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RESEARCH ARTICLE

Genetic diversity, variability and trait associations in rice (*Oryza sativa* L.) genotypes

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Abstract

This study assessed genetic divergence, variability and trait associations for 12 morphological characters in 30 rice (*Oryza sativa* L.) genotypes. Genetic divergence was estimated using Mahalanobis' D^2 analysis. Genotype TKM 13 exhibited superior performance for traits such as days to 50 % flowering, plant height, number of productive tillers per plant, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant. D^2 analysis revealed no clear relationship between geographic origin and genetic diversity. Traits including 100 grain weight, grain yield per plant and grain length contributed substantially to genetic divergence. High to moderate phenotypic (PVC) and genotypic (GCV) coefficient of variation, along with high heritability coupled with high genetic advance as a percentage of mean, were observed for traits such as grain L/B ratio, 100 grain weight and kernel traits. Most traits were predominantly controlled by additive gene action, indicating that selection would be effective for their improvement.

Keywords: correlation; D^2 analysis; path analysis; rice

Introduction

Profound appreciation is due to the cereal breeders of India, whose tireless efforts have made the nation self-sufficient in cereal grain production, enhancing food security and empowering millions of farmers. Rice, the lifeline of Asia, remains central to India's agriculture and nutrition, cultivated over 47.8 million hectares in 2023-24, producing 137.8 million tonnes with an average productivity of 4.32 t/ha slightly below the global average of 4.7 t/ha. (1–3). In Tamil Nadu, rice covers 18 lakh hectares with a higher productivity of 4.60 t/ha. Despite being a major exporter, India's per capita rice availability (190.5 g/day) remains below the recommended 250–300 g/day as for ICMR-NIN2020, FAO2021. The primarily due to issues of accessibility and distribution rather than production (4). Alarmingly, many still struggle for adequate meals, even with the Public Distribution System in place, underscoring the continued relevance of food equity advocates like N G Ranga. Ensuring 3 adequate meals a day for every citizen remains a pressing goal and it underlines the urgent need to further increase food grain production, particularly in cereals, which form the dietary foundation for most Indians (5, 6).

The success of the Green Revolution during the 1970s and 1980s fueled by the development of semi-dwarf varieties exploiting pleiotropic effects of dwarfing genes ushered in substantial improvements in rice production and productivity. This was achieved through meticulous selection of superior lines via pure-line selection and hybridization. To sustain the gains of the Green Revolution, rice breeders have increasingly turned to hybrid breeding technologies (7). In this context, the choice of parents and selection of traits are the 2 pivotal elements in achieving successful crop improvement through gene manipulation. Multivariate analyses provide vital insights for this process. Mahalanobis' D^2 statistic is particularly valuable as it measures generalized distances among genotypes and helps identify the most divergent parents. Such divergent parents are likely to produce heterotic hybrids and/or transgressive segregants. Moreover, studies on correlation and path coefficient analysis provide crucial information on the relative importance of component traits in achieving high grain yield per plant. Assessing genetic variability among genotypes further supports the selection process by revealing the extent of genetic differences for target traits, guiding effective breeding strategies through both correlation and causation approaches (8).

Materials and Methods

The experimental materials for this genetic divergence study comprised 30 rice genotypes collected from various locations, as detailed in Table 1. Uniform, healthy, selfed seeds of these genotypes were sown on raised nursery beds in December 2022

Table 1. List of genotypes selected for D^2 analysis

Genotype code	Genotype names	Origin
G1	ADT-36	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G2	ADT-37	
G3	ADT-38	
G4	ADT-39	
G5	ADT-40	
G6	ADT-41	
G7	ADT-42	
G8	ADT-43	
G9	ADT-44	
G10	ADT-45	
G11	ADT-46	
G12	ADT-47	
G13	ADT-48	
G14	ADT-50	
G15	ADT-51	
G16	ADT-53	
G17	ASD-16	Rice Research Station, Ambasamuthiram, Tamil Nadu, India
G18	CO-49	Paddy Breeding Station, Coimbatore, Tamil Nadu, India
G19	CO-51	
G20	TKM-13	
G21	CR-1009	Central Rice Research Institute (CRRI), Cuttack, Orissa, India
G22	IR-64	International Rice Research Institute (IRRI), Philippines
G23	Thuyamalli	Collected from local farmers – Origin not traceable
G24	Kalanamak	
G25	Seeraga Samba	
G26	Bhavani	
G27	White Ponni	Paddy Breeding Station, Coimbatore, Tamil Nadu, India
G28	TRY-1	Agricultural College and Research Institute, Trichy, Tamil Nadu, India
G29	TRY-2	
G30	TRY-3	

highly fertile soil at Annamalai University. Twenty five day old seedlings were transplanted into 2 row plots of 3 m length, arranged in 3 replications. A spacing of 20 cm × 15 cm was adopted. The experiment was laid out in a randomized block design (RBD). The crop was observed during the period from January to April 2023. Observations were recorded on 12 morphological traits, namely, days to 50 % flowering, plant height, number of productive tillers per plant, panicle length, hundred grain weight, grain length, grain breadth, grain length/ breadth (L/B) ratio, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant. The data was collected from 5 randomly selected plants per entry per replication. Genetic divergence among the 30 genotypes was estimated using Mahalanobis D^2 statistics (9). Grouping genotypes into clusters was performed using Tocher's method, based on the mean values of the measured traits for each genotype (10). Genotypic and phenotypic coefficients of variation, correlation coefficients and path analysis were calculated using the variance and covariance components following the methods described previously, respectively (11).

Results and Discussion

The analysis of variance revealed significant differences among all the traits, indicating the existence of considerable variability among the genotypes (Table 2). These results align with earlier findings (12–17), where significant variation was reported for multiple traits across diverse rice genotypes. For instance, highly significant ANOVA results were recorded for 11 traits in 45 rice lines (18). It reveals, the genotypes G_{23} (28.20 g), G_2 (28.05 g) and G_1 (27.60 g) recorded the highest grain yield per plant (Table 3 and Fig. 1). Out of 30 genotypes, 9 showed significantly high mean values for this trait. Genotype G_{20} exhibited significant mean values for several key traits, including days to 50 % flowering, plant height, number of productive tillers per plant, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant. Genotype G_{22} showed the lowest mean value for days to 50 % flowering (60 days), indicating its earliness. These genotypes may be utilized in future breeding programs (19–21).

Cluster analysis grouped the 30 genotypes into 4 distinct clusters (Table 4). The clustering pattern revealed no parallelism between genetic and geographical diversity, consistent with previous studies (21, 22). Cluster I was the largest, comprising 25 genotypes, while Clusters II and III included 2 genotypes each and Cluster IV was monogenotypic. Intra-cluster distances ranged from 0.000 (Cluster IV) to 196.440 (Cluster I), whereas the minimum inter-cluster distance was observed between Clusters I and III (155.999), followed by Clusters I and II (196.022). The maximum inter-cluster distances occurred between Clusters II and IV (550.796) and between Clusters I and IV (421.826) (Table 5), indicating broad genetic diversity. Therefore, hybridization between genotypes from divergent clusters (e.g. Clusters II and IV) is recommended to exploit this variability. This agrees with the findings of earlier researchers (23–27). Furthermore, genotypes from the same geographic origin were scattered across different clusters, while those from different regions were grouped together, reinforcing the lack of correlation between geographic origin and genetic diversity (25–30).

Cluster means varied widely for all 12 traits studied (Table 6). Earliness in flowering was observed in Cluster IV, while late flowering occurred in Cluster III. Cluster III recorded the highest plant height, whereas Cluster I recorded the lowest. Cluster I had the highest number of productive tillers per plant, while Cluster IV had the fewest. Cluster IV showed maximum panicle length and Cluster III the minimum. Hundred grain weight was highest in Cluster II and lowest in Cluster IV. Maximum grain length occurred in Cluster II, while minimum was recorded in Cluster IV. Cluster III showed the lowest grain breadth, while Clusters I and II recorded

Table 2. Analysis of variance for 12 morphological characters in 30 rice genotypes

Source	df	MSS											
		DFF	PH	NPT	PL	HGW	GL	GB	GLBR	KL	KB	KLBR	GYD
Replication	2	4.9566	4.0881	0.6333	0.8253	0.0025	0.0021	0.0001	0.0012	0.0032	0.0015	0.0037	0.3945
Genotype	29	744.2835**	359.6180**	14.8180**	5.5672**	0.6854**	0.0488**	0.0054**	2.4449**	0.0307**	0.0022**	0.7643**	18.1605**
Error	58	2.3054	3.9959	0.8729	0.8453	0.0028	0.0025	0.0002	0.0028	0.0065	0.0026	0.0021	0.5620

*Significant at 5 % level ; **Significant at 1 % level.

Table 3. Mean performance of genotypes for various characters in rice

Genotypes	DFF	PH	NPT	PL	HGW	GL	GB	GLBR	KL	KB	KLBR	GYD
G1	67.33**	83.04**	27.27**	20.14	1.96	0.79	0.29	2.76	0.73**	0.26	2.84	27.60**
G2	68.33**	88.54**	27.60**	20.13	2.17**	0.64	0.28	2.29	0.48	0.26	1.84	28.05**
G3	92.00	96.45*	26.33**	22.69	2.13**	0.89**	0.29	3.06	0.78**	0.22	3.48**	22.53
G4	89.33	95.89**	22.33	23.13	1.88	0.79	0.20**	3.90**	0.51	0.20**	2.47	26.33**
G5	104.00	105.82	22.93	24.45*	2.60**	0.80	0.29	2.74	0.60	0.20**	2.98	22.65
G6	67.33**	96.05**	21.80	22.69	2.05**	1.20**	0.21**	5.87**	0.80**	0.20**	3.96**	21.73
G7	67.67**	98.61	23.20	23.11	2.66**	0.89**	0.29	3.10	0.68**	0.26	2.59	24.07
G8	66.33**	87.31**	27.07**	22.12	1.65	0.79	0.22**	3.60**	0.66**	0.25	2.62	23.17
G9	103.00	106.57	22.27	23.60	2.36**	0.71	0.30	2.33	0.52	0.21*	2.51	22.18
G10	68.00**	87.57**	22.53	20.97	1.61	0.79	0.24**	3.38	0.61	0.22	2.79	22.57
G11	92.00	111.82	21.40	23.97	2.50**	1.05**	0.21**	5.08**	0.70**	0.21*	3.43**	23.84
G12	85.00	94.05**	19.53	22.58	1.48	0.70	0.23**	3.13	0.50	0.20**	2.49	21.87
G13	62.00**	84.45**	22.67	21.84	2.29**	1.06**	0.21**	5.08**	0.78**	0.22	3.54**	22.72
G14	102.00	106.63	22.73	22.94	1.59	0.73	0.29	2.49	0.60	0.20**	2.96	25.95**
G15	103.00	104.55	22.40	23.21	2.39**	0.63	0.23**	2.72	0.50	0.21*	2.46	22.89
G16	89.33	90.05**	21.40	22.46	1.47	0.79	0.22**	3.54**	0.62	0.20**	3.01	21.84
G17	70.00**	92.34**	19.87	21.80	2.56**	0.79	0.29	2.70	0.59	0.26	2.29	25.03
G18	93.00	105.65	26.00**	21.51	1.93	0.79	0.21**	3.83**	0.60	0.20**	2.95	22.55
G19	77.33**	100.21	19.93	24.85**	1.61	0.78	0.29	2.74	0.76**	0.27	2.81	26.51**
G20	69.00**	93.84**	24.80**	23.70	1.34	0.80	0.30	2.72	0.71**	0.21*	3.44**	25.63**
G21	105.33	105.38	21.73	22.53	2.57**	0.80	0.31	2.62	0.60	0.20**	2.96	21.99
G22	60.00**	105.55	22.67	24.71**	2.40**	0.80	0.31	2.61	0.61	0.21*	2.96	27.33**
G23	75.33**	105.33	21.40	22.62	1.90	0.81	0.31	2.64	0.61	0.20**	3.09**	28.20**
G24	82.00	103.31	21.27	25.47**	1.91	0.71	0.22**	3.14	0.61	0.21*	2.85	24.26
G25	66.67**	101.32	20.60	23.53	1.70	0.61	0.20**	2.96	0.40	0.15**	2.79	16.43
G26	91.00	105.05	22.33	23.15	2.14**	0.95**	0.20**	4.68**	0.80**	0.18**	4.38**	23.47
G27	91.33	129.34	20.67	21.61	1.66	0.80	0.20**	3.96**	0.61	0.20**	2.97	22.43
G28	92.33	103.17	21.67	22.35	2.58**	0.80	0.30	2.65	0.60	0.20**	2.95	25.73**
G29	70.67**	99.41	20.73	21.43	2.57**	0.91**	0.22**	4.21**	0.71**	0.20**	3.53**	23.05
G30	91.67	130.35	24.07*	25.43**	2.58**	0.90**	0.31	2.96	0.60	0.21*	2.82	22.84
General mean	81.44	100.59	22.71	22.82	2.04	0.82	0.25	3.32	0.63	0.22	2.96	23.85
S.Ed	0.88	1.15	0.54	0.53	0.03	0.03	0.02	0.03	0.06	0.02	0.03	0.43
CD 5 %	2.4546	3.2317	1.5104	1.4864	0.0071	0.0087	0.0051	0.0858	0.0159	0.0062	0.0738	1.2120
CD 1 %	3.2605	4.2926	2.0063	1.9743	0.0095	0.0116	0.0068	0.1139	0.0212	0.0082	0.0981	1.6098

*Significant at 5 % level ; **Significant at 1 % level.

Table 4. Composition of D2 clusters for 30 rice genotypes

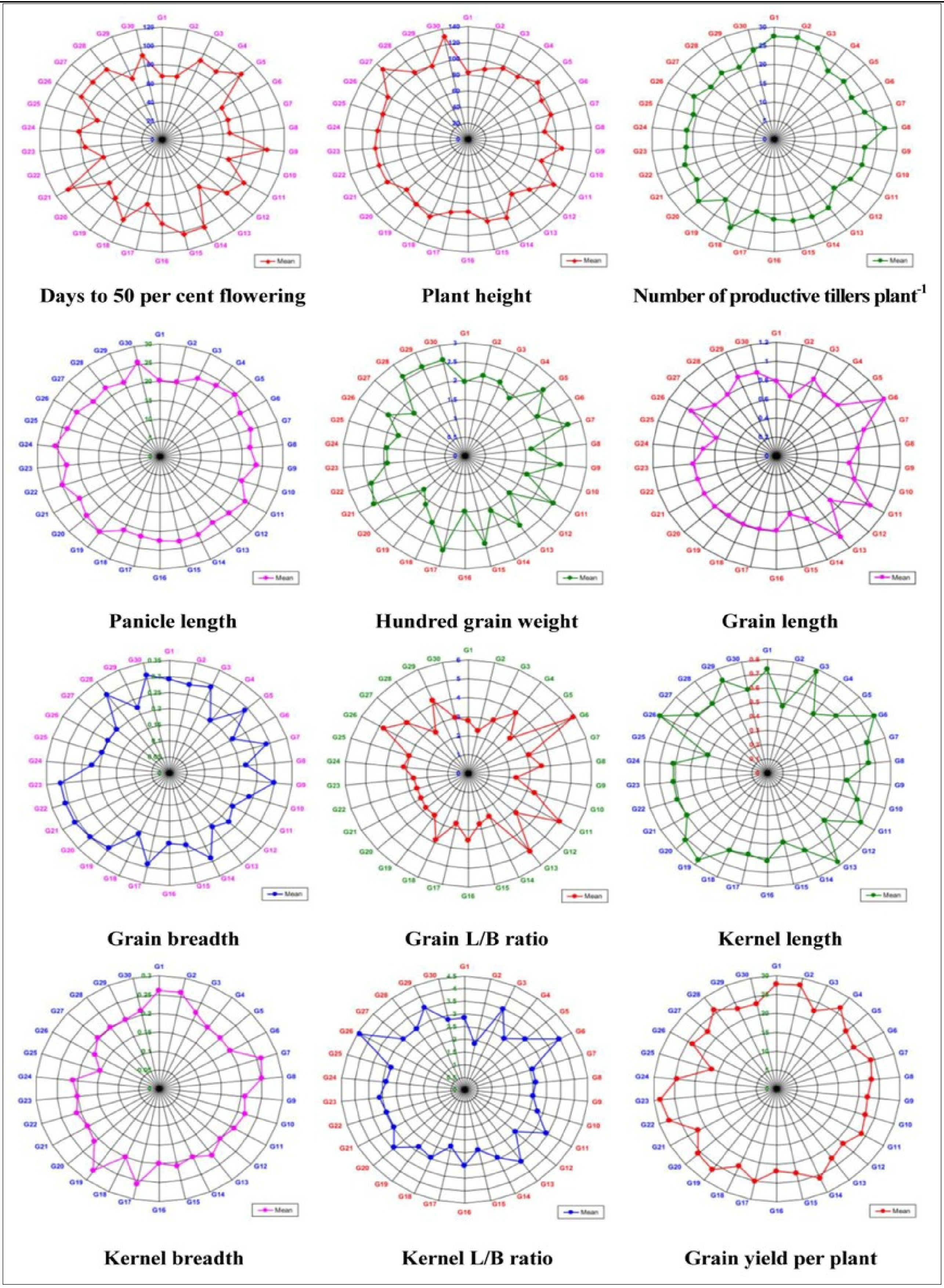
Cluster	Number of genotypes	Name of genotypes
I	25	ADT 36, ADT 37, ADT 38, ADT 39, ADT 40, ADT 41, ADT 42, ADT 43, ADT 44, ADT 45, ADT 46, ADT 47, ADT 48, ADT 50, ADT 51, ADT 53, ASD 16, CO 49, CO 51, TKM 13, CR 1009, IR 64, Thuyamalli, Kalanamak, TRY 1
II	2	TRY 2, TRY 3
III	2	Bhavani, White Ponni
IV	1	Seeraga Samba

Table 5. Average inter (D^2) and intra (D) cluster values for 30 rice genotypes

Cluster	I	II	III	IV
I	38588.531 (196.440)	38424.809 (196.022)	24335.730 (155.999)	177937.516 (421.826)
II		1635.715 (40.444)	44594.438 (211.174)	303376.250 (550.796)
III			20306.828 (142.502)	131922.531 (363.211)
IV				0.000 (0.000)

Table 6. Cluster means of 30 rice genotypes for various characters

Cluster	DFF (Days)	PH (cm)	NPT	PL (cm)	HGW (g)	GL (mm)	GB (mm)	GLBR	KL (mm)	KB (mm)	KLBR	GYD (g)
I	81.28	98.09	22.91	22.78	2.06	0.81	0.26	3.23	0.63	0.23	2.89	24.29
II	81.17	114.88	22.40	23.43	2.57	0.91	0.26	3.59	0.66	0.21	3.17	23.94
III	91.17	117.19	21.50	22.38	1.90	0.88	0.20	4.32	0.71	0.19	3.67	22.95
IV	66.67	101.32	20.60	23.53	1.71	0.61	0.21	2.96	0.41	0.15	2.79	16.43
General mean	81.44	100.59	22.71	22.82	2.04	0.82	0.25	3.32	0.63	0.22	2.96	23.85



Days to 50 per cent flowering

Plant height

Number of productive tillers plant^{-1}

Panicle length

Hundred grain weight

Grain length

Grain breadth

Grain L/B ratio

Kernel length

Kernel breadth

Kernel L/B ratio

Grain yield per plant

Fig. 1. Mean performance of 30 rice genotypes.

the highest. Cluster III had the maximum grain and kernel L/B ratios, while Cluster IV had the minimum. Similarly, maximum kernel length and breadth were recorded in Clusters III and I, respectively, while Cluster IV recorded the minimum for both. Cluster I showed the highest grain yield per plant, whereas Cluster IV had the lowest. Among the clusters, Clusters I and II outperformed the general mean for grain yield per plant. These findings suggest that no single cluster possessed all desirable traits. Notably, the highest and lowest mean values for traits were distributed across distant clusters. Cluster I showed favorable mean values for number of productive tillers per plant, grain breadth, kernel breadth and grain yield per plant. Cluster II, the second-best for yield, showed high mean values for 100 grain weight, grain length, grain breadth and grain yield per plant. These findings further indicate that no cluster contained genotypes with all desirable traits. Therefore, hybridization between genotypes from distinct clusters is necessary to combine multiple favorable traits.

Assessing the relative contribution of individual traits to total genetic diversity using D^2 statistics helps identify which characteristics most strongly differentiate genotypes. Traits that contribute more to genetic divergence are biologically important because they often control key processes such as growth, reproduction, stress tolerance, or resource-use efficiency. Agronomically, these traits matter because they influence crop performance yield potential, adaptability, resilience to biotic and abiotic stresses and overall productivity. By focusing on traits with high diversity contributions, breeders can efficiently select parent lines that maximize heterosis and develop improved varieties with superior performance under diverse cultivation conditions. Hundred grain weight (39.14 %), grain yield per plant (35.18 %) and grain length (6.21 %) contributed most to divergence among genotypes (Table 7 and Fig. 2). Similar results were reported by earlier studies (17, 26, 29–31). Biologically, these traits are important as they directly influence grain productivity and market value. Hundred grain weight reflects seed size and density are linked to assimilate partitioning efficiency and grain filling capacity. Grain yield per plant integrates multiple physiological and morphological processes, serving as a key determinant of overall productivity. Grain length affects both yield components and consumer preference, making it agronomically and economically relevant. It has been noted that traits with high contributions to divergence may not always directly influence complex traits like yield (26, 30, 31). Therefore, while selecting parents for hybridization, yield potential must also be considered (24, 28, 30). Effective parent selection for hybridization requires evaluating both cluster diversity and individual genotype performance for key traits. The study revealed considerable diversity within and between clusters. Based on grain yield and associated traits, hybridization between Clusters I and II is recommended to develop high yielding.

Table 7. Contribution of different characters to genetic divergence

Characters	Contribution of each characters (%)
Days to 50 % flowering (days)	1.38
Plant height (cm)	1.21
Number of productive tillers per plant	0.22
Panicle length (cm)	1.28
Hundred grain weight (g)	39.14
Grain length (mm)	6.21
Grain breadth (mm)	4.59
Grain L/B ratio	0.17
Kernel length (mm)	0.68
Kernel breadth (mm)	5.74
Kernel L/B ratio	4.20
Grain yield per plant (g)	35.18

Significant differences at the genotypic level confirmed the presence of wide genetic variability. High GCV values were recorded for grain L/B ratio and 100 grain weight. Moderate GCV was observed for productive tillers per plant, grain yield per plant, plant height, kernel breadth, grain and kernel lengths, grain breadth, kernel L/B ratio and days to 50 % flowering (Table 8). These findings are consistent with earlier reports (32–36). High estimates of PCV (Phenotypic Coefficient of Variation) and GCV (Genotypic Coefficient of Variation) for grain L/B ratio and 100 grain weight were also reported previously (34–36). Low PCV and GCV were observed for productive tillers per plant and panicle length, confirming earlier results (32, 37–40). Traits with low environmental sensitivity are largely controlled by genetic factors, as seen in this study, corroborating previous findings (38–42). High heritability was recorded for 100 grain weight, grain length, grain L/B ratio, grain breadth, kernel L/B ratio, days to 50 % flowering, kernel length, kernel breadth, plant height, grain yield per plant, number of productive tillers and panicle length. High genetic advance as percent of mean was observed for grain L/B ratio, 100 grain weight, days to 50 % flowering, kernel L/B ratio and grain and kernel dimensions. These traits, mostly governed by additive gene action, can be improved through simple selection as reported earlier (Table 8 and Fig. 3a and 3b) (38–45).

Days to 50 % flowering exhibited high heritability and genetic advance, indicating additive gene effects, consistent with earlier findings (32, 35). Genotypic correlations were generally higher than phenotypic correlations, supporting previous reports (Table 9) (36, 38). The Grain yield correlated positively with grain and kernel breadths, suggesting their utility as selection criteria (46, 47). Days to 50 % flowering showed a non-significant negative correlation with grain yield, aligning with earlier studies

Table 8. Mean, range, PCV, GCV, heritability and genetic advance as per cent of mean for 12 characters in rice

	Mean ± SE	Range	PCV (%)	GCV (%)	h^2 (%)	GA as mean
Days to 50 % flowering (days)	81.44±0.88	60.00-105.33	19.31	19.39	99.08	39.59
Plant height (cm)	100.59±1.15	83.04-130.35	10.82	11.01	96.73	21.93
Number of productive tillers per plant	22.71±0.54	19.53-27.60	9.49	10.35	84.19	17.95
Panicle length (cm)	22.82±0.53	20.13-25.47	5.49	6.81	65.06	9.13
Hundred grain weight (g)	2.04±0.03	1.34-2.66	23.42	23.42	99.99	48.24
Grain length (mm)	0.82±0.03	0.61-1.20	15.61	15.62	99.82	32.12
Grain breadth (mm)	0.25±0.02	0.20-0.31	16.64	16.68	99.44	34.17
Grain L/B ratio	3.32±0.03	2.29-5.87	27.21	27.25	99.66	55.95
Kernel length (mm)	0.63±0.06	0.40-0.80	16.03	16.11	99.06	32.87
Kernel breadth (mm)	0.22±0.02	0.15-0.27	12.46	12.58	98.01	25.41
Kernel L/B ratio	2.96±0.03	1.84-4.38	17.04	17.11	99.19	34.95
Grain yield per plant (g)	23.85±0.43	16.43-28.20	10.16	10.63	91.26	19.99

PCV- Phenotypic Coefficient of Variation; GCV- Genotypic Coefficient of Variation.

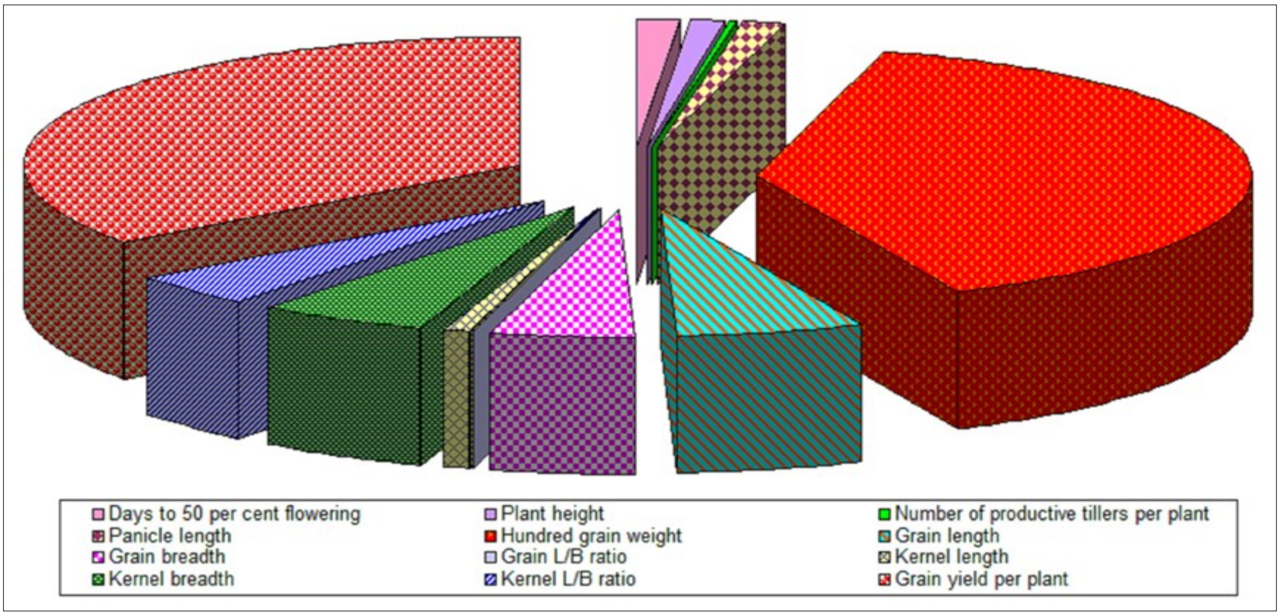


Fig. 2. Character contribution of 30 rice genotypes.

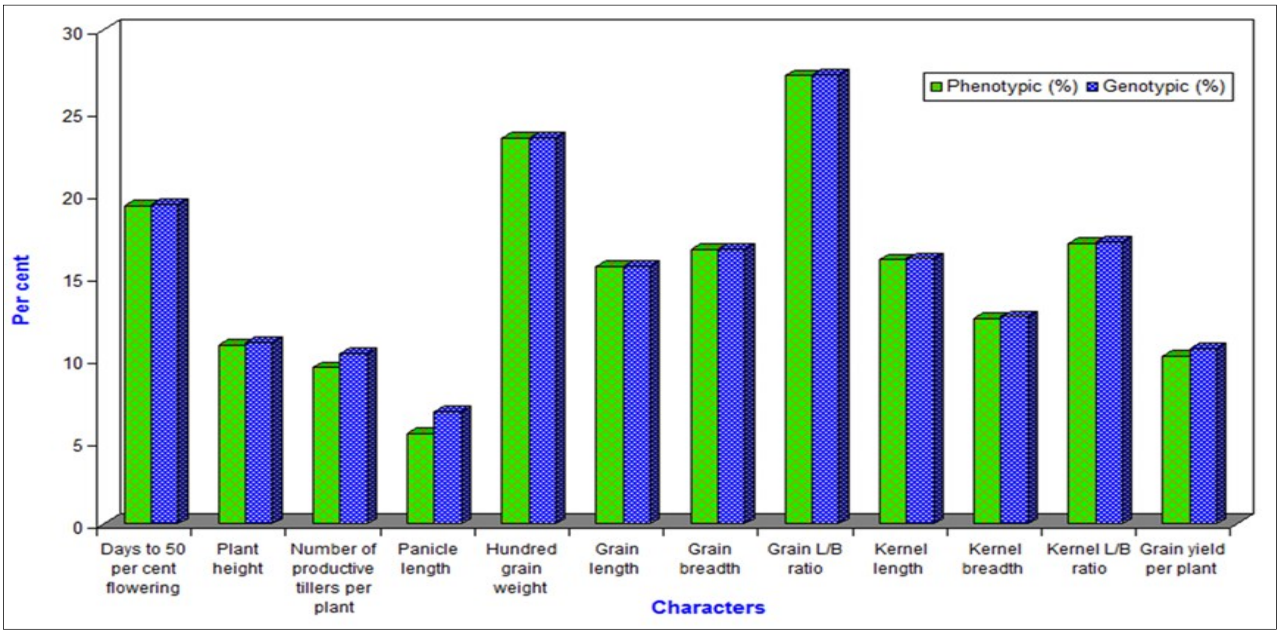


Fig. 3a. Magnitude of variability for various morphological characters in 30 rice genotypes.

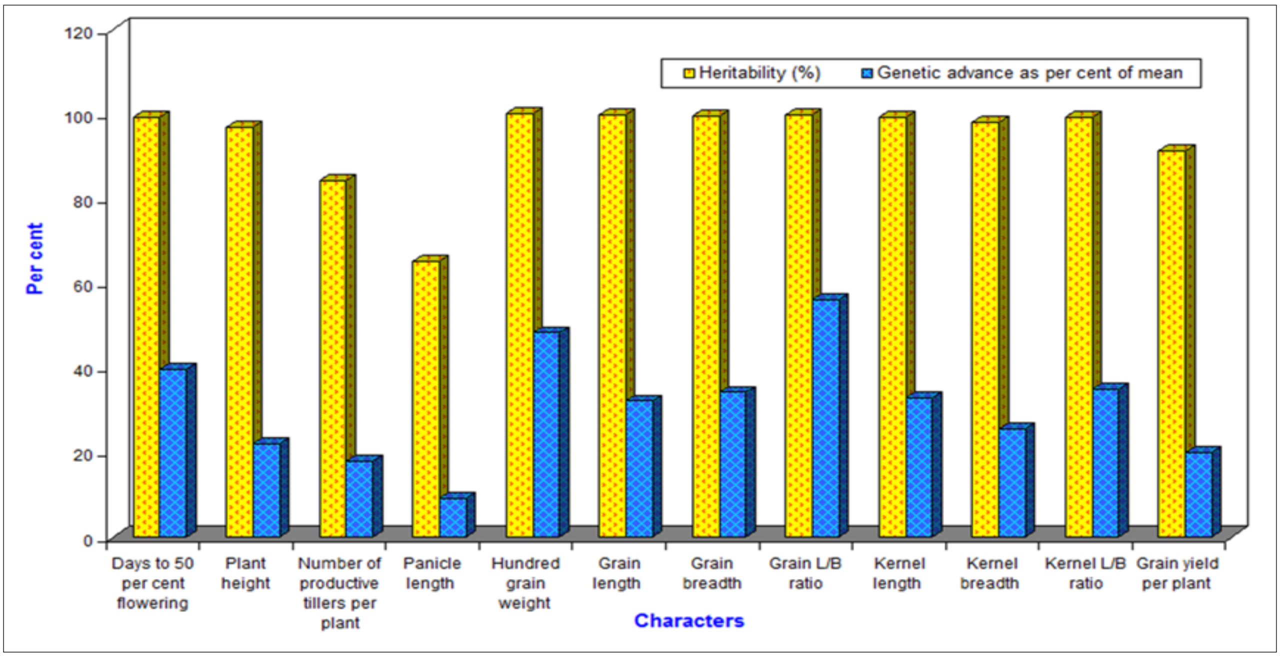


Fig. 3b. Estimated heritability and genetic advance as per cent of mean for various characters in rice.

Table 9. Phenotypic and genotypic correlation among various morphological characters in 30 rice genotypes

Characters		DFF (Days)	PH (cm)	NPT	PL (cm)	HGW (g)	GL (mm)	GB (mm)	GLBR	KL (mm)	KB (mm)	KLBR	GYD (g)
Days to 50 % flowering	P	1.000	0.466**	-0.105	0.156	0.173	-0.160	0.031	-0.121	-0.187	-0.281	-0.003	-0.217
	G	1.000	0.475**	-0.130	0.199	0.174	-0.159	0.032	-0.122	-0.189	-0.284	-0.004	-0.227
Plant height	P		1.000	-0.257	0.412**	0.213	0.026	0.085	-0.031	-0.152	-0.377*	0.104	-0.141
	G		1.000	-0.290	0.558**	0.216	0.027	0.088	-0.030	-0.155	-0.381*	0.105	-0.149
Number of productive tillers per plant	P			1.000	-0.308	0.046	-0.044	0.169	-0.141	0.127	0.340	-0.103	0.253
	G			1.000	-0.360	0.051	-0.046	0.182	-0.150	0.147	0.385*	-0.113	0.272
Panicle length	P				1.000	0.056	0.021	0.149	-0.089	-0.009	-0.203	0.107	-0.076
	G				1.000	0.070	0.027	0.182	-0.111	-0.010	-0.281	0.150	0.114
Hundred grain weight	P					1.000	0.359	0.341	0.031	0.211	0.260	0.034	0.245
	G					1.000	0.359	0.342	0.032	0.211	0.263	0.034	0.256
Grain length	P						1.000	-0.223	0.800**	0.779**	0.023	0.729**	-0.045
	G						1.000	0.224	0.801**	0.783**	0.023	0.732**	-0.047
Grain breadth	P							1.000	-0.758**	-0.045	0.329	-0.281	0.472**
	G							1.000	-0.758**	-0.044	0.330	-0.279	0.492**
Grain L/B ratio	P								1.000	0.533**	-0.200	0.657**	-0.299
	G								1.000	0.536**	-0.202	0.660**	0.314
Kernel length	P									1.000	0.288	0.750**	0.152
	G									1.000	0.287	0.752**	0.166
Kernel breadth	P										1.000	-0.407*	0.505**
	G										1.000	-0.407*	0.532**
Kernel L/B ratio	P											1.000	-0.186
	G											1.000	-0.192
Grain yield per plant	P												1.000
	G												1.000

(48, 49). Genotypic correlation between days to 50 % flowering and plant height and between plant height and panicle length, was significantly positive, consistent with earlier reports (32, 46–50). Productive tillers per plant showed significant positive correlation with kernel breadth. Grain length positively correlated with grain L/B ratio, kernel length and kernel L/B ratio, which also correlated positively among themselves, as noted in other studies (32, 48, 49).

Path coefficient analysis revealed that grain breadth and grain L/B ratio exerted strong direct effects on grain yield per plant, while other traits like days to 50 % flowering, grain length and kernel L/B ratio had negative direct effects (Table 10 and Fig. 4). Similar observations were reported in previous studies (32, 35–36, 52–55). Indirect effects were also notable: the 100 grain weight via grain breadth, grain length via grain L/B ratio and kernel breadth via grain breadth showed strong positive indirect effects. These findings emphasize the importance of specific traits in yield improvement (45–46, 56–61). In conclusion, traits such as grain breadth and grain L/B ratio, showing both significant correlations and high direct effects, should be prioritized in selection strategies to enhance grain yield in rice.

Conclusion

The present study revealed substantial genetic diversity among the evaluated rice genotypes, indicating ample scope for genetic improvement through hybridization and selection. Genotype G20 exhibited superior performance for key agronomic traits such as grain yield per plant, 100 grain weight and grain length, making it a promising parent for future breeding programs. Crosses between genetically divergent clusters, particularly Clusters I and II, are recommended to develop transgressive segregants and exploit heterosis for yield enhancement. Traits such as the grain length-to-breadth ratio, 100 grain weight, kernel characteristics and overall grain yield showed high variability and heritability, suggesting their suitability as selection targets in rice improvement programs. To ensure the stability and adaptability of promising genotypes, multi-environment testing across diverse agro-climatic zones is essential. Furthermore, integrating hybrid development strategies

Table 10. Path co-efficient analysis depicting the direct, indirect effects and genotypic correlations of various morphological characters on grain yield per plant in 30 rice genotypes

Characters	DFF (Days)	PH (cm)	NPT	PL (cm)	HGW (g)	GL (mm)	GB (mm)	GLBR	KL (mm)	KB (mm)	KLBR	GYD (g)
Days to 50 % flowering	-0.189	0.018	-0.011	0.017	0.024	0.623	0.111	-0.656	-0.082	-0.083	0.001	-0.227
Plant height	-0.089	0.038	-0.024	0.049	0.030	-0.106	0.309	-0.164	-0.673	-0.112	-0.012	-0.149
Number of productive tillers per plant	0.024	-0.011	0.083	0.031	0.007	0.179	0.640	-0.809	0.064	0.113	0.013	0.272
Panicle length	-0.038	0.022	-0.029	0.087	0.009	-0.104	0.640	-0.596	-0.004	-0.082	-0.018	-0.114
Hundred grain weight	-0.033	0.008	0.004	0.006	0.139	-1.405	1.201	0.170	0.092	0.077	-0.004	0.256
Grain length	0.030	0.001	-0.004	0.002	0.049	-3.915	0.785	4.313	0.341	0.007	-0.086	-0.047
Grain breadth	-0.006	0.003	0.004	0.016	0.048	0.875	3.514	-4.084	-0.019	0.097	0.033	0.492**
Grain L/B ratio	0.023	-0.001	-0.015	0.009	0.004	-3.134	-2.665	5.386	0.233	-0.059	-0.078	-0.314
Kernel length	0.035	-0.006	0.012	0.001	0.029	-3.066	-0.153	2.884	0.435	0.084	-0.089	0.166
Kernel breadth	0.053	-0.015	0.032	0.024	0.037	-0.091	1.159	-1.085	0.125	0.293	0.048	0.532**
Kernel L/B ratio	0.001	0.004	-0.009	0.013	0.004	-2.867	-0.981	3.552	0.327	-0.119	-0.118	-0.192

Residual effect = 0.6647775

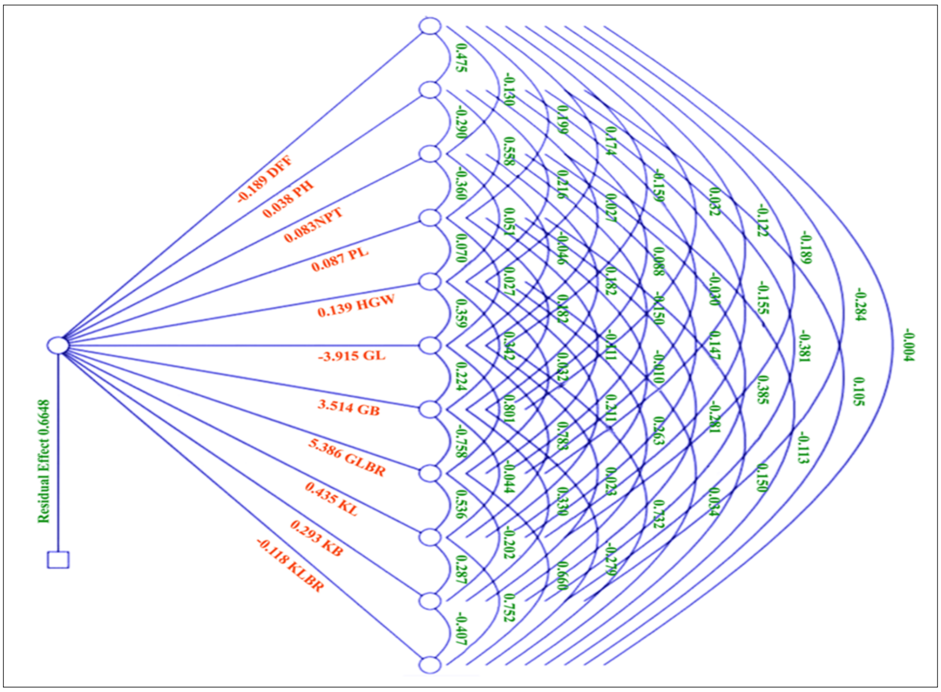


Fig. 4. Diagram of factors influencing yield at the genotypic level.

with molecular tools such as marker-assisted selection, genomic prediction and trait-linked QTL mapping will accelerate the development of high-yielding, climate-resilient and quality rice cultivars.

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Authors' contributions

PS and AH performed the study. PS wrote the manuscript. KS, SS and BR conceived of the study and participated in its design and coordination. All authors read and approved the final manuscript.

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