield per plant. Hence, it is suggested that due consideration should be given to biological yield and harvest index while exercising selection. Similar findings were reported by Singh *et al.*, (2018) [16], Thuy *et al.*, (2023) [17] and Kujur *et al.*, (2023) [18].

Table 4. Estimates of correlation coefficient among different characters in rice genotypes

Characters	DFF	DOM	PH	FLL	FLW	NTPP	NPPP	PL	NSPP	BY	HI	TW
DFF	1	0.811**	-0.370**	-0.202**	0.041	-0.053	-0.018	-0.073	0.081	0.009	-0.319**	-0.013
DOM			-0.206**	-0.012	0.092	-0.046	0.038	0.043	0.055	-0.045	-0.299**	-0.019

PH				0.153*	-0.027	0.232**	0.069	0.025	0.138*	0.088	0.115*	0.066
FLL					0.194*	0.081	0.025	0.037	0.024	0.088	0.028	0.201*
FLW						0.057	0.037	-0.04	0.157*	0.084	-0.116	0.008
NTPP							0.659**	0.220**	0.007	0.023	-0.033	0.196*
NPPP								0.324**	0.062	0.188*	0.11	0.313**
PL									0.143*	0.206**	0.064	0.409**
NSPP										0.873**	0.183*	0.441**
BY											0.231**	0.489**
HI												0.224**
TW												
GY												

*,** significance at 5% and 1% level, respectively.

DFF= Days to 50% flowering, **DOM**= Days to maturity, **PH**= Plant height, **FLL**= Flag leaf length, **FLW**= Flag leaf width, **NTPP**= Number of tillers per plant, **NPPP**= Number of panicles per plant, **PL**= Panicle length, **NSPP**= Number of spikelets per panicle, **BY**= Biological yield per plant, **HI**= Harvest index, **TW**= Test weight, **GY**= Grain yield per plant

Table 5. Direct and indirect effect of different characters on grain yield in rice genotypes

Characters	DFF	DOM	PH	FLL	FLW	NTPP	NPPP	PL	NSPP	BY	HI	TW
DFF	**-0.0199**	0.0068	0.0007	0.001	0.001	0.0003	-0.0003	0.0003	-0.0037	0.0087	-0.0853	0.0018
DOM	-0.0161	**0.0084**	0.0004	0.0001	0.0023	0.0003	0.0006	-0.0002	-0.0025	-0.0429	-0.0798	0.0016
PH	0.0074	-0.0017	**-0.002**	-0.0008	-0.0007	-0.0014	0.0011	0.0001	0.0063	0.0827	0.0307	0.0012
FLL	0.004	-0.0001	-0.0003	**0.005**	0.0048	-0.0005	0.0004	-0.0002	-0.0011	-0.0833	0.0075	0.0005
FLW	-0.0008	0.0008	0.0001	0.001	**0.0246**	-0.0004	0.0006	0.0002	-0.0071	0.079	-0.0311	-0.0011
NTPP	0.0011	-0.0004	-0.0005	-0.0004	0.0014	**-0.006**	0.0103	-0.001	-0.0003	-0.0218	-0.0087	0.0023
NPPP	0.0004	0.0003	-0.0001	-0.0001	0.0009	-0.004	**0.0156**	-0.0015	0.0028	0.177	0.0295	0.0029
PL	0.0014	0.0004	0.0001	-0.0002	-0.001	-0.0013	0.0051	**0.0047**	0.0065	0.1944	0.0172	0.0031
NSPP	-0.0016	0.0005	0.0003	-0.0001	0.0039	0.002	0.001	0.0007	**0.0453**	0.8223	0.0489	0.004
BY	-0.0002	-0.0004	0.0002	0.0004	0.0021	0.0001	-0.0029	-0.001	0.0396	**0.9421**	0.0618	0.0045
HI	0.0063	-0.0025	-0.0002	-0.0001	-0.0029	0.0002	-0.0017	-0.0003	0.0083	0.2177	**0.2673**	0.004
TW	0.0003	-0.0002	0.0001	0.001	0.0002	-0.0012	0.0049	-0.0019	-0.02	0.4603	0.0598	**0.009**

Residual effects-0.00466

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

Bold values showing direct and normal values showing indirect effect.

Mahalnobis (1928) followed by clustering of genotypes into various non-overlapping clusters by Tocher's method. The 64 genotypes were grouped in to seven non-overlapping clusters and their details are presented in table 6. The highest number of 15 genotypes appeared in cluster-II, while cluster-V contained lowest number of 4 entries. The maximum intra-cluster distance was observed in case of Cluster-VII indicating the presence of wide genetic diversity among the genotypes present in the same. The maximum inter-cluster distance was observed between the Cluster-II and III followed by cluster-V and VII which are presented in table 7. Based on these findings, crosses between Cluster-II and III and Cluster-V and VII is recommended to obtain robust heterotic recombinants and transgressive segregants in future breeding programmes. To realize maximum variability and high heterotic effect, Mishra *et al.* (2003) [19] and Chaturvedi and Maurya (2005) [20] recommended that parents should be selected from two clusters having wider inter cluster distance.

Table 6. Clustering pattern of 64 rice genotypes on the basis of non-hierarchical Euclidean cluster analysis

Clusters	No of genotypes	Genotypes (as mentioned in Table 1)
I	11	11 16 17 26 27 31 41 42 56 57 63
II	15	5 6 10 12 13 25 28 29 30 36 37 40 48 58 64
III	5	1 2 34 35 59
IV	10	14 22 23 24 32 33 52 53 54 61
V	4	7 38 39 49
VI	7	3 4 15 21 43 50 51
VII	12	8 9 18 19 20 44 45 46 47 55 60 62

Table 7. Estimates of inter and intra-cluster distance

Clusters	I	II	III	IV	V	VI	VII
I	**2.286**	2.903	3.887	4.132	3.544	2.958	3.997
II		**2.572**	4.727	4.39	4.028	3.492	3.938
III			**2.798**	3.527	3.87	4.201	3.409
IV				**2.651**	4.281	2.935	3.483
V					**2.113**	3.343	4.436
VI						**2.54**	4.038
VII							**2.942**

Bold figures indicating the intra-cluster distance while normal figure showing inter-cluster distances

The selection and choice of parents mainly depends upon contribution of characters towards divergence. The highest contribution towards genetic divergence was exhibited by harvest index followed by plant height, number of panicles per plant, flag leaf length, number of tillers per plant, days to 50% flowering, panicle length and grain yield. Remaining characters contributed comparatively low towards total divergence which is presented in table 8 and depicted through pie chart in fig.1.

Table 8. Contribution of 13 different characters towards total divergence in rice genotypes

S.No.	Characters	% contribution
1	Days to flowering	7.35
2	Days to maturity	5.69

3	Plant height (cm)	10.44
4	Flag Leaf Length (cm)	8.17
5	Flag Leaf Width (cm)	6.51
6	No. of tillers /plant	7.57
7	No. of panicle/plant	9.25
8	Panicle length (cm)	7.24
9	No. of spikelet/ panicle	6.51
10	Biological yield per plant (g)	6.53
11	Harvest index (%)	11.54
12	Test weight (g)	6.18
13	Grain yield per plant (g)	7.01

Fig.1: Pie chart representation of different traits and their contribution towards genetic divergence

Fig.2: Bar diagram of GCV, PCV, broad sense heritability and genetic advance as percent of mean

4. CONCLUSION

In the present study, the analysis of variance (ANOVA) revealed existence of highly significant variations among 64 genotypes of rice. Among these genotypes, RP 6459-C2-sel 12 followed by KMP 252 and RNR 38966 are regarded as best for grain yield per plant. These genotypes also exhibited consistently high mean performance for other traits related to yield; indicating their potential for being effective in terms of yield. High estimates of GCV and PCV along with high values of heritability and genetic advance were observed for grain yield per plant, biological yield per plant and number of spikelets per panicle. Correlation coefficient analysis exhibited positive and significant association of grain yield per plant with NSPP (0.827), BY (0.963), HI (0.475) and TW (0.503). Whereas, path coefficient analysis revealed that BY (0.942) and HI (0.267) had positive and direct effect on grain yield. The genotypes were grouped in 7 clusters. In case of intra and inter-cluster distance, the maximum intra-cluster distance was observed in case of Cluster-VII (2.942) while maximum inter-cluster distance was observed between the Cluster-II and III(4.727). The highest percentage contribution towards genetic divergence was exhibited by harvest index followed by plant height, number of panicles per plant, panicle length and grain yield. The genetic variation found among rice genotypes provides a crucial basis for creating new varieties with enhanced characteristics. By leveraging this diversity in breeding programs, breeders can effectively utilize the genetic potential of various genotypes to develop superior rice varieties.

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