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GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN ADVANCED BREEDING LINES OF RICE (*Oryza sativa* L.)

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ABSTRACT

Genetic variability and character association are fundamental for identifying useful selection criteria in rice improvement. The present study was conducted during *Kharif* 2025 at the Zonal Agricultural and Horticultural Research Station, Shivamogga, Karnataka, to assess the genetic variability, correlation and path coefficients for yield and yield attributing traits in seventeen advanced breeding lines of rice derived from the cross combinations Tunga × KHP-13, KPR-1 × KHP-13 and Sahyadri Kempumukthi × Swarna Sub 1, along with three checks, Tunga, KHP-13 and Sahyadri Kempumukthi. The experiment was laid out in a randomized complete block design with two replications, and observations were recorded on fourteen yield and yield attributing characters. Analysis of variance revealed significant differences among the genotypes for all the characters studied. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters, indicating some influence of environment on their expression. High heritability coupled with high genetic advance as percentage of mean was recorded for days to 50 per cent flowering, plant height, number of tillers per plant, number of productive tillers per plant, test weight and grain length to breadth ratio, suggesting the predominance of additive gene action for these traits. Grain yield per plant showed a significant positive correlation with panicle length, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle, panicle fertility and test weight, and a significant negative correlation with days to 50 per cent flowering, days to maturity and grain length to breadth ratio. Path coefficient analysis revealed that number of filled grains per panicle exerted the highest positive direct effect on grain yield per plant, followed by number of productive tillers per plant and test weight, while panicle length also recorded a fairly high positive direct effect. The low residual effect indicated that the characters included in the study accounted for most of the variation in grain yield per plant. Number of tillers per plant and days to 50 per cent flowering, despite showing a strong correlation with yield, exerted their influence mainly through indirect effects rather than direct effects. Based on these results, number of filled grains per panicle, number of productive tillers per plant, test weight and panicle length were identified as the traits with the strongest direct positive effect on grain yield and are recommended as reliable selection criteria for yield improvement, while grain yield itself, being more influenced by environment, would be better improved through indirect selection based on these component traits.

***Key words*:** Rice; Genetic variability; Heritability; Correlation; Path analysis

Introduction

Rice (*Oryza sativa* L., 2n = 24) is one of the most important cereal crops in the world and plays a central role in global food and nutritional security. It belongs to the genus Oryza of the tribe Oryzeae under the family Poaceae, and is grown under a wide range of agro-ecological conditions, contributing more than one-fifth of the calorific requirement of the world's population. Global

rice production has continued to increase in recent years, with global production for 2025-26 estimated at 541.2 million tonnes on a milled basis (Anonymous, 2026). India has emerged as the world's largest rice producer, with production placed at 150.18 million tonnes during 2024-25 from a harvested area of 51.27 million hectares (Anonymous, 2025a), and the first advance estimates for 2025-26 place Kharif rice production at a fresh record of 124.50 million tonnes (Anonymous, 2025b).

Despite these record production levels, India continues to face the challenge of feeding a growing population under variable climatic conditions, and the yield plateau observed in several regions highlights the need to continuously develop improved, high yielding cultivars. Grain yield is a complex quantitative trait governed by polygenes and strongly influenced by environmental factors along with several interrelated component traits. The first step in any crop improvement programme is, therefore, to understand the nature and extent of genetic variability present in the available breeding material, since selection is effective only when adequate variability exists for the trait under improvement. Partitioning the observed phenotypic variability into its genotypic and environmental components, along with heritability and genetic advance, provides a useful basis for planning selection strategies (Johnson *et al.*, 1955b). Recent studies have confirmed considerable genetic variability for grain yield and its component traits in rice; Soundharya *et al.*, (2024) reported moderate genotypic variability for grain related traits along with low environmental influence, while Sao *et al.*, (2024), working with a large germplasm collection, observed high heritability coupled with high genetic advance for hundred seed weight, seedling height and length to breadth ratio, indicating strong additive gene effects for these traits.

Since grain yield results from the combined effect of several component characters, selection based on yield alone may not always be reliable, making it important to understand how yield is associated with its contributing traits. Correlation studies help identify the traits associated with yield, while path coefficient analysis partitions these relationships into direct and indirect effects and helps in identifying useful criteria for selection. Gupta *et al.*, (2020) reported high genotypic and phenotypic coefficients of variation for filled grains per panicle and effective tillers in rice germplasm, with these traits also showing a strong direct positive effect on yield through path analysis, while Shanmugam *et al.*, (2024) identified kernel breadth, length to breadth ratio and days to fifty per cent flowering as traits with a favourable direct effect on single plant yield in rice landraces.

Table 1: List of advanced breeding lines and checks of rice used in the study.

Cross combination	Code	Genotype / Breeding line
Tunga × KHP-13	G1	Tunga×KHP-13-3-6-7-3-1-5
	G2	Tunga×KHP-13-5-2-4-2-5-6
	G3	Tunga×KHP-13-2-6-11-7-18-8
	G4	Tunga×KHP-13-4-8-3-14-20-15
	G5	Tunga×KHP-13-7-17-18-16-25-11
KPR-1 × KHP-13	G6	KPR-1×KHP-13-7-5-3-12-1-10
	G7	KPR-1×KHP-13-5-2-6-7-9-8-6
	G8	KPR-1×KHP-13-4-7-3-15-29-10
Sahyadri Kempumukthi × Swarna Sub 1	G9	K×S-8-3-1
	G10	K×S-6-2-1
	G11	K×S-11-3-2
	G12	K×S-12-4-1
	G13	K×S-10-4-1
	G14	K×S-11-4-2
	G15	K×S-5-2-4
	G16	K×S-4-1-3
	G17	K×S-4-3-5
Checks	G18	Tunga
	G19	KHP-13
	G20	Sahyadri Kempumukthi

In this context, a set of seventeen advanced breeding lines derived from the cross combinations Tunga × KHP-13, KPR-1 × KHP-13 and Sahyadri Kempumukthi × Swarna Sub 1, along with the checks Tunga, KHP-13 and Sahyadri Kempumukthi, was evaluated at the Zonal Agricultural and Horticultural Research Station, Shivamogga, Karnataka to assess the extent of genetic variability and the pattern of character association for yield and its component traits. With this background, the present investigation was undertaken with the objectives of (i) assessing the genetic variability present in advanced breeding lines of rice for yield and yield attributing traits, and (ii) studying the character association and path analysis for yield and yield attributing traits in these advanced breeding lines of rice.

Materials and Methods

The experimental material comprised seventeen advanced breeding lines of rice of the F_7 and BC_1F_4 generations, derived from the cross combinations Tunga × KHP-13, KPR-1 × KHP-13 and Sahyadri Kempumukthi × Swarna Sub 1, along with three checks, Tunga, KHP-13 and Sahyadri Kempumukthi (Table 1). The experimental material was obtained from the Department of Genetics and Plant Breeding, College of Agriculture, Shivamogga. The experiment was conducted during *Kharif* 2025 at the Zonal Agricultural and Horticultural Research Station (ZAHRS), Shivamogga,

Table 2: Genetic variability parameters for yield and yield attributing traits in advanced breeding lines of rice.

Sl. No.	Character	Mean	Range		Coefficient of Variation		h^2_{bs} (%)	GAM (%)
			Min	Max	PCV (%)	GCV (%)		
1	Days to 50 per cent flowering	105.79	85.00	133.00	16.19	16.18	99.91	33.32
2	Days to maturity	143.33	128.00	163.00	6.76	6.75	99.64	13.89
3	Plant height (cm)	140.44	119.40	163.90	10.29	10.27	99.67	21.13
4	Panicle length (cm)	27.37	23.61	31.87	7.98	7.92	98.53	16.21
5	Number of tillers per plant	16.40	12.90	22.20	13.44	13.20	96.44	26.70
6	Number of productive tillers per plant	15.28	12.70	19.70	12.44	12.32	98.06	25.13
7	Number of spikelets per panicle	177.97	126.40	254.80	15.31	9.98	42.52	13.41
8	Number of filled grains per panicle	164.65	140.00	204.00	9.54	9.41	97.26	19.11
9	Panicle fertility (%)	89.82	86.70	95.28	2.21	2.17	96.03	4.39
10	Test weight (g)	24.86	20.04	30.55	12.02	11.92	98.55	24.39
11	Grain length and breadth ratio	3.63	2.99	5.50	18.36	18.29	99.28	37.55
12	Grain yield per plant (g)	53.05	30.62	60.56	14.32	9.82	46.98	13.86
13	Grain yield (kg/ha)	5817.00	4487.51	6554.17	9.86	8.55	75.17	15.27
14	Straw yield (kg/ha)	6516.10	4886.65	9713.31	23.07	15.61	45.77	21.75

PCV: Phenotypic coefficient of variation; GCV: Genotypic coefficient of variation; h^2bs: Broad sense heritability; GAM: Genetic advance as per cent of mean.

Karnataka (13°55' N latitude, 75°34' E longitude, 650 m above mean sea level), which received an average rainfall of 567 mm and recorded an average temperature of 24.8°C during the crop season.

The twenty genotypes were evaluated in a randomized complete block design with two replications under puddled field conditions. Seeds were sown in raised nursery beds and healthy seedlings were transplanted to the main field at the rate of one seedling per hill, following a spacing of 20 cm × 15 cm. Recommended package of practices was followed to raise a normal, healthy crop.

Five plants were selected at random from each genotype in each replication for recording observations. Observations were recorded on fourteen yield and yield attributing characters, namely, days to 50 per cent flowering, days to maturity, plant height (cm), panicle length (cm), number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle, panicle fertility (%), test weight (g), grain length to breadth (L/B) ratio, grain yield per plant (g), grain yield (kg/ha) and straw yield (kg/ha), following standard procedures.

Genotypic and phenotypic components of variance were estimated as suggested by Cochran and Cox (1957). Genotypic (GCV) and phenotypic (PCV) coefficients of variation were calculated as per Burton and De Vane (1953) and classified as low (0–10%), moderate (10–20%) and high (>20%) following Sivasubramanian and Menon (1973). Broad sense heritability (h^2) was estimated as the ratio of genotypic variance to phenotypic variance (Lush, 1949; Hanson *et al*., 1956) and classified as low (0–30%), moderate (30.1–60%) and high (>60%) as suggested by Robinson and Comstock (1949). Genetic advance was estimated following Johnson *et al*., (1955a) as $GA = h^2 \times K \times \sigma p$, where K is the selection differential (2.06 at 5 per cent selection intensity) and σp is the phenotypic standard deviation; genetic advance as per cent of mean (GAM) was classified as low (0–10%), moderate (10.1–20%) and high (>20%), as suggested by Johnson *et al*., (1955a).

Phenotypic correlation coefficients among all pairs of characters, with grain yield per plant considered as the dependent trait, were computed following Al-Jibouri *et al*., (1958) using R software, and tested for significance at 5 and 1 per cent probability levels. Path coefficient analysis was carried out at the phenotypic level following Wright (1934) and Dewey and Lu (1959), with grain yield per plant taken as the dependent character (Y) and the remaining eleven characters, namely, days to 50 per cent flowering, days to maturity, plant height, panicle length, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle, panicle fertility, test weight and grain length to breadth ratio, taken as causal variables. The residual effect, representing the variation in yield not accounted for by the causal factors considered, was also worked out. Direct and indirect effects were classified as negligible (0.00–0.09), low (0.10–0.19), moderate (0.20–0.29), high (0.30–0.99) and very high (>1.00) as suggested by Lenka and Mishra (1973).

Results and Discussion

Genetic variability for yield and yield attributing traits

The extent of genetic variability present in breeding

Table 3: Phenotypic correlation coefficients among yield and yield attributing traits in advanced breeding lines of rice.

Traits	DFF	DM	PH	PL	TPP	PTP	SPP	FGP	PF	TW	GYP
DFF	1.000										
DM	0.802**	1.000									
PH	0.836**	0.803**	1.000								
PL	-0.580**	-0.491**	-0.432**	1.000							
TPP	-0.492**	-0.368*	-0.334*	0.656**	1.000						
PTP	-0.486**	-0.340*	-0.271	0.740**	0.951**	1.000					
SPP	-0.370*	0.022	-0.270	0.330*	-0.010	0.093	1.000				
FGP	-0.573**	-0.269	-0.341*	0.700**	0.584**	0.684**	0.706**	1.000			
PF	-0.396*	-0.305	-0.186	0.483**	0.408**	0.492**	0.269	0.701**	1.000		
TW	-0.635**	-0.540**	-0.370*	0.387*	0.704**	0.695**	-0.020	0.540**	0.477**	1.000	
GYP	-0.565**	-0.367*	-0.293	0.762**	0.804**	0.886**	0.354*	0.881**	0.639**	0.762**	1.000

*, **: Significant at 5 and 1 per cent levels, respectively. DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; PL: Panicle length; TPP: Number of tillers per plant; PTP: Number of productive tillers per plant; SPP: No. of spikelets per panicle; FGP: Number of filled grains per panicle; PF: Panicle fertility; TW: Test weight; GYP: Grain yield per plant.

material governs the scope for effective selection through simple methods. Analysis of variance revealed highly significant differences among the twenty genotypes for all the fourteen characters studied, confirming the presence of substantial genetic variability in the material. The estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h^2bs) and genetic advance as per cent of mean (GAM) for the fourteen characters are presented in Table 2.

A wide range of variation was recorded for all the characters studied. Days to 50 per cent flowering ranged from 85 to 133 days (mean 105.79 days) with moderate PCV (16.19%) and GCV (16.18%), and recorded high heritability (99.91%) coupled with high GAM (33.32%). Days to maturity (mean 143.33 days) and panicle length (mean 27.37 cm) recorded low PCV and GCV together with high heritability but only moderate GAM. Plant height (mean 140.44 cm), number of tillers per plant (mean 16.40) and number of productive tillers per plant (mean 15.28) recorded moderate PCV and GCV coupled with high heritability and high GAM. Number of spikelets per panicle showed a comparatively wider gap between PCV (15.31%) and GCV (9.98%), with only moderate heritability (42.52%), indicating a greater role of environment in the expression of this trait. Number of filled grains per panicle and panicle fertility recorded low PCV and GCV with high heritability, though genetic advance was moderate for the former and low for the latter. Test weight (mean 24.86 g) and grain length to breadth ratio (mean 3.63) recorded moderate to high PCV and GCV coupled with high heritability and high GAM, the latter recording the highest GAM (37.55%) among all the characters studied. Grain yield per plant showed a moderate PCV (14.32%) against a comparatively low GCV (9.82%) and moderate heritability (46.98%), while grain yield per hectare recorded low PCV and GCV with high heritability (75.17%) but moderate GAM. Straw yield per hectare recorded the highest PCV (23.07%) among all the characters, together with moderate heritability and high GAM, indicating a considerable role of environment along with non-additive gene action in the expression of this trait.

In general, PCV was higher than the corresponding GCV for all the characters studied, reflecting some influence of environment on their expression, although the difference was narrow for most of the morphological and grain characters. This wide range of variation among the advanced breeding lines derived from Tunga × KHP-13, KPR-1 × KHP-13 and Sahyadri Kempumukthi × Swarna Sub 1 indicates that the material forms a genetically diverse group offering good scope for selection, which is in agreement with the findings of Chandramohan *et al*., (2016), Bhinda *et al*., (2017) and Chamar *et al*., (2021), who also reported significant genotypic differences for most yield related characters in rice. Dhavaleshvar *et al*., (2019), who evaluated advanced breeding lines at Shivamogga and allied stations, similarly reported a wide range of variation for yield attributing traits, supporting the present findings.

For days to 50 per cent flowering, plant height, number of tillers per plant, number of productive tillers per plant, test weight and grain length to breadth ratio, the close correspondence between PCV and GCV, together with high heritability and high genetic advance, indicates that the variation for these traits is largely genetic in nature, so that simple selection based on phenotypic performance would be effective, which is in agreement with Johnson *et al*., (1955a). Grain length to breadth ratio recorded the

Table 4: Direct and indirect effects of yield attributing traits on grain yield per plant in advanced breeding lines of rice (path coefficient analysis).

Traits	DFF	DM	PH	PL	TPP	PTP	SPP	FGP	PF	TW	'r' value
DFF	**0.199**	0.035	0.009	-0.131	0.072	-0.203	0.002	-0.279	0.028	-0.216	-0.565
DM	0.160	**0.044**	0.008	-0.111	0.054	-0.142	0.001	-0.131	0.021	-0.184	-0.367
PH	0.166	0.036	**0.010**	-0.098	0.049	-0.113	0.001	-0.166	0.013	-0.126	-0.293
PL	-0.115	-0.022	-0.004	**0.226**	-0.097	0.309	-0.001	0.341	-0.034	0.132	0.762
TPP	-0.098	-0.016	-0.003	0.148	**-0.147**	0.397	0.002	0.284	-0.028	0.240	0.804
PTP	-0.097	-0.015	-0.003	0.168	-0.140	**0.417**	0.002	0.333	-0.034	0.237	0.886
SPP	-0.074	0.001	-0.003	0.075	0.001	0.039	**-0.004**	0.343	-0.019	-0.007	0.354
FGP	-0.114	-0.012	-0.004	0.158	-0.086	0.285	-0.003	**0.486**	-0.049	0.184	0.881
PF	-0.079	-0.014	-0.002	0.109	-0.060	0.205	-0.001	0.340	**0.069**	0.162	0.639
TW	-0.126	-0.024	-0.004	0.088	-0.104	0.290	0.001	0.263	-0.033	**0.341**	0.762

Diagonal, bold values indicate direct effects; off-diagonal values indicate indirect effects; 'r' value indicates correlation of the trait with grain yield per plant. Residual effect = 0.216. DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; PL: Panicle length; TPP: Number of tillers per plant; PTP: Number of productive tillers per plant; SPP: Number of spikelets per panicle; FGP: Number of filled grains per panicle; PF: Panicle fertility; TW: Test weight.

highest genetic advance among all the characters studied, similar to the finding of Sao *et al*., (2024) for the same trait, while the high heritability and genetic advance recorded for number of tillers and number of productive tillers per plant agrees with Sandeep *et al*., (2018) and Chamar *et al*., (2021), who reported tiller number to be one of the easier traits to improve through direct selection.

Days to maturity, panicle length and number of filled grains per panicle recorded high heritability with only moderate genetic advance, suggesting that although these traits are under fairly good genetic control, improvement through simple selection would be comparatively slower. Number of spikelets per panicle, grain yield per plant and straw yield showed a wider gap between PCV and GCV along with moderate heritability, indicating greater environmental influence on these traits; straw yield recorded the highest PCV among all the characters, in agreement with Barik *et al*., (2019), who also reported PCV to be higher than GCV for yield related traits in rice. Panicle fertility recorded high heritability but the lowest genetic advance among the characters studied, which may be attributed to the narrow range of variation already present for this trait; a similar observation was made by Nath and Kole (2021), who cautioned that heritability alone should not be used to judge the scope for selection.

Overall, number of tillers per plant, number of productive tillers per plant, test weight and grain length to breadth ratio appear to be the traits where direct phenotypic selection would be most rewarding in the present material, whereas grain yield per plant, being comparatively more influenced by environment, would be better improved indirectly through its component traits, as discussed in the following section. This is also supported by Niharika *et al*., (2022) and Sudeepthi *et al*., (2020), who recommended selection based on yield components rather than yield alone in advanced breeding material.

Correlation among yield and yield attributing traits

Since grain yield is a complex, polygenically controlled character resulting from the combined action of several interrelated component traits, phenotypic correlation coefficients were worked out among the characters, with grain yield per plant considered as the dependent trait, to understand the nature and magnitude of their association (Table 3).

Grain yield per plant exhibited significant and positive correlation with panicle length (0.762), number of tillers per plant (0.804), number of productive tillers per plant (0.886), number of spikelets per panicle (0.354), number of filled grains per panicle (0.881), panicle fertility (0.639) and test weight (0.762), while it recorded significant negative correlation with days to 50 per cent flowering (-0.565), days to maturity (-0.367) and grain length to breadth ratio (-0.342). This indicates that, in the present material, genotypes that flower and mature relatively early and carry a greater number of productive tillers with well filled panicles tend to record higher grain yield. Similar positive relationships between yield and productive tiller number, filled grain number and test weight have been reported by Parimala *et al*., (2016), Lahari *et al*., (2017) and Chamar *et al*., (2021), while the negative relationship of yield with days to flowering and maturity is in agreement with Chamar *et al*., (2021).

Among the yield components, number of productive tillers per plant recorded a strong positive correlation with number of tillers per plant (0.951), panicle length (0.740), number of filled grains per panicle (0.684) and test weight

(0.695). Number of filled grains per panicle was significantly and positively associated with panicle length (0.700), number of spikelets per panicle (0.706) and panicle fertility (0.701). Days to 50 per cent flowering and days to maturity showed a close positive association with each other (0.802) and with plant height (0.836 and 0.803, respectively), and a significant negative association with panicle length, tiller related traits, filled grain number, panicle fertility and test weight, indicating that early flowering and early maturing genotypes tended to carry more productive tillers and better filled panicles. Grain length to breadth ratio recorded significant positive correlation with days to 50 per cent flowering (0.549), days to maturity (0.585) and plant height (0.447), and significant negative correlation with panicle fertility (-0.320) and test weight (-0.495), so that genotypes with slender grains in this material tended to flower and mature comparatively later, with somewhat lower panicle fertility and test weight.

Path coefficient analysis

Path coefficient analysis was carried out at the phenotypic level, with grain yield per plant as the dependent character and the remaining eleven characters as causal variables, to partition the correlation coefficients into their direct and indirect components (Table 4). The residual effect was low (0.216), indicating that the characters included in the present study accounted for a substantial proportion of the variation in grain yield per plant.

Number of filled grains per panicle recorded the highest positive direct effect on grain yield per plant (0.486), followed by number of productive tillers per plant (0.417) and test weight (0.341), while panicle length also recorded a moderate positive direct effect (0.226). Since these traits also carried a strong positive correlation with grain yield, their association with yield appears to be largely a direct one and not merely a reflection of their relationship with other component traits. Similar results, with filled grains per panicle and productive tiller number among the traits recording the highest direct effect on yield, have been reported by Parimala *et al*., (2016), Khanal *et al*., (2025) and Nanda *et al*., (2026).

Some traits showed a marked difference between their correlation with yield and their direct effect, illustrating the usefulness of path analysis over simple correlation. Days to 50 per cent flowering recorded a negative correlation with yield but a low positive direct effect (0.199), its negative association with yield being largely mediated through negative indirect effects via number of productive tillers per plant, number of filled grains per panicle and test weight; this indicates that late flowering lowers yield mainly by reducing these component traits rather than through a direct effect. Number of tillers per plant showed the opposite trend, recording a strong positive correlation with yield (0.804) but a low negative direct effect (-0.147), its influence on yield being transmitted mainly through number of productive tillers per plant. Such differences between correlation and direct effect for tiller related and flowering related traits have also been reported by Khanal *et al*., (2025) and Shanmugam *et al*., (2024), who suggested that productive tiller number, rather than total tiller number, should be preferred as a selection criterion, a view also supported by the present findings.

Number of spikelets per panicle had a significant positive correlation with yield but a negligible direct effect (-0.004), its influence being carried mainly through number of filled grains per panicle (0.343), indicating that spikelet number is important mainly through its role in determining the number of filled grains rather than as an independent yield component. Grain length to breadth ratio recorded both a negative correlation and a low negative direct effect on grain yield per plant (-0.146), in agreement with the general observation of Gour *et al*., (2017) that slender grain types tend to record comparatively lower yield per plant.

Taken together, number of filled grains per panicle, number of productive tillers per plant, test weight and panicle length appear to be the most reliable traits for direct phenotypic selection to improve grain yield in the present material, while days to 50 per cent flowering and number of tillers per plant would be better used along with their component traits rather than on their own. These conclusions are in broad agreement with the correlation and path analysis literature discussed above (Parimala *et al*., 2016; Lahari *et al*., 2017; Katkani *et al*., 2023; Shanmugam *et al*., 2024; Khanal *et al*., 2025).

Conclusion

The present investigation revealed the presence of adequate genetic variability among the advanced breeding lines , as evident from significant differences observed for all fourteen characters studied. Traits such as number of tillers per plant, number of productive tillers per plant, test weight and grain length to breadth ratio recorded high heritability coupled with high genetic advance, indicating that these characters are governed largely by additive gene action and can be improved through direct phenotypic selection. Correlation studies showed that grain yield per plant was significantly and positively associated with number of productive tillers per plant, number of

filled grains per panicle, panicle length and test weight, while it was negatively associated with days to flowering and maturity. Path analysis further confirmed that number of filled grains per panicle, number of productive tillers per plant and test weight exerted high positive direct effects on grain yield, establishing their association with yield as largely direct rather than indirect. Taken together, these findings indicate that number of filled grains per panicle, number of productive tillers per plant, test weight and panicle length may be effectively employed as reliable indirect selection criteria for enhancing grain yield in this breeding material.

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References

Al-Jibouri, H.A., Miller P.A. and Robinson H.F. (1958). Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. *Agron. J.*, **50(10)**, 633-636.

Anonymous (2025a). Final estimates of crop production for 2024-25. Ministry of Agriculture and Farmers Welfare, Government of India, New Delhi.

Anonymous (2025b). First advance estimates of production of major kharif crops for 2025-26. Ministry of Agriculture and Farmers Welfare, Government of India, New Delhi.

Anonymous (2026). Rice outlook: January 2026, RCS-26A. Economic Research Service, United States Department of Agriculture, Washington, D.C.

Barik, J., Kumar V., Sangram K., Lenka, C. and Panda D. (2019). Assessment of variation in morpho-physiological traits and genetic diversity in relation to submergence tolerance of five indigenous lowland rice landraces. *Rice Sci*., **27(1)**, 2-43.

Bhinda, M.S., Karnwal M.K. and Chaudhary M.K. (2017). Estimates of genetic variability, heritability and genetic advance for yield contributing and quality traits in advance breeding lines of rice (Oryza sativa L.). *Int. J. Appl. Biol. Pharm. Technol*., **7(2)**, 229-233.

Burton, G.W. and De Vane E.W. (1953). Estimating heritability in tall fescue (Festuca arundinacea) from replicated clonal material. *Agron. J.*, **45**, 478-481.

Chamar, J.P., Joshi R.P., aKatikani D., Sahu D. and Patel V. (2021). Genetic variability, heritability and correlation coefficient analysis in rice (*Oryza sativa* L.) germplasm. *J. Pharma Innov*., **10(5)**, 763-769.

Chandramohan, Y., Srinivas B., Thippeswamy S. and Padmaja D. (2016). Diversity and variability analysis for yield parameters in rice (*Oryza sativa* L.) genotypes. *Indian J. Agric. Res*., **50(6)**, 609-613.

Cochran, W.G. and Cox G.M. (1957). Experimental Designs. 2nd edition. J. Wiley & Sons, Inc., New York. 611.

Dewey, D.R. and Lu K.H. (1959). A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agron. J.*, **51(9)**, 515-518.

Dhavaleshvar, M., Malleshappa C. and Kumar D.M.B. (2019). Variability, correlation and path analysis studies of yield and yield attributing traits in advanced breeding lines of rice (*Oryza sativa* L.). *Int. J. Pure App. Biosci*., **7(1)**, 267-273.

Gour, L., Koutu G.K., Singh S.K., Patel D.D., Shrivastava A. and Singh Y. (2017). Genetic variability, correlation and path analyses for selection in elite breeding materials of rice (*Oryza sativa* L.) genotypes in Madhya Pradesh. *The Pharm. Innov. J*., **6(11)**, 693-696.

Gupta, S., Upadhyay S., Koli G.K., Rathi S.R., Bisen P., Loitongbam B., Singh P.K. and Sinha B. (2020). Trait association and path analysis studies of yield attributing traits in rice (*Oryza sativa* L.) germplasm. Int. J. Bio-resour. *Stress Manag*., **11(6)**, 508-517.

Hanson, G.H., Robinson H.F. and Comstock R.E. (1956). Biometrical studies on yield in segregating populations of Korean lespedeza. *J. Agron*., **48(6)**, 268-272.

Johnson, H.W., Robinson H.F. and Comstock R.E. (1955a). Estimation of genetic and environmental variability in soybean. *Agron. J*., **47**, 314-318.

Johnson, H.W., Robinson H.F. and Comstock R.E. (1955b). Genotypic and phenotypic correlations in soybeans and their implications in selection. *Agron. J*., **47(10)**, 477-483.

Katkani, D., Payasi S.K., Hamidi A. and Singh Y. (2023). Character association studies among yield and yield attributing traits in advanced breeding lines of rice (*Oryza sativa* L.) across environments. *J. Soil Water Conserv*., **24(1)**, 189-197.

Khanal, S., Subedi N., Sapkota R., Dura R. and Nepali S. (2025). Genetic variability, character association and path analysis of yield and yield attributes of rice genotypes at Lalitpur, Nepal. *Arch. Agric. Environ. Sci*., **10(1)**, 113-119.

Lahari, T., Sekhar M.R., Kumar S.S. and Reddy C.V.C.M. (2017). Character association and path analysis for yield and yield attributing traits under submergence in rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci*., **6(10)**, 3333-3340.

Lenka, D. and Mishra B. (1973). Path coefficient analysis of yield in rice varieties. *Indian J. Agric. Sci*., **43(4)**, 376-379.

Lush, J.L. (1949). Inter size correlation, regression of offspring on dams as a method of estimating heritability of characters. *Proc. Amer. Soc. Anim. Prod*., **33**, 293-301.

Nanda, K.P., Vavdiya P.A., Jadav R.V., Sorathia A.M., Mungra K.S. and Naghera Y.V. (2026). Correlation and path

coefficient analysis of yield and its contributing traits in red rice (*Oryza sativa* L.). *J. Adv. Biol. Biotechnol*., **29(1)**, 962-972.

Nath, S. and Kole P.C. (2021). Genetic variability and yield analysis in rice. *Electron. J. Plant Breed*., **12(1)**, 253-258.

Niharika, B., Dushyantha Kumar B.M., Veeranna H.K., Manjunatha B. and Halingali B.I. (2022). Genetic variability, character association and path analysis of advanced breeding lines (MAGIC lines) of rice (*Oryza sativa* L.). *J. Pharma Innov*., **11(9)**, 2442-2446.

Parimala, K., Sudheer Kuamr S., Damodar Raju C., Kuamr S.S. and Vijay D. (2016). Correlation and path coefficient analysis of yield and yield components in rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci*., **5(11)**, 887-892.

Robinson H.E. and Comstock R.S. (1949). Biometrical studies of yield in segregating population of Korean lespedeza. *Agron. J*., **48**, 268-272.

Sandeep, S., Sujatha M., Subbarao L.V. and Neeraja C.N. (2018). Genetic variability, heritability and genetic advance studies in rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci*., **6**, 3719-3727.

Sao, A., Singh G., Nair S.K. and Harish G.D. (2024). Estimation of genetic variability parameters for various yield attributing traits in germplasm collection of rice (*Oryza sativa* L.). *Int. J. Plant Soil Sci*., **36(3)**, 158-165.

Shanmugam, A., Suresh R., Ramanathan A., Anandhi P., Pushpa R. and Sassikumar D. (2024). Correlation and path coefficient analysis among yield and yield attributing traits of rice landraces. *Curr. Innov. Agric. Sci*., **1(1)**, 35-42.

Sivasubramanian, S. and Menon M. (1973). Heterosis and inbreeding depression in rice. *Madras Agric. J*., **60(7)**, 1139-1140.

Soundharya, B., Edukondalu B., Narender G. and Dinesh A. (2024). Genetic variability, heritability and genetic advance for yield and yield related traits in rice (*Oryza sativa* L.). *J. Adv. Biol. Biotechnol*., **27(12)**, 1083-1090.

Sudeepthi, K., Srinivas T., Kumar B.R., Jyothula D.P.B. and Umar S.N. (2020). Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). *Electron. J. Plant Breed*., **11(2)**, 144-148.

Wright, S. (1934). The method of path coefficients. *Ann. Math. Stat*., **5(3)**, 161-215.