International Journal of Bioresource Science
Citation: IJBS: **12**(01): 41-47, June 2025
DOI: 10.30954/2347-9655.01.2025.5

ASSOCIATION FOR AGRICULTURE ENVIRONMENT AND BIOTECHNOLOGY

RESEARCH PAPER

Genetic Variability, Correlation and Diversity Analysis for Yield and Grain Quality Traits among the Advanced Breeding Lines of Rice (*Oryza sativa* L.) in Upland Condition

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Received: 22-02-2025 **Revised:** 30-05-2025 **Accepted:** 09-06-2025

ABSTRACT

Genetic variability, correlation and diversity studies were carried out during *kharif* 2022 using sixty advanced breeding lines of rice for yield component traits and grain quality traits under upland condition. Analysis of variance revealed the presence of significant variability among the genotypes for all the traits under study. High values of GCV and PCV observed for number of productive tillers per hill and grain yield indicated the wider range of variability for these traits. High heritability coupled with high genetic advance for plant height, number of tillers per hill, number of productive tillers per hill, panicles per sqm, test weight, grain yield, grain iron content, zinc content and protein content suggested the scope for improvement of these traits through selection. Correlation analysis unveiled positive significant association of grain yield with spikelet fertility percentage and negative significant association with grain zinc content. Genetic diversity analysis using K-means clustering formed six clusters, with highest number of genotypes grouped in cluster I. The maximum inter-cluster distance was seen between cluster IV and cluster VI (7.25) showing broader genetic diversity between the genotypes of these clusters and such genotypes can serve as divergent parents in hybridization programmes to get high heterosis and superior segregants.

HIGHLIGHTS

- Genetic variability and heritability in yield and quality traits of upland rice.
- Trait association of grain yield with spikelet fertility and zinc content.
- Genetic divergence among rice genotypes through K-means clustering.

Keywords: Advanced breeding lines, correlation, K-means, diversity and clusters

Rice, the world's most important cereal crop, is the primary source of food and calories for about half of the mankind. In the current context of climate change, rice cultivation faces problem due to climatic burdens under dwindling and degrading natural resources conditions (Sairam *et al.* 2023; Gaikwad *et al.* 2022; Santosh *et al.* 2024). For the cultivation of rice, average annual rainfall required is around 1500 mm. On an average, to produce 1 kg of rough rice 2500 litre of water is required (Bouman, 2009; Shankar *et al.* 2020; Ram *et al.* 2020). In Asia, 17 million hectares of irrigated rice might experience

How to cite this article: Shashidhara, N., Vilas, G.M., Uday, G., Nethra, P., Sainath, K. and Santosh, D.T. (2025). Genetic Variability, Correlation and Diversity Analysis for Yield and Grain Quality Traits among the Advanced Breeding Lines of Rice (*Oryza sativa* L.) in Upland Condition. *Int. J. Bioresource Sci.*, **12**(01): 41-47.

Source of Support: IUCEA; **Conflict of Interest:** None

"physical water scarcity" by 2025, whereas 22 million hectares could face "economic water scarcity" (Tuong and Bouman, 2003). Therefore, for achieving long term rice production, efficient water utilization is need of the hour. Upland rice is a strategy to reduce water requirements in rice production, which is normally grown in rainfed, naturally well-drained soils in sloppy, undulated or terraced land, without surface water accumulation (Zaman *et al*. 2017; Durgude *et al*. 2022). But the amount of research put into upland rice is very limited. To boost the cultivation of upland rice, it is quintessential to breed for the varieties that could perform on par with lowland rice varieties both in terms of yield and nutritional traits.

Tapping the genetic variability present in the breeding material would provide a great array of genotypes that could be selected to develop new varieties. Estimates of phenotypic and genotypic coefficients of variances provide an account on the variability present in the material. Heritability and genetic advance give an idea about the amount of progress expected under selection. Since, yield is a complex trait it is governed by several other component traits. Correlation analysis helps to deduce the nature and degree of association between yields and yield related traits, which in-turn aid in improving yield by practicing indirect selection of its component traits which are highly correlated. And also the idea of association between yield and quality traits helps in deciding whether or not simultaneous improvement of yield and quality traits could be performed in a single breeding programme. Genetic diversity present in the population plays a vital role in the selection of diverse parents which could be used in hybridization programme to create different combination of superior transgressive segregants. K-means is a centroid-based clustering algorithm. 'K' represents the number of clusters, and it is also an input parameter (Kanavi *et al.* 2020). Genotype selection in large numbers has a high level of difficulty. Cluster analysis can be used to classify genotypes and determine the best cluster (Kozak *et al.* 2008).

MATERIALS AND METHODS

The study was conducted at Agricultural Research Station, Mugad, Dharwad, Karnataka. It encompassed sixty advanced breeding lines of rice with five checks namely, BPT5204, IR64, DRR Dhan 45, Chittimutyalu and Kagisali, which were evaluated under upland condition in an augmented block design with a spacing of 20 cm X 10 cm. Morphological observations were recorded on the yield related traits *viz.*, days to 50 % flowering (DFF), plant height (PH), panicle length (PL), number of tillers per hill (TPH), number of productive tillers per hill (PTH), panicles per sqm (PSM), spikelet fertility percentage (SF), test weight (TW), days to maturity (DTM) and grain yield (GY) and grain quality traits like grain length (GL), grain breadth (GB) and grain L/B ratio (L/B). The other three grain quality traits *viz.*,grain iron content (GFeC), zinc content (GZnC) and protein content (GPC) were measured by the standard protocol given by Yankanchi *et al*. 2022 for iron and zinc content and Arunima *et al*. 2022 for protein content. The mean values of all the traits recorded were used for analysis of variability and genetic diversity using R software and OPSTAT for correlation analysis.

RESULTS AND DISCUSSION

Analysis of variance revealed the existence of significant variation among the genotypes for all the traits included in the study. PCV and GCV values were observed to be high for number of productive tillers per hill and grain yield indicating the presence of wider range of variability for these traits. Similar results were reported by Ajmera *et al.* (2017) and Islam *et al.* (2015) for productive tillers per hill and grain yield respectively. Moderate range of variability was seen for plant height, number of tillers per hill, panicles per sqm, test weight, grain L/B ratio, grain iron content, zinc content and protein content, since these traits had moderate values of GCV and PCV. The estimates of mean, range and genetic variability parameters for yield component traits and grain quality traits are given in Table 1 and Table 2 respectively. PCV values were found to be slightly higher than GCV values for all the traits indicating the least influence of environment on these traits.

Genetic variability is the raw material upon which selection operates. Estimates of heritability in broad sense along with genetic advance as a percent of mean gives an account on the progress expected under selection (Yadav *et al.* 2010). High heritability

Table 1: The estimates of mean, range and genetic variability parameters for yield and its component traits

Characters	Mean	Range		PCV	GCV	Heritability (bs)	Genetic advance over mean
		Min.	Max.				
DFF	90.91	81.65	94.45	3.82	3.49	83.42	6.57
PH	61.98	42.03	93.75	15.82	14.98	89.66	29.25
PL	20.73	15.04	25.36	8.25	6.78	67.48	11.48
TPH	14.68	10.34	22.13	16.37	14.97	83.56	28.23
PTH	12.59	5.20	21.98	29.63	25.32	73.02	44.63
PSM	234.52	153.80	313.80	19.10	17.02	79.39	31.29
SF	87.52	79.98	96.03	4.63	4.21	82.73	7.90
TW	24.07	16.05	33.25	14.94	13.93	86.95	26.81
DTM	134.32	122.25	140.10	2.15	1.70	62.49	2.77
GY	3118.21	1089.47	5486.98	32.10	29.68	85.53	56.63

DFF- *days to 50 % flowering,* **PH**- *plant height (cm),* **PL**- *panicle length (cm),* **TPH**- *number of tillers per hill,* **PTH**- *number of productive tillers per hill,* **PSM**- *panicles per sqm,* **SF**- *spikelet fertility percentage (%),* **TW**- *test weight (g),* **DTM**- *days to maturity and* **GY**- *grain yield (kg/ha).*

PCV- *Phenotypic coefficient of variability and* **GCV**- *Genotypic coefficient of variability*

Table 2: The estimates of mean, range and genetic variability parameters for grain quality traits

Characters	Mean	Range		PCV	GCV	Heritability (bs)	Genetic advance over mean
		Min.	Max.				
GL	8.88	7.05	10.77	7.81	7.62	95.31	15.36
GB	2.52	2.17	3.05	7.50	6.27	69.92	10.82
L/B ratio	3.54	2.65	4.45	10.84	10.09	86.60	19.37
GFeC	13.29	9.33	17.21	15.52	15.31	97.29	31.15
GZnC	15.69	10.72	23.85	17.58	16.89	92.31	33.48
GPC	7.08	5.22	8.40	10.51	10.15	93.26	20.21

GL- *grain length (mm),* **GB**- *grain breadth (mm),* **L/B**- *length to breadth ratio (mm),* **GFeC**- *grain iron concentration (ppm),***GZnC**- *grain zinc concentration (ppm) and* **GPC**- *grain protein concentration (%).*

coupled with high genetic advance was seen for plant height, number of tillers per hill, number of productive tillers per hill, panicles per sqm, test weight, grain yield, grain iron content, zinc content and protein content. Thus, these traits were considered to be under the action of additive genes and selection would be effective in improving these characters. These results corroborate with those reported by Uday *et al*. (2016) for plant height, Srujana *et al*. (2017) for number of tillers per hill, Ajmera *et al.* (2017) for number of productive tillers per hill, Quadri *et al.* (2023) for panicles per sqm, Singh *et al.* (2020) for test weight, Islam *et al.* (2015) for grain yield, Akshay *et al.* (2022) for grain iron content, Babu *et al.* (2012) for zinc content and Shashidhara *et al.* (2013) for protein content.

Correlation analysis revealed positive significant association of grain yield only with spikelet fertility percentage and positive non-significant association with all other yield related traits except plant height. Thus, these positively related traits could be considered for indirect selection for the improvement grain yield. Similar results were reported by Sravan *et al*. (2012) for spikelet fertility, Dhavaleshvar *et al.* (2019) for days to 50 % flowering, days to maturity, panicle length and test weight, Talekar *et al.* (2022) for panicles per sqm, Bhati *et al.* (2015) for number of tillers per hill, Abdul *et al.* (2011) for number of productive tillers per hill and Adhikari *et al.* (2018) for plant height. Also, positive significant association was seen between plant height and panicle length similar to Singh *et al.* (2020) and between tillers per hill and productive tillers per hill similar to Thuy *et al.* (2023). Estimates of phenotypic correlation coefficients are given in Table 3. Grain yield showed negative significant

Table 3: Estimates of phenotypic correlation coefficients for yield traits and grain quality traits

	DFF	PH	PL	TPH	PTH	PSM	SF	TW	DTM	GL	GB	L/B	GFeC	GZnC	GPC	GY
DFF	1															
PH	0.285*	1														
PL	0.399**	0.344**	1													
TPH	0.076	0.236	0.145	1												
PTH	-0.112	-0.003	-0.127	0.336*	1											
PSM	-0.160	-0.091	-0.150	0.161	0.084	1										
SF	0.103	-0.036	0.217	0.014	-0.042	-0.032	1									
TW	0.204	0.013	0.027	0.107	0.087	-0.093	0.092	1								
DTM	0.057	0.017	0.017	0.065	0.037	0.129	-0.012	0.203	1							
GL	0.093	-0.035	-0.092	-0.012	-0.066	-0.147	0.109	0.468**	-0.101	1						
GB	0.067	0.212	0.187	0.024	-0.088	-0.148	-0.123	0.313*	0.067	-0.049	1					
L/B	0.047	-0.132	-0.169	-0.023	-0.007	-0.035	0.165	0.133	-0.132	0.759**	-0.680**	1				
GFeC	-0.191	-0.051	-0.149	-0.226	0.088	-0.142	-0.190	0.153	0.025	0.030	0.138	-0.090	1			
GZnC	0.063	0.069	0.069	-0.084	-0.021	-0.004	-0.075	-0.014	-0.310*	0.004	0.272*	-0.161	-0.028	1		
GPC	-0.077	-0.023	-0.086	0.241	0.133	0.019	-0.193	-0.103	0.042	0.022	-0.171	0.115	-0.030	-0.102	1	
GY	0.008	-0.037	0.177	0.115	0.048	0.113	0.733**	0.224	0.103	0.203	-0.085	0.188	-0.113	-0.280*	-0.127	1

Table 4: Intra cluster (Diagonal) and inter cluster distances for 6 clusters formed by advanced breeding lines of rice for yield, yield related traits and quality traits

Cluster	I	II	III	IV	V	VI
I	4.74	5.96	5.74	5.82	5.36	6.19
II		5.20	6.55	6.65	5.44	6.72
III			5.32	6.76	5.89	6.53
IV				5.14	6.34	7.25
V					4.50	6.37
VI						5.50

Table 5: Cluster mean values for yield and its component traits

Cluster No.	DFF	PH	PL	TPH	PTH	PSM	SF	TW	DTM	GY
I	91.67	62.18	20.24	14.70	12.30	245.91	85.27	22.49	134.72	2432.56
II	92.00	57.57	20.41	13.62	11.12	216.75	90.79	25.88	132.00	3541.62
III	92.25	67.05	20.77	14.65	13.23	241.00	86.32	28.93	136.00	3157.81
IV	82.00	50.48	18.75	13.30	11.54	248.33	86.46	21.65	133.00	2881.08
V	91.33	61.20	21.74	15.65	14.29	230.00	89.78	24.53	136.40	4120.83
VI	92.95	76.04	22.73	15.08	11.36	197.20	89.06	22.13	128.75	2807.97

Table 6: Cluster mean values for grain quality traits

Cluster No.	GL	GB	L/B	GFeC	GZnC	GPC
I	8.70	2.48	3.51	12.97	15.48	7.38
II	9.73	2.39	4.07	13.37	14.60	6.42
III	8.58	2.74	3.13	13.34	16.51	6.24
IV	8.69	2.54	3.42	14.26	16.21	7.31
V	8.96	2.46	3.64	13.46	13.99	7.23
VI	8.79	2.66	3.32	12.85	21.54	7.30

association with a quality trait *i.e.*, grain zinc content similar to the result reported by Namata, 2022. All other quality traits except grain length and grain L/B ratio showed negative non-significant association with grain yield similar to the results reported by Sabesan *et al.* (2009) forgrain breadth, Bhattacharjee *et al.* (2020) for grain iron content and Srihari *et al.* (2023) for grain protein content. Therefore, simultaneous improvement of grain yield and these quality traits cannot be carried out and selection should have to be executed separately.

Genetic diversity is an effective tool which aids in the selection of genetically divergent parents to be used in hybridization programme for obtaining high heterosis and superior segregants. To enumerate and quantify the amount of genetic diversity in the population, D^2 statistics is a potential tool. Genetic diversity analysis was carried out using K-means clustering. Dendrogram depicting the clustering pattern of advanced breeding lines is given in Fig. 1.

Based on the D^2 values genotypes were grouped into six clusters, where highest number of genotypes were found to be present in cluster I (23) followed by cluster V (15), cluster II (8), cluster III (8), cluster IV (6) and cluster VI (5). The intra and inter cluster distances are presented in Table 4. The maximum inter-cluster distance was recorded between cluster IV and VI (7.25) followed by cluster III and IV (6.76). Thus, genotypes belonging to these clusters are genetically divergent and hold a promise to serve as parents in hybridization to get higher amount of heterosis and superior segregants. The maximum intra-cluster distance was seen in cluster VI (5.50) followed by cluster III (5.32). Hence, selection within these clusters may be exercised based on the highest areas for the desirable traits, which would be made use of in improvement through inter-varietal hybridization (Joshi *et al.* 2008).

Cluster mean analysis results for yield component traits and quality traits are given in Table 5 and Table 6 respectively. None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. Maximum and minimum cluster means were distributed in relatively distant clusters indicating the presence of wide range of variation for all the traits under study. Cluster IV and cluster VI had lowest mean values for days to 50 % flowering and days to maturity respectively. Thus, genotypes from these clusters can be used to breed for early flowering and early maturing types respectively. Lowest mean value for plant height was found in cluster IV, which indicates that genotypes of these cluster can be made use of in breeding for semi dwarf plant type. The outcomes

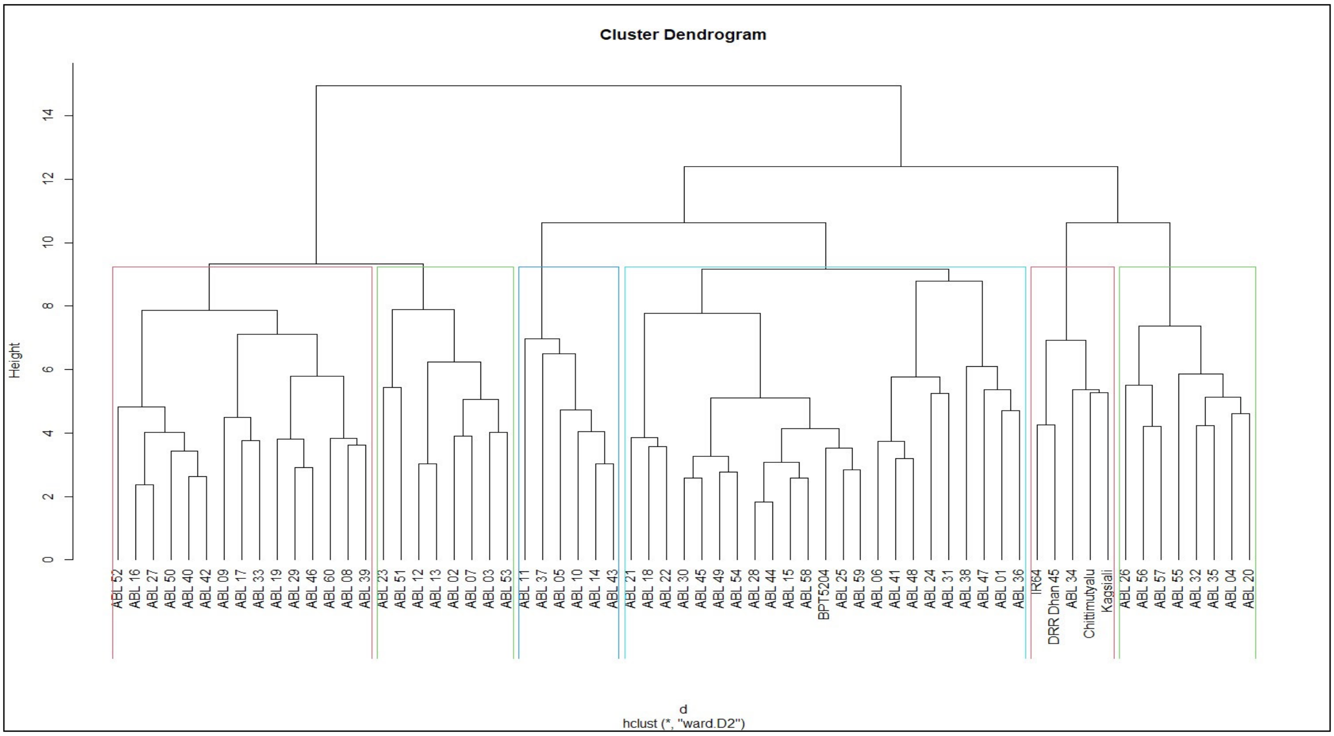

Fig. 1: Clustering pattern of advanced breeding lines of rice

of diversity analysis were in close agreement with those quoted by Chandramohan *et al.* (2016) and Ranjith *et al.* (2018).

This study concluded that significant variation was present for all the traits under study among the advanced breeding lines of rice. Most of the traits showed high heritability twinned with high genetic advance as a percent of mean, which indicated the fixation of genes and presence of additive gene action in these traits. Thus, selection for these characters would be fruitful. Yield showed negative significant association with grain zinc content and negative non-significant association with grain iron and protein content. This indicated that yield and quality improvement cannot be done simultaneously and selection must be executed separately. Diversity study showed highest inter-cluster distance between cluster IV and VI, crossing between the genotypes of these clusters would result in high heterosis and superior segregants.

ACKNOWLEDGEMENTS

Agricultural Research Station, Mugad, Dharwad, India for providing place to carry out the experiment.

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