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Genetic variability and yield-determining traits in rice (*Oryza sativa* L.) genotypes under Bastar Plateau agro-climatic conditions

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Abstract

Rice (*Oryza sativa* L.) is a major staple crop worldwide and improving grain yield (GY) through the identification of superior genotypes and yield-contributing traits is essential for sustainable production. This study evaluated genetic variability, character association, path coefficients and genetic diversity among 64 lowland rice genotypes under transplanted conditions using a randomised complete block design (RCBD) with two replications. Significant variability was observed among the genotypes for yield and related traits. The highest GY values were recorded in AD 21303, TKR 35, MTU 1436, RP6811-8-1-3-2-1-1-B and OR 2573-3, indicating their potential for use in breeding programmes. High heritability coupled with high genetic advance (GA) was observed for kernel length-to-breadth ratio (KLB), grain length-to-breadth ratio (GLB), kernel breadth (KB) and related traits, suggesting the predominance of additive gene action. The genotypic coefficient of variation (GCV) was slightly lower than the phenotypic coefficient of variation (PCV), indicating environmental influence on trait expression. Grain yield showed significant positive correlations with days to 50 % flowering (DFF), days to maturity (DM), number of effective tillers per plant (NET), panicle length (PL), flag leaf length (FLL), number of grains per panicle (NGPP), test weight (TW), biological yield (BY) and harvest index (HI). Path coefficient analysis revealed that BY had the highest positive direct effect on GY, followed by HI, TW, flag leaf width (FLW), FLL, NGPP, PL, kernel length (KL) and KLB ratio. Cluster analysis grouped the genotypes into seven clusters, with Cluster III exhibiting superior mean performance for GY and associated traits. The DFF, DM and plant height (PH) contributed most to genetic divergence. The results indicate substantial genetic variability and identify BY, HI, TW and grain traits as important selection criteria for improving rice yield.

Keywords: genetic diversity; genetic variability; heritability; rice breeding; trait association; yield components

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1. Introduction

Rice (*Oryza sativa* L.) is the primary staple food for more than half of the world's population, particularly in Asian countries. It is a monocotyledonous, self-pollinated crop belonging to the Poaceae family and is widely cultivated in tropical and subtropical regions (1). Rice grows well under warm and humid climatic conditions, with an optimum temperature range of 21–37 °C and an annual rainfall requirement of at least 1000 mm (2). Owing to its adaptability, rice is cultivated in more than 100 countries worldwide (3). In India, rice plays a vital role in ensuring food security, especially in rainfed and lowland ecosystems where productivity is often constrained by environmental variability and limited genetic improvement. India contributes approximately 27.43 % of global rice production, with rice cultivated over 51.42 Mha and an estimated production of 150 Mt during 2024–25.

Chhattisgarh, popularly known as the "Rice Bowl of India," has an agriculture-based economy in which nearly 82 % of the population depends on farming for their livelihood (4). Rice is cultivated over an area of about 4.4 Mha in the state, producing nearly 10 Mt annually with an average productivity of 2.3 t ha^{-1}. Lowland rice ecosystems, particularly those dependent on rainfall, contribute significantly to the state's agricultural production; however, their productivity remains lower than the national average (5). The Bastar Plateau region represents a unique agro-climatic zone characterised by undulating topography, acidic soils, erratic rainfall distribution and traditional low-input cultivation practices (6). These environmental conditions greatly influence crop performance and necessitate the identification and development of rice genotypes specifically adapted to this region.

Grain yield (GY) in rice is a complex quantitative trait governed by several interacting component characters and strongly influenced by environmental conditions. Therefore, direct selection based solely on GY is often ineffective because of its low heritability and high environmental sensitivity. In rice breeding programmes, traits such as number of effective tillers per plant (NET), panicle length (PL), number of grains per panicle (NGPP), TW, biological yield (BY) and harvest index (HI) are considered important selection criteria for improving yield potential. Genetic variability is the basic prerequisite for any successful crop improvement programme. Estimation of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability and genetic advance (GA) provides valuable information regarding the magnitude of variability present in breeding materials and the relative influence of genetic and environmental factors on trait expression. Similarly, correlation and path coefficient analyses are useful statistical approaches for understanding the association among traits and determining their direct and indirect effects on GY. Path coefficient analysis helps in identifying traits with true causal influence on yield by partitioning correlation coefficients into direct and indirect effects.

Despite the importance of lowland rice cultivation in the Bastar Plateau region, limited information is available regarding the genetic variability, yield relationships and genetic divergence among rice genotypes specifically adapted to this agro-climatic condition. Most earlier studies have focused on broader agro-ecological regions, with comparatively less emphasis on area-specific evaluation under Bastar Plateau conditions. Therefore, systematic evaluation of elite and locally adapted rice genotypes is essential for identifying promising breeding materials suitable for this ecologically distinct region. The objective of this study was to evaluate genetic variability, heritability, correlation among yield traits, path coefficients and genetic divergence among rice genotypes grown under Bastar Plateau agro-climatic conditions to identify important traits contributing to GY and to identify promising genotypes for future rice improvement programmes.

2. Materials and Methods

A total of 64 rice genotypes, including three standard checks (Swarna, NDR8002 and CG1919), were used as the experimental material for this study (Table 1). The set of genotypes included released varieties, advanced breeding lines and mutant lines representing diverse genetic backgrounds. The genotypes were obtained from the rice germplasm section of the All India Coordinated Research Project at Shaheed Gundadhur (S.G.) College of Agriculture and Research Station, Jagdalpur. The genotypes were evaluated for 18 traits encompassing phenological, morphological, yield and grain quality parameters (Table 2). The study was conducted during the kharif season of 2024 at the Instructional cum Research Farm associated with S.G. College of Agriculture and Research Station, Jagdalpur, Chhattisgarh (Fig. 1). The site is located at an altitude of 552 metres above mean sea level, with geographical coordinates of 19°5'34" N latitude and 81°57'52" E longitude. During the crop growth period (July), the temperature ranged from 10.8–35.7 °C and a total rainfall of 1486.7 mm was received. The plants were maintained at a spacing of 20 cm between rows and 15 cm between plants. Each plot measured 2 × 5 m. All recommended agronomic and crop protection practices were followed to ensure a healthy and successful crop. The experimental site was characterised by lateritic soil with a pH ranging from 5.5–6.5. The observations recorded were as follows: days to maturity (DM): the number of days from sowing to physiological maturity, defined as the stage at which approximately 85–90 % of the grains in the panicle turned straw-coloured; days to 50 % flowering (DFF): the number of days from sowing until 50 % of the plants in a plot exhibited at least one flowering spikelet per panicle; plant height (PH, cm): measured at maturity from the base of the plant to the tip of the tallest panicle, excluding awns, in five randomly selected plants per genotype; number of ear-bearing tillers (NET): recorded from five randomly selected plants per genotype and the average was calculated; PL (cm): measured at maturity from the base to the tip of the panicle, excluding awns, in five randomly selected plants per genotype; flag leaf length (FLL, cm): measured from the ligule to the tip of the leaf blade in five randomly selected plants per genotype, seven days after anthesis; flag leaf width (FLW, cm): measured at the widest portion of the flag leaf in five randomly selected plants per genotype, seven days after anthesis; number of filled grains per panicle: determined by counting the filled grains in five randomly selected panicles after harvest and the average was calculated; BY (q ha^{-1}): the total above-ground biomass, including grain and straw but excluding roots, recorded after harvest; test weight (TW, g): determined by weighing 1000 fully dried grains at 13 % moisture content using a precision balance; HI (%): calculated as the ratio of economic yield (GY) to BY, expressed as a percentage, using the following formula:

$$\text{Harvest index (\%)} = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

Grain yield per hectare (q ha^{-1}) was calculated from the GY obtained from each plot after threshing. Grain length (GL) was measured from 10 randomly selected grains with husks and the average value was recorded. Grain breadth (GB) was measured from 10 randomly selected grains with husks and the average value was recorded. Grain length-to-breadth (GLB) ratio was calculated using the following formula:

$$\text{Grain length-to-breadth ratio} = \frac{\text{Grain length}}{\text{Grain breadth}}$$

Kernel length (KL) was measured from 10 randomly selected milled kernels and the average value was recorded. Kernel breadth (KB) was measured from ten randomly selected milled kernels and the average

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value was recorded. Kernel length-to-breadth (KLB) ratio was calculated using the following formula:

$$\text{Kernel length-to-breadth ratio} = \frac{\text{Kernel length}}{\text{Kernel breadth}}$$

Table 1. List of rice genotypes evaluated under Bastar Plateau agro-climatic conditions during kharif 2024

Sl. No.	Genotypes
1.	BPT 3485
2.	NP 126
3.	HURS 24-11-IR143526-168-1-1-245-13-1
4.	R 2447-1027-1-456-1
5.	SPE-27
6.	NDR 2023-CP-6
7.	CR 2916-92-2-1-1
8.	BAYR 4511
9.	CR 3987-6-3-1-1-2
10.	NP 7315
11.	K2020SY23
12.	AD 21303
13.	MLD 270-IR16F1053
14.	SRPV-1818
15.	RP 6615-45-6-7-1
16.	BAYR 4513
17.	RP6811-8-1-3-2-1-1-B
18.	KNM 12466
19.	National Check (Swarna)
20.	RGL 7042 (MTU RM 403-8-1-1-1)
21.	BAS 54
22.	BRR-2028
23.	RP 6458-DB-C1-234
24.	NVSR-1299
25.	BAYR 4510
26.	CR4491-6-1-1-1-2-1-1-1
27.	BAYR 4509
28.	MTU 1436 (MTU 2823-23-1-1)
29.	CR 4205-229-110-6-3
30.	AD 20364
31.	PHI 24104
32.	CR 4626-9-1-1-1-1-2
33.	BAYR 4512
34.	RP5285-142-4-2-2-1-1-B
35.	RGL 7043 (MTU RM 410-25-1-1-1)
36.	Makdo Mutant-29
37.	HURS 24-12-IR143529-190-10-10-416 26-12
38.	R 2358-109-1-86-1
39.	Zonal Check (NDR8002)
40.	TRC 2024-8/TRC TNTJ 5370-B-B-1-17
41.	NVSR-1222
42.	CR 4492-3-1-1-1
43.	CRHR 702
44.	MTU 1431 (MTU 2632-15-1-4-2)
45.	WGL-1750
46.	MLD 268-IR22LT1511
47.	CR 6324-3-2-1-2-1
48.	MTU 1432 (MTU 2681-15-1-1)
49.	BAYR 4514
50.	VDN 2018
51.	BKR 455
52.	OR 2573-3
53.	RP 6835-62-10-5-3-22
54.	TRC 2024-7/TRC TNTJ 5370-B-B-11-9
55.	NDR 2023-9-CP-22
56.	VPSY 21
57.	CR4413-1-2-1-1-2
58.	TKR 35
59.	ORS-MBB 12
60.	MSN-124
61.	CR 3969-24-1-2-1-1-2-1
62.	NP 7373
63.	SYE-723-33-14
64.	Local Check (CG1919)

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Table 2. Mean performance, range, standard error, critical difference and coefficient of variation for 18 traits in rice genotypes

Characters	Mean ($\bar{X}$)	Minimum	Maximum	Standard error	Critical difference	Coefficient of variation
Days to 50 % flowering	109.44	94	120	0.876	1.75	6.405
Days to maturity	141.48	128	153	0.832	1.665	4.707
Plant height (cm)	117.07	93.50	130	1.165	2.330	7.962
Number of effective tillers per plant	5.85	3.90	9.59	0.143	0.287	19.63
Flag leaf length (cm)	25.11	20.25	29.49	0.257	0.514	8.191
Flag leaf width (cm)	30.39	22.70	39.55	0.525	1.05	13.824
Panicle length (cm)	1.79	1.37	3.24	0.030	0.061	13.655
Number of grains per panicle	278.69	174	417.01	6.966	13.933	19.99
Test weight (g)	22.28	15.65	34.67	0.484	0.969	17.93
Grain length (mm)	7.96	6.21	10	0.103	0.206	10.385
Grain breadth (mm)	2.57	1.90	3.30	0.036	0.073	11.449
Grain length-to-breadth ratio	3.14	2.14	4.53	3.144	0.129	16.463
Kernel length (mm)	6.01	4.30	7.70	6.008	0.205	13.65
Kernel breadth (mm)	2.21	1.70	3	2.205	0.070	12.839
Kernel length-to-breadth ratio	2.76	1.78	3.85	0.061	1.232	17.73
Biological yield (q ha^{-1})	130.08	88.11	170.05	2.675	5.35	16.45
Harvest index (%)	44.09	29.60	54.58	0.858	1.717	15.57
Grain yield (q ha^{-1})	57.84	40.16	74.6	1.318	2.637	18.24



Fig. 1. Experimental field view of 64 lowland rice genotypes evaluated under transplanted conditions.

Statistical analysis

The experimental data recorded for all the traits were subjected to analysis of variance (ANOVA) under a randomised complete block design (RCBD) to determine the existence of significant differences among the genotypes at 5 % and 1 % probability levels and descriptive statistics were computed using Microsoft excel (2007) (7). The PCV and GCV (8), heritability (h^2) in the broad sense (9) and GA (10) were calculated. The PCV and GCV were calculated using the following formulae:

$$PCV = \sqrt{\sigma^2 p} \times 100 \div \bar{x}$$

$$GCV = \sqrt{\sigma^2 g} \times 100 \div \bar{x}$$

Where, $\sigma^2 p$ = phenotypic variance, $\sigma^2 g$ = genotypic variance, $\bar{x}$ = grand mean of the trait

Broad-sense heritability was estimated as follows:

$$h^2 (\%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Genetic advance was calculated using the formula:

$$GA = k\sigma p h^2$$

Where, k = selection differential at 5 % selection intensity (2.06), σp = phenotypic standard deviation and h^2 = heritability in broad sense 3.6.3.4

$$\text{Genetic advance as percent of mean (GAM)} = \frac{GA}{\bar{x}} \times 100$$

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Where, GA = genetic advance $\bar{x}$

All statistical analyses, such as correlation analysis (11), path coefficient analysis (12), cluster analysis (13) and principal component analysis (PCA) (14) were performed using SPAR 2.0 software (https://iasri.res.in/Saleble_technology1.aspx).

3. Results and Discussion

Analysis of variance

The ANOVA revealed highly significant differences among the 64 lowland rice genotypes for all 18 traits studied, indicating the presence of substantial genetic variability among the genotypes (Table 3). The significant variability for yield, phenological, morphological and grain quality traits provide ample scope for effective selection and genetic improvement in lowland rice breeding programmes (15, 16). Grain yield exhibited wide variation ranging from 40.16–74.16 q ha^{-1}, demonstrating the diverse yield potential of the evaluated genotypes under Bastar Plateau conditions.

The superior performance of genotypes such as AD 21303, TKR 35, MTU 1436, RP6811-8-1-3-2-1-1-B and OR 2573-3 indicates their adaptability and suitability for lowland ecosystems of the Bastar Plateau. These genotypes can be utilised directly in varietal evaluation trials or employed as donor parents in hybridisation programmes aimed at improving GY and adaptability under rainfed lowland conditions. The relatively low coefficient of variation observed for DM suggested greater stability of this trait across environments, whereas higher variability for NGPP indicated wider opportunities for selection and yield improvement.

The slightly higher PCV compared to GCV for all traits indicated some environmental influence on trait expression; however, the narrow differences between PCV and GCV for most characters suggested that most of the observed variability was genetic in nature (Fig. 2). This is advantageous in breeding programmes because genetically controlled traits can be effectively improved through phenotypic selection.

Genetic variability, heritability and genetic advance

The estimates of variability, heritability and GA demonstrated the presence of exploitable genetic variation among the evaluated rice genotypes (Table 4). Moderate to high GCV and PCV values observed for GY and related traits suggested sufficient variability for effective selection under lowland conditions. Similar findings have also been reported in earlier studies (15–17).

Moderate GCV for yield-related characters indicates sufficient genetic variability, which can be exploited in breeding programmes (18). High heritability coupled with high GA was observed for GY, BY, KLB ratio, GLB ratio, KB and HI, indicating the predominance of additive gene action (Fig. 3). Such traits can be effectively improved through direct phenotypic selection because their expression is largely governed by genetic factors rather than environmental influence. This enhances the efficiency of selection and allows reliable improvement through phenotypic performance (19).

The high heritability and GA recorded for KLB ratio and grain quality traits are particularly important for the Bastar Plateau region, where consumer preference and market value are strongly influenced by grain shape and cooking quality. Slender and desirable grain types generally receive better market acceptance and premium prices. Therefore, improvement of KLB ratio through selection may contribute not only to yield enhancement but also to improved grain quality and farmer profitability in this region. Furthermore, precise identification of superior genotypes accelerates genetic gain and support the development of rice varieties with enhanced yield, adaptability and stress tolerance, thereby strengthening breeding efficiency and genetic improvement programmes (20).

In contrast, traits such as PH and FLL exhibited comparatively lower heritability, indicating greater environmental influence on their expression. Such traits may require selection across multiple environments or improvement through hybridisation and heterosis breeding approaches (21).

The results suggest that GY, BY, HI, KLB ratio and grain quality traits can serve as reliable selection criteria for developing high-yielding and market-preferred rice varieties suitable for Bastar Plateau agro-climatic conditions.

Correlation analysis

Correlation analysis revealed significant positive associations between GY and several important yield-contributing traits including BY, HI, TW, NGPP, NET, PL and flag leaf traits (Table 5). These relationships provide important biological insights into yield determination under lowland conditions (22).

The strong positive association between BY and GY indicated that genotypes with greater biomass accumulation tended to produce higher GY. Under rainfed lowland ecosystems such as the Bastar Plateau, efficient biomass production is particularly important because fluctuating moisture availability and environmental stress can limit assimilate production. Genotypes capable of producing greater dry matter are therefore better able to support grain filling and sustain productivity.

Similarly, the positive correlation between HI and GY emphasised the importance of efficient assimilate partitioning from vegetative organs to reproductive sinks. Genotypes with higher HI utilise accumulated biomass more efficiently for grain production, thereby improving yield performance under resource-limited environments.

The positive association of NET with GY indicated that productive tillers directly enhanced sink capacity and grain production. Likewise, the strong association of NGPP and TW with GY demonstrated the importance of

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both grain number and grain size in determining final productivity (23).

Table 3. Analysis of variance for yield and yield-attributing traits in lowland rice genotypes

Source of variation	DF	Days to 50 % flowering	Days to maturity	Plant height (cm)	Effective tillers per plant	Panicle length (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Grains per panicle	Test weight (g)
Replication	1	11.85	312.5	58.29	0.86	0.52	3.96	0.005	473.04	16.85
Treatment	63	98.92**	88.73**	173.77**	2.64**	8.46**	35.31**	0.119**	6212.66**	30.05**
Error	63	17.57	24.06	100.60	0.28	4.21	6.96	0.025	623.43	3.67
Total	127	57.88	58.41	136.57	1.46	6.29	21.00	0.072	3394.86	16.86

Source of variation	DF	Grain length (mm)	Grain breadth (mm)	Grain length-to-breadth ratio	Kernel length (mm)	Kernel breadth (mm)	Kernel length-to-breadth ratio	Biological yield (q ha^{-1})	Harvest index (%)	Grain yield (q ha^{-1})
Replication	1	0.047	0.01	0.019	0.003	0.01	0.008	320.07	11.24	32.16
Treatment	63	1.369**	0.173**	0.536**	1.347**	0.160**	0.481**	888.08**	67.99**	222.86**
Error	63	0.089	0.01	0.017	0.066	0.007	0.013	135.8	16.08	35.67
Total	127	0.724	0.091	0.275	0.701	0.083	0.245	510.43	41.80	128.50

*$p < 0.05$; **$p < 0.01$; DF: degree of freedom.

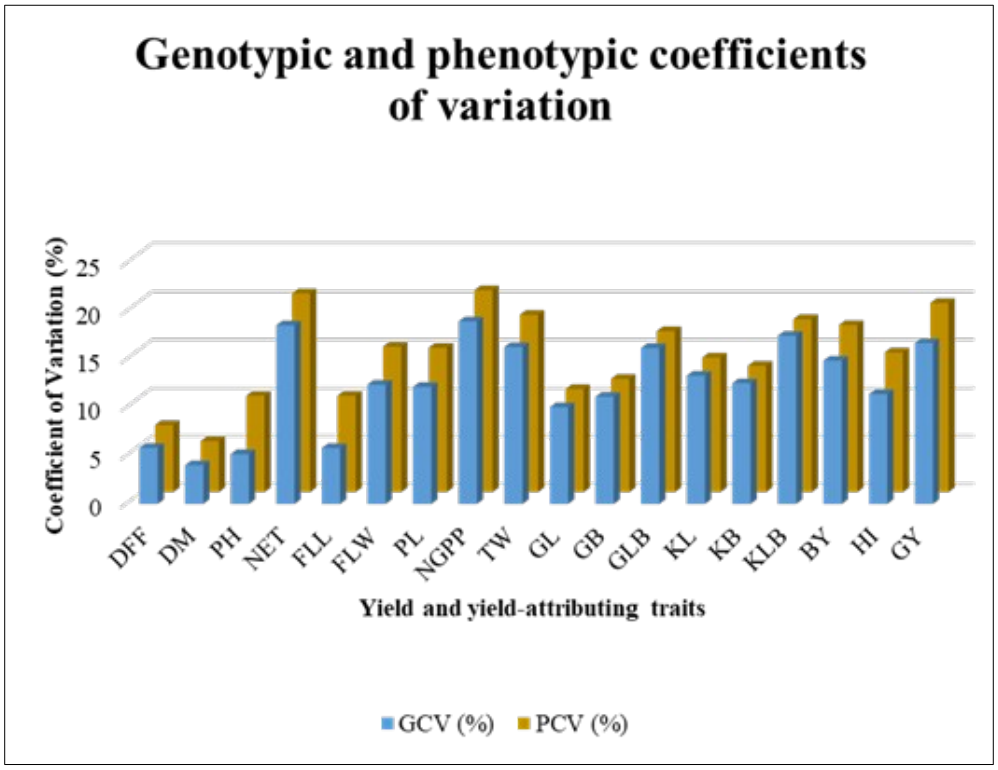


Fig. 2. Bar diagram representing the genotypic coefficient of variation and phenotypic coefficient of variation for yield and yield-attributing traits.

DFF: days to 50 % flowering; DM: days to maturity; PH: plant height; NET: number of effective tillers per plant; FLL: flag leaf length; FLW: flag leaf width; PL: panicle length; NGPP: number of grains per panicle; TW: test weight; GL: grain length; GB: grain breadth; GLB: grain length-to-breadth ratio; KL: kernel length; KB: kernel breadth; KLB: kernel length-to-breadth ratio; BY: biological yield; HI: harvest index; GY: grain yield; GCV: genotypic coefficient of variation; PCV: phenotypic coefficient of variation.

Table 4. Estimates of genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance for yield and yield-attributing traits

Characters	GCV (%)	PCV (%)	Heritability (%)	GA % mean
Days to 50 % flowering	5.83	6.97	69.84	10.03
Days to maturity	4.02	5.31	57.34	6.27
Plant height (cm)	5.17	10.01	26.67	5.50

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Number of effective tillers per plant	18.56	20.66	80.64	34.33
Flag leaf length (cm)	5.81	10.02	33.56	6.93
Flag leaf width (cm)	12.39	15.13	67.08	20.90
Panicle length (cm)	12.16	15.01	65.59	20.28
Number of grains per panicle	18.97	20.98	81.76	35.33
Test weight (g)	16.30	18.43	78.25	29.71
Grain length (mm)	10.05	10.72	87.79	19.39
Grain breadth (mm)	11.13	11.77	89.41	21.67
Grain length-to-breadth ratio	16.20	16.72	93.84	32.33
Kernel length (mm)	13.32	13.99	90.69	26.13
Kernel breadth (mm)	12.54	13.13	91.22	24.68
Kernel length-to-breadth ratio	17.48	17.98	94.59	35.03
Biological yield (q ha^{-1})	14.89	17.37	73.47	26.29
Harvest index (%)	11.41	14.52	61.74	18.46
Grain yield (q ha^{-1})	16.72	19.65	72.40	29.30

GCV: genotypic coefficient of variation; PCV: phenotypic coefficient of variation; GA: genetic advance.

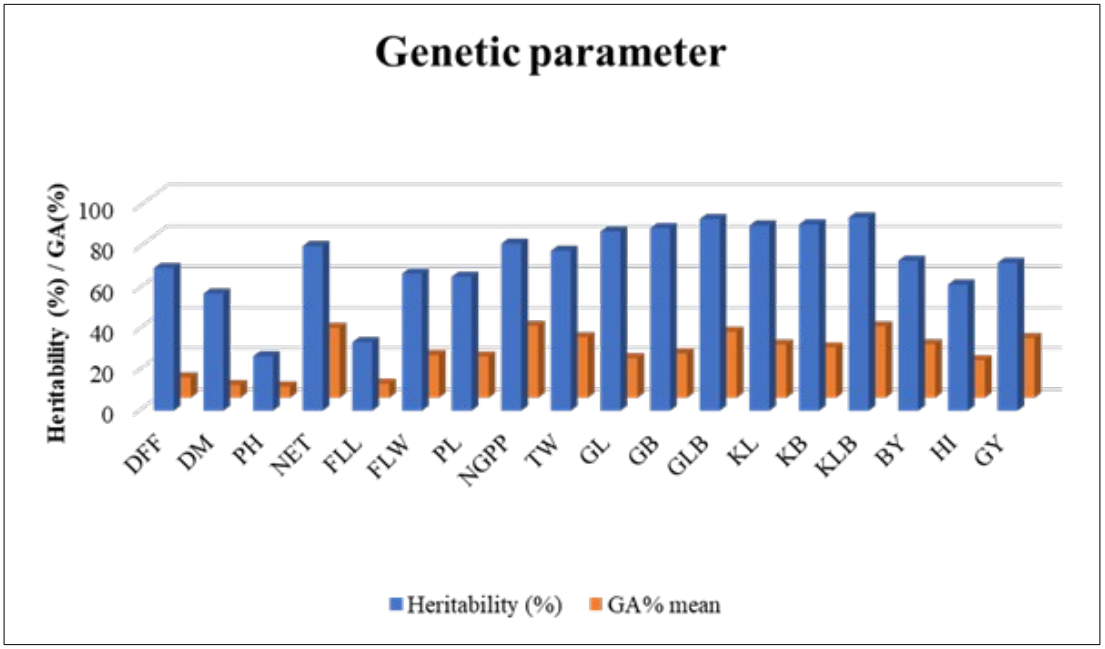


Fig. 3. Genetic parameter estimates showing heritability (%) and genetic advance as percent of mean (GA % mean) for yield and yield-attributing traits.

DFF: days to 50 % flowering; DM: days to maturity; PH: plant height; NET: number of effective tillers per plant; FLL: flag leaf length; FLW: flag leaf width; PL: panicle length; NGPP: number of grains per panicle; TW: test weight; GL: grain length; GB: grain breadth; GLB: grain length-to-breadth ratio; KL: kernel length; KB: kernel breadth; KLB: kernel length-to-breadth ratio; BY: biological yield; HI: harvest index; GY: grain yield; GA: genetic advance.

Table 5. Phenotypic correlation coefficients among yield and yield-attributing traits in rice genotypes

Character	DFF	DM	PH	NET	FLL	FLW	PL	NGPP	TW	GL	GB	GLB	KL	KB	KLB	BY	HI	GY
DFF	1.000	0.752 **	-0.075	-0.110	0.338 **	0.244 **	-0.123	0.197*	0.239 **	-0.226*	0.090	-0.104	0.170	-0.187*	-0.174*	0.462**	-0.022	0.396**
DM			-0.066	-0.120	0.199*	0.169	-0.163	0.211*	0.202*	-0.272**	0.114	-0.152	0.154	-0.246**	-0.199*	0.395**	-0.095	0.299**
PH				0.109	0.155	0.203*	0.047	0.126	0.021	0.127	0.209*	0.243**	0.075	-0.018	0.104	-0.063	-0.049	-0.132

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NET	0.147	0.251**	0.389**	0.231**	0.146	0.162	-0.105	0.120	-0.105	0.190*	0.182*	0.072	0.236**	0.198*
FLL		0.237**	0.025	0.252**	0.198*	-0.029	0.004	0.060	0.050	-0.060	0.017	0.299**	0.049	0.336**
FLW			-0.060	0.329**	0.248**	0.002	-0.041	0.200*	0.029	0.066	0.122	0.203*	0.163	0.344**
PL				-0.205*	-0.050	0.265**	-0.202*	0.148	-0.140	0.296**	0.219*	0.004	0.022	-0.001
NGPP					0.520**	0.015	-0.014	0.087	0.050	0.030	0.014	0.282**	0.268**	0.451**
TW						0.126	0.109	0.236**	0.123	0.010	0.059	0.283**	0.303**	0.549**
GL							-0.144	0.713**	0.038	0.683**	0.527**	-0.128	-0.018	-0.146
GB								-0.009	0.536**	-0.731**	-0.382**	0.092	0.082	0.139
GLB									0.053	0.423**	0.679**	-0.011	0.035	0.020
KL										-0.366**	-0.618**	0.093	0.090	0.152
KB											0.595**	-0.147	-0.031	-0.159
KLB												-0.086	-0.027	-0.096
BY													-0.263**	0.560**
HI														0.367**
GY														1

*$p < 0.05$ %; **$p < 0.01$ %.

DFF: days to 50 % flowering; DM: days to maturity; PH: plant height; NET: number of effective tillers per plant; FLL: flag leaf length; FLW: flag leaf width; PL: panicle length; NGPP: number of grains per panicle; TW: test weight; GL: grain length; GB: grain breadth; GLB: grain length-to-breadth ratio; KL: kernel length; KB: kernel breadth; KLB: kernel length-to-breadth ratio; BY: biological yield; HI: harvest index; GY: grain yield.

Flag leaf length and PL also showed positive correlations with GY, suggesting the importance of source-sink relationships. Longer flag leaves may enhance photosynthetic activity and assimilate supply, while longer panicles can accommodate a higher number of grains, ultimately contributing to improved GY (24).

These findings collectively indicate that simultaneous selection for BY, HI, productive tillers, NGPP and TW would be highly effective for improving rice productivity under Bastar Plateau conditions.

Path coefficient analysis

Path coefficient analysis provided a clearer understanding of the direct and indirect contributions of different traits towards GY (Table 6). Biological yield exerted the highest positive direct effect on GY, followed by HI, TW, FLW, FLL, NGPP and PL (Fig. 4).

The strong direct effect of BY on GY indicates that biomass accumulation is a major determinant of productivity under lowland conditions. In the Bastar Plateau ecosystem, where rice cultivation is often constrained by erratic rainfall and low-input management, genotypes capable of producing higher biomass may better withstand environmental fluctuations and maintain grain production. Increased biomass production enhances assimilate availability for grain filling, thereby directly improving yield performance.

Harvest index also exhibited a strong positive direct effect, indicating that efficient partitioning of assimilates towards grains plays a vital role in yield improvement. This suggests that both biomass production and efficient assimilate utilisation are critical for developing high-yielding rice genotypes adapted to lowland ecosystems.

Traits such as FLL, FLW and PL contributed indirectly to GY through BY and HI, highlighting the importance of photosynthetic efficiency and source-sink balance in rice productivity. The positive indirect effects of effective tillers and NGPP further emphasised their role in enhancing sink capacity and assimilate utilisation.

Therefore, traits exhibiting high positive direct effects, along with significant positive correlations with GY should receive greater emphasis during selection and breeding programmes aimed at improving lowland rice productivity (12).

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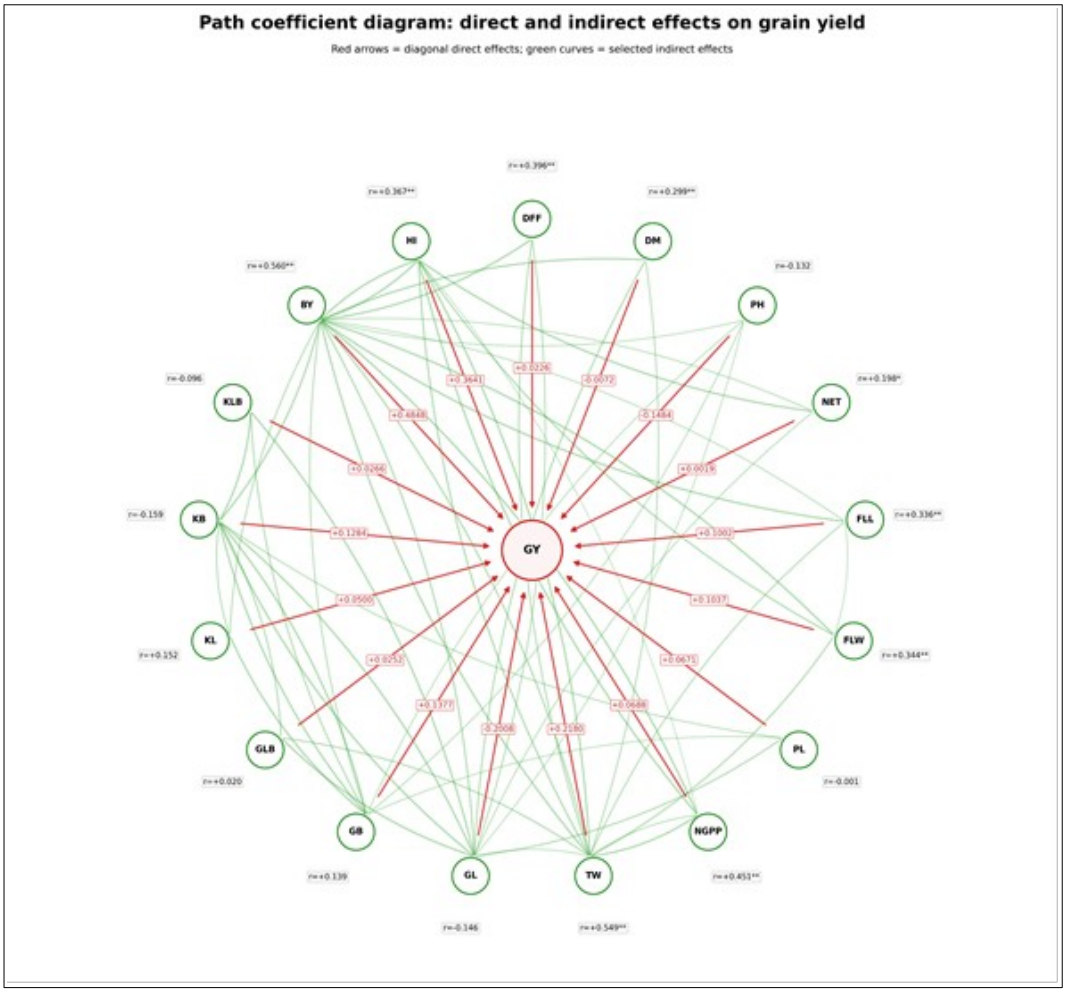


Fig. 4. Path coefficient diagram showing the direct and indirect effects of yield-attributing traits on grain yield. Red lines indicate direct effects, while green lines indicate indirect effects.

DFF: days to 50 % flowering; DM: days to maturity; PH: plant height; NET: number of effective tillers per plant; FLL: flag leaf length; FLW: flag leaf width; PL: panicle length; NGPP: number of grains per panicle; TW: test weight; GL: grain length; GB: grain breadth; GLB: grain length-to-breadth ratio; KL: kernel length; KB: kernel breadth; KLB: kernel length-to-breadth ratio; BY: biological yield; HI: harvest index.

Table 6. Direct and indirect effects of yield and yield-attributing traits on grain yield through path coefficient analysis

Character	DFF	DM	PH	NET	FLL	FLW	PL	NGPP	TW	GL	GB	GLB	KL	KB	KLB	BY	HI	GY
DFF	0.0226	-0.0054	0.0111	-0.0002	0.0339	0.0253	-0.0083	0.0136	0.0521	0.0453	0.0124	-0.0026	0.0085	-0.0240	-0.0046	0.2238	-0.0080	0.396**
DM	0.0170	-0.0072	0.0098	-0.0002	0.0199	0.0175	-0.0110	0.0145	0.0441	0.0547	0.0157	-0.0038	0.0077	-0.0316	-0.0053	0.1914	-0.0346	0.299**
PH	-0.0017	0.0005	-0.1484	0.0002	0.0155	0.0210	0.0032	0.0087	0.0045	-0.0255	0.0287	0.0061	0.0038	-0.0023	0.0028	-0.0308	-0.0178	-0.132
NET	-0.0025	0.0009	-0.0162	0.0019	0.0148	0.0260	0.0261	0.0159	0.0317	-0.0325	-0.0144	0.0030	-0.0052	0.0244	0.0049	0.0350	0.0858	0.198*
FLL	0.0077	-0.0014	-0.0230	0.0003	0.1002	0.0245	0.0017	0.0174	0.0432	0.0059	0.0005	0.0015	0.0025	-0.0076	0.0004	0.1448	0.0180	0.336**
FLW	0.0055	-0.0012	-0.0301	0.0005	0.0237	0.1037	-0.0040	0.0226	0.0541	-0.0004	-0.0057	0.0050	0.0014	0.0085	0.0032	0.0985	0.0592	0.344**
PL	-0.0028	0.0012	-0.0070	0.0008	0.0025	-0.0062	0.0671	-0.0141	-0.0109	-0.0532	-0.0279	0.0037	-0.0070	0.0380	0.0058	0.0019	0.0082	-0.001
NGPP	0.0045	-0.0015	-0.0187	0.0004	0.0253	0.0341	-0.0137	0.0688	0.1133	-0.0029	-0.0019	0.0022	0.0025	0.0039	0.0004	0.1368	0.0977	0.451**
TW	0.0054	-0.0015	-0.0031	0.0003	0.0199	0.0257	-0.0034	0.0358	0.2180	-0.0252	0.0150	0.0059	0.0062	0.0012	0.0016	0.1371	0.1102	0.549**
GL	-0.0051	0.0020	-0.0188	0.0003	-0.0029	0.0002	0.0178	0.0010	0.0274	-0.2008	-0.0198	0.0179	0.0019	0.0876	0.0140	-0.0620	-0.0065	-0.146
GB	0.0020	-0.0008	-0.0310	-0.0002	0.0004	-0.0043	-0.0136	-0.0010	0.0238	0.0288	0.1377	-0.0002	0.0268	-0.0938	-0.0102	0.0448	0.0299	0.139
GLB	-0.0024	0.0011	-0.0361	0.0002	0.0061	0.0207	0.0099	0.0060	0.0515	-0.1431	-0.0013	0.0252	0.0027	0.0543	0.0181	-0.0054	0.0126	0.020
KL	0.0038	-0.0011	-0.0112	-0.0002	0.0050	0.0030	-0.0094	0.0034	0.0269	-0.0076	0.0738	0.0013	0.0500	-0.0470	-0.0165	0.0449	0.0328	0.152
KB	-0.0042	0.0018	0.0027	0.0004	-0.0060	0.0069	0.0198	0.0021	0.0021	-0.1371	-0.1006	0.0107	-0.0183	0.1284	0.0159	-0.0714	-0.0114	-0.159

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KLB	-0.0039	0.0014	-0.0155	0.0004	0.0017	0.0126	0.0147	0.0010	0.0129	-0.1058	-0.0526	0.0171	-0.0309	0.0764	0.0266	-0.0415	-0.0100	-0.096
BY	0.0105	-0.0028	0.0094	0.0001	0.0299	0.0211	0.0003	0.0194	0.0617	0.0257	0.0127	-0.0003	0.0046	-0.0189	-0.0023	0.4848	-0.0958	0.560**
HI	-0.0005	0.0007	0.0073	0.0005	0.0050	0.0169	0.0015	0.0185	0.0660	0.0036	0.0113	0.0009	0.0045	-0.0040	-0.0007	-0.1275	0.3641	0.367**

*$p < 0.05$ %; **$p < 0.01$ %.

DFF: days to 50 % flowering; DM: days to maturity; PH: plant height; NET: number of effective tillers per plant; FLL: flag leaf length; FLW: flag leaf width; PL: panicle length; NGPP: number of grains per panicle; TW: test weight; GL: grain length; GB: grain breadth; GLB: grain length-to-breadth ratio; KL: kernel length; KB: kernel breadth; KLB: kernel length-to-breadth ratio; BY: biological yield; HI: harvest index; GY: grain yield.

Cluster analysis

Cluster analysis grouped the 64 rice genotypes into seven distinct clusters, confirming the presence of substantial genetic divergence among the evaluated material (Fig. 5). The existence of wide genetic diversity among clusters provides opportunities for selecting diverse parents in hybridisation programmes.

The maximum inter-cluster distance observed between Cluster V and Cluster VI indicated greater genetic divergence between these groups (Table 7). Crosses involving genotypes from highly divergent clusters are expected to generate greater heterosis, broader variability and superior transgressive segregants in subsequent generations (25, 26). Therefore, genotypes belonging to these clusters may serve as valuable parental combinations for developing improved rice varieties with enhanced yield potential and adaptability.

Cluster III exhibited superior mean performance for several important yield-contributing traits including PH, PL and GB, indicating the high agronomic potential of genotypes grouped within this cluster (Table 8). Such genotypes can be directly utilised in selection programmes or incorporated into breeding programmes aimed at improving yield and grain quality.

The clustering pattern also demonstrated that genetic diversity was not strictly associated with geographical origin, suggesting that selection history, pedigree background and adaptation patterns may have contributed significantly to genetic divergence among the genotypes.

Principal component analysis

Principal component analysis revealed that flowering time, maturity duration, PH, PL and grain quality traits contributed substantially towards total genetic divergence among the rice genotypes (Fig. 6). The first two principal components explained a major proportion of total variability, indicating the multidimensional nature of genetic diversity present in the evaluated germplasm.

Table 7. Intra- and inter-cluster distances among 7 clusters based on Mahalanobis D^2 analysis

Clusters	I	II	III	IV	V	VI	VII
I	**330.66**						
II	792.27	**392.12**					
III	481.31	1052.32	**306.88**				
IV	788.64	1029.96	1573.97	**569.10**			
V	2029.71	839.93	2642.20	1741.49	**383.40**		
VI	869.84	2377.92	1068.50	1361.98	4515.64	0.00	
VII	1769.65	947.85	2660.33	1135.79	819.37	3397.40	0.00

Table 8. Cluster mean values for yield and yield-attributing traits among rice genotypes

Cluster	DFF	DM	PH	NET	FLL	FLW	PL	NGPP	TW	GL	GB	GLB	KL	KB	KLB	BY	HI	GY
I	109.04	141.41	114.53	5.60	29.67	1.74	24.82	278.00	21.17	7.46	2.51	3.00	5.44	2.15	2.56	130.70	43.73	56.81
II	109.03	140.84	119.67	5.88	30.89	1.78	25.32	281.07	23.20	8.39	2.68	3.17	6.58	2.28	2.93	127.83	45.50	57.85
III	115.00	147.50	120.60	5.85	30.85	1.64	26.12	274.00	23.27	7.05	3.15	2.24	4.90	2.50	1.98	143.69	44.75	65.10
IV	117.50	150.50	110.50	5.75	30.45	1.77	25.65	296.50	21.78	7.85	1.95	4.03	5.85	1.70	3.44	143.46	43.19	61.10
V	112.50	142.50	117.70	6.30	33.30	1.86	24.93	313.00	25.87	9.80	2.30	4.26	7.15	2.70	2.70	133.61	46.27	62.18
VI	110.00	142.50	115.50	7.30	30.95	2.06	26.07	227.00	19.82	6.21	2.10	2.96	4.30	1.70	2.53	139.12	41.23	57.35
VII	99.00	129.00	116.40	9.59	28.00	3.24	23.42	185.00	19.99	9.50	2.10	4.53	6.50	1.70	3.83	118.94	48.71	57.93

DFF: days to 50 % flowering; DM: days to maturity; PH: plant height; NET: number of effective tillers per plant; FLL: flag leaf length; FLW: flag leaf width; PL: panicle length; NGPP: number of grains per panicle; TW: test weight; GL: grain length; GB: grain breadth; GLB: grain length-to-breadth ratio; KL: kernel length; KB: kernel breadth; KLB: kernel length-to-breadth ratio; BY: biological yield; HI: harvest index; GY: grain yield.

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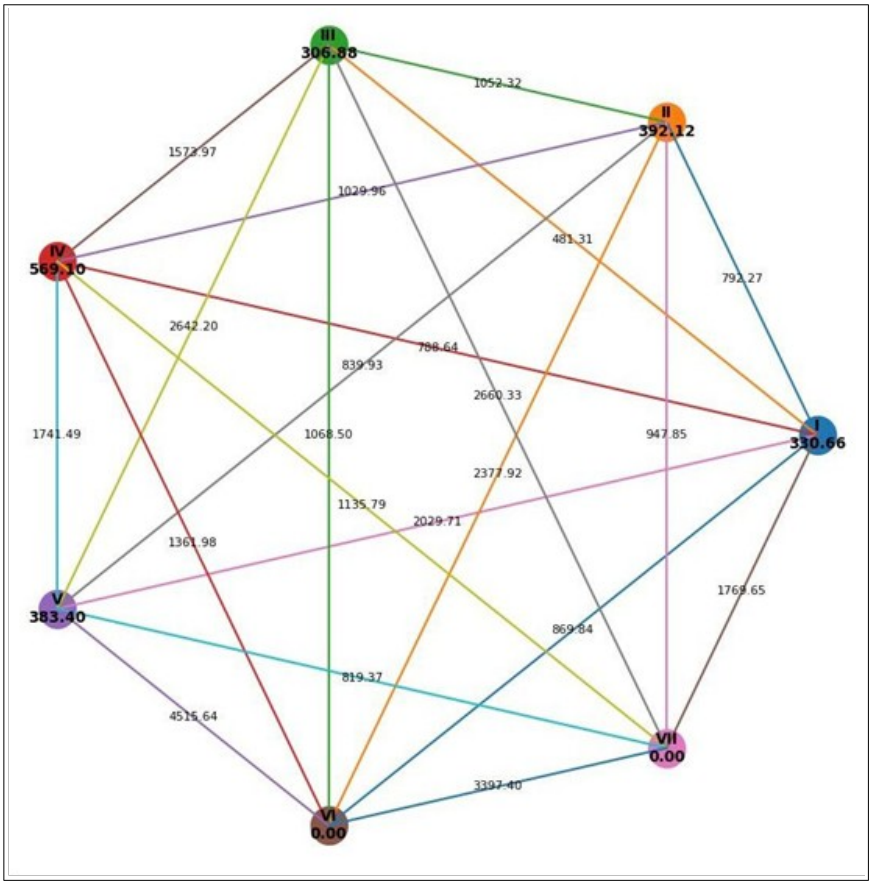


Fig. 5. Cluster diagram showing intra- and inter-cluster distances among rice genotypes based on Mahalanobis *D²* statistics.

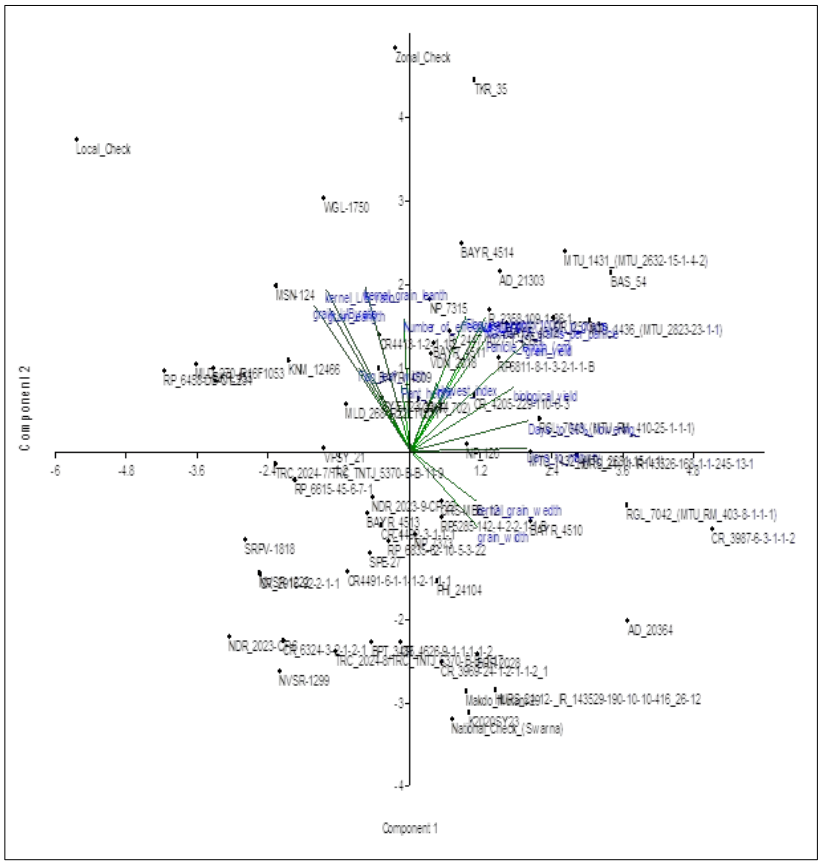


Fig. 6. Principal component analysis plot showing distribution of 64 rice genotypes across the first two principal components.

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The greater contribution of DFF, DM and PH towards divergence suggested that phenological and plant architectural traits played major roles in differentiating genotypes under Bastar Plateau conditions. These traits are particularly important under rainfed lowland ecosystems because they influence crop duration, adaptation to rainfall patterns and stress escape mechanisms.

The contribution of GY and grain quality traits towards PCA divergence further indicated the availability of substantial variability for economically important characters. Genotypes occupying distant positions in the PCA scatter plot may possess complementary traits and can therefore be utilised as potential parents in hybridisation programmes aimed at broadening the genetic base and developing superior recombinants.

The PCA results complemented cluster analysis by confirming that both yield-related and grain quality traits contributed significantly towards overall genetic diversity (Fig. 7). Such information is highly valuable for designing efficient breeding strategies targeting high yield, adaptability and grain quality improvement in lowland rice ecosystems of the Bastar Plateau (25, 26).

4. Conclusion

The study revealed substantial genetic variability among 64 lowland rice genotypes evaluated under Bastar Plateau conditions, indicating significant potential for genetic improvement. High heritability coupled with high genetic advance (GA) for grain yield (GY), biological yield (BY), harvest index (HI), kernel length-to-breadth (KLB) ratio, grain length-to-breadth (GLB) ratio and kernel breadth (KB) suggested the predominance of additive gene action and the effectiveness of direct phenotypic selection for these traits. Correlation and path coefficient analyses identified BY, HI, number of effective tillers per plant (NET), number of grains per panicle (NGPP), panicle length (PL) and test weight (TW) as key determinants of GY. Biological yield and HI exhibited the highest positive direct effects on GY, highlighting their importance as reliable selection criteria for improving productivity in lowland rice. Among the genotypes evaluated, AD 21303, TKR 35, MTU 1436, RP6811-8-1-3-2-1-1-B and OR 2573-3 were identified as superior performers and potential donor parents for future breeding programmes. Cluster analysis grouped the genotypes into 7 clusters, with considerable genetic divergence observed between Clusters V and VI, suggesting their suitability for hybridisation to generate superior recombinants. Overall, the study identified important yield-contributing traits, promising high-yielding genotypes and genetically diverse parental groups that can be utilised for developing improved rice varieties with enhanced yield, grain quality and adaptability to lowland ecosystems. Future research should focus on multi-environment testing and the integration of molecular breeding approaches to accelerate the development of climate-resilient rice varieties.

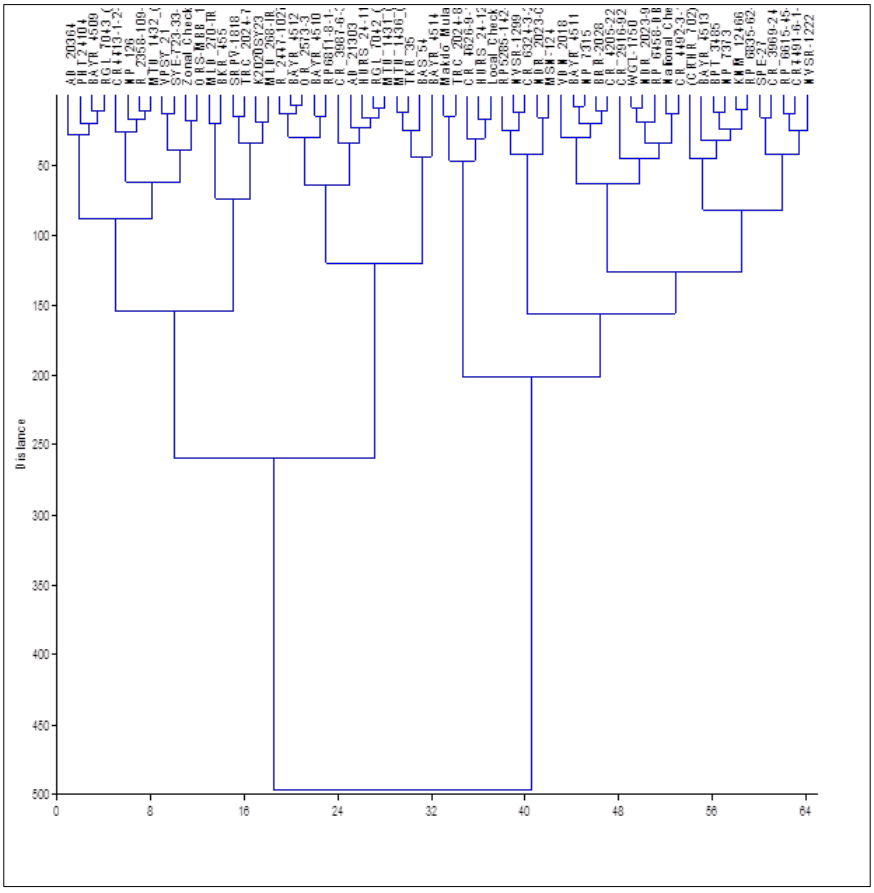


Fig. 7. Dendrogram illustrating genetic divergence among 64 rice genotypes based on cluster analysis.

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Authors' contributions

UK carried out the experiment, data collection, analyses and manuscript writing. SK provided valuable help with the experimental design, data analysis and interpretation of results. SK, RP, RRK and NCM provided their invaluable assistance in designing of the study, analyses, supervision and guidance to identify the research problems. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest

Authors do not have any conflict of interests to declare.

Ethical issues

None

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