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ASSESSMENT OF GENETIC VARIABILITY, CHARACTER ASSOCIATION AND GENETIC DIVERGENCE IN RICE (*Oryza sativa* L.) UNDER SEMI-DEEP WATER CONDITION

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ABSTRACT

Thirty rice genotypes, including 3 checks were evaluated for 11 quantitative traits to study genetic variability, character association, path analysis and divergence under semi deep water conditions. The analysis of variance confirmed the presence of substantial variation for all the traits. High estimates of heritability with high genetic advance were observed for grain yield per plant, harvest index, number of productive tillers, 1000-grain weight and biological yield which indicated the presence of additive gene effects. Grain yield per plant exhibited significant positive correlation with spikelet fertility, harvest index, 1000-grain weight, number of spikelets per panicle and panicle length at both genotypic and phenotypic levels. Path coefficient analysis indicated that biological yield per plant, harvest index, spikelet fertility, number of spikelets per panicle and 1000-grain weight had high positive direct effects on grain yield, revealing their importance as selection parameters for yield enhancement. The genotypes were grouped into 3 non overlapping clusters revealing the presence of diversity in the population. The present study aimed to identify promising rice genotypes with desirable trait combinations to enhance ongoing breeding programmes through the estimation of variability and genetic diversity.

Key words: Rice, Genetic variability, Character association, Divergence

Introduction

Rice serves as the dietary staple for more than half of the world's population and is the most important food grain for millions of people across Asia, Africa, and Latin America, contributing substantially to the daily caloric intake of over half of the total global population. As population growth rates are high and are expected to continue increasing at least for the next decade in these regions, rice remains to be their primary source of food. The development of high-yielding, lodging-resistant, and fertilizer-responsive rice varieties (along with wheat)

during the 1960s, laid the foundation for the Green Revolution. Rice contains 70-80 % carbohydrates, 6-7 % protein, 1.2-2.0% mineral matter. In addition to calories, it is a good source of magnesium, phosphorus, manganese, selenium, iron and Vitamin-B complex such as thiamine, riboflavin and niacin (Fresco, 2005).

Total production of rice in India during 2025-26 (3rd Advance estimates) is recorded at 1540.24 Lakh tonnes. It is higher by 38.4 Lakh tonnes than previous year's rice production of 1501.84 Lakh tonnes (Unified Portal for Agricultural Statistics (UPAg), Deptt. Of Agriculture &

Farmers Welfare). According to the latest data provided, Uttar Pradesh is the highest rice producing state, followed by Telangana and West Bengal on the basis of order of percentage share of production during 2024-25.

Semi-deep water rice is a kind of rice that is adapted to grow in areas where the standing depth of water in the field varies between 20-60 cm (Sarangi *et al.*, 2020). It has special adaptations that allow it to produce better yields with less irrigation. This water regime of rice crop has the potential to offer a more sustainable option for cultivation, particularly in areas where water is scarce or where irrigation is expensive. Semi-deep water rice cultivation involves managing nutrient inputs effectively to optimize crop productivity and maintain soil health.

The presence of considerable genetic variability in a population is a fundamental pre-requisite for development of new varieties that outperform the currently existing varieties. The assessment of character association and path analysis aids a breeder in understanding the contribution and effect of each character to yield, and thereby making appropriate selection for them. All these analysis helps in designing an efficient breeding programme by allowing the selection of elite parental lines which can be further exploited in breeding programmes to develop superior varieties.

Materials and Methods

The present investigation was done at CRS, Masodha of Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar, Ayodhya in course of *Kharif* season, 2023. Geographically this place situated between 26.48°N latitude, 82.13°E longitude and at an elevation of 113 meters above mean sea level in the Gangetic plains of eastern U.P. The district of Ayodhya experiences a semi-arid climate with hot summer and cold winter. About 80% of total rainfall is received during the monsoon season (upto September) with occasional showers in the winter.

The soil of experimental site had a pH of 7.4 which makes it slightly alkaline, with electrical conductivity (EC) of 0.2dsm⁻¹, rich in potash K₂O (232.5 kg/ha) with available nitrogen N (205.4 kg/ha), phosphorus P₂O₅ (23.5 kg/ha) and organic carbon (0.3). Observations were recorded for eleven quantitative characters namely, days to 50% flowering, days to maturity, plant height (cm), number of productive tillers, panicle length (cm), number of spikelets per panicle, spikelets fertility (%), 1000-grain weight (g), biological yield per plant (g), harvest index (%) and grain yield per plant (g).

The experimental material for the present study consisted of 30 genotypes including 3 check varieties

Table 1: List of genotypes.

S. No.	Genotype Name
1	RP Bio 4919-NSR 53-1
2	NDR 2022-10-6
3	MTU 1422 (MTU 2481-14-1-1-1)
4	CRU-BCKV-15 (15-Sw/Sa-17-8-5-5)
5	RGL 7038 (MTURM428-53-1-1)
6	CR 3993-151-5-3
7	CN 2164-54-3-1-1
8	CR 2667-4-1-2-2-1
9	TTB 2013-33
10	CR-2839-1-5-B-1-5-1-B-9-1-1-1-2
11	MTU 1388 (MTU 2527-22-1-1-1) (Check)
12	NDR 2022-10-4
13	OR 2765
14	MTU 1424 (MTU 2433-1-3-1)
15	CR 4378-2-1-1-6
16	TTB 2010-56
17	RP Bio 4918-NPK 24
18	CR 4492-3-1-1-1
19	MALI-4
20	MTU 1423 (MTU 2527-22-1-1-1)
21	CN 2164-21-3-1-1
22	Sambha Sub-1 (Check)
23	CR 2889-208-11-17
24	NDR 2022-8-2
25	CR 3993-133-15-8
26	CR-3478-M-11-B-1-2
27	OR 2606-1
28	CSRC(D) 12-8-12-1
29	CR 2667-8-5-3-2-1
30	NDR 9930111 (MSD) (Check)

namely MTU 1388, Sambha Sub-1 and NDR 9930111 (MSD) (Table 1). The experimental trial was laid out in Randomized Block Design (RBD) with three replications. The analysis of variance for various traits in the randomised block design followed the methodology outlined by Panse and Sukhatme (1967). To assess variability in different traits, the approach recommended by Burton and de Vane (1953) was employed. The heritability in the broad sense (h^2_b) was calculated using the formula proposed by Allard *et al.*, (1960). The expected genetic advance (GA%) was estimated based on the formula suggested by Robinson *et al.*, 1949; Johnson *et al.*, (1955). The association among different traits at both genotypic and phenotypic levels was determined as per the methodology outlined by Searle (1961). Path coefficient analysis was carried out according to Dewey and Lu (1959). The Mahalanobis' D² cluster analysis (1936) was used to assess the genetic diversity existing among thirty genotypes on the basis of eleven quantitative characters.

Table 2: Analysis of variance of randomized block design for 11 traits in rice.

Source of variation	Repli- cation	Treat- ments	Error
	df 2	df 29	df 58
Days to 50% flowering	7.81	65.92**	6.01
Days to maturity	0.58	66.32**	5.22
Plant height (cm)	17.48	532.75**	19.31
No. of productive tillers	0.01	6.77**	0.00
Panicle length (cm)	0.07	6.30**	0.06
No. of spikelets/panicle	21.94	365.35**	1.55
Spikelets fertility (%)	0.62	167.76**	0.98
1000-grain weight (g)	0.01	29.22**	0.14
Biological yield/plant (g)	3.57	293.68**	3.62
Harvest Index (%)	0.61	224.60**	0.37
Grain yield/plant (g)	0.14	63.31**	0.11

Results and Discussion

Analysis of Variance (ANOVA)

The Analysis of Variance revealed that treatment mean squares were highly significant for all the eleven traits. The mean squares due to replications, however, were non-significant for the all the traits (Table 2).

Genetic variability, heritability, genetic advance and coefficient of variance

The high estimates of heritability in broad sense (>80%) were recorded for no. of productive tillers (99.80%), harvest index (99.34%), grain yield/plant (99.29%), no. of spikelets/panicle (98.33), 1000-grain weight (98.08), spikelet fertility (97.69%), panicle length (96.26%), biological yield/plant (95.24%), plant height (86.93%). The moderate estimates of heritability (<80% and >50%) were observed for traits days to maturity (74.52%) and days to 50% flowering (71.38%). The results are in similarity with the findings of Venkanna *et al.*, (2022) and Chendake *et al.*, (2023), they found high estimates of heritability for number of spikelets per

panicle, spikelet fertility, grain yield per plant.

The high estimates of genetic advance in per cent of mean (>20%) were recorded by harvest index (35.99%), grain yield/plant (31.40), no. of productive tillers (26.66%), 1000 grain weight (27.58%), biological yield/plant (27.50%). The moderate estimate for genetic advance (10-20%) in per cent of mean was shown by plant height (19.52%), no. of spikelets/panicle (18.37%), panicle length (11.05%) while lower estimates for genetic advance (<10%) were obtained for days to 50% flowering (5.51%) and days to maturity (4.67%). These findings were in similarity with Prasad *et al.*, (2017) and Venkanna *et al.*, (2022).

In general, the magnitude of phenotypic coefficient of variance (PCV) was higher than genotypic coefficient of variance (GCV) for all eleven traits studied in the present experiment. For genotypic coefficient of variation, the characters that exhibited the higher estimates (>15%) were harvest index (17.53%) and grain yield/plant (15.30%). The characters which exhibited moderate estimates (10-15%) were biological yield (13.68%), 1000-grain weight (13.52%), No. of productive tillers (12.95%) and plant height (10.17%). The remaining characters showed low estimates (<10%). The higher estimates for phenotypic coefficient of variation (>15%) were exhibited by harvest index (17.59%) and grain yield/plant (15.35%). The characters which exhibited moderate estimates (10-15%) were biological yield (14.02%), 1000 grain weight (13.65%), No. of productive tillers (12.97%) and plant height (10.90%). The remaining characters showed low estimates (<10%) (Table 3).

Correlation coefficient

The coefficient of variation was observed for 11 characters for all the genotypes with grain yield per plant as presented in (Table 4.1 and 4.2). The grain yield/plant showed highly significant positive correlation with spikelet fertility (0.783), followed by harvest index (0.718), 1000

Table 3: Estimation of coefficient of variance, heritability.in broad sense, genetic advance and genetic advance as mean.

Genotypes	Mean	Range		GCV (%)	PCV (%)	Heritability (%)	GA% mean
		Minimum	Maximum				
Days to 50% flowering	122.19	112.00	129.00	3.17	3.75	71.38	5.51
Days to maturity	148.82	138.00	155.00	2.63	3.04	74.52	4.67
Plant height (cm)	111.46	89.00	150.00	10.17	10.90	86.93	19.52
No. of productive tillers	10.04	6.60	13.69	12.95	12.97	99.80	26.66
Panicle length(cm)	22.84	19.70	25.66	5.47	5.57	96.26	11.05
No. of spikelets/panicle	106.04	70.68	124.94	8.99	9.07	98.33	18.37
Spikelet fertility (%)	86.88	61.09	94.38	7.43	7.52	97.69	15.13
1000 grain weight (g)	19.95	9.12	23.58	13.52	13.65	98.08	27.58
Biological yield/plant (g)	62.25	44.19	84.83	13.68	14.02	95.24	27.50
Harvest Index (%)	42.72	14.11	51.40	17.53	17.59	99.34	35.99
Grain yield/plant (g)	25.95	11.97	32.10	15.30	15.35	99.29	31.40

Characters	DM	PH	NPT	PL	NSP	SF	GW	BYP	HI	GY
Days to 50% flowering	0.979**	-0.065	0.293**	0.219*	0.046	0.067	0.103	0.034	-0.047	-0.063
Days to maturity		-0.053	0.354**	0.058	0.081	0.093	0.187	0.047	-0.033	-0.017
Plant height (cm)			0.280**	0.171	0.185	0.031	0.180	-0.243*	0.215*	0.059
No. of productive tillers				0.290**	0.293**	0.080	0.194	-0.050	0.212*	0.201
Panicle length(cm)					0.622**	0.154	0.003	0.124	0.109	0.293**
No. of spikelets/panicle						0.485**	0.443**	0.024	0.381**	0.652**
Spikelet fertility (%)							0.709**	-0.508**	0.820**	0.783**
1000-grain weight (g)								-0.473**	0.719**	0.661**
Biological yield/plant (g)									-0.773**	-0.124
Harvest Index (%)										0.718**

DM: Days to maturity; PH: Plant height (cm); NPT: No. of productive tillers; PL: Panicle length(cm);
NSP: No. of spikelets/panicle; SF: Spikelet fertility (%); GW: 1000-grain weight (g); BYP: Biological yield/ plant (g);
HI: Harvest Index (%); GY: Grain yield/ plant (g)

Characters	DM	PH	NPT	PL	NSP	SF	GW	BYP	HI	GY
Days to 50% flowering	0.887**	-0.051	0.259*	0.178	0.042	0.066	0.097	0.016	-0.038	-0.056
Days to maturity		-0.053	0.318**	0.044	0.071	0.082	0.164	0.048	-0.027	-0.008
Plant height (cm)			0.264*	0.161	0.172	0.028	0.171	-0.222*	0.206	0.060
No. of productive tillers				0.286**	0.290**	0.078	0.193	-0.049	0.212*	0.200
Panicle length(cm)					0.609**	0.150	0.005	0.148	0.098	0.286**
No. of spikelets/panicle						0.477**	0.435**	0.024	0.379**	0.648**
Spikelet fertility (%)							0.700**	-0.496**	0.811**	0.774**
1000-grain weight (g)								-0.459**	0.710**	0.652**
Biological yield/plant (g)									-0.764**	-0.118
Harvest Index (%)										0.718**

DM: Days to maturity; PH: Plant height (cm); NPT: No. of productive tillers; PL: Panicle length(cm);
NSP: No. of spikelets/panicle; SF: Spikelet fertility (%); GW: 1000-grain weight (g); BYP: Biological yield/ plant (g);
HI: Harvest Index (%); GY: Grain yield/ plant (g)

(0.063), followed by plant height (0.059) and-days to maturity (0.017). The grain yield/plant showed highly significant positive phenotypic correlation with spikelet fertility (0.774), followed by harvest index (0.718), 1000

Characters	DF	DM	PH	NPT	PL	NSP	SF	GW	BYP	HI	GY
DF	0.2212	-0.2600	-0.0008	-0.0079	-0.0168	0.0042	0.0114	0.0100	0.0341	-0.0587	-0.063
DM	0.2165	-0.2656	-0.0006	-0.0095	-0.0044	0.0074	0.0156	0.0182	0.0466	-0.0409	-0.017
PH	-0.0143	0.0140	0.0117	-0.0075	-0.0130	0.0168	0.0053	0.0175	-0.2409	0.2695	0.059
NPT	0.0649	-0.0940	0.0033	-0.0268	-0.0222	0.0265	0.0135	0.0189	-0.0500	0.2665	0.201
PL	0.0485	-0.0154	0.0020	-0.0078	-0.0764	0.0563	0.0261	0.0003	0.1231	0.1366	0.293**
NSP	0.0102	-0.0216	0.0022	-0.0079	-0.0475	0.0905	0.0819	0.0432	0.0233	0.4778	0.652**
SF	0.0149	-0.0246	0.0004	-0.0021	-0.0118	0.0439	0.1688	0.0691	-0.5036	1.0283	0.783**
GW	0.0228	-0.0496	0.0021	-0.0052	-0.0002	0.0401	0.1197	0.0975	-0.4686	0.9020	0.661**
BYP	0.0076	-0.0125	-0.0028	0.0014	-0.0095	0.0021	-0.0858	-0.0461	0.9912	-0.9693	-0.124
HI	-0.0104	0.0087	0.0025	-0.0057	-0.0083	0.0345	0.1384	0.0701	-0.3659	0.8544	0.718**

DF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NPT: No. of productive tillers; PL: Panicle length(cm); NSP: No. of spikelets/panicle; SF: Spikelet fertility (%); GW: 1000-grain weight (g); BYP: Biological yield/ plant (g); HI: Harvest Index (%); GY: Grain yield/ plant (g)
Resi = 0.00261; *, ** significant at 5% and 1% level, respectively.

plant height, no. of spikelets per panicle, panicle length and low for days to 50% flowering and days to maturity days. The grain yield/plant showed highly significant positive genotypic correlation with spikelet fertility (0.783), followed by harvest index (0.718), 1000 grain weight (0.661), no. of spikelets/panicle (0.652) and panicle length (0.293). High value positive direct effect on grain yield/plant was shown by biological yield/plant (0.991), harvest index (0.854), days to 50%-flowering (0.221), spikelet fertility (0.168), 1000 grain weight (0.097), no. of spikelets/panicle (0.09) and plant height (0.011). This indicated greater reliance on these characters in selection programme. Using Mahalanobis' D^2 cluster analysis, the 30 genotypes were grouped into three different non-overlapping clusters which revealed the presence of substantial genetic diversity among the rice germplasm lines screened and indicated that this material may serve as good source for selecting the desirable promising segregants for grain yield and its contributing traits. Out of all, the genotypes NDR 2022-10-4 (32.10), CR-2839-1-5-B-1-5-1-B-9-1-1-1-2 (32.03), CR 2889-208-11-17 (31.50), MTU 1423 (MTU 2527-22-1-1-1) (31.45) and RP Bio 4919-NSR 53-1 (30.33) produced highest grain yield per plant. These lines may be used as parents in hybridization programme aimed at development of high yielding varieties.

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