Assessment of yield and yield attributing traits among local upland rice cultivars in Indo-Gangetic plains of UP, India

Abstract

Assessing variation within a crop's germplasm is crucial for enhancing crop improvement through breeding programs. This study explores the genetic variability among landrace rice genotypes across twelve yield and yield-contributing traits. ANOVA analysis revealed significant variation across all traits, indicating diverse genetic sources and potential for future breeding initiatives. The results identified genotype LC-61 demonstrated the highest grain yield per plant, suggesting its suitability for breeding programs focused on high yield. The study also assessed the genetic variability, with PCV estimates surpassing GCV for all traits, indicating a higher influence of genetic factors on trait expression. Heritability and genetic advance analysis highlighted traits with predominant additive gene action, suggesting their suitability for improvement through simple selection methods. Association analysis identified traits correlated with grain yield, guiding future breeding efforts towards genotypes exhibiting high performance in these traits. The study concludes by identifying superior-performing genotypes and highlighting traits with the potential for enhancing rice yield and production through targeted breeding strategies.

Keywords–Rice, Heritability, GCV, PCV, Grain yield

1.Introduction

Rice (Oryza sativa L., 2n=2x=24) holds the position of being the most dominant staple cereal crop for approximately 3.5 billion people worldwide (Seck et al., 2012). It constitutes a significant portion of their daily caloric intake (Hoogenkamp et al., 2017). To support its enormous production, rice cultivation covers more than 150 million hectares globally, with annual rice production totaling around 600 million tons (Virmani et al., 2007). Particularly crucial in Asia (Gnanamanickam&Gnanamanickam, 2009), where its cultivation spans millennia (Bouman et al., 2007), rice dominates both in cultivation area and production volume, with Asia contributing approximately 90% of the global output (Fahad et al., 2019), led by India and China (Shahbandeh, 2024).

Despite the substantial production increases witnessed since the Green Revolution (Muthayya et al., 2014), the escalating demand driven by a projected 2% annual population growth, estimated to reach 4.6 billion rice consumers by 2050 (Lampe, 1995), underscores the imperative for a substantial upsurge in production to meet global rice security. Addressing this demand necessitates genetic enhancement approaches that can be effectively applied to the existing approximately 50,000 rice landraces of India (http://www.igmoris.nic.in, 2017), which predominantly relies on the extent of genetic variability, a phenomenon governed by polygenic influences susceptible to environmental factors (Singha & Singha, 2024).

Statistical methodologies such as heritability estimation guide breeders toward identifying promising traits, thereby elucidating the intricate relationship between yield and morphological attributes through correlation analyses (Hossain et al., 2015). Employing statistical tools, this study aims to unravel the genetic variability inherent in rice landraces over known checks to identify better-performing genotypes, thereby augmenting future breeding initiatives to enhance yield and resilience through novel gene sources (Singha & Singha, 2024; Tuhina-Khatun et al., 2015; Hossain et al., 2015).

The objectives of the study include the analysis of mean performances for twelve yield and yield-contributing traits across twenty-three rice genotypes, as well as assessing genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heterosis, genetic advances (GA), and trait associations.

2. Material and Method

2.1 Experiment location and design

The field experiments were conducted at the Agricultural Research Farm of the Institute of Agricultural Sciences, Banaras Hindu University, located in Varanasi, Uttar Pradesh, India. The farm is situated at 25.28°N latitude, 83.08°E longitude, and an elevation of 76 meters above mean sea level. The eastern Indo-Gangetic Plains, where the farm is situated, benefit from the annual low-level floods of the Ganges, contributing to its high productivity. All trials were conducted in irrigated ecosystems and on medium upland topographic sequences, utilizing transplanted nursery establishment techniques. The research spanned two years, covering the Kharif seasons of 2021 and 2022. Twenty-three local upland rice cultivars were included in the study, along with two check cultivars for comparison. The experimental design was a randomized complete block design (RCBD) with two trials and three replications for each genotype. A spacing of 20 cm between rows and 15 cm between plants was maintained, following recommended cultural practices to ensure optimal crop growth.

2.2 Data collection

Three were randomly selected from each entry, with observations taken from the middle rows to minimize border effects. Twelve yield and yield-contributing traits were recorded. Days to 50 percent flowering were counted from seed sowing in the nursery to the emergence of the first panicle in 50 percent of the plants. In contrast, days to maturity represented the duration from seeding to grain ripening, with 80 percent grain maturity in a panicle. Plant height, measured from the ground to the tip of the tallest panicle (excluding awn), and panicle length, measured from the panicle base to the tip at maturity (excluding awn), were recorded. The number of effective tillers per plant, excluding late tillers and filled grains per panicle,was estimated based on data from three randomly selected panicles per plant. Similarly, the number of unfilled grains per panicle, total grains per panicle, and spikelet fertility percentage were determined using the same method. The weight of 1000 well-developed grains at 12-14 percent moisture content and grain yield per plant at the same moisture content were recorded using an electronic balance. Additionally, the grain weight per panicle was measured using an electronic balance after the panicle matured and dried.

2.3 Data Analysis

The Levene test assessed the homogeneity of variance between trials, which were later combined for means. ANOVA was conducted using R software for all traits to test for significant differences. The coefficient of variation (CV) was calculated using the method suggested by Burton and Devane (1953). The phenotypic coefficient of variation (PCV) was determined as the phenotypic standard deviation divided by the general mean. In contrast, the genotypic coefficient of variation (GCV) was calculated as the genotypic standard deviation divided by the general mean multiplied by 100. The GCV and PCV were classified into three scales: low (0-10%), moderate (10-20%), and high (>20%), according to Robinson et al. (1949). Heritability (h^2) was estimated using Allard's formula (1960).

$$H = \frac{\sigma 2\ g}{\sigma 2\mathrm{p}}$$

Where H equals the ratio of genotypic variance (σ2g) to phenotypic variance (σ2p). The genotypic variance was calculated as (MST-MSE)/r, where MST is the mean square treatment, MSE is the mean square error, and r is the number of replications. The phenotypic variance was σ2g plus σ2e, where σ2e is the error variance. Heritability values were classified into three scales: low (0-30%), medium (30-60%), and high (>60%). The genetic advance (GA), representing the expected genetic gain, was determined using Allard's formula (1960), incorporating heritability, phenotypic standard deviation, and selection differential. The genetic advance as a percentage of the mean was calculated as the genetic advance divided by the general mean of the character in the population, multiplied by 100. The scale for genetic advance as a percentage of the mean was categorized as low (less than 10%), medium (10-20%), and high (above 20%), as per Johannson et al. (1955).

The simple phenotypic correlation coefficients among pairs of characters were calculated according to the formula suggested by Searle (1961).

$$\mathrm{r}(\mathrm{X}_1\mathrm{X}_2) = \frac{Cov\ (X_1X_2)}{\sqrt{V(X_1).V(X_2)}}$$

According to the scale, for the correlation coefficient proposed by Searle (1965), correlation coefficients greater than 0.65 were categorized as very strong, coefficients ranging from 0.50 to 0.64 were considered moderately strong, coefficients between 0.30 to 0.49 were classified as moderately weak, and coefficients below 0.30 were labeled as very weak.

3. Results

3.1 Mean performance of yield attributing traits

Analysis of mean performances for twelve yield and yield-contributing traits across twenty-three rice genotypes revealed significant variations. Notably, genotype LC-65 displayed the shortest days to 50% flowering (DF) at 95 days, closely resembling the CRMAS-1 check, while genotype HUR-917 exhibited the longest days to maturity (DM) at 143 days. LC-65 also demonstrated the shortest days to maturity at 126 days, placing it in the medium maturity range compared to CRMAS-1 (https://ccari.icar.gov.in/dss/rice.html). In terms of plant height (PH), LC-61 exhibited the tallest plants at 117.95 cm, whereas the CRMAS-1 check had the shortest at 83.85 cm. Panicle length (PL) ranged from 22 cm for LC-64 to 26.95 cm for LC-80. LC-61 and LC-63 displayed the highest number of effective tillers per plant (ETP) at 11.5, while LC-68 exhibited the lowest at 7.5. LC-61 recorded the highest total grains per panicle (TGP) at 177.5, significantly surpassing the mean. Conversely, LC-80 had the lowest at 140.5. LC-61 also exhibited the highest filled grains per panicle (FGP) at 156, surpassing the CRMAS-1 check, while LC-71 had the fewest at 113. LC-82 displayed the lowest grain weight per panicle (WP) at 2.94, whereas LC-71 had the highest at 4.62. Spikelet fertility percent (SF%) was highest in HUR-917 at 92.75% and lowest in LC-70 at 75.16%. LC-79 showed the highest test weight (TW) at 29.115g, while HUR-917 had the lowest at 14.255g. LC-61 exhibited the maximum grain weight per panicle (GYP) at 49.05g, significantly higher than CRMAS-1, HUR-917, and the mean at 28.46g, 36.34g, and 33.86g respectively, while LC-64 showed the minimum at 24.84g. Across all traits, mean values were 101.50 days (DF), 131.96 days (DM), 110.92 cm (PH), 23.65 cm (PL), 9.78 (ETP), 137.12 (FGP), 25.51 (UGP), 162.90 (TGP), 84.09% (SF%), 25.33g (TW), 3.43g (WP), and 33.87g

Table 1. Mean performance analysis of yield and yield attributing traits.

Genotypes	DF[1]	DM[2]	PH[3]	PL[4]	ETP[5]	FGP[6]	UGP[7]	TGP[8]	SF%[9]	TW[10]	WP[11]	GYP[12]
LC-61	99.5	128.5	117.95	23.6	11.5	156	21.5	177.5	87.8848	25.03	4.305	49.05
LC-62	101	131	115.2	24.6	9	150.5	17.5	168	89.5918	24	3.49	34.45
LC-63	105	134	112.4	23.3	11.5	135.5	24.5	160	84.7114	25.955	3.74	42.91
LC-64	103	132	112.15	22	7.5	126.5	31.5	158	80.1227	25.535	3.365	24.84
LC-65	95	126	115	23.5	12	136	22	158	86.0589	23.015	3.56	42.79
LC-66	105	136	115.7	23.5	9.5	136.5	27	163.5	83.5311	26.61	3.495	33.255
LC-67	101.5	131	111.85	23.8	8	129	25.5	154.5	83.4842	26.355	3.22	25.425
LC-68	103	134	112.4	25.1	7.5	131.5	20.5	152	86.4086	25.635	3.05	25.875
LC-69	100	131	107.95	22.8	10.5	123.5	23	146.5	84.3065	26.045	3.14	33.07
LC-70	98	129	107.9	23.05	9.5	113.5	37.5	151	75.1656	25.73	3.295	31.075
LC-71	102	132.5	110.55	22.9	11	113	29.5	142.5	79.3144	26.745	4.62	41.9
LC-72	100	132	110.65	23.35	10	124	31	155	80.1853	25.585	3.51	35.135
LC-73	102	132	114.5	25.1	10.5	148.5	19.5	168	88.4157	24.07	3.31	37.805
LC-74	102.5	133	115.85	25.25	10	147.5	22.5	170	86.7647	25.205	2.99	33.965
LC-75	103	132	110.6	23.2	9.5	128	17.5	145.5	87.9512	25.89	2.99	31.07
LC-76	96	127	114.35	23.85	8	139	29	168	82.7583	25.22	2.97	24.56
LC-77	104	135	120.2	23	10.5	142.5	26	168.5	84.5746	25.155	3.38	34.405
LC-78	103	134	110.55	22.8	10	133.5	28	161.5	82.6668	24.72	3.585	35.31
LC-79	104	135	109.65	23.55	10	125.5	26.5	152	82.5671	29.115	3.465	34.72
LC-80	103	133	114.8	26.95	10	122	18.5	140.5	86.9399	28	3.9	33.58
LC-81	96.5	128	112.05	22.9	9.5	129	35	164	78.7954	24.935	3.23	33.435
LC-82	105	134	111.1	23.95	10.5	135	34	169	79.8774	26.695	2.94	30.555
LC-83	104	135	107.5	23.25	9.5	125	32	157	79.5636	26.925	3.5	32.725
CRMAS-1	89.5	121	83.85	22.75	8.5	149.5	20.5	170	87.939	26.83	3.345	28.465
HUR-917	112	143	98.2	23.15	10.5	227.5	17.8	252	92.7521	14.255	3.24	36.345
Mean	101.5	131.96	110.916	23.648	9.78	137.12	25.512	162.9	84.09324	25.3302	3.4254	33.8686

Where,[1](DF)= Days of 50% flowering; [2](DM)= Days of maturity; [3](PH)= Plant height; [4](PL)= Panicle length; [5](ETP)= Effective tillers per plant; [6](FGP)= Filled grain per plant; [7](UGP)= Unfilled grain per plant; [8](TGP)= Total grain per panicle; [9](SF%)= Spikelet fertility; [10](TW)= Test weight; [11](WP)= Grain weight per panicle; [12](GYP)= Grain yield per plant.

3.2 Genetic Variability

The study conducted an exhaustive analysis of various agricultural traits in the plant species under examination. Notably, traits like days to 50% flowering and days to maturity showcased low levels of phenotypic and genotypic variability, with coefficients of variation (CV) of 5.55 and 5.53 days, respectively (Table 2). However, despite this low variability, the study found exceptionally high heritability for both traits, with values of 99.24% and 99.44%, respectively (Table 2). Moreover, the examination of panicle length revealed a similar trend of low PCV of 4.73 but moderate heritability of 64.28% (Table 2). Conversely, effective tiller per plant displayed moderate levels ofPCV and heritabilitywith 17.83 and 46.56% (Table 2). Traits associated with grain production, such as filled grains per panicle and total grains per panicle, exhibited high levels of variability coupled with high heritability. Filled grains per panicle showed high PCV of 17.17and GCV of 16.8, with heritability and genetic advance as percent mean values of 95.73% and 33.87%, respectively (Table 2). Total grains per panicle also demonstrated high PCV of 13.54 and GCV of 13.02, with heritability and genetic advance as percent mean values of 92.45% and 25.8%, respectively (Table 2). These findings suggest substantial genetic diversity within the population for these traits and a high potential for genetic improvement to enhance grain yield. On the other hand, spikelet fertility percent showed low variability PCV and GCV with 5.55 and 4.89 but moderate heritability (77.72) (Table 2). Furthermore, traits like test weight and grain yield per plant demonstrated high variability and heritability. Test weight exhibited a high PCV of 10.68 and GCV of 10.24, with heritability and genetic advance as percent mean values of 91.94% and 20.24%, respectively (Table 2). Grain yield per plant showed a high PCV of 19.39 and GCV of16.55, with heritability and genetic advance as percent mean values of 72.81% and 29.09%, respectively. Similarly, grain weight per panicle showed high variability (PCV = 14.04, GCV = 11.36) and heritability (65.45%), indicating its significance in determining grain yield and quality (Table 2).

Table 2. Genetic variability parameters

Traits	GCV	Scale	PCV	Scale	GA	Scale	GAM%	h^2(bs)%	Scale
Days to flowering	5.532	L	5.55279	L	11.4321	M	11.3518	99.2399	H
Days to maturity	4.013	L	4.02435	L	10.822	M	8.243705	99.4396	H
Plant height	7.038	L	7.28668	L	15.3855	M	14.00434	93.2966	H
Panicle length	3.791	L	4.72768	L	1.48382	L	6.260847	64.2862	H
Effective tiller per plant	12.169	M	17.8337	M	1.69887	L	17.10665	46.5646	M
Filled grain per panicle	16.805	M	17.1751	M	46.9869	H	33.87073	95.7323	H
Unfilled grain per panicle	22.192	H	27.3976	H	9.11213	L	37.03078	65.6121	H
Total grain per panicle	13.025	M	13.5457	M	42.2008	H	25.80002	92.4593	H
Spikelet fertility	4.894	L	5.55127	L	7.52197	L	8.888144	77.7233	H
Test weight	10.248	M	10.6869	M	5.08509	L	20.24264	91.949	H
Weight per panicle	11.36	M	14.0408	M	0.64803	L	18.93305	65.4578	H
Grain yield per plant	16.553	M	19.3986	M	9.85302	L	29.09648	72.8121	H

GCV = Genetic coefficient variation, PCV = Phenotypic coefficient variation, GA = Genetic advancement,
GAM% = Genetic advance as a percentage of the mean, h^2(bs)% = Broad sense heritability, L = Low, M = Medium, H = High.

3.3 Trait association

Trait association studies were conducted to discern the genetic basis for yield enhancement by examining the interaction between distinct plant yield attributing traits. The phenotypic correlation coefficients between yield and its component characteristics were estimated and summarized in Table 3. Notably, days to 50% flowering exhibited significant positive correlations with days to maturity (0.4858), plant height (0.3346), number of filled grains per panicle (0.3974), total grains per panicle (0.4214), grain weight per panicle (0.2284), and spikelet fertility percent (0.1232), while displaying negative correlations with effective tillers per plant (-0.2595) and grain yield per plant (-0.1224). Days to maturity also showed positive and highly significant associations with several traits, including plant height (0.2784), number of filled grains per panicle (0.4171), total grains per panicle (0.4462), and spikelet fertility percent (0.2124), while exhibiting negative correlations with effective tillers per plant (-0.2571), test weight (-0.339), and grain yield per plant (0.1308). Plant height correlated positively and significantly with days to 50% flowering (0.3346), days to maturity (0.2784), panicle length (0.2972), number of filled grains per panicle (0.1256), and grain weight per panicle (0.2419), but negatively with test weight (-0.2266) and spikelet fertility percent (-0.1127). Furthermore, traits like panicle length, effective tillers per plant, filled grains per panicle, unfilled grains per panicle, total grains per panicle, spikelet fertility percent, test weight, and grain weight per panicle were also evaluated for their correlations with other traits, revealing significant associations indicative of potential genetic interactions influencing yield-related traits in the plant species under study.

Table 3. Estimation of trait correlation for yield and yield contributing traits in rice genotypes

	DF	DM	PH	PL	ETP	FGP	UGP	TGP	SF%	TW	WP	GYP
DF	1	0.9858	0.3346	0.0599	-0.2595	0.3974	-0.0898	0.4214	0.2132**	-0.296	0.2284**	-0.1225*
DM		1	0.2784	0.0515	-0.2571	0.4171	-0.0846	0.4462	0.2124**	-0.339	0.2033**	-0.0739
PH			1	0.2972	0.0052	-0.1256	0.1384	-0.1109	-0.1127*	0.2266**	0.2419**	-0.0169
PL				1	0.0687	0.0978	-0.3346	-0.0046	0.3146**	0.0648	-0.054	0.0276
ETP					1	0.0148	0.0026	0.0194	-0.0042	-0.0689	-0.0748	0.7578
FGP						1	-0.5068	0.9614	0.7290	-0.7909	0.1027*	0.6916
UGP							1	-0.2526	-0.9484	0.3356**	-0.157	-0.0538
TGP								1	0.5147	-0.7912	0.06	0.3109**
SF%									1	-0.4963	0.1412*	0.2051**
TW										1	0.0625	0.3035**
WP											1	0.1219*
GYP												1

Significant at * P <= 0.05; ** P <= 0.01; Where, (DF)= Days of 50% flowering; (DM)= Days of maturity; (PH)= Plant height; (PL)= Panicle length; (ETP)= Effective tillers per plant; (FGP)= Filled grain per plant; (UGP)= Unfilled grain per plant; (TGP)= Grain per panicle; (SF%) = Spikelet fertility; (GYP)= Grain yield per plant; (TW)= Test weight; (WP)= Grain weight per panicle.

Table 4.: Analysis of variance (ANOVA) for yield and yield contributing traits in rice genotypes

Source of variation	df	Mean sum of square											
		DF	DM	PH	PL	ETP	FGP	UGP	TGP	SF%	GYP	TW	WP
Replication	5	0.844	0.621	13.324	1.655	0.068	11.655	3.575	4.982	2.685	4.586	2.248	0.181
Treatment	24	62.304	55.663	123.873	2.062	4.597	1111.128	75.271	944.811	39.225	74.571	13.834	0.382
Error	24	0.237	0.156	4.295	0.448	1.676	24.226	15.629	37.018	4.916	11.732	0.581	0.079

Where, (df)= Degree of freedom; (DF)= Days of 50% flowering; (DM)= Days of maturity; (PH)= Plant height; (PL)= Panicle length; (ETP)= Effective tillers per plant; (FGP)= Filled grain per plant; (UGP)= Unfilled grain per plant; (TGP)= Grain per panicle; (SF%) = Spikelet fertility; (GYP)= Grain yield per plant; (TW)= Test weight; (WP)= Grain weight per panicle.

4. Discussion and Conclusion

Assessing diversity within a crop's germplasm is vital for enhancing crop improvement through breeding programs, necessitating collecting, preserving, and evaluating genetically diverse germplasm. While a small fraction of accessions is typically utilized extensively due to possessing valuable traits, a significant portion of diversity often remains untapped. Identifying and utilizing potential genotypes within the germplasm collection is crucial for crop improvement initiatives. Genetic variability within experimental material provides essential information for selecting parent plants in breeding programs, contributing to more efficient use of genetic resources and expanding the gene pool. Divergence among individual plants, influenced by genetic makeup and environmental conditions, plays a significant role in breeding programs.

ANOVA analysis unveiled significant variation across all twelve traits among the twenty five rice genotypes, indicating diverse genetic sources and potential for future breeding, hybridization, and creation of transgressive segregants (Table 4). This genotypic diversity underscores the importance of leveraging these materials in breeding programs. This finding resonates with prior research by Sumanth et al. (2017), Ajmera et al. (2017), Adhikari et al. (2018), Nihad et al. (2021), Gupta et al. (2022), and Thakur et al. (2023), all reporting substantial variability in rice yield and yield-contributing traits.

The genotype LC-61 demonstrated the highest grain yield per plant, suggesting its potential for utilization in breeding programs aimed at achieving high yield. Conversely, LC-76 exhibited the lowest yield, indicating its unsuitability for such programs. LC-80 possessed the most extended panicle length, while LC-64 had the shortest. The highest number of unfilled grains per panicle was observed in LC-70, which recorded the highest. LC-79 demonstrated the highest test weight, contrasting with HUR-917, which exhibited the lowest. LC-71 displayed the highest performance for this trait. This information underscores the importance of considering mean performance to identify high-performing genotypes.

The assessment of genetic variability aimed to enhance the efficiency of the selection process by leveraging greater variability among genotypes, which holds promise for further crop improvement.In this study, PCV estimates exceeded those of GCV for all traits examined, aligning with similar findings by previous researchers. The difference between PCV and GCV values for most characters was low, suggesting a higher influence of genetic factors on trait expression. Traits like unfilled grains per panicle, filled grains per panicle, total grains per panicle, grain yield, and spikelet fertility % exhibited high GCV values, consistent with prior studies. Moderate GCV values were observed for effective tillers and plant height, while other characteristics displayed low GCV values.Heritability and genetic advance, when expressed as a percentage of the mean, are key factors in selecting desirable traits. They provide valuable insights into potential improvements achievable through selection. Considering both parameters together yields more accurate predictions than relying solely on heritability estimates because they encompass both additive and non-additive gene actions. Thus, breeders need to consider these aspects during selection carefully. Studies by Souroush et al. (2004) and Satyanarayana et al. (2005) in rice highlight the importance of evaluating both parameters. Traits showing high heritability and significant genetic advances, like the number of effective tillers per plant, number of grains per panicle, grain weight per panicle, test weight, and grain yield per plant, suggest predominant additive gene action. This implies that simple recurrent selection could effectively enhance these traits, which is consistent with findings by Krishna et al. (2013), Chouhan et al. (2014), Kumar et al. (2015), and Pratap et al. (2018).

Different plant traits are related to grain yield, which is vital for breeders aiming to enhance variety performance where natural selection is limited. Hence, we conducted an association analysis to identify traits correlated with grain yield. Yield, a complex trait, is influenced by various component traits, making it crucial to grasp their relationships with each other and grain yield. Our study found moderate and positive correlations between traits like spikelet fertility percentage (0.1951), filled grains per panicle (0.3514), and effective tillers (0.7505) with grain yield per plant. These results mirrored previous research by Mustafa et al. (2007), Naseer et al. (2015), Biswajit et al. (2017) and Bhandari et al. (2020). Conversely, traits such as test weight (0.1422), total grains per panicle (0.1421), and panicle length (0.0319) showed weak correlations with yield, consistent with earlier studies. Additionally, days to 50% flowering, days to maturity, and plant height displayed weak, negative correlations with yield, while unfilled grains per panicle exhibited a moderate, weak negative correlation, in line with findings by Zahid et al. (2006).

In conclusion, the present study identifies genotypes LC-61, LC-63, and LC-65 as superior performers, suggesting their potential as parent lines in hybridization programs to yield transgressive segregants. Traits such as number of filled grains per panicle, total grains per panicle, plant height, days to 50% flowering, days to maturity, and grain yield per plant exhibited high heritability and genetic advance, indicating their suitability for improvement through simple selection methods, given their reduced susceptibility to environmental influences. Phenotypic correlation analysis revealed strong positive associations between grain yield per plant and filled grains per panicle, total grains per panicle, and plant height, guiding future breeding efforts towards genotypes exhibiting high performance in these traits. Additionally, traits such as effective tillers per plant, number of grains per panicle, test weight, and spikelet fertility exhibited notablypositive effects on grain yield per plant, suggesting that targeted selection for these traits could significantly enhance rice yield and production.

Ethical standards. Not applicable.

Consent for publication. Not applicable.

Availability of data and materials. All data produced during this study were included this article.

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