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Integrated multivariate dissection of genetic variability, trait interrelationships and path effects on grain yield in rice

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Abstract

The present investigation was conducted to assess the extent of genetic variability, associations, and interrelationships among thirty-three rice (*Oryza sativa* L.) genotypes for yield and related traits under field conditions. Considerable differences have been identified among genotypes for all parameters, supporting the presence of significant genetic variability. Traits such as biological yield, harvest index, and grain yield per hill exhibited high coefficients of variation, high heritability and high genetic advance, indicating predominance of additive gene action and potential for effective selection. Grain yield displayed an efficient and positive correlation with biological yield, harvest index, and the number of panicles per hill. Harvest index and test weight were identified as the most important traits exerting strong direct effects on yield, while other traits contributed indirectly. The integrated analysis of variability, correlation, and path effects provides a strong basis for identifying key selection indices and formulating efficient breeding strategies for enhancing rice productivity.

Keywords: Rice; genetic variability; correlation; path coefficient analysis; yield components

1. Introduction

Rice (*Oryza sativa* L.) is a major staple crop across the globe, nourishing nearly half of the world's population and serving as the principal source of calories in Asia. India ranks among the largest rice producers, cultivating the crop across diverse agro-climatic zones during *Kharif*, Rabi, and Boro seasons. In 2023-24, India achieved a record production of 137.8 million metric tonnes, contributing nearly one-fifth of the global supply [1]. Production is further projected to reach 149 million metric tonnes in 2024-25, reflecting continued gains but also highlighting the need for sustained productivity growth [2]. Despite these achievements, rice productivity faces persistent challenges from population pressure, climate change, declining factor productivity, and yield plateaus in major varieties, necessitating continuous genetic improvement for food and livelihood security.

Crop improvement programs fundamentally rely on the availability and effective utilization of genetic variability. Estimates of the genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, and genetic advance (GA) provide insights into the nature of trait inheritance and the potential response to selection. Traits that exhibit high heritability along with high GA are usually governed by additive gene action, making them reliable for phenotypic selection in early generations [3-6]. Several recent studies in rice have confirmed high heritability and genetic advance for grain yield and related traits, including biological yield and harvest index, thereby emphasizing their importance in selection programs [7-9].

Grain yield is a complex polygenic trait influenced by multiple yield components and their interactions. Correlation analysis provides an understanding of the strength and direction of relationships between yield and its component traits, thereby identifying useful indirect selection criteria [10]. However, correlation alone does not partition direct and indirect contributions. Path coefficient analysis, originally proposed by Dewey and Lu (1959), partitions correlation into direct and indirect effects, enabling a more precise identification of traits that directly influence yield [11]. Recent studies in rice have consistently identified harvest index, test weight, and biological yield as major direct contributors to grain yield, while traits like panicle length and number of tillers exert indirect effects [7, 12, 13].

Although several researchers have reported variability and trait associations in rice germplasm under different environments, genotype-specific information under local conditions remains limited. An integrated assessment of genetic variability, correlation, and path analysis is therefore necessary to refine trait-based selection strategies for developing high-yielding rice varieties suitable for regional agro-climatic conditions.

1.1 Objectives

The present investigation was carried out with the following primary objectives:

1. To assess the genetic variability among rice genotypes for yield and its component traits.
2. To assess the phenotypic and genotypic relationships between grain yield and associated characteristics.
3. To estimate the direct and indirect effects of component traits on grain yield using

2. Materials and Methods

2.1 Experimental Site and Materials

The present investigation was carried out during *Kharif* 2024 at the Field Experimental Centre, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences (SHUATS), Prayagraj, Uttar Pradesh, India (25.45°N, 81.85°E, 98 m above sea level). The site has a sandy loamy soil with medium fertility status, and the climate is humid subtropical with hot summers and cool winters.

The experimental material consisted of 33 rice (*Oryza sativa* L.) genotypes, including advanced breeding lines and varieties obtained from SHUATS and collaborating institutions.

2.2 Experimental Design and Crop Management

The trial was laid out in a Randomized Block Design (RBD) with three replications. Each genotype was sown in a plot of two rows, 3 m in length, with spacing of 20 × 15 cm between rows and plants. Recommended agronomic practices were followed, including timely irrigation, fertilizer application, and plant protection measures, to ensure optimal crop growth and minimize environmental variation.

2.3 Traits Recorded

Data were recorded on five randomly selected plants per genotype per replication for the following yield and yield-related traits:

Days to 50% flowering, Plant height (cm), Number of tillers per hill, Number of panicles per hill, Panicle length (cm), Number of grains per panicle, Test weight (g), Biological yield per hill (g), Harvest index (%) and Grain yield per hill (g)

2.4 Statistical Analysis

The data were subjected to analysis of variance (ANOVA) following the procedure of Panse and Sukhatme, 1985 [6] to test the significance of genotypic differences. Genetic parameters including the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability, and genetic advance were estimated as described by Burton and DeVane, 1953 [3], Johnson *et al*., 1955 [4], and Hanson *et al*., 1956 [5]. Correlation coefficients at genotypic and phenotypic levels were calculated according to the method of Al-Jibouri *et al*., 1958 [10]. Path coefficient analysis was conducted following Dewey and Lu, 1959 [11] to partition correlation coefficients into direct and indirect effects on grain yield.

All statistical computations were carried out using OPSTAT software, while supplementary analyses and graphical visualization were performed in R (version 4.3.1) and Microsoft Excel 2019, ensuring robustness and reproducibility of results.

3. Results and Discussion

3.1 Genetic Variability Parameters

The ANOVA revealed (Table 1) highly significant differences among the 33 rice genotypes for all 13 quantitative traits, highlighting the presence of substantial genetic variability. Such variability is critical for sustained genetic improvement, as it forms the basis for effective selection.

The range of variation and estimates of GCV, PCV, heritability, and GA are presented in Table 2. Across traits, the PCV values were slightly higher than GCV, which suggests environmental influences on expression. However, the narrow PCV and GCV gap for plant height, days to 50% flowering, panicle length, and grain yield per hill indicates that these traits are mainly under genetic control and less prone to environmental fluctuations.

High GCV and PCV were found for traits such as number of panicles per hill, biological yield per hill, and grain yield per hill, indicating broad genetic variation and more room for selection. Similar results were reported in recent studies, where yield and biomass traits consistently showed high variability and heritability in rice landraces and advanced breeding lines (Mandal *et al*., 2023; Singh *et al*., 2023) [8, 9].

High heritability (>95%) coupled with high GA% was recorded for grain yield per hill, biological yield per hill, and number of panicles per hill. This implies a predominance of additive gene action, suggesting that simple phenotypic selection would be effective in early generations. Comparable findings have been reported by Mandal *et al*. (2023) [8] and Anwar *et al*. (2022) [7], who observed high heritability and GA for yield traits in rice.

Conversely, flag leaf width, test weight, and spikelets per panicle expressed moderate heritability with moderate GA, reflecting possible non-additive effects and stronger environmental interaction. These traits may require recurrent selection or hybridization strategies rather than simple selection for improvement.

Overall, the combination of high genetic variability, heritability, and genetic advance for yield and biomass traits strongly supports their role as key targets for direct selection in rice improvement programs.

3.2 Correlation Coefficient Analysis

Correlation analysis provided deeper insights into trait inter-relationships. At the genotypic and phenotypic levels, there were substantial and positive correlations between grain yield per hill and biological yield per hill, Number of panicles per hill, Harvest index, Number of tillers per hill, Panicle length (Table 3 and Table 4).

This indicates that simultaneous improvement in these traits would directly enhance yield potential. Similar correlations have been documented in irrigated and lowland rice environments, where biomass and harvest index emerged as strong contributors to yield (Mandal *et al*., 2023; Devi *et al*., 2024) [8, 13].

Additionally, number of tillers per hill correlated strongly with panicles per hill, confirming their close developmental relationship. Plant height also correlated with flag leaf length, reflecting the structural and physiological linkage.

Notably, days to 50% flowering, days to maturity, and flag leaf width exhibited weak or negative correlations with yield, suggesting limited utility in direct selection. These findings are consistent with past reports that earliness may not always enhance yield under irrigated systems (Kumar *et al*., 2023) [14].

The general trend of higher genotypic correlations compared to phenotypic further underlines that environmental factors tend to mask true genetic associations, a pattern also observed in recent multivariate studies (Mandal *et al*., 2023; Singh *et al*., 2024) [8, 9].

3.3 Path Coefficient Analysis

Correlation alone does not reveal causal relationships; hence, path analysis was conducted to partition direct and indirect effects.

Phenotypic Level (Table 5)

- Harvest index (0.3954) again recorded the strongest direct effect, followed by test weight (0.1285) and biological yield (0.1264).
- Moderate indirect contributions through panicle number and tillers per hill confirmed their secondary but significant role.

Genotypic Level (Table 6)

- Harvest index (0.5154) exerted the strongest positive direct effect on grain yield, followed by test weight (0.2082), biological yield (0.1117), and number of panicles per hill (0.1002).
- Traits such as flag leaf width and plant height showed negative direct effects, despite weak correlations with yield, suggesting undesirable pleiotropic effects or trade-offs.
- Traits like tillers per hill and panicle length had low or negative direct effects but contributed indirectly through harvest index and biological yield.

The low residual effects (0.1117 at genotypic and 0.1737 at phenotypic level) confirmed that most of the variation in yield was well-explained by the traits included in the model.

Recent rice studies also reported harvest index and biological yield as the most reliable direct contributors to grain yield, while panicle length and tillering influenced yield mostly through indirect pathways (Mandal *et al*., 2023; Anwar *et al*., 2022) [8, 7].

Table 1: Analysis of Variance among 33 rice genotypes for 13 quantitative traits

S. No.	Source	Mean sum of squares		
		Replication	**Genotypes**	**Error**
	Degrees of freedom	2	32	64
1	Day to 50% flowering	0.25	114.35 **	0.83
2	Days to Maturity	0.62	240.59 **	0.24
3	Flag leaf length	0.78	122.17 **	2.98
4	Flag leaf width	0	0.13 **	0
5	Plant height	30.75	1244.5 **	40.31
6	Number of total tillers per hill	0.85	1.32 **	0.3
7	Number of panicles per hill	0.3	2.01 **	0.21
8	Panicle length	1.17	34.7 **	0.93
9	Number of spikelets per panicles	100.22	2554.53 **	108.22
10	Test weight	0.06	8.82 **	0.21
11	Harvest Index	4.14	150.49 **	9.05
12	Biological yield per hill	32.98	859.26 **	30.43
13	Grain yield per hill	11.78	182.8 **	4.62

** indicates significance at 1% level of significance

Table 2: Genetic parameters for 13 quantitative characters in rice genotypes

S. No	Character	GCV	PCV	h² (Broad Sense)	GA	Gen. Adv as% of Mean
1	Day to 50% flowering	8.04	8.13	97.87	12.64	16.38
2	Days to Maturity	7.09	7.1	99.7	16.41	14.59
3	Flag leaf length	18.32	19	93.03	12.52	36.41
4	Flag leaf width	19.38	19.66	96.89	0.42	39.25
5	Plant height	18.87	19.800	90.870	39.340	37.060
6	Number of total tillers per hill	7.28	10.01	52.86	0.87	10.9
7	Number of panicles per hill	10.88	12.63	74.2	1.37	19.3
8	Panicle length	11.21	11.67	92.34	6.64	22.19
9	Number of spikelets per panicles	21.57	22.95	88.28	55.27	41.74
10	Test weight	7.77	8.05	93.12	3.37	15.44
11	Harvest Index	20.98	22.9	83.9	12.96	39.58
12	Biological yield per plant	24.72	26.05	90.08	32.5	48.33
13	Grain yield per hill	35.06	36.4	92.78	15.29	69.56

GCV: Genotypic Coefficient of Variation, PCV: Phenotypic Coefficient of Variation,
h^2: Heritability, GA% of Mean: Genetic Advance as percent of mean

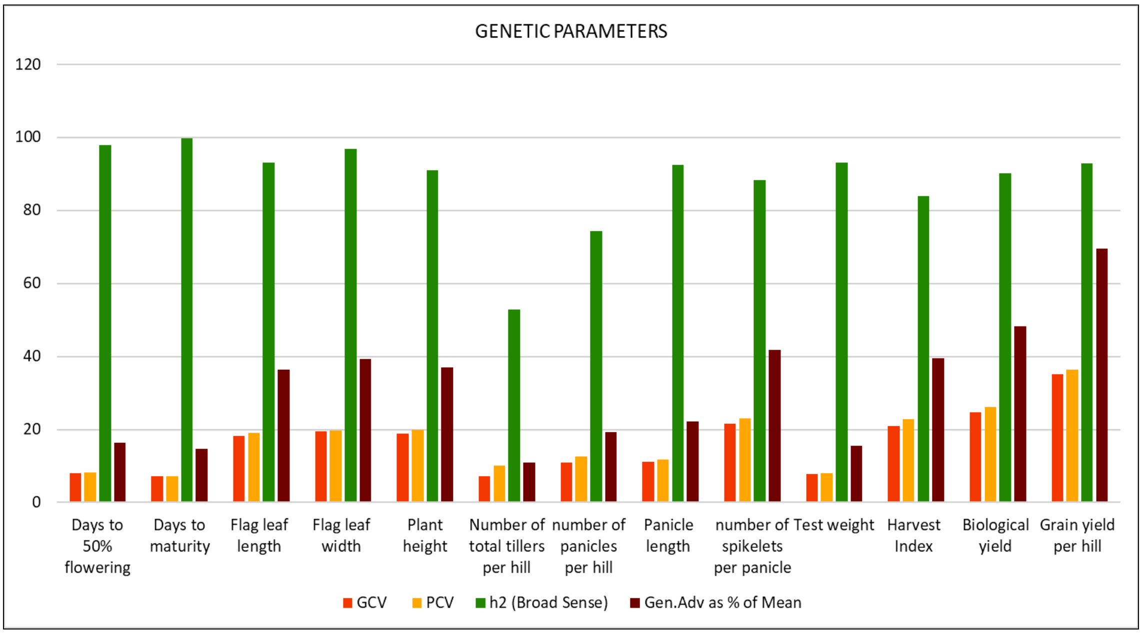

Fig 1: Bar diagram depicting GCV, PCV, heritability and genetic advance as% of mean for 13 quantitative characters of rice

Table 3: Estimation of Phenotypic correlation coefficient for grain yield and its related traits in 33 rice genotypes.

Characters	Day to 50% flowering	Days to Maturity	Flag leaf length	Flag leaf width	Plant height	Number of total tillers per hill	Number of panicles per hill	Panicle length	Number of spikelets per panicles	Test weight	Harvest Index	Biological yield per plant
Days to Maturity	0.33 **											
Flag leaf length	0.079	-0.319 **										
Flag leaf width	-0.109	-0.427 **	0.681**									
Plant height	0.306 **	0.042	0.187	-0.051								
Number of total tillers per hill	0.109	-0.327 **	0.609 **	0.525 **	-0.010							
Number of panicles per hill	0.334**	-0.276 **	0.641 **	0.581**	0.171	0.629 **						
Panicle length	-0.134	-0.016	-0.086	-0.253 *	0.285 **	-0.092	-0.157					
Number of spikelets per panicles	-0.238 *	-0.426 **	0.704 **	0.719 **	-0.119	0.458 **	0.433 **	-0.335 **				
Test weight	-0.011	-0.481 **	0.650 **	0.690 **	-0.221 *	0.501 **	0.520 **	-0.254 *	0.613 **			
Harvest Index	-0.1304	-0.4664 **	0.689 **	0.679 **	-0.029	0.551 **	0.547 **	-0.19	0.642 **	0.748 **		
Biological yield per plant	-0.1517	-0.4846 **	0.164	0.490 **	-0.392 **	0.324 **	0.271 **	-0.181	0.361 **	0.461 **	0.286 **	
Grain yield per hill	-0.1251	-0.4914 **	0.660 **	0.720 **	-0.167	0.532 **	0.555 **	-0.269 **	0.686 **	0.804 **	0.804 **	0.555 **

**1% Level of significance *5% Level of significance

Table 4: Estimation of Genotypical correlation coefficient for grain yield and its related traits in 33 rice genotypes

Characters	Day to 50% flowering	Days to Maturity	Flag leaf length	Flag leaf width	Plant height	Number of total tillers per hill	Number of panicles per hill	Panicle length	Number of spikelets per panicles	Test weight	Harvest Index	Biological yield per plant
Days to Maturity	0.333											
Flag leaf length	0.093	-0.331										
Flag leaf width	-0.11	-0.435 *	0.720 **									
Plant height	0.316	0.043	0.217	-0.054								
Number of total tillers per hill	0.136	-0.449 **	0.863**	0.731 **	-0.054							
Number of panicles per hill	0.374 *	-0.323	0.785 **	0.705 **	0.191	0.895 **						
Panicle length	-0.139	-0.015	-0.101	-0.271	0.311	-0.153	-0.138					
Number of spikelets per panicles	-0.251	-0.459 **	0.748 **	0.782 **	-0.133	0.625 **	0.524 **	-0.368 *				
Test weight	-0.011	-0.498 **	0.702 **	0.730 **	-0.245	0.723 **	0.645 **	-0.286	0.689 **			
Harvest Index	-0.141	-0.509 **	0.776 **	0.745 **	-0.032	0.842 **	0.746 **	-0.213	0.773 **	0.840 **		
Biological yield per plant	-0.158	-0.508 **	0.185	0.526 **	-0.439 *	0.483 **	0.328	-0.210	0.417 *	0.515 **	0.412*	
Grain yield per hill	-0.132	-0.512 **	0.726 **	0.754 **	-0.182	0.780 **	0.661 **	-0.287	0.77 **	0.866 **	0.904 **	0.570 **

**1% Level of significance *5% Level of significance

Table 5: Estimation of Phenotypic Path analysis for grain yield and its related traits in 33 rice genotypes.

Characters	Day to 50% flowering	Days to Maturity	Flag leaf length (cm)	Flag leaf width (cm)	Plant height (cm)	Number of total tillers per hill	Number of panicles per hill	Panicle length (cm)	Number of spikelets per panicles	Test weight (g)	Harvest Index (%)	Biological yield per plant
Day to 50% flowering	-0.0828	0.01768	0.0102	0.00523	0.00802	-0.00353	0.02849	0.00777	-0.01723	-0.0029	-0.05102	-0.04503
Days to Maturity	-0.02732	0.05357	-0.0409	0.02038	0.0011	0.0106	-0.02353	0.00096	-0.03085	-0.1291	-0.18247	-0.14385
Flag leaf length (cm)	-0.0066	-0.01712	0.12801	-0.03249	0.00491	-0.01971	0.05467	0.005	0.051	0.17442	0.26955	0.04886
Flag leaf width (cm)	0.00909	-0.02291	0.08725	-0.04756	-0.00135	-0.01695	0.04957	0.01463	0.05214	0.1856	0.26591	0.14557
Plant height (cm)	-0.02538	0.00224	0.02401	0.00245	0.02618	0.00033	0.01461	-0.01645	-0.00868	-0.05929	-0.01131	-0.11633
Number of total tillers per hill	-0.00902	-0.01753	0.07791	-0.02495	-0.00027	-0.03239	0.05367	0.00532	0.03324	0.13417	0.21568	0.09617
Number of panicles per hill	-0.02768	-0.01479	0.08212	-0.02773	0.00449	-0.02039	0.08518	0.00903	0.03135	0.13942	0.21392	0.08038
Panicle length (cm)	0.01115	-0.00089	-0.01109	0.01209	0.00746	0.00299	-0.01334	-0.05768	-0.02425	-0.06825	-0.07433	-0.05367
Number of spikelets per panicles	0.01969	-0.02281	0.09012	-0.03431	-0.00314	-0.01486	0.03688	0.01931	0.07244	0.16439	0.25105	0.10704
Test weight (g)	0.00089	-0.02579	0.08326	-0.03299	-0.00579	-0.0162	0.0443	0.01468	0.04441	0.2682	0.29267	0.13675
Harvest Index (%)	0.0108	-0.02499	0.0882	-0.0324	-0.00076	-0.01785	0.0466	0.01096	0.04649	0.20062	0.39122	0.08501
Biological yield per plant	0.01256	-0.02596	0.02107	-0.02338	-0.01026	-0.01049	0.02308	0.01043	0.02612	0.12355	0.11205	0.29684

Table 6: Estimation of Genotypic Path analysis for grain yield and its related traits in 33 rice genotypes

Characters	Day to 50% flowering	Days to Maturity	Flag leaf length (cm)	Flag leaf width (cm)	Plant height (cm)	Number of total tillers per hill	Number of panicles per hill	Panicle length (cm)	Number of spikelets per panicles	Test weight (g)	Harvest Index (%)	Biological yield per plant
Day to 50% flowering	-0.03804	0.02986	-0.01598	0.00585	0.03957	0.04644	-0.0623	0.00266	-0.05992	-0.00466	-0.05169	-0.02396
Days to Maturity	-0.01267	0.08964	0.05654	0.02316	0.00542	-0.15365	0.05385	0.0003	-0.10953	-0.20155	-0.18697	-0.07685
Flag leaf length (cm)	-0.00356	-0.02965	-0.17091	-0.03832	0.02719	0.29503	-0.13078	0.00191	0.17815	0.28426	0.28484	0.02796
Flag leaf width (cm)	0.00418	-0.03903	-0.12313	-0.05319	-0.00672	0.2499	-0.11745	0.00514	0.18625	0.29553	0.27321	0.07952
Plant height (cm)	-0.01203	0.00389	-0.03714	0.00286	0.12511	-0.01845	-0.03193	-0.00591	-0.0318	-0.09904	-0.01173	-0.06637
Number of total tillers per hill	-0.00517	-0.04028	-0.14746	-0.03887	-0.00675	0.34193	-0.14925	0.0029	0.14896	0.29284	0.30874	0.07294
Number of panicles per hill	-0.01422	-0.02897	-0.13415	-0.03749	0.02397	0.30631	-0.16661	0.00263	0.12476	0.26127	0.27374	0.04963
Panicle length (cm)	0.00532	-0.0014	0.01722	0.01442	0.03897	-0.05229	0.02305	-0.01898	-0.08771	-0.1159	-0.07836	-0.03175
Number of spikelets per panicles	0.00957	-0.04123	-0.12784	-0.04159	-0.0167	0.21386	-0.08728	0.00699	0.23817	0.27882	0.28358	0.06307
Test weight (g)	0.00044	-0.04464	-0.12003	-0.03883	-0.03061	0.2474	-0.10755	0.00543	0.16407	0.40475	0.3081	0.07783
Harvest Index (%)	0.00536	-0.0457	-0.13275	-0.03962	-0.004	0.28787	-0.12437	0.00406	0.18417	0.34004	0.36673	0.06226
Biological yield per plant	0.00603	-0.0456	-0.03163	-0.02799	-0.05496	0.1651	-0.05474	0.00399	0.09944	0.20852	0.15114	0.15107

4. Conclusion

The present study on 33 rice genotypes revealed significant genetic variability for yield and related traits, confirming sufficient scope for improvement through selection. Traits such as grain yield per hill, biological yield, and number of panicles per hill exhibited high genetic variability, heritability, and genetic advance, indicating predominance of additive gene action and their amenability to direct phenotypic selection.

Correlation analysis highlighted biological yield, harvest index, and number of panicles per hill as the most reliable associates of grain yield, while path coefficient analysis identified harvest index and test weight as the strongest direct contributors to yield, with other traits acting indirectly through them. The consistency of these traits across correlation and path analyses underscores their central role in determining rice productivity.

Overall, the integration of variability parameters, correlation, and path analysis provides clear evidence that harvest index, test weight, and biological yield should be prioritized as selection criteria in breeding programs. Focusing on these traits will accelerate the development of high-yielding rice cultivars adapted to the target environments.

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