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ASSESSMENT OF GENETIC VARIABILITY, CHARACTER ASSOCIATION, PATH COEFFICIENT ANALYSIS OF GRAIN YIELD AND ITS CONTRIBUTING TRAITS IN MEDIUM SLENDER RICE (*ORYZA SATIVA L.*)

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ABSTRACT

Rice (*Oryza sativa* L.) is a major global cereal crop with over 40,000 varieties, primarily classified into two subspecies: *Indica* (long-grain) and *Japonica* (medium- and short-grain). Fine-grain rice, known for its superior quality and market value, is in high demand, especially in urban areas. A study was conducted at the Crop Research Station, Masodha, Ayodhya, during the 2024 *Kharif* season which analyzed 63 rice germplasm lines and three check varieties using Augmented Design. Twelve quantitative traits were observed, including flowering time, plant height, yield components, and spikelet fertility. Variance analysis indicated significant treatment effects on biological yield, harvest index, and productive tillers per plant. The top five genotypes for grain yield were Samba sub-1 (20.78g), NVSR 934 (20.5g), RP 6770-960-22-10-3-1 (18.15g), AD 19566 (17.6g), and NVSR-933 (17.17g), making them promising candidates for hybrid breeding.

Phenotypic coefficient of variation (PCV) was generally higher than genotypic coefficient of variation (GCV), except for fertile spikelets per panicle. High PCV and GCV were observed for fertile spikelets, biological yield, and harvest index, while moderate values were found for productive tillers and flag leaf area. Heritability was highest for biological yield per plant, moderate for spikelet fertility and harvest index, and lowest for plant height and grain yield. Traits with high genetic advance included biological yield and fertile spikelets.

Grain yield showed a strong positive correlation with biological yield, fertile spikelets, and plant height. Path coefficient analysis confirmed that biological yield, harvest index, and fertile spikelets had the most direct influence on grain yield. Genetic divergence analysis grouped genotypes into six clusters, with maximum diversity between Clusters II and VI. Crossbreeding between distant clusters is recommended for improving rice yield and quality.

***Keywords*:** Genetic Variability, Heritability, Harvest index, Correlation, Path coefficient analysis, Genetic Divergence.

Introduction

Rice (*Oryza sativa* L.), belonging to the Poaceae family, is a staple food for a large portion of the global population. Its cultivation dates back thousands of years, primarily originating in Asia, particularly China and India. As a self-pollinated, short-day, C3 plant, rice thrives in humid tropical and subtropical climates with abundant sunlight and a steady water supply. Optimal growth occurs between 21°C and 37°C, with specific temperature needs at different stages: 20°C–35°C during tillering, 26°C–29°C at flowering, and 20°C–25°C at ripening (Verma *et al*., 2017).

Rice is rich in carbohydrates, proteins (mainly oryzenin), vitamins, and minerals, and contributes over 30% of global caloric intake. It also supports various industries, including food processing, brewing, paper production, and livestock care. Globally, rice is cultivated on about 165 million hectares, yielding over 519 million tonnes (FAO, 2022). In India, it covers 48 million hectares, producing 135.76 million tonnes (USDA, 2022).

Modern breeding focuses on creating genetic variability and selecting traits related to yield. Understanding variability, heritability, genetic advance, divergence, and trait relationships through correlation and path analysis is essential for improving rice varieties and developing efficient breeding strategies**.**

Materials and Method

The present study, was conducted during the Kharif 2023–24 season at the Crop Research Station, Masodha, in Ayodhya district, Eastern Uttar Pradesh. Geographically, the site is located at 26.48° N latitude and 82.13° E longitude, with an elevation of 113 meters. The area lies in the Gangetic alluvial zone and experiences a semi-arid climate, typified by hot summers, cold winters, and a monsoon season from July to September, which contributes most of the annual rainfall. The soil was sandy loam with an approximate pH of 8.0. Weekly weather parameters including rainfall, temperature, humidity, and sunshine duration were documented throughout the season.

The experimental material consisted of 63 medium slender rice genotypes, including three check varieties BPT 5204, Samba Sub 1, and Keteki Joha. The trial was laid out using an Augmented Block Design across six blocks. Each entry was sown at 20 × 15 cm spacing in 10 m² plots. Observations on twelve yield-contributing traits were recorded from five randomly selected plants and averaged for statistical analysis.

At crop maturity, key agronomic traits were recorded using standard methodologies. Productive tillers were counted as the number of panicle-bearing tillers per plant. Panicle length was measured from the base to the apex excluding awns, while the leaf area index was calculated by multiplying the flag leaf's length and maximum width, then applying a correction factor of 0.75. The number of spikelets per panicle was averaged from five representative panicles, and spikelet fertility was calculated as the ratio of filled to total spikelets, expressed as a percentage. The 1000-grain weight was determined using an analytical balance on dried seeds. Biological yield included the total above-ground dry biomass excluding roots, and harvest index was computed as the ratio of grain yield to biological yield.

Statistical and biometrical analyses were conducted using data from 60 genotypes and three checks. Analysis of variance was performed as per the Augmented Block Design (Federer, 1956). Variability parameters including phenotypic, genotypic, and environmental coefficients of variation were calculated following Burton and De Vane (1953). Heritability estimates followed Allard *et al.* (1960), and genetic advance was assessed as per Robinson *et al.* (1949). Correlation and path coefficient analyses were carried out following Searle (1961) and Dewey and Lu (1959), while genetic divergence was assessed through non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973).

Results and Discussion

The analysis of variance (ANOVA) conducted using an Augmented Block Design revealed significant differences among the genotypes, indicating the presence of substantial genetic variability. Specifically, block effects were found to be significant for traits such as the number of productive tillers per plant, flag leaf area, spikelet fertility, and biological yield. Similarly, the check varieties exhibited significant variation for most traits, except for days to 50% flowering, days to maturity, number of fertile spikelets per panicle, spikelet fertility, and 1000-grain weight.

The mean performance analysis indicated notable variation among genotypes for all observed traits. Days to 50% flowering ranged from 85 to 128 days, while days to maturity ranged from 109 to 156 days. Plant height varied between 64.2 cm and 125.5 cm. Productive tillers ranged from 4.4 to 15.5 per plant, and panicle length varied from 19.3 cm to 27.4 cm. Similarly, significant differences were noted in leaf area index, spikelet count per panicle, spikelet fertility percentage, and 1000-grain weight. Grain yield per plant ranged from 9.09 g to 20.8 g, while biological yield ranged from 20.5 g to 82 g, and harvest index from 16.05% to 59.9%.

These findings highlight the rich genetic diversity among the tested genotypes, offering opportunities for selecting superior lines for future breeding programs. Such variability is essential for improving complex traits like grain yield, as it enables the identification of desirable genotypes with optimal trait combinations (Babu *et al.*, 2012; Kumar *et al.*, 2020; Yadav *et al.*, 2021).

Heritability and genetic advance were assessed for twelve agronomic traits in rice . Biological yield per plant showed the highest broad-sense heritability (92.56%), indicating strong genetic control. Moderate heritability was found in spikelet fertility (58%), harvest index (52.30%), and flag leaf area (52%), while lower heritability was recorded for traits such as number of productive tillers (40.30%), plant height (28%), and grain yield per plant (19.10%). Genetic advance as a percentage of mean was highest for biological yield (50.69%), fertile spikelets per panicle (46.22%), and harvest index (31.27%), suggesting good scope for improvement through selection. Generally, phenotypic coefficients of variation (PCV) exceeded genotypic coefficients (GCV), indicating the influence of environmental factors, with the exception of fertile spikelets per panicle. Similar findings were reported by Girma *et al.* (2018), Behera *et al.* (2018), and Nanda *et al.* (2021).

Correlation analysis revealed that grain yield per plant had a significant and positive association with biological yield, fertile spikelets per panicle, flag leaf area, productive tillers, and plant height. Conversely, days to 50% flowering and maturity showed negative but non-significant correlations. Other key traits, such as harvest index and 1000-grain weight, also displayed notable relationships with components influencing yield. These results support earlier studies by Singh *et al.* (2022), Kranthi Kiran *et al.* (2023), and Paramanik *et al.* (2023), emphasizing the complex interplay of traits influencing grain yield in medium slender rice.

Path coefficient analysis was used to separate the total correlation into direct and indirect effects of various traits on grain yield. Biological yield per plant and number of fertile spikelets per panicle showed strong positive direct effects, highlighting their importance as major yield contributors. Harvest index and number of productive tillers also had indirect positive effects through biological yield and spikelet number. In contrast, traits like 1000-grain weight and days to maturity had negative direct effects. Some traits, such as biological yield, showed negative indirect effects via harvest index.

The genetic divergence among 63 rice genotypes (60 germplasm lines and 3 checks) was analyzed using Non-hierarchical Euclidean cluster analysis based on 12 quantitative traits. The analysis grouped the genotypes into six clusters, Cluster IV contained the most genotypes (28), followed by cluster V (13) and cluster I (8). Clusters II and III had 5 genotypes each, while cluster VI included 4 genotypes. Intra-cluster distance was lowest in cluster III (5.586) and highest in cluster I (20.766). The highest inter-cluster distance was observed between clusters II and VI (52.209), indicating significant diversity between these groups.

Cluster mean performance for traits showed noticeable variation. For days to 50% flowering, cluster VI recorded the highest mean (125.625 days), followed by cluster I (117.813), while cluster IV had the lowest mean (95.750). Similarly, for days to maturity, cluster VI again showed the highest mean (152.5), followed by cluster I (142.375), with cluster IV showing the earliest maturity (121.821). These findings suggest that clusters VI and I comprise late-maturing genotypes, while clusters IV and III include early-maturing ones. The results align with earlier studies by Chandraker *et al.* (2024), Sar *et al.* (2023), and Mandal *et al.* (2022).

The cluster-wise mean analysis of 63 rice genotypes showed significant variation across 12 traits. Plant height ranged from 77.93 cm (cluster VI) to 114.31 cm (cluster I), while productive tillers per plant varied from 8.03 (cluster V) to 15.75 (cluster II). Cluster III had the highest grain yield (20.86 g) and number of fertile spikelets (172.71), whereas cluster VI had the highest biological yield (77.55 g). Cluster II recorded the highest spikelet fertility (83.08%) and harvest index (47.03%). The 1000-grain weight was highest in cluster I (21.22 g).

Table 1: List of the 63 germplasm resources under study

1.	AD 21039	16.	NP 9993	31.	NWGR 19219	46.	Samba Early	61.	**Samba Sub-1**
2.	BPT 3159	17.	BKR 245	32.	TRC 2023-37	47.	CRAC 3998-325-3	62.	**BPT 5204**
3.	CB 20166	18.	R 2370-115-1-93-1	33.	CR 4376-1-1-1-2-1-1	48.	RP 6767-CGR 25-CGIL-70-CGK2-1- 2131-21	63	**Keteki joha**
4.	Pusa 5477-28-30-2-1-1-3-3	19.	RNR 41216	34.	RGL 7033 (MTU RM 428-2-1-1)	49.	BRR 2135		
5.	RP 6747-19487-1-1	20.	BRR 0285	35.	SYE 930-8-25	50.	RP 6449-db-235		
6.	KPS 10320	21.	WGL 1722	36.	CR 3573-3-1-3-1-1-1	51.	KPS 10375		
7.	CSR-MGC-63	22.	CR 3583-3-2-2-1-1-1	37.	RP 6766-CGR 27-CGIL-92-CGK 143- 2135-5 S	52.	TRC 2023-26 / TRC SMTC 5488-B-B- 11-41		
8.	P.3334	23.	RP 6528-RMS-2-7-11-3	38.	Pusa 5377-4-1-1-2-2-1	53.	NDR 2022-1-2		
9.	TRC 2023-39 / TRC SMTC 5387-9-20	24.	CB 20143	39.	AD 19566	54..	NWGR 17121		
10.	RP 6681-RMS-1-79-64-43	25.	BPT 3127	40.	RP 6768-RMS 3-6-9-18	55.	RNR 38123		

11.	MTU 1419 (MTU 2632-43-2-2)	26.	AD 21193	41.	KNM 12368	56.	WGL 1724	
12.	NVSR-933	27.	RP 6460-C3-345-12	42.	CRAC 3998-247-2	57.	NVSR 991	
13..	NWGR 18121	28.	CR 3856-44-22-2-1-11-4-5-5	43.	NP 6161	58.	RP 6769-1144-12-1-2-1-2	
14.	CRAC 3998-128-2	29.	RAU 1407-13-3	44.	RGL 7034 (RGL 3035 – 56-4-1)	59.	RP 6770-960-22-10-3-1	
15.	CR 4479-3-2-1-1-1-1	30.	MTU 1418 (MTU 2789-6-1-2)	45.	NVSR 3606	60.	NVSR 934	

Table 2: Analysis of variance of augmented design for 12 characters in rice germplasm

Source of variation	DF	Days to 50% flowering	Days to maturity	Plant Height (cm)	No. of productive tillers /plant	Panicle length (cm)	Flag leaf area (cm^2)	No. of fertile spikelet Per plant	Spikelet fertility (%)	Biological yield (g)	Harvest index (%)	1000 grain weight (g)	Grain yield perplant (g)
Block	5	79.77	108.02	242.99	6. 797*	3.15	67.41**	495.40	241.817**	421.16**	42.74	4.55	10.53
Treatment	62	168.72	169.444	250.57	8.015**	3.62	26.092	1703.47	94.278	310.76**	107.83*	11.15	10.44
Checks	2	660.792	460.722	2079.06**	41.513**	16.74*	235.469**	970.50	92.356	3036.94**	615.02**	24.71	59.50**
Varieties	59	146.487	151.881	106.66	3.288	3.283	24.585	251.71	101.78*	248.29**	74.88	10.67	6.59
Check vs. varieties	1	110.501	14.944	4750.98**	235.538**	0.001	10.74	87506.27**	760.87**	470.28**	1124.61**	5.180	167.35**
Error	10	171.259	141.322	145.55	1.803	3.249	10.654	683.51	37.486	15.349	31.97	11.05	5.11

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

Table 3: Mean performance of 60 genotypes and 3 checks for 12 characters in rice germplasm

S No.	Genotype	Days to 50% flowering	Days to maturity	Plant Height (cm)	No. of productive tillers /plant	Panicle length (cm)	Flag leaf area (cm^2)	No. of fertile Spikelet Per plant	Spikelet fertility (%)	Biological yield (g)	Harvest index (%)	1000 grain weight (g)	Grain yield per plant (g)
1	AD 21039	92	118	93.4	9.6	21.2	37.0	70.4	88.3	64.80	20.01	17.8	16.09
2	BPT 3159	121	146	95.8	8.8	22.5	21.2	78.0	86.66	28.00	33.66	17.6	9.09
3	CB 20166	113	138	87.3	7.2	19.8	27.6	77.0	79.38	40.00	27.63	17.4	10.70
4	Pusa 5477-28-30-2-1-1-3-3	118	146	87.3	8.0	20.1	34.2	85.6	86.46	52.00	27.00	20.0	13.60
5	RP 6747-19487-1-1	104	128	99.5	9.2	25.4	32.6	95.0	79.16	52.40	26.93	23.8	13.60
6	KPS 10320	87	112	86.7	11.6	22.3	33.4	71.2	80.9	51.00	25.15	20.8	12.12
7	CSR-MGC-63	96	120	83.4	10.8	21.4	33.4	81.0	82.65	48.60	29.23	19.6	12.82
8	P.3334	96	122	106.1	11.2	22.8	37.4	111.0	88.8	58.00	23.52	25.0	13.14
9	TRC 2023-39 / TRC SMTC 5387-9-20	110	136	92.9	8.2	23.4	26.8	74.8	78.73	49.40	28.81	24.0	13.90
10	RP 6681-RMS-1-79-64-43	95	121	95.4	4.4	21.0	23.6	99.2	76.3	47.00	28.75	24.6	12.70
11	MTU 1419 (MTU 2632-43-2-2)	125	153	92.2	11.0	23.7	33.6	106.6	88.83	50.00	29.63	22.0	14.20
12	NVSR-933	89	117	76.6	5.0	20.4	38.2	88.8	74.0	54.00	32.18	18.8	17.17
13	NWGR 18121	93	121	88.8	7.0	23.2	26.0	85.6	65.8	30.00	47.20	20.8	13.34
14	CRAC 3998-128-2	101	127	72.4	8.4	21.2	32.8	66.6	75.6	33.0	37.74	17.6	12.14
15	CR 4479-3-2-1-1-1-1	96	119	95.9	11.2	21.8	32.6	101.0	77.69	40.00	26.26	20.8	10.17
16	NP 9993	118	144	94.8	9.0	21.1	32.8	99.4	82.83	69.00	24.51	20.8	16.79
17	BKR 245	89	118	99.1	9.0	25.1	32.0	101.2	77.84	58.00	21.61	24.0	12.36
18	R 2370-115-1-93-1	98	124	89.0	5.8	21.5	32.2	74.4	62.2	68.00	22.36	22.8	15.12
19	RNR 41216	94	120	106.2	8.8	24.9	30.0	99.2	76.3	39.00	37.53	26.2	13.44
20	BRR 0285	97	122	90.8	6.2	23.3	40.2	87.2	67.07	35.00	42.88	19	14.38
21	WGL 1722	119	146	99.4	7.0	24.5	26.2	92.8	61.86	26.00	45.508	25.6	11.27
22	CR 3583-3-2-2-1-1-1	91	117	94.2	8.2	24.0	34.6	91.0	56.87	68.00	23.94	23.8	16.19
23	RP 6528-RMS-2-7-11-3	118	144	102.0	9	27.4	24.8	103.2	79.38	35.00	34.44	21	10.09
24	CB 20143	100	128	85.5	8.8	24.26	24.2	84.6	70.5	50.00	26.25	17.4	12.86
25	BPT 3127	102	130	77.5	4.8	21.9	35.2	76.6	85.11	36.00	36.42	18.8	12.78
26	AD 21193	127	155	72.1	8	20.8	38.6	61.8	51.5	68.60	24.28	17.4	16.55
27	RP 6460-C3-345-12	100	125	81.6	5.2	25.2	31.8	82.6	68.83	40.00	35.01	18	13.56
28	CR 3856-44-22-2-1-11-4-5-5	109	133	76.7	8	21.0	32.2	61.6	69.21	57.00	26.66	17.6	14.96
29	RAU 1407-13-3	113	138	71.9	7.4	19.3	27	70.4	64.43	68.00	19.01	16.8	12.86
30	MTU 1418 (MTU 2789-6-1-2)	119	144	77.2	8	23.2	30.6	81	64.8	63.00	20.82	17.6	13.10
31	NWGR 19219	127	152	72.9	6.6	24.4	30.8	78.8	54.72	82.00	20.85	16.6	17.09
32	TRC 2023-37	110	134	81.8	6	21.5	34.8	91.4	73.12	62.00	23.02	16.2	14.10
33	CR 4376-1-1-1-2-1-1	102	127	64.2	6.2	22.5	33.4	64.6	73.4	63.00	16.05	17	10.07
34	RGL 7033 (MTU RM 428-2-1-1)	91	117	80.6	9.4	19.8	36	70.6	79.32	62.00	21.93	21.2	13.30

35	SYE 930-8-25	128	156	79.9	7.4	21.9	39.4	89.2	72.52	80.00	21.01	16	16.71
36	CR 3573-3-1-3-1-1-1	122	147	86.8	9.4	23.8	32.8	77	51.33	79.60	20.59	24	16.15
37	RP 6766-CGR 27-CGIL-92-CGK 143-2135-5 S	115	138	95.8	9.8	24.1	40.8	108.2	67.62	40.00	46.71	27	16.11
38	Pusa 5377-4-1-1-2-2-1	95	120	89.5	8.2	21.9	34	83	59.28	56.00	29.07	22	16.40
39	AD 19566	105	130	95.4	7	24.9	33.6	111.4	84.39	70.40	25.03	23.6	17.6
40	RP 6768-RMS 3-6-9-18	100	126	85.6	7.4	20.9	23.4	109.4	83.51	66.00	20.02	20	13.12
41	KNM 12368	119	145	82.9	7.6	24.3	24	96	76.19	50.00	23.24	16.6	11.34
42	CRAC 3998-247-2	85	109	91.8	6	23.1	25.2	80.8	82.44	54.00	25.53	16.8	13.30
43	NP 6161	95	121	80.0	9	23.1	31.4	57	74.02	25.00	22.76	16.4	15.20
44	RGL 7034 (RGL 3035 – 56-4-1)	96	121	84.7	7.6	24.8	24.8	75	87.2	74.00	19.37	17.4	14.08
45	NVSR 3606	118	144	74.9	6.4	21.4	24	76.2	80.21	40.00	35.55	16.6	12.26
46	Samba Early	125	152	105.0	10.8	21.4	26	110	81.48	68.00	19.28	27	13.04
47	CRAC 3998-325-3	92	116	71.6	8.2	22.3	26.2	77.6	87.19	60.00	30.71	17.4	15.18
48	RP 6767-CGR 25-CGIL-70-CGK2-1-2131-21	100	126	75.4	7.6	26	31.4	67	76.13	40.00	33.36	16.6	12.92
49	BRR 2135	101	127	103.2	8.8	26.0	27.8	97	78.22	35.00	36.32	25	12.18
50	RP 6449-db-235	94	118	73.0	10.4	23.5	24.2	89.2	85.76	68.00	24.00	16.6	16.23
51	KPS 10375	119	137	84.4	10.6	24.1	25.6	74.8	68.4	50.00	26.62	16.6	12.20
52	TRC 2023-26 / TRC SMTC 5488-B-B-11-41	107	135	98.2	11.6	25.2	33.2	120	72.72	68.00	20.02	24.4	13.36
53	NDR 2022-1-2	102	128	86.2	10.6	21.1	36.8	110.4	81.17	80.00	20.56	22.8	16.37
54	NWGR 17121	97	121	72.8	9.80	21.8	22.8	83	55.33	67.40	20.43	16.4	13.44
55	RNR 38123	128	154	80.0	8.60	22.1	25.8	61.4	62.25	70.00	22.93	17.4	15.80
56	WGL 1724	92	118	87.8	8.20	24.4	31.2	110.6	61.44	63.00	23.69	19.8	14.78
57	NVSR 991	110	136	83.2	9.40	24.6	30.2	74.2	72.74	70.00	24.63	17.4	17.07
58	RP 6769-1144-12-1-2-1-2	111	138	75.8	7.80	20.5	23.8	85.8	72.80	20.50	46.78	16.6	9.59
59	RP 6770-960-22-10-3-1	99	125	100.5	11.5	23.5	28.5	102.5	86.80	30.31	59.88	18.4	18.15
60	NVSR 934	109	131	101.5	10.8	24.5	30.5	120.5	88.50	67.50	30.37	20.5	20.50
61	Keteki joha©	120	142.16	125.5	10.64	24.67	30.21	171.85	85.27	34.89	39.13	19.45	14.67
62	BPT 5204©	103	127.33	88.6	15.52	21.38	26.17	151.8	83.19	35.49	46.33	17.27	16.40
63	Samba sub-1©	104	126.66	102.3	11.38	22.52	38.38	175.39	77.68	74.15	26.34	21.32	20.78
	Mean	105	131.06	87.8	8.58	22.85	30.53	90.642	74.98	53.73	28.68	19.93	13.97
	Lowest Range	85	109	64.20	4.40	19.30	21.20	57.00	51.33	20.50	16.05	16.00	9.09
	Highest Range	128	156.0	125.5	15.50	27.40	40.80	175.4	88.80	82.0	59.90	27.00	20.80
	C.V	8.87	10.89	7.80	4.25	12.85	6.31	3.94	7.56	3.39	3.26	6.25	5.86
	SE(d)	7.55	6.86	6.96	0.77	1.04	1.88	15.09	3.53	2.26	3.26	1.91	1.30
	C.D 5%	16.83	15.29	15.52	1.72	2.31	4.199	33.63	7.87	5.03	7.27	4.27	2.90

Table 4: Heritability, genetic advance and coefficient of variability analysis

Character	Range minimum	Range maximum	Grand mean	GCV %	PCV %	Heritability (Broad sense)	Genetic advance	Genetic advance as percentage of mean
Days to 50% flowering	85.00	128.0	105.0	4.287	11.69	13.40	3.403	3.238
Days to maturity	109.0	156.0	131.06	2.245	9.347	5.700	1.455	1.110
Plant height (cm)	64.20	125.5	87.80	6.493	12.26	28.00	6.150	7.081
No. of productive tiller per plant	4.400	15.50	8.580	13.15	20.70	40.30	1.443	17.19
Panicle length (cm)	19.30	27.40	22.85	0.723	7.921	0.083	0.031	0.136
Flag leaf area (cm^2)	21.20	40.80	30.53	11.04	15.36	52.00	5.005	16.36
Number of fertile spikelet per Panicle	57.00	175.4	90.64	21.65	20.90	10.73	40.14	46.22
Spikelet fertility (%)	51.33	88.80	74.98	9.720	12.72	58.00	11.43	15.31
Biological yield per plant (g)	20.50	82.00	53.73	25.58	26.59	92.56	27.38	50.69
Harvest index (%)	16.05	59.90	28.68	20.98	28.99	52.30	8.840	31.27
1000 grain weight (g)	16.00	27.00	19.93	2.781	16.41	2.800	0.194	0.970
Grain yield per plant (g)	5.200	20.80	13.97	7.972	18.20	19.10	0.993	7.200

Table 5: Simple correlation coefficient between 12 characters of rice genotypes

Traits	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of Productive Tillers per plant	Panicle length (cm)	Leaf Area Index (cm^2)	No. of fertile spikelet per panicle	Spikelet fertility (%)	Biological yield Per plant(g)	Harvest Index (%)	1000-grain weight (g)	Grain yield per plant (g)
Days to 50%flowering	**1.000**	0.981**	0.097	-0.029	0.037	-0.090	0.086	-0.061	-0.029	0.012	-0.085	-0.073
Days to maturity		**1.000**	0.027	-0.064	0.029	-0.073	0.023	-0.096	-0.008	-0.013	-0.053	-0.091
Plant height(cm)			**1.000**	0.319*	0.352**	0.110	0.625**	-0.333**	-0.185	0.287*	0.431**	0.233*
No. of ProductiveTillers per plant				**1.000**	-0.070	-0.052	0.552**	0.334**	-0.114	0.378**	0.040	0.354**
Panicle length (cm)					**1.000**	-0.093	0.187	-0.008	-0.117	0.041	0.144	-0.057
Leaf area index(cm^2)						**1.000**	0.124	-0.124	0.374**	-0.203	0.287**	0.419**
No. of fertile spikelet per panicle							**1.000**	0.391**	-0.067	0.290*	0.079	0.484**
Spikelet fertility(%)								**1.000**	-0.265*	0.217	-0.029	0.031
Biological yield per plant(g)									**1.000**	-0.758**	0.123	0.518**
Harvest Index (%)										**1.000**	-0.002	0.088
1000-grainweight(g)											**1.000**	0.154

*&** Significant at 5% and 1 % probability level respectively

Table 6: Direct and indirect effect of different characters on grain yield per plant in rice germplasm

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of Productive Tillers per plant	Panicle length (cm)	Leaf Area Index (cm^2)	No. of fertile spikelet Per panicle	Spikelet fertility (%)	Biological yield Per plant(g)	Harvest Index (%)	1000-grain weight (g)	Grain yield per plant(g)
Days to 50% flowering	**-0.0016**	-0.066	0.0036	0.0011	-0.0006	-0.0124	0.0205	-0.0040	-0.0370	0.0121	0.0066	-0.073
Days to maturity	0.00016	**-0.0673**	0.0010	0.0023	-0.0005	-0.0101	0.0056	-0.0063	-0.0096	-0.0130	0.0041	-0.091
Plant height(cm)	0.0002	-0.0018	**0.0371**	-0.0116	0.0056	0.0153	0.1494	0.0220	-0.2348	0.2854	-0.0333	0.233*
No. of Productive Tillers/plant	0.0000	0.0043	0.0118	**-0.0363**	-0.0011	-0.0073	0.1321	0.0220	-0.1443	0.3758	-0.0031	0.354**
Panicle length (cm)	0.0001	-0.0020	0.0130	0.0025	**0.0160**	-0.0129	0.0448	-0.0005	-0.1479	0.0405	-0.0111	-0.057
Leaf Area Index (cm^2)	-0.0001	0.0049	0.0041	0.0019	-0.0015	**0.1387**	0.0298	-0.0082	0.4743	-0.2024	0.0222	0.419**
No. of fertile spikelet per panicle	0.0001	-0.0016	0.0231	-0.0201	0.0030	0.0173	**0.2392**	0.0258	-0.0846	0.2881	-0.0061	0.484**
Spikelet fertility (%)	-0.0001	0.0065	0.0123	-0.0121	-0.0001	-0.0172	0.0936	**0.0659**	-0.3354	0.2158	0.0023	0.031
Biological yield /plant(g)	0.0000	0.0005	-0.0069	0.0041	-0.0019	0.0519	-0.0160	-0.0174	**1.2672**	-0.7545	-0.0095	0.518**
Harvest Index (%)	0.0000	0.0009	0.0106	-0.0137	0.0007	-0.0282	0.0693	0.0143	-0.9611	**0.9948**	0.0001	0.088
1000-grain weight(g)	-0.0001	0.0036	0.0160	-0.0015	0.0023	0.0398	-0.0189	-0.0019	0.1557	-0.0018	**-0.0773**	0.154

Residual Effect= 0.30314 Bold values shows direct and normal values shows indirect effects

Table 7: Clustering pattern of 63 rice genotype on the basis of Non-hierarchical Euclidean cluster analysis of 12 characters

Clusters	Genotype Number	Genotype
I	8	AD 21039, CRAC 3998-128-2, NDR 2022-1-2, RP 6460-C3-345-12, TRC 2023-37, MTU 1418, RP 6768-RMS-3-6-9-18, BRR 2135
II	5	BPT 3159, CR 4479-3-2-1-1-1-1, CR 3856-44-22-2-1-11-4-5-5, NWGR 17121, KNM 12368
III	5	CB 20166, NP 9993, CRAC 3998-247-2, RNR 38123, RAU 1407-13-3
IV	28	Pusa 5477-28-30-2-1-1-3-3,Samba early, TRC 2023-39,RP 6681-RMS-1-79-64-43,WGL 1722,NWGR 18121,TRC 2023-26,NVSR 991,BPT 5204,RP 6770-960-22-10-3-1,P.3334,RP 6568-RMS-2-7-11-3,BPT 3127,MTU 1419,NVSR-933,KPS 10375,CB 20143,RP 6449-db-235,NWGR 19219,R 2370-115-1-93-1,AD 21193,BRR 0285,RGL 7033,CR 3573-3-1-3-1-1-1,Samba Sub -1,CR 4376-1-1-1-2-1-1,RNR 41216,RP 6769-1144-12-1-2-1-2
V	13	KPS 10320, NVSR 934, RP 6747-19487-1-1, RP 6766-CGR 27-CGIL-92-CGK 143-2135-5-5-S, RGL 7034, Pusa 5377-4-1-1-2-2-1, NVSR 3606, AD 19566, WGL 1724, CSR-MGC-63, CR 3583-3-2-2-1-1-1, BKR 245, Ketekijoha
VI	4	SYE 930-8-25, CRAC 3998-325-3,NP 6161,RP 6767-CGR 25-CGIL-70-CGK2-1-2131-21

Table 8: Estimates of average intra and inter-cluster distance for 6 clusters in rice germplasm

Clusters	I	II	III	IV	V	VI
I	**20.766**	32.816	34.493	31.431	30.267	43.731
II		**15.438**	32.780	33.700	32.809	52.209
III			**5.586**	25.807	28.600	28.616
IV				**12.946**	18.182	30.998
V					**12.201**	20.229
VI						**9.154**

Bold figure shows intra-cluster distance

Table 9: Cluster mean for different characters in rice germplasm

Cluster	Days to 50% flowering	Days to Maturity	Plant height (cm)	No.of Productive tillers /plant	Panicle length	leaf area index (cm^2)	No.of fertile spikelet per plant	Spikelet fertility (%)	Biological yield (g)	Harvest index (%)	1000 grain weight (g)	Grain yield per plant (g)
Cluster I	117.813	142.375	114.313	9.779	25.215	30.323	141.855	78.431	33.175	40.405	21.224	13.541
Cluster II	107.200	132.400	87.434	15.748	20.998	26.296	151.262	83.082	33.888	47.028	17.226	15.956
Cluster III	104.200	130.800	95.842	11.218	22.470	37.960	172.714	78.456	74.548	25.974	21.080	20.856
Cluster IV	95.750	121.821	88.201	7.993	22.899	31.429	84.757	76.647	51.057	28.556	20.536	13.535
Cluster V	115.769	141.846	84.000	8.031	21.677	29.338	84.446	77.462	54.615	25.082	18.708	12.778
Cluster VI	125.625	152.500	77.935	7.850	22.725	35.400	76.700	57.517	77.550	21.682	18.500	16.625

Conclusion

The study's findings indicate that the genotypes Samba sub-1, NVSR 934, RP 6770-960-22-10-3-1, AD 19566, and NVSR-933 demonstrated the highest potential for grain yield. A significant genotypic and phenotypic coefficient of variability was observed in biological yield per plant, harvest index, and the number of fertile spikelets per panicle. Additionally, high heritability coupled with considerable genetic advance was noted in biological yield per plant, the number of fertile spikelets per panicle, and harvest index, suggesting a predominant influence of additive gene effects and promising prospects for effective selection to enhance these traits.

The correlation study identified biological yield per plant, followed by the number of fertile spikelets per panicle, leaf area index, the number of productive tillers per plant, and plant height, as the most critical traits directly contributing to grain yield per plant. Path analysis further highlighted the harvest index as the most significant direct and indirect yield-contributing factor. Therefore, these traits play a crucial role in determining higher yields and can be utilized for crop improvement. The study concludes that the 63 genotypes exhibit substantial genetic variability, making them valuable candidates for hybridization programs.

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