



Genetic Variability, Correlation and Path Coefficient Analysis for Grain Yield and its Component Traits in Rice (*Oryza sativa* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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Abstract

The present investigation was undertaken to assess genetic variability among thirty rice (*Oryza sativa* L.) genotypes and to identify reliable indirect selection criteria for grain yield through correlation and path coefficient analysis. Thirty genotypes were evaluated in a randomised block design with three replications during Kharif 2025 at the Field Experimentation Centre, Naini Agricultural Institute, Prayagraj, Uttar Pradesh, for thirteen quantitative traits. Analysis of variance showed highly significant genotypic differences for twelve of the thirteen characters, confirming substantial genetic variability in the material. High heritability coupled with high genetic advance as a percentage of the mean was recorded for number of spikelets per panicle (98.4%; 41.1%), biological yield per plant (71.2%; 23.6%) and grain yield per plant (69.9%; 22.8%), indicating predominantly additive gene action and good scope for direct phenotypic selection for these traits. Grain yield showed a strong positive genotypic correlation with test weight (1.09), biological yield (0.871) and harvest index (0.715), and path analysis confirmed biological yield and harvest index as the traits with the largest positive direct effects on grain yield at both genotypic and phenotypic levels; test weight, despite its strong correlation with yield, acted mainly through indirect effects channelled via these two traits. The genotype DRRH2 combined the highest grain yield with high biological yield, harvest index and test weight and,

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together with 72-Dhan-59, 80-NLR-40024 and Vikramarya, is proposed as a promising donor for future hybridisation programmes aimed at raising grain yield in rice.

Keywords: Correlation; genetic advance; genetic variability; grain yield; heritability; path coefficient.

1. Introduction

Rice (*Oryza sativa* L.) is the staple food of more than half of the world's population and supplies close to one-fifth of global dietary energy from cereals, with Asia accounting for about 90% of world production (Food and Agriculture Organization of the United Nations, 2023). India is the largest rice-growing country by area, cultivating roughly 44-45 million hectares annually, though it trails China in total output owing to comparatively lower productivity, with a national average yield of around 2.6-2.8 t/ha (Government of India, 2024). The Green Revolution, driven by semi-dwarf, nitrogen-responsive varieties carrying dwarfing genes such as *sd1*, sharply raised rice yields from the 1960s onward (Khush, 1999, 2005), but realised farm yields in high-yielding varieties have since begun to plateau despite continued input intensification (Peng et al., 1999), prompting renewed interest in the systematic exploitation of genetic variability for further gains (Khush, 2001).

Grain yield is a complex quantitative trait governed by polygenes and expressed through the interaction of several component characters, which makes direct selection for yield alone slow and often unreliable (Johnson et al., 1955). Reliable genetic improvement therefore depends on quantifying the extent of variability present in the breeding material and on identifying component traits that can serve as indirect selection criteria. Genotypic and phenotypic coefficients of variation, together with heritability in the broad sense (Burton & DeVane, 1953; Lush, 1949) and genetic advance (Johnson et al., 1955), jointly indicate which traits are governed by additive gene action and are therefore amenable to improvement through simple selection. Because phenotypic correlation alone cannot distinguish true genetic association from environmentally induced covariation, correlation coefficients were partitioned into genotypic and phenotypic components (Al-Jibouri et al., 1958), and path coefficient analysis (Wright, 1921; Dewey & Lu, 1959) was used to resolve these correlations into direct and indirect effects. The present investigation was undertaken with this approach to assess genetic variability among thirty diverse rice genotypes and to identify dependable selection criteria for grain yield improvement.

Recent evaluations of diverse rice germplasm have further demonstrated the value of genetic variability, heritability and genetic advance in identifying traits with selection potential for yield improvement (SaiVenkat et al., 2024; Raj et al., 2025). Likewise, recent studies using correlation and path analysis in rice have shown that yield-component traits can differ in their associations and direct effects on grain yield, supporting their joint evaluation when defining selection criteria (Parmar et al., 2025; Deepika et al., 2026). In the present investigation, a research gap remains in determining which of the measured yield-related traits provide the most dependable selection criteria for the thirty rice genotypes when genetic variability, trait associations, and direct and indirect effects on grain yield are considered together. Addressing this gap through an integrated assessment is necessary to identify selection criteria specific to the evaluated material and experimental conditions.

1.1 Objective

- To estimate genetic variability, heritability and genetic advance for yield and its related traits in rice cultivars
- To assess the direct and indirect contributions of yield-attributing traits to grain yield
- To study the correlations among quantitative traits and grain yield

2. Materials and Methods

The field experiment was conducted during Kharif 2025 at the Field Experimentation Centre of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh (25.57°N, 81.51°E; 98 m amsl), a subtropical zone with mean annual rainfall of about 1013 mm concentrated between July and September. Thirty rice genotypes, including two check varieties, procured from SHUATS were evaluated in a randomised block design with three replications, using 20 cm row-to-row and 15 cm plant-to-plant spacing and a fertiliser dose of N:P:K @ 120:60:60 kg/ha. Observations were recorded on five randomly selected competitive plants per genotype per replication for thirteen quantitative traits, viz. days to 50% flowering, days to maturity, plant height (cm), flag leaf length (cm), flag leaf width (cm), number of tillers per hill, number of panicles per tiller, panicle length (cm), number of spikelets per panicle, biological yield per plant (g), harvest index (%), test weight (g) and grain yield per plant (g).

Genotype mean values were subjected to analysis of variance for a randomised block design (Fisher, 1935). Genotypic and phenotypic coefficients of variation (GCV, PCV) were estimated following Burton (1952) and Burton and DeVane (1953) and categorised as low (<10%), moderate (10-20%) or high (>20%) as suggested by Sivasubramanian and Menon (1973). Broad-sense heritability (h^2) was estimated as the ratio of genotypic to phenotypic variance (Lush, 1949) and classified as low (<30%), moderate (30-60%) or high (>60%) following Robinson et al. (1951). Genetic advance at 5% selection intensity and genetic advance as a percentage of the mean were computed following Johnson et al. (1955). Genotypic and phenotypic correlation coefficients among the thirteen characters were estimated following Al-Jibouri et al. (1958), and path coefficient analysis, partitioning the correlation of each component trait with grain yield into direct and indirect effects, was carried out following Dewey and Lu (1959).

3. Results and Discussion

Analysis of variance revealed highly significant ($p < 0.01$) differences among the thirty genotypes for twelve of the thirteen characters studied; number of tillers per hill was significant only at $p < 0.05$ (Table 1). This confirmed the presence of substantial

genetic variability in the material and indicated good scope for selection for grain yield improvement. Treatment mean squares were highest for number of spikelets per panicle and plant height, followed by days to maturity and days to 50% flowering, while biological yield, harvest index, test weight and grain yield per plant also showed highly significant treatment effects.

Table 1. Analysis of variance (treatment mean squares), genotypic and phenotypic coefficients of variation, broad-sense heritability and genetic advance for thirteen quantitative characters in rice

S. No.	Character	Treatment MS	GCV (%)	PCV (%)	h ² (%)	GA	GA % Mean
1	Days to 50% flowering	218.839**	7.74	7.74	99.97	17.59	15.95
2	Days to maturity	499.482**	9.62	9.69	98.48	26.31	19.67
3	Plant height (cm)	1439.614**	16.50	26.51	38.74	22.73	21.16
4	Flag leaf length (cm)	34.748**	8.03	14.32	31.44	2.99	9.28
5	Flag leaf width (cm)	0.012**	4.65	8.45	30.28	0.06	5.27
6	No. of tillers per hill	9.300*	10.55	23.46	20.23	1.07	9.78
7	No. of panicles per tiller	3.949**	10.71	20.61	26.99	0.89	11.46
8	Panicle length (cm)	11.008**	7.29	10.35	49.64	2.40	10.59
9	No. of spikelets per panicle	2100.723**	20.13	20.30	98.36	53.91	41.13
10	Biological yield (g)	113.413**	13.60	16.11	71.24	10.04	23.64
11	Harvest index (%)	19.401**	5.65	8.30	46.24	3.02	7.91
12	Test weight (g)	3.321**	3.50	6.49	29.08	0.87	3.89
13	Grain yield (g)	17.488**	13.25	15.84	69.90	3.89	22.82

GCV = genotypic coefficient of variation; PCV = phenotypic coefficient of variation; h² = broad-sense heritability; GA = genetic advance at 5% selection intensity. *Significant at $p < 0.05$; **Significant at $p < 0.01$

Wide ranges of variation were recorded for all thirteen traits (Table 2). Grain yield per plant ranged from 12.00 g (JGL-3828) to 21.33 g (DRRH2), with a grand mean of 17.04 g; DRRH2, 72-Dhan-59, 80-NLR-40024 and Vikramarya were the highest-yielding genotypes. Days to 50% flowering ranged from 89.0 to 125.0 days and days to maturity from 114.7 to 162.7 days, with Kasturi being the earliest genotype for both traits and thus a potential donor for short-duration breeding. Plant height varied from 84.1 cm (NLR-34449) to 186.9 cm (72-Dhan-59), and comparably wide variation was recorded for the remaining component traits, confirming the broad genetic base of the material evaluated.

Phenotypic coefficients of variation exceeded the corresponding genotypic coefficients for every trait (Table 1), reflecting an environmental contribution to total variability, though the narrow GCV-PCV gap for most characters indicated good correspondence between the two. PCV ranged from 6.49% (test weight) to 26.51% (plant height); GCV ranged from 3.50% (test weight) to 20.13% (number of spikelets per panicle). Heritability in the broad sense was very high for days to 50% flowering (99.97%), days to maturity (98.48%) and number of spikelets per panicle (98.36%), and high for biological yield (71.24%) and grain yield (69.90%), whereas number of tillers per hill, number of panicles per tiller and test weight showed low heritability, indicating comparatively larger environmental influence. Since high heritability need not translate into high selection gain unless accompanied by adequate genetic advance (Johnson et al., 1955), genetic advance as a percentage of the mean was examined jointly with heritability. High heritability coupled with high genetic advance as a percentage of the mean was recorded for number of spikelets per panicle (41.13%), biological yield (23.64%) and grain yield (22.82%), indicating additive gene action and good scope for direct phenotypic selection for these traits, whereas test weight, number of tillers per hill and number of panicles per tiller combined low heritability with low genetic advance, suggesting limited value for direct single-trait selection.

At the genotypic level (Table 3), grain yield showed a strong positive association with test weight (1.09), biological yield (0.871) and harvest index (0.715). At the phenotypic level (Table 4), grain yield was positively correlated with days to 50% flowering (0.416), harvest index (0.467) and test weight (0.391), but showed a negative association with biological yield (-0.174), in contrast to the strong positive genotypic correlation between these two traits. This genotypic-phenotypic divergence for biological yield illustrates how environmental covariation can mask an underlying favourable genetic association and underlines the importance of genotypic, rather than phenotypic, correlation for identifying dependable indirect selection criteria (Falconer & Mackay, 1996). Days to 50% flowering, days to maturity, biological yield, harvest index and test weight consistently showed mutually positive and significant genotypic associations, indicating scope for simultaneous improvement of these traits. These results agree with the trends reported by Johnson et al. (1955), Singh and Chaudhary (1985), Akinwale et al. (2011) and Bekele et al. (2013) in rice.

Path coefficient analysis (Tables 5 and 6) partitioned the correlation of each component character with grain yield into direct and indirect effects. At the genotypic level, panicle length (0.650) and biological yield (0.650) exerted the highest positive direct effects on grain yield, followed by harvest index (0.483), whereas days to maturity (-0.828) and flag leaf length (-0.828) showed the highest negative direct effects. Test weight, despite its strong positive correlation with grain yield, showed only a small negative direct effect (-0.179), its association with yield being mediated almost entirely through large positive indirect effects via biological yield (0.724) and harvest index (0.463) — a case where the trait is more useful for indirect than direct selection. At the phenotypic level, biological yield exerted by far the largest positive direct effect on grain yield (0.651), consistent with its genotypic direct effect, confirming it as the single most reliable component trait for both genotypic and phenotypic selection. Taken together, biological yield and harvest index emerge as the traits combining favourable heritability, genetic advance, strong positive correlation with grain yield, and substantial positive direct effects, making them the most dependable direct selection indices, while test weight and number of spikelets per panicle are better exploited as indirect selection parameters. These findings agree with the classical framework of Wright (1921) and Dewey and Lu (1959), and with reports on the primacy of biological yield and harvest index as yield determinants in rice by Sabesan et al. (2009), Akinwale et al. (2011), Bekele et al. (2013) and Babu et al. (2012).

Table 2. Mean performance of thirty rice genotypes for thirteen quantitative traits, Kharif 2025

S.No.	Genotype	DDF	DM	PH (cm)	FLL (cm)	FLW (cm)	TPH	PPT	PL (cm)	SPP	BY (g)	HI (%)	TW (g)	GY (g)
1	Indrani	109	128.33	95.46	30.51	1.13	12.33	8.13	21.8	166.93	38.33	37	21	15
2	AK Dhan	107	125.33	120.04	37.99	1.16	11.4	8.8	27.18	167.4	34.67	34.67	22	13.67
3	80-NLR-40024	108	122.67	84.68	31.25	1.01	13.67	9.47	18.36	90	41.67	38.67	22.67	20
4	JGL-3828	105	127.33	90.21	36.94	1.08	11.93	9.4	22.44	126.2	33.67	36.67	21.33	12
5	Bina Dhan-10	94	116.33	103.51	36.01	0.97	9.93	7.13	24.69	155.93	35.67	34	21.33	15.33
6	Lage Dhan	125	162.67	137.29	29.53	1.11	14.27	9.13	22.89	123.53	43	39	22	17
7	Talmunfar	122.33	157	125.4	36.15	1.02	14.2	9.53	24.69	112.6	49	41.33	23	19
8	Jarava	119	140	105.33	37.98	1.06	11.8	6.4	21.23	111.73	34.33	38	21.33	14.67
9	84-NLR-3354	113	138	92.25	33.26	1.08	11.6	6.6	22.72	87.53	40.33	39.33	23	17.67
10	Gautam	95	117.33	95.08	34.49	0.93	10.67	6.73	21.15	121.33	48.33	42	22.33	17.67
11	Boichi	113	131.33	100.27	29.65	1.04	12.53	7.87	23.07	111.87	40.67	38.33	23	17.33
12	Vikramarya	114	131.33	91.11	30.94	1.12	12.8	7.47	22.93	148.07	52.33	39.67	23	20
13	DRRH2	113	131	92.77	38.43	1.11	11.07	6.53	22.88	156	56	41.67	24.33	21.33
14	74-NLR-33359	113	131	92.4	30.28	1	12.13	7	20.81	94.93	41.33	40.67	22.33	16.67
15	81-NLR-33641	114	133	89.69	31.85	0.96	11.47	6.87	21.33	106.6	42.67	38.33	21.67	19.33
16	Lal Bhuna	115	134.67	132.17	31.95	1	13.07	7.53	23.08	116.33	35.67	37	21.33	13
17	Ranukasel	119	151	137.75	33.76	1.02	11.2	7.13	21.94	111.67	40.67	37.33	22.33	14.33
18	Sampada	115	142.67	93.51	30.81	1.03	10.2	7	22.23	93.8	43.67	39.33	23.33	17.33
19	Suraksha	114	145.33	91.28	35.39	1.01	9.93	8.47	24.92	134.2	43.67	39.67	21.67	15.67
20	Mandhya Vijaya	119	155	119.85	34.38	1.06	10.93	9.93	22.61	111.47	53.67	42	23.67	18.67
21	Signet-5455	110	131	103.77	31.37	1.07	8.13	6.93	24.29	142.87	53.67	43	24.33	18.67
22	Dhan-74	106.33	129.33	115.77	31.25	0.99	11	9.53	24.23	151.67	42	39	22	17
23	NLR	103	122	106.34	29.24	1.02	7.67	6.13	23.48	159	39.67	37	21.67	15.33
24	MTU-1035	119	148.67	94.35	26.55	1.18	10.33	9.07	19.63	144.8	42	37.33	20	15.67
25	79-NLR-30491	115	136.33	88.34	28.74	1.04	8.2	8.2	19.61	123.07	42	37.67	22.33	19.67
26	Kasturi	89	114.67	120.42	32.95	0.96	8.47	7.2	25.75	187.4	30.67	31	20.33	13.67
27	Dhan-38	105	122	125.19	33.65	1.05	10.4	8.07	25.03	165.93	45.33	37.67	23.33	18.33
28	NLR-34449	114	149.67	84.09	26.71	0.91	9.13	7	20.99	114.6	42.33	36.33	22.67	17.33
29	72-Dhan-59	97	118.67	186.93	26.46	1.06	9.27	6	23.01	158.87	43.67	37.67	23	20.33
30	Dhan-53 (C)	105	120	107.55	29.15	1.09	9.33	7.8	22.13	135.67	43	36	23.33	19.67
	Mean	110.32	133.79	107.43	32.25	1.04	10.97	7.77	22.7	131.07	42.46	38.24	22.32	17.04
	Minimum	89	114.67	84.09	26.46	0.91	7.67	6	18.36	87.53	30.67	31	20	12
	Maximum	125	162.67	186.93	38.43	1.18	14.27	9.93	27.18	187.4	56	43	24.33	21.33
	SEm±	0.08	0.92	12.87	2.21	0.04	1.33	0.79	0.96	1.97	2.12	1.34	0.7	0.86
	CD (5%)	0.24	2.62	36.44	6.25	0.12	3.76	2.24	2.73	5.57	5.99	3.8	1.99	2.42
	CV (%)	0.13	1.2	20.75	11.86	7.05	20.95	17.61	7.35	2.6	8.64	6.09	5.47	8.69

DDF = Days to 50% flowering; DM = Days to maturity; PH = Plant height; FLL = Flag leaf length; FLW = Flag leaf width; TPH = No. of tillers/hill; PPT = No. of panicles/tiller; PL = Panicle length; SPP = No. of spikelets/panicle; BY = Biological yield; HI = Harvest index; TW = Test weight; GY = Grain yield. (C) = Check variety

Table 3. Genotypic correlation coefficients among thirteen quantitative characters in rice

Character	DFF	DM	PH	FLL	FLW	TPH	PPT	PL	SPP	BY	HI	TW	GY
DFF	1	0.890**	-0.15	-0.05	0.441**	0.735**	0.423**	-0.347**	-0.558**	0.326**	0.555**	0.235*	0.14
DM		1	0.02	-0.04	0.19	0.564**	0.527**	-0.2	-0.481**	0.286**	0.446**	0.1	0.01
PH			1	-0.1	0.2	0.232*	-0.04	0.507**	0.371**	-0.07	-0.258*	0.233*	-0.08
FLL				1	0.06	0.453**	-0.11	0.608**	0.06	-0.05	0.18	0.248*	-0.403**
FLW					1	0.655**	0.573**	0.07	0.324**	0.12	0.12	0	0
TPH						1	0.670**	-0.14	-0.637**	0.09	0.435**	-0.08	-0.09
PPT							1	-0.05	-0.08	-0.02	0.12	-0.07	-0.09
PL								1	0.674**	-0.1	-0.347**	0.270*	-0.408**
SPP									1	-0.12	-0.535**	-0.322**	-0.17
BY										1	1.08	1.12	0.871**
HI											1	0.958**	0.715**
TW												1	1.09
GY													1

DFF=Days to 50% flowering; DM=Days to maturity; PH=Plant height; FLL=Flag leaf length; FLW=Flag leaf width; TPH=No. of tillers/hill; PPT=No. of panicles/tiller; PL=Panicle length; SPP=No. of spikelets/panicle; BY=Biological yield; HI=Harvest index; TW=Test weight; GY=Grain yield. * $p < 0.05$; ** $p < 0.01$

Table 4. Phenotypic correlation coefficients among thirteen quantitative characters in rice

Character	DFF	DM	PH	FLL	FLW	TPH	PPT	PL	SPP	BY	HI	TW	GY
DFF	1	0.113	0.02	-0.006	-0.137	0.04	0.005	-0.089	-0.113	-0.15	0.624**	0.343**	0.416**
DM		1	0.884**	-0.091	-0.028	0.241**	0.331**	0.219**	-0.246**	-0.554**	0.275**	0.376**	0.13
PH			1	0.023	-0.05	0.133	0.215*	0.221*	-0.136	-0.475**	0.238*	0.297*	0.059
FLL				1	-0.078	0.006	-0.10	-0.04	0.291**	0.221*	-0.042	-0.051	-0.074
FLW					1	0.023	0.153	0.222*	0.296**	0.041	-0.024	0.009	-0.076
TPH						1	-0.005	0.085	0.035	0.183	0.146	0.051	0.089
PPT							1	0.317**	-0.122	-0.276**	-0.053	0.148	0.001
PL								1	0.083	-0.027	0.075	0.025	-0.152
SPP									1	0.455**	-0.063	-0.11	-0.111
HI										1	-0.079	-0.358**	-0.174
TW											1	0.522**	0.467**
GY												1	0.391**

DFF=Days to 50% flowering; DM=Days to maturity; PH=Plant height; FLL=Flag leaf length; FLW=Flag leaf width; TPH=No. of tillers/hill; PPT=No. of panicles/tiller; PL=Panicle length; SPP=No. of spikelets/panicle; BY=Biological yield; HI=Harvest index; TW=Test weight; GY=Grain yield. * $p < 0.05$; ** $p < 0.01$

Table 5. Direct (diagonal) and indirect effects of thirteen quantitative characters on grain yield at the genotypic level

Character	DFF	DM	PH	FLL	FLW	TPH	PPT	PL	SPP	BY	HI	TW	GY
DFF	0.335	-0.737	0.008	0.04	-0.019	0.042	0.022	-0.226	0.232	0.212	0.268	-0.042	0.14
DM	0.298	-0.828	-0.001	0.034	-0.008	0.032	0.027	-0.13	0.2	0.186	0.216	-0.018	0.01
PH	-0.049	-0.014	-0.056	0.079	-0.009	0.013	-0.002	0.329	-0.154	-0.048	-0.125	-0.042	-0.08
FLL	-0.016	0.034	0.005	-0.828	-0.003	0.026	-0.005	0.395	-0.025	-0.031	0.088	-0.044	-0.403
FLW	0.148	-0.159	-0.011	-0.048	-0.043	0.037	0.029	0.042	-0.135	0.078	0.059	0	0
TPH	0.246	-0.467	-0.013	-0.375	-0.028	0.057	0.034	-0.088	0.265	0.059	0.21	0.015	-0.09
PPT	0.142	-0.436	0.002	0.088	-0.025	0.038	0.051	-0.034	0.033	-0.015	0.056	0.012	-0.09
PL	-0.116	0.165	-0.029	-0.503	-0.003	-0.008	-0.003	0.65	-0.28	-0.066	-0.168	-0.048	-0.408
SPP	-0.187	0.398	-0.021	-0.049	-0.014	-0.036	-0.004	0.438	-0.416	-0.078	-0.258	0.057	-0.17
BY	0.109	-0.236	0.004	0.04	-0.005	0.005	-0.001	-0.066	0.05	0.65	0.521	-0.199	0.871
HI	0.186	-0.369	0.015	-0.151	-0.005	0.025	0.006	-0.226	0.222	0.701	0.483	-0.171	0.715
TW	0.079	-0.081	-0.013	-0.205	0	-0.005	-0.003	0.176	0.134	0.724	0.463	-0.179	1.09

Abbreviations as in Table 3. Diagonal values denote direct effects; off-diagonal values denote indirect effects via the respective character

Table 6. Direct (diagonal) and indirect effects of thirteen quantitative characters on grain yield at the phenotypic level

Character	DFF	DM	PH	FLL	FLW	TPH	PPT	PL	SPP	BY	HI	TW	GY
DFF	0.159	-0.315	-0.007	0.003	-0.002	0.024	-0.018	-0.01	0.108	0.179	-0.02	0.012	0.416
DM	0.14	-0.356	0.002	0.006	-0.001	0.016	-0.018	-0.006	0.092	0.155	-0.016	0.005	0.13
PH	-0.014	-0.008	0.073	0.009	0	-0.007	0.003	0.012	-0.043	-0.027	0.003	-0.007	0.059
FLL	-0.004	0.018	-0.006	-0.118	0	0.011	-0.018	0.012	-0.008	-0.016	-0.001	-0.007	-0.074
FLW	0.038	-0.048	0	-0.003	-0.008	0	-0.007	0.001	-0.035	0.095	-0.003	0.008	-0.076
TPH	0.053	-0.076	-0.007	-0.018	0	0.074	-0.026	-0.005	0.053	-0.034	-0.008	0	0.089
PPT	0.035	-0.079	-0.003	-0.026	-0.001	0.023	-0.081	0.003	0.005	0.049	-0.001	-0.014	0.001
PL	-0.039	0.048	0.021	-0.035	0	-0.009	-0.007	0.04	-0.088	-0.041	0.006	-0.01	-0.152
SPP	-0.088	0.169	0.016	-0.005	-0.001	-0.02	0.002	0.018	-0.194	-0.051	0.019	-0.016	-0.111
BY	0.044	-0.085	-0.003	0.003	-0.001	-0.004	-0.006	-0.003	0.015	0.651	-0.028	0.042	-0.174
HI	0.06	-0.106	-0.004	-0.001	0	0.011	-0.002	-0.004	0.069	0.34	-0.054	0.035	0.467
TW	0.021	-0.021	-0.005	0.009	-0.001	0	0.012	-0.005	0.034	0.304	-0.021	0.089	0.391

Abbreviations as in Table 3

Biological yield and harvest index, showing favourable heritability, genetic advance, strong positive genotypic correlation with grain yield and the largest positive direct effects, are the most reliable direct selection criteria for improving grain yield in rice, while test weight is better used as a supportive indirect selection parameter. A multi-trait, index-based selection strategy combining these traits, rather than single-character selection, would be more effective for achieving genetic gain. Among the genotypes evaluated, DRRH2 combined the highest grain yield with high biological yield, harvest index and test weight and may be exploited as a promising donor in future rice hybridisation programmes, along with 72-Dhan-59, 80-NLR-40024 and Vikramarya.

4. Conclusion

The present study, undertaken to estimate genetic variability, heritability and genetic advance, assess the direct and indirect contribution of yield-attributing traits, and study correlations among quantitative traits in relation to grain yield, led to the following conclusions. High heritability coupled with high genetic advance as a percentage of the mean was recorded for number of spikelets per panicle, biological yield and grain yield, indicating that these traits are governed predominantly by additive gene action and can be reliably improved through simple phenotypic selection, thereby fulfilling the first objective of the study. Correlation studies revealed that grain yield had a strong positive genotypic association with test weight, biological yield and harvest index, confirming these as the most dependable component traits for indirect selection, in line with the second objective. Path coefficient analysis further showed that biological yield and harvest index exerted the highest positive direct effects on grain yield at both genotypic and phenotypic levels, while test weight, despite its strong correlation, contributed to yield mainly through indirect effects via these two traits — addressing the third objective on direct and indirect trait contributions. Taken together, biological yield and harvest index emerge as the most effective direct selection criteria for improving grain yield in rice, with test weight serving as a useful supportive indirect selection parameter. The genotype DRRH2, which combined high grain yield with favourable biological yield, harvest index and test weight, along with 72-Dhan-59, 80-NLR-40024 and Vikramarya, may be exploited as promising donors in future rice hybridisation programmes aimed at genetic improvement of grain yield.

5. Limitations

The study was conducted with thirty genotypes at a single location during Kharif 2025; therefore, the estimates describe the evaluated genetic material and environment. Multi-environment and multi-season evaluation would be required to establish the stability of trait associations, heritability estimates, and genotype performance across contrasting conditions. Accordingly, the selection implications should be interpreted within the experimental conditions of this investigation.

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Declaration of AI Use

This manuscript was prepared through the intellectual contributions of the author(s) to the study design, data analysis, interpretation of results, and scholarly content. Grammarly and ChatGPT were used solely to assist with grammatical refinement and reference formatting during manuscript revision. The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

Competing Interests

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper.

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