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Bharath Kumar S
M.Sc. Scholar, Section of Genetics and Plant breeding, S.G. College of Agriculture and Research Station, IGKV, Jagdalpur, Chhattisgarh, India

Chiranjivi DS
M.Sc. Scholar, Section of Genetics and Plant breeding, S.G. College of Agriculture and Research Station, IGKV, Jagdalpur, Chhattisgarh, India

Umesha K
M.Sc. Scholar, Section of Genetics and Plant breeding, S.G. College of Agriculture and Research Station, IGKV, Jagdalpur, Chhattisgarh, India

Shravan Kumar
M.Sc. Scholar, Section of Genetics and Plant breeding, S.G. College of Agriculture and Research Station, IGKV, Jagdalpur, Chhattisgarh, India

Sameer Das
M.Sc. Scholar, Section of Genetics and Plant breeding, S.G. College of Agriculture and Research Station, IGKV, Jagdalpur, Chhattisgarh, India

Raja Ram Kanwar
Scientist, Section of Genetics and Plant breeding, S.G. College of Agriculture and Research Station, IGKV, Jagdalpur, Chhattisgarh, India

Prafull Kumar
Scientist, Section of Genetics and Plant breeding, S.G. College of Agriculture and Research Station, IGKV, Jagdalpur, Chhattisgarh, India

Corresponding Author:
Bharath Kumar S
M.Sc. Scholar, Section of Genetics and Plant breeding, S.G. College of Agriculture and Research Station, IGKV, Jagdalpur, Chhattisgarh, India

Studies of upland rice (*Oryza sativa* L.) for yield potential and associated traits under Bastar plateau conditions

Bharath Kumar S, Chiranjivi DS, Umesha K, Shravan Kumar, Sameer Das, Raja Ram Kanwar and Prafull Kumar

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Abstract

The present study, evaluated 57 upland rice (*Oryza sativa* L.) genotypes under direct seeding conditions using a Randomized Complete Block Design. Genotypes R2748-1-1, IR18A1068, JDP-1212, R2735-56-1 and IR18A1073 recorded the highest grain yields, indicating potential for selection. High heritability and genetic advance were noted for number of effective tillers per plant, number of grains per panicle, grain yield and related traits, suggesting additive gene action. PCV values slightly exceeded GCV, indicating environmental influence. Moderate to high variability was found in key yield-contributing traits. Grain yield showed significant positive correlation with traits like days to 50% flowering, number of effective tillers, flag leaf length, flag leaf width, panicle length, number of grains per panicle, test weight, biological yield and harvest index. Path analysis revealed that biological yield followed by harvest index, number of grains per panicle, flag leaf length, flag leaf width, panicle length, number of effective tillers, test weight, days to 50% flowering, days to maturity, plant height, kernel breadth, grain L/B ratio, grain length and kernel length exhibited positive direct effect on grain yield. Cluster analysis grouped the genotypes into six clusters, with Cluster VI showing the best mean performance for grain yield and contributing traits. Grain L/B ratio, kernel L/B ratio and days to maturity were major contributors to genetic diversity.

Keywords: Heritability, genetic advance, GCV, PCV, correlation, path analysis, cluster analysis

Introduction

Rice (*Oryza sativa* L.), a monocotyledonous member of the Poaceae family, is a self-pollinated crop cultivated extensively across tropical and subtropical regions. It thrives under hot, humid conditions with an optimal temperature range of 21-37 °C and requires a minimum annual rainfall of 1000 mm. Globally, rice is grown in more than 100 countries, across latitudes 50°N to 40°S and altitudes up to 3000 m above mean sea level. The crop occupies 171.25 million hectares with a projected production of 541.51 million metric tons (Anonymous, 2025) [3], of which Asia contributes 85%. India alone accounts for over 27% of global output, with 51.42 million hectares under cultivation and an estimated production of 150 million metric tons in 2024-25. Chhattisgarh, known as the "Rice Bowl of India," exemplifies rice's socio-economic significance, with 82 % of its population dependent on agriculture. Here, rice occupies 4.4 million hectares, producing nearly 10 million tons at an average productivity of 2.3 t/ha (Anonymous, 2024b) [2].

Upland rice, cultivated without irrigation, spans about 14 million hectares worldwide and contributes 11% of total production. Its importance lies in its suitability for low-input systems, owing to reduced water requirements and lower cultivation costs. Improving upland rice productivity necessitates the exploitation of genetic variability and identification of key yield-contributing traits. Given the polygenic and complex nature of yield, analytical tools such as correlation and path coefficient analysis are indispensable. While correlation quantifies trait associations, path analysis partitions these relationships into direct and indirect effects, thereby enabling more effective trait-based selection and guiding the development of high-yielding, stress-resilient upland rice cultivars.

Materials and Methods

The present study was conducted during *Kharif* 2023 at the Instructional cum Research Farm, S.G. College of Agriculture and Research Station, Jagdalpur, Chhattisgarh (19°05′15″N, 81°58′1″E; 552 m above mean sea level). The experiment was laid out in a Randomized Block Design with two replications. A total of 57 rice genotypes, including checks, were evaluated for 18 traits covering phenological, morphological, yield and grain quality parameters. Plot-based observations were recorded for days to 50% flowering and days to maturity, while other traits were recorded from five random plants. Yield-related traits such as plant height, panicle length, number of effective tillers per plant, number of grains per panicle, biological yield, harvest index and test weight were observed. During the cropping season, temperatures ranged from 10.8-35.7 °C, with 1486.7 mm rainfall, peaking in July (398.3 mm). Statistical analyses included: ANOVA (Panse and Sukhatme, 1967) [17], phenotypic and genotypic coefficients of variation (Fisher, 1918) [7], correlation and path analyses (Dewey and Lu, 1959) [5] and genetic divergence using Mahalanobis's D² analysis (Mahalanobis, 1936) [15].

Results and Discussion

The analysis of variance (ANOVA) revealed highly significant differences among the 57 upland rice genotypes for all 18 evaluated traits, confirming the presence of considerable genetic variability. At 1% level of significance, traits such as days to 50% flowering, days to maturity, plant height, flag leaf length, number of effective tillers per plant, panicle length, number of grains per panicle, harvest index, test weight, grain L/B ratio, kernel length, biological yield and grain yield were highly significant. At 5% level, flag leaf width, grain length, grain breadth, kernel breadth and kernel L/B ratio exhibited significant genotypic differences. These findings indicate the presence of sufficient variation within the studied germplasm, offering scope for effective selection and improvement of yield-contributing traits (Singh and Chaudhary, 1985; Falconer and Mackay, 1996).

Grain yield, the most important economic trait in rice breeding, exhibited wide variation, ranging from 19.19 q/ha in the check variety Vandana to 38.31 q/ha in R2748-1-1. The top five high-yielding genotypes included R2748-1-1 (38.31 q/ha), IR18A1068 (36.88 q/ha), JDP-1212 (36.69 q/ha), R2735-56-1 (35.97 q/ha) and IR18A1073 (35.22 q/ha). The mean yield across all genotypes was 28.64 q/ha with a coefficient of variation (CV) of 8.65%. This observed yield variability highlights the opportunity to select superior genotypes suitable for diverse agro-ecological environments. The CV for all traits ranged between 1.22% and 8.65%. The lowest variability was observed for grain length (1.22%), while grain yield showed the highest among yield-contributing traits (8.65%). Overall, the low to moderate CV values reflect high experimental precision and minimal environmental influence, further validating the reliability of the observed genetic variation (Allard, 1999) [1].

Phenotypic coefficient of variation (PCV) values were consistently higher than genotypic coefficient of variation (GCV), though the differences were marginal, indicating limited environmental influence on the expression of these traits. Moderate PCV and GCV values were observed for most yield-related traits, whereas days to 50% flowering, days to maturity, and traits associated with grain and kernel dimensions exhibited lower values (<4%). The closeness between PCV and GCV estimates for most traits suggests that their variation is primarily genetic in origin, which is advantageous for breeders as it enhances the predictability of selection response (Burton and DeVane, 1953) [4]. Moderate GCV for yield-related characters such as number of effective tillers per plant, number of grains per panicle, biological yield and harvest index indicates sufficient genetic variability, which can be exploited in breeding programs. Conversely, the low GCV for kernel breadth and days to maturity reflects limited scope for improvement through simple selection.

Broad-sense heritability estimates ranged from 41.84% for panicle length to 97.68% for grain length. Out of the 18 traits, 16 exhibited high heritability (>60%). Traits with particularly high heritability included grain length (97.68%), number of effective tillers per plant (96.35%), grain L/B ratio (92.34%) and kernel length (91.69%). Moderate heritability was observed for kernel breadth (55.10%) and panicle length (41.84%). High heritability implies that most of the observed phenotypic variation is due to genetic differences rather than environmental effects. This enhances the efficiency of selection and allows reliable improvement through phenotypic performance (Johnson *et al.*, 1955) [9]. For breeders, traits such as number of effective tillers per plant, grain length and biological yield, which exhibited high heritability, represent stable and dependable targets for genetic advancement. Traits with moderate heritability may require additional testing across environments to ensure accurate selection.

Genetic advance as percent of mean (GAM) ranged from 6.89% (kernel breadth) to 35.77% (number of effective tillers per plant). High GAM (>20%) was recorded for number of effective tillers per plant (35.77%), number of grains per panicle (34.22%), flag leaf length (25.71%), grain yield (25.15%), grain L/B ratio (22.33%), biological yield (22.24%) and kernel L/B ratio (20.40%). Traits with moderate GAM (10-20%) included flag leaf width, plant height, test weight, grain length, harvest index, kernel length and days to 50% flowering. Low GAM (<10%) was recorded for panicle length, days to maturity and kernel breadth. High genetic advance coupled with high heritability indicates predominance of additive gene action, enabling effective phenotypic selection. Such traits facilitate precise identification of superior genotypes, accelerate genetic gain and support the development of rice varieties with enhanced yield, adaptability and stress tolerance, thereby strengthening breeding efficiency and genetic improvement programs.

The combination of high heritability with high genetic advance as percent of mean, observed for traits such as number of effective tillers per plant, number of grains per panicle, grain yield, flag leaf length, biological yield and grain yield, indicates predominant additive gene action. This suggests that these characters can be effectively improved through simple selection procedures (Panse and Sukhatme, 1967) [17]. On the other hand, traits with high heritability but low GAM may be under non-additive gene control, where improvement would be more effectively achieved through hybridization and exploitation of heterosis.

Correlation analysis revealed significant associations of grain yield with several key traits. Grain yield was positively and significantly correlated with days to 50% flowering (0.280**), number of effective tillers per plant

(0.493**), flag leaf length (0.518**), flag leaf width (0.500*), panicle length (0.493*), number of grains per panicle (0.521**), test weight (0.415**), biological yield (0.766**) and harvest index (0.539**). These results highlight the importance of foliage traits, reproductive efficiency and assimilate partitioning in determining yield potential. The strong positive correlation with biological yield and harvest index emphasizes the importance of both total biomass production and efficient partitioning toward grain formation. Non-significant positive correlations were observed with days to maturity, plant height, grain length, grain L/B ratio, kernel length and kernel breadth, suggesting limited but occasionally favorable contributions to yield. Negative but non-significant correlations were noted with grain breadth (-0.036) and kernel L/B ratio (-0.029), indicating minimal or inconsistent influence on yield. These findings collectively underscore the need for a multi-trait selection approach, integrating yield-contributing traits that show strong positive associations with grain yield (Dewey and Lu, 1959) [5].

Path coefficient analysis was employed to assess the direct and indirect contributions of traits to grain yield. Biological yield exerted the highest positive direct effect (0.8299) on grain yield, establishing it as the most influential trait. Harvest index (0.6299) also showed a strong positive direct contribution, underscoring the critical role of assimilate partitioning. Smaller but positive direct effects were observed for kernel length (0.0927), grain length (0.0439), test weight (0.0222), number of effective tillers per plant (0.0141), flag leaf width (0.0113), panicle length (0.0097) and days to maturity (0.0054). Traits with small but positive direct effects may also serve as supportive selection criteria, whereas traits with negative direct effects warrant cautious consideration (Dewey and Lu, 1959) [5]. In contrast, negative direct effects were observed for kernel L/B ratio (-0.1631), kernel breadth (-0.0940), grain L/B ratio (-0.0722), grain breadth (-0.0301), days to 50% flowering (-0.0115), plant height (-0.0059), flag leaf length (-0.0054) and number of grains per panicle (-0.0020). These traits may contribute indirectly to yield but are less reliable as direct selection targets.

Based on cluster analysis, the 57 genotypes were grouped into six clusters, reflecting their genetic divergence. Cluster I was the largest, comprising 17 genotypes, followed by Cluster V (13 genotypes), Cluster II (9 genotypes), Cluster IV (8 genotypes), and Clusters III and VI (5 genotypes each). Intra-cluster distances ranged from 2.777 (Cluster I) to 3.473 (Cluster III), reflecting moderate genetic heterogeneity within groups. The highest inter-cluster distances were recorded between Cluster I and Cluster VI (7.084) followed by Cluster II and Cluster III (6.692), Cluster I and III (6.264), Cluster III and VI (6.263), Cluster V and VI (6.099), suggesting these combinations possess the greatest potential for heterotic expression when used as parental lines (Mahalanobis, 1936; Murty and Arunachalam, 1966) [15, 16]. Cluster VI was superior for most yield-contributing traits, including plant height (109.18 cm), number of effective tillers per plant (6.24), flag leaf length (30.95 cm), flag leaf width (1.53 cm), panicle length (23.42 cm), number of grains per panicle (77.36), test weight (31.73 g), biological yield (78.94 q/ha), harvest index (46.17%) and grain yield (36.40 q/ha). This demonstrates the high agronomic potential of genotypes in this cluster, making them ideal candidates for direct selection and use in hybridization programs. Cluster III excelled in grain length, grain L/B ratio, kernel L/B ratio and kernel length; Cluster IV in days to 50% flowering, days to maturity and grain breadth; Cluster II in grain breadth and kernel width; and Cluster I in grain breadth. Such differentiation underscores the potential of utilizing divergent clusters for combining complementary traits in breeding programs.

Principal component analysis identified the traits contributing most to overall genetic divergence. Grain L/B ratio (7.48%), kernel L/B ratio (7.30%), days to maturity (6.88%), test weight (6.85%) and flag leaf width (6.22%) accounted for the highest proportions of variability. Plant height (6.01%), days to 50% flowering (5.90%), kernel breadth (5.67%), grain yield (5.66%) and panicle length (5.59%) were also important contributors. The remaining traits contributed between 2.63% and 5.58%, highlighting the multifaceted nature of variability in this upland rice germplasm. The PCA findings complement the cluster analysis, revealing that both morphological and yield-related traits contribute to genetic diversity. Such knowledge is crucial for designing crossing programs that exploit complementary traits while maximizing heterosis and variability in segregating generations (Jolliffe, 2002) [10].

Table 1: Mean sum of squares of 18 yield and yield attributing traits

Source of variation	DF	Days to 50% flowering	Days to maturity	Plant height (cm)	Effective tillers/plant	Panicle length (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Grains per panicle	Test weight (g)
Replication	1	6.40	13.34	9.05	0.02	6.46	0.01	0.002	14.73	1.15
Treatment	56	69.75**	50.98**	236.13**	1.31**	6.97**	29.45**	0.042*	279.46**	15.74**
Error	56	5.23	4.09	20.61	0.02	1.36	3.69	0.004	18.07	3.53
Total	113	38.03	27.41	127.31	0.66	5.04	17.05	0.023	148.71	8.85

Source of variation	DF	Grain length (mm)	Grain breadth (mm)	Grain L/B ratio	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio	Biological yield (q/ha)	Harvest index (%)	Grain yield (q/ha)
Replication	1	0.531	0.406	0.154	1.573	0.383	0.080	23.25	8.30	5.66
Treatment	56	1.048*	0.066*	0.256**	0.571**	0.034*	0.233*	151.66**	34.98**	39.56**
Error	56	0.012	0.008	0.010	0.025	0.010	0.024	15.81	6.23	2.89
Total	113	0.530	0.040	0.133	0.309	0.025	0.128	72.20	35.17	26.25

Table 2: Mean, Minimum, Maximum, Standard error, Critical difference and coefficient of variation of 18 traits under study

Characters	Mean ($\bar{X}$)	X_{min}	X_{max}	Std. Error (deviation)	Critical Difference	Coefficient of Variation
Days to 50% flowering	92.25	80	110	2.65	5.32	2.87
Days to maturity	124.22	113.5	140	2.02	4.06	1.63
Plant height (cm)	99.60	85.23	131.32	4.54	9.12	4.56
Number of effective tillers per plant	4.53	3.40	7.70	0.16	0.31	3.45
Flag leaf length (cm)	24.43	18.61	37.15	2.09	4.20	8.56
Flag leaf width (cm)	1.30	0.97	1.67	0.07	0.13	5.02
Panicle length (cm)	21.17	17.63	26.18	1.69	3.40	7.99
Number of grains per panicle	64.08	38.2	91.15	4.39	8.81	6.85
Test weight (g)	27.59	21.4	37.78	1.44	2.88	5.20
Grain length (mm)	9.08	7.70	10.85	0.11	0.22	1.22
Grain breadth (mm)	2.94	2.20	3.35	0.09	0.19	3.13
Grain L/B ratio	3.11	2.60	4.57	0.10	0.20	3.25
Kernel length (mm)	7.18	6.25	8.35	0.16	0.32	2.19
Kernel breadth (mm)	2.45	2.15	2.75	0.10	0.20	4.07
Kernel L/B ratio	2.95	2.48	3.78	0.15	0.31	5.23
Biological yield (q/ha)	67.89	42.07	82.79	4.13	8.29	6.08
Harvest index (%)	42.26	29.08	51.51	2.44	4.89	5.76
Grain yield (q/ha)	28.64	19.19	38.31	2.48	4.97	8.65

Table 3: Phenotypic correlation coefficients of yield and yield attributing characters

Traits	DFF	DM	PH	NET	FLL	FLW	PL	NGPP	TW	GL	GB	GLB	KL	KB	KLB	BY	HI	GY
DFF	1																	
DM	0.872**																	
PH	0.241**	0.257**																
NET	0.064	-0.007	0.143															
PL	0.332**	0.326**	0.373**	0.422**														
FLL	0.006	-0.04	0.133	0.405**	0.554**													
FLW	0.230*	0.197*	0.304**	0.208*	0.522**	0.450**												
NGPP	0.275**	0.16	0.056	0.395**	0.335**	0.314**	0.270**											
TW	0.227*	0.113	0.15	0.386**	0.261**	0.251**	0.147	0.452**										
GL	0.079	0.083	0.248**	0.15	0.072	-0.057	-0.018	0.136	0.264**									
GB	0.025	0.047	0.011	-0.032	-0.123	-0.101	-0.15	0.193*	0.108	-0.132								
GLB	0.024	0.015	0.169	0.12	0.117	0.02	0.081	-0.051	0.099	0.784**	-0.706**							
KL	0.113	0.095	0.294**	0.169	0.118	-0.092	0.06	0.125	0.236*	0.824**	-0.151	0.675**						
KB	-0.025	-0.016	-0.099	-0.034	-0.137	0.09	-0.011	0.066	0.011	-0.386**	0.459**	-0.555**	-0.427**					
KLB	0.079	0.063	0.227*	0.125	0.134	-0.114	0.037	0.035	0.146	0.733**	-0.351**	0.739**	0.874**	-0.803**				
BY	0.195*	0.046	-0.027	0.450**	0.448**	0.477**	0.377**	0.442**	0.310**	0.013	-0.098	0.08	0.04	0.099	-0.031			
HI	0.189*	0.218*	0.157	0.154	0.211*	0.129	0.267**	0.215*	0.210*	0.044	0.049	-0.031	0.004	-0.045	0.019	-0.124		
GY	0.280**	0.173	0.074	0.493**	0.518**	0.500*	0.493*	0.521**	0.415**	0.028	-0.036	0.028	0.021	0.063	-0.029	0.766**	0.539**	1

Table 4: Estimation path coefficient of grain yield with different traits in rice genotypes

Traits	DFF	DM	PH	NET	FLL	FLW	PL	NGPP	TW	GL	GB	GLB	KL	KB	KLB	BY	HI	GY
DFF	-0.0115	0.0047	-0.0014	0.0009	-0.0018	0.0001	0.0022	-0.0006	0.0051	0.0035	-0.0008	-0.0017	0.0105	0.0024	-0.0129	0.1622	0.1191	0.280**
DM	-0.0101	0.0054	-0.0015	-0.0001	-0.0018	-0.0005	0.0019	-0.0003	0.0025	0.0037	-0.0014	-0.0011	0.0088	0.0015	-0.0104	0.0386	0.1373	0.173
PH	-0.0028	0.0014	-0.0059	0.002	-0.002	0.0015	0.003	-0.0001	0.0033	0.0109	-0.0003	-0.0122	0.0273	0.0093	-0.037	-0.0226	0.0988	0.074
NET	-0.0007	0.0000	-0.0009	0.0141	-0.0023	0.0046	0.002	-0.0008	0.0086	0.0066	0.001	-0.0087	0.0157	0.0032	-0.0204	0.3736	0.0972	0.493**
FLL	-0.0038	0.0018	-0.0022	0.0059	-0.0054	0.0063	0.0051	-0.0007	0.0058	0.0032	0.0037	-0.0085	0.0109	0.0129	-0.0219	0.372	0.1329	0.518**
FLW	-0.0001	-0.0002	-0.0008	0.0057	-0.003	0.0113	0.0044	-0.0006	0.0056	-0.0025	0.003	-0.0014	-0.0085	-0.0085	0.0187	0.3956	0.0815	0.500*
PL	-0.0027	0.0011	-0.0018	0.0029	-0.0028	0.0051	0.0097	-0.0006	0.0033	-0.0008	0.0045	-0.0059	0.0055	0.001	-0.006	0.3127	0.1679	0.493*
NGPP	-0.0032	0.0009	-0.0003	0.0056	-0.0018	0.0036	0.0026	-0.002	0.0101	0.006	-0.0058	0.0037	0.0116	-0.0062	-0.0057	0.3666	0.1357	0.521**
TW	-0.0026	0.0006	-0.0009	0.0054	-0.0014	0.0028	0.0014	-0.0009	0.0222	0.0116	-0.0032	-0.0072	0.0219	-0.0011	-0.0237	0.2574	0.1324	0.415**
GL	-0.0009	0.0005	-0.0015	0.0021	-0.0004	-0.0007	-0.0002	-0.0003	0.0059	0.0439	0.004	-0.0566	0.0764	0.0363	-0.1196	0.0111	0.0276	0.028
GB	-0.0003	0.0003	-0.0001	-0.0005	0.0007	-0.0011	-0.0015	-0.0004	0.0024	-0.0058	-0.0301	0.0510	-0.014	-0.0432	0.0573	-0.0813	0.0309	-0.036
GLB	-0.0003	0.0001	-0.001	0.0017	-0.0006	0.0002	0.0008	0.0001	0.0022	0.0344	0.0212	-0.0722	0.0626	0.0521	-0.1205	0.0666	-0.0193	0.028
KL	-0.0013	0.0005	-0.0018	0.0024	-0.0006	-0.001	0.0006	-0.0003	0.0052	0.0361	0.0046	-0.0487	0.0927	0.0402	-0.1426	0.0332	0.0022	0.021
KB	0.0003	-0.0001	0.0006	-0.0005	0.0007	0.001	-0.0001	-0.0001	0.0003	-0.0169	-0.0138	0.0401	-0.0397	-0.094	0.1309	0.0825	-0.0282	0.063
KLB	-0.0009	0.0003	-0.0014	0.0018	-0.0007	-0.0013	0.0004	-0.0001	0.0032	0.0322	0.0106	-0.0533	0.0811	0.0754	-0.1631	-0.0255	0.012	-0.029
BY	-0.0023	0.0003	0.0002	0.0063	-0.0024	0.0054	0.0037	-0.0009	0.0069	0.0006	0.003	-0.0058	0.0037	-0.0093	0.005	0.8299	-0.078	0.766**
HI	-0.0022	0.0012	-0.0009	0.0022	-0.0011	0.0015	0.0026	-0.0004	0.0047	0.0019	-0.0015	0.0022	0.0003	0.0042	-0.0031	-0.1028	0.6299	0.539**

Table 5: Grouping of genotypes into 6 clusters on the basis of D^2 analysis

Clusters	No. of genotypes	Genotypes
I	17	R2744-118-1, R2759-20-1, R 2300-377-2-261-1, R 1670-3269-2-3926, R 2341-281-2-332-1, R 2322-180-1-169-1, IR18A1061, R 2775-C6-2-3, R 2341-337-3-180-1, R 2340-284-1-151-1, R 2774-C 3-1-1, Sahbhagi Dhan-1 (ch), Narendra 97 (ch), Annada (ch), Vandana (ch), R-RHZ-MI-95, Zinco Rice-MS (ch)
II	9	R2739-86-1, R2739-115-1, R2756-27-1, IR18A1073, IR17A3050, R 2485-PHD-SPS-15-1, Samleshwari (ch), JDP-5925, R-RHZ-CC-162
III	5	IR18A1072, IR17A2769, R 2297-4-1-2-1, R 2297-6-1-3-1, IR17A2891
IV	8	R2739-120-1, IR17A3105, IR18A1076, CR-Dhan-310, Protezin (ch), R-RHZ-RKC-211, R-RGY-IS-110, R-RHZ-RKC-212
V	13	R2739-43-1, R2743-78-1, R2744-19-1, R2744-119-1, R 1877-41-1-13-1, R 2307-46-1-24-1, R 2341-339-2-182-1, R 2321-154-1-94-1, JDP 2018, Bastar Dhan (ch), Danteshwari (ch), R-RHZ-CC-164, IR18A1423
VI	5	R2735-56-1,R2748-1-1, IR18A1068, JDP-1212, IR18A1042

Table 6: Estimation of intra (diagonal and bold) and inter cluster distances among 6 clusters

Clusters	I	II	III	IV	V	VI
I	2.777					
II	3.672	2.939				
III	6.264	6.692	3.473			
IV	4.027	3.516	5.833	3.279		
V	2.819	4.264	4.132	3.706	2.863	
VI	7.084	4.421	6.263	5.146	6.099	3.375

Note: Data in the bold digits represent intra-cluster distances.

Table 7: Cluster mean performance of yield and yield attributing characters

Cluster		DFF	DM	PH	NET	FLL	FLW	PL	NGPP	TW	GL	GB	GLB	KL	KB	KLB	BY	HI	GY
I	Mean	89.26	122.15	94.15	4.14	22.21	1.27	20.08	56.76	26.47	8.44	2.98	2.84	6.68	2.49	2.69	63.91	42.04	26.77
	SE ±	4.00	2.90	7.43	0.46	2.49	0.10	1.35	9.23	1.99	0.41	0.16	0.18	0.17	0.11	0.13	7.81	2.92	3.15
II	Mean	91.83	123.28	95.73	4.89	26.90	1.41	22.86	76.53	27.94	8.64	2.98	2.90	6.92	2.52	2.76	75.93	43.93	33.37
	SE ±	4.10	4.51	5.45	0.73	2.11	0.10	1.68	7.37	3.34	0.52	0.17	0.18	0.44	0.12	0.22	2.31	1.85	1.48
III	Mean	91.70	123.80	98.86	4.42	23.63	1.23	20.53	58.48	27.48	10.05	2.63	3.85	8.10	2.19	3.72	65.34	41.17	26.35
	SE ±	4.10	4.09	10.49	0.19	2.48	0.15	1.68	10.28	1.90	0.51	0.25	0.42	0.27	0.04	0.06	10.86	7.58	2.51
IV	Mean	101.75	132.31	107.63	4.27	25.07	1.28	21.93	67.46	27.97	9.16	2.98	3.08	7.19	2.51	2.87	67.83	43.84	29.61
	SE ±	5.32	4.87	15.96	0.59	4.56	0.13	0.92	9.44	2.40	0.59	0.08	0.20	0.31	0.07	0.18	8.63	2.86	3.21
V	Mean	89.69	122.23	101.04	4.34	23.02	1.22	20.33	60.02	27.03	9.52	2.97	3.22	7.45	2.45	3.05	64.3	39.32	25.09
	SE ±	3.89	3.53	8.70	0.39	1.68	0.12	1.51	8.51	1.81	0.36	0.16	0.16	0.27	0.11	0.19	6.27	4.80	2.32
VI	Mean	95.20	125.60	109.18	6.24	30.95	1.53	23.42	77.36	31.73	9.84	2.90	3.40	7.73	2.39	3.24	78.94	46.17	36.40
	SE ±	5.25	4.49	13.37	1.14	5.06	0.12	1.72	10.71	4.48	0.38	0.08	0.16	0.41	0.07	0.21	5.03	1.73	1.52

Note: Data in the bold digits represents the highest mean values recorded for particular traits.

Key words: 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; BY = Biological yield; GL = Grain length; GB = Grain breadth; GLB = Grain L/B ratio; KL = Kernel length; KB = Kernel breadth; KLB = Kernel L/B ratio; HI = Harvest index; GY = Grain yield.

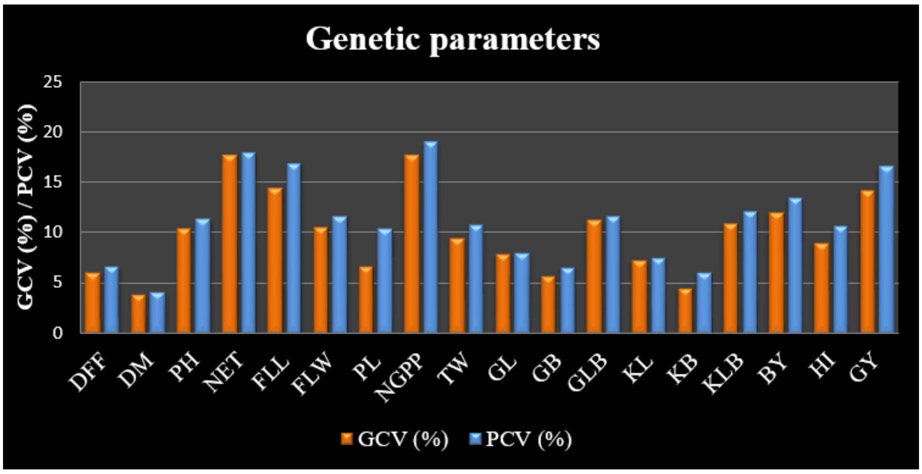

Fig 1: Bar diagram representing phenotypic and genotypic coefficient of variability for yield and yield attributing characters

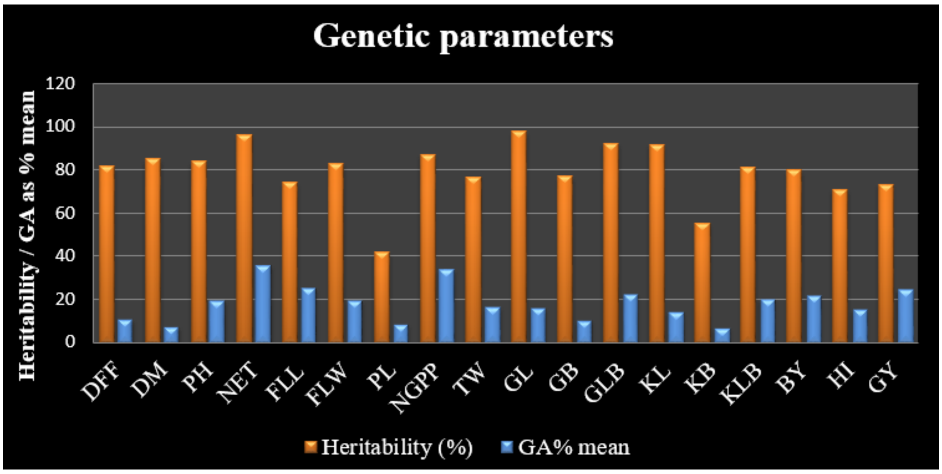

Fig 2: Bar graph representing heritability coupled with genetic advance as percent of mean for yield and yield attributing traits.

Conclusion

Significant variability was observed for all 18 traits, with 13 traits highly significant at 1% and 5 traits at 5% level of significance. High heritability coupled with high genetic advance was noted for number of effective tillers per plant, number of grains per panicle, grain yield, grain L/B ratio, biological yield and kernel L/B ratio, indicating additive gene action. Grain yield showed significant positive correlation with traits like biological yield, harvest index, number of effective tillers per plant and flag leaf length. Path analysis revealed biological yield and harvest index as major direct contributors to grain yield. Genetic divergence grouped genotypes into six clusters, with maximum inter-cluster distance between Clusters I and VI, whereas maximum intra-cluster distance was found in Cluster III. Cluster VI showed superior performance for most of the yield-related traits. Grain L/B ratio contributed most to genetic divergence, followed by kernel L/B ratio and days to maturity. The study suggests the presence of substantial genetic variability, which can be exploited through strategic hybridization to develop high-yielding and diverse rice genotypes suitable for upland conditions.

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