Exploring genetic variability and diversity in advanced breeding lines of rice for yield-attributing and grain quality traits

ABSTRACT

Genetic variability and diversity are crucial for enhancing yield and grain quality in rice (*Oryza sativa* L.). A field experiment was conducted during *Kharif*, 2023 at the Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.). Thirty-three advanced breeding lines were evaluated for 30 yield-attributing and grain quality traits using a Randomized Block Design (RBD) with two replications. Analysis of variance revealed highly significant differences among the lines, indicating substantial genetic variability. Genetic parameter evaluation showed higher PCV values than GCV, indicating the influence of environmental factors on the trait expression. Gel consistency, alkali spreading value and amylose percentage exhibited high GCV and PCV values, indicating a strong genetic influence and potential for selection. Traits with high heritability and high genetic advance as % of the mean included number of effective tillers per plant, panicle length (cm), breadth of flag leaf (cm), 100 seed weight (g), biological yield per plant (g), grain yield per plant (g), gel consistency, alkali spreading value, amylose percentage and head rice recovery (%), indicating the predominance of additive gene action. Genetic diversity analysis through agglomerative hierarchical clustering based on Euclidean Distance grouped the lines into five distinct clusters. Cluster II was the largest, followed by Cluster I, while Clusters III, IV, and V contained 2, 5, and 1 line(s), respectively. Intra-cluster distances ranged from 0.00 (Cluster V) to 18.381 (Cluster IV), while the maximum inter-cluster distance was between Clusters I and V. Cluster III had the highest mean values for several traits, including grain yield per plant, making these lines promising candidates for hybrid breeding programs to improve yield and grain quality.

Key words: Rice, RBD, Advanced breeding lines, Variance, GCV, PCV, heritability, Genetic advance as % of mean, Genetic diversity, Agglomerative hierarchical clustering, Euclidean Distance, Intra-cluster, Inter-cluster.

Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops globally, serving as a staple food for over 3.5 billion people. It plays a crucial role in ensuring food security, particularly in Asia, which accounts for approximately 90% of the world's total rice production. More than 75% of the global rice supply is consumed in Asian countries, highlighting its critical importance to the region's food security. Rice (*Oryza sativa* L.) is the primary staple food for one third of the world population and is often referred to as “Global Grain” (Ajmera *et al*., 2017). It thrives in hot and humid climates with high humidity, prolonged sunshine, and an adequate water supply. Nutritionally, rice is a significant source of carbohydrates and proteins along with some essential micronutrients such as manganese, niacin, thiamine, selenium, magnesium and trace amounts of pantothenic acid, phosphorous, riboflavin, vitamin B-6, copper and folate.

USDA’s Global rice production during 2023-24 is projected at a record 513.5 million tonnes (milled basis), in which India stands at second position with 132 million tonnes (Anonymous, 2024). The Chhattisgarh state, known as the "Rice Bowl of India," as it plays a major role in contributing to the country’s total rice production and houses a rich diversity of rice germplasm. By 2050, it is predicted that 160 million tons of rice needed to feed ever increasing Indian population (Muthu *et al*., 2020). Consequently, improving rice yield and quality remains a primary focus of national and international breeding programmes.

Grain yield improvement is the prime objective of plant breeders for several decades but demand for good quality of rice is also increased in current decade as living standard of people are being gradually improved (Rathi *et al*., 2010). Variability in yield and quality traits can arise due to differences in the genetic constitution of plant populations or environmental factors. Identifying and exploiting genetic variability is critical to selecting superior genotypes. The success of any breeding programme mainly depends on the quantum of genetic variability available for exploitation and the extent to which the desirable characters are heritable (Tiwari *et al*., 2011).

The variability in the breeding material is extremely important in the selection of superior plant type, where selection is based not only on yield but also on its component traits. Genetic parameters such as Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) are useful in determining the amount of variability exists in the genotypes (Idris *et al*., 2012). For efficient selection it becomes essential to know about heritable portion of total variability in the germplasm for different traits. Heritability is the heritable portion of phenotypic variance. It serves as a key indicator of the transmission of traits from parents to their offspring and plays a crucial role in the selection process in plant breeding. Heritability estimates provide the information on the proportion of variation that is transmissible to the progenies in subsequent generations (Kumar *et al*., 2014).

Genetic advance refers to the improvement in the mean genotypic value of selected plants compared to the parental population. Heritability enables us to predict the degree of correspondence between phenotypic value of the genotype and its breeding value. High heritability with high genetic advance indicates that heritability is most likely due to additive gene effects and selection for such character will be effective. A critical analysis of genetic variability parameters, heritability, and genetic advance for various economically important traits is a crucial prerequisite for any crop improvement effort.

Genetic diversity plays an important role in plant breeding since progeny originating from diverse parents exhibit greater heterosis and provide broad spectrum of variability in segregating generations. Studies on genetic diversity help assess species diversity, genetic composition, and variability among genotypes, which are essential for identifying and conserving promising parental lines. Thus, understanding genetic diversity is crucial for achieving systematic agricultural growth and enhancing the productivity and quality of rice. Therefore, this study aimed to evaluate 33 advanced breeding lines for yield and quality traits, providing insights into genetic variability, estimating key genetic parameters, and assessing genetic diversity to aid in the selection of superior genotypes for rice improvement.

Materials and Methods

The research experiment was conducted during the *kharif* season of 2023 at the Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.). The experiment was laid out in Randomized Block Design using 33 genotypes or treatments in two replications for studying 11 yield-attributing traits and 19 grain quality traits. The statistical analysis was performed using Agri Analyze software for analysis of variance, genetic parameters and XLSTAT software for genetic diversity.

Analysis of Variance (ANOVA)

The analysis of variance (ANOVA) was done on the basis of model described by Cochran and Cox (1950) for randomized complete block design.

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where, Y_{ij} = phenotypic observation of $i\ th$ genotype and $j\ th$ replication

μ = general mean

g_i = effect of i^{th} genotype

r_j = effect of j^{th} replication

e_{ij} = random error associated with i^{th} genotype and j^{th} replication.

The level of significance was tested at 5% and 1% levels of probability against error degree of freedom using F table values given by Fisher and Yates (1963).

Assessment of variability

Range: It is the difference between the largest and the smallest values in the data.

$$Range = Largest\ value - Smallest\ value$$

Mean ($\bar{X}$): Mean is simply the average of a given data. It is defined as the ratio of sum of total observations to the total number of observations.

$$\bar{X} = \frac{\Sigma X}{N}$$

Where, $\bar{X}$= Mean

ΣX = sum of individual observations

N = Total number of observations.

Genotypic and Phenotypic Coefficient of variation (GCV% and PCV%):

$$GCV = \frac{Genotypic\ Standard\ Deviation}{General\ Mean} \times 100 = \frac{\sigma g}{\bar{x}} \times 100$$

$$PCV = \frac{Phenotypic\ Standard\ Deviation}{General\ Mean} \times 100 = \frac{\sigma p}{\bar{x}} \times 100$$

The estimates of phenotypic and genotypic coefficient of variation were classified as low, medium and high (Sivasubramanian and Madhavamenon, 1973).

Less than 10% = Low

10-20% = Moderate

Greater than 20% = High

Heritability in broadsense (h^2_{bs}): It is the proportion of phenotypic variability that is due to genetic reasons or in other words ratio of genotypic variance to the total observed variance.

$$\mathrm{h}^2_{\mathrm{bs}}(\%) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where, $\mathrm{h}^2_{\mathrm{bs}}$= heritability in broad sense

σ_g^2 = genotypic variance

σ_p^2 = phenotypic variance = (σ_g^2) + (σ_e^2)

σ_e^2 = environmental variance

The heritability in broad sense can be categorized as (Johnson *et al.*, 1955)

Low = 0 to 30%,

Intermediate = 30 to 60% and

High = above 60%

Genetic Advance as percent of Mean (GAM): Genetic advance as % of mean was calculated using the formula given by Robinson and Comstock, 1949.

$$\text{GAM} = \frac{GA}{\bar{x}} \times 100$$

Where, GAM = Genetic advance as % of mean,

GA = Genetic advance under selection and

$\bar{x}$ = Grand Mean of the trait.

Genetic advance as % mean was categorized as (Johnson *et al.*, 1955)

Low - (0-10%),

Moderate - (10-20%) and

High - (≥20%)

Genetic Diversity

Genetic diversity analysis was done by agglomerative hierarchical clustering, based on the similarity or dissimilarity between objects, often calculated from quantitative traits using a Euclidean distance matrix, which was calculated by the formula,

$$ED_{jk} = \sqrt{\sum_{i=1}^{n} \left(X_{ij} - X_{ik}\right)^2}$$

where, ED_{jk} = distance between genotypes j and k,

X_{ij} and X_{ik} = phenotype traits values of the i$^{\text{th}}$ character for genotypes *j* and *k*, respectively,

n = number of phenotype traits used to calculate the distance.

The distance matrix from phenotype traits was used to construct Dendrogram based on the Unweighted Pair-group Method with Arithmetic Means (UPGMA). The results of cluster analysis were presented in the form of Dendrogram.

Intra-cluster distance was measured by taking the average distance between all the points in the cluster. Inter-cluster distances were measured by considering the average distance between all points in two different clusters. In addition, mean ED was calculated for each genotype by averaging of a particular genotype to the other genotypes.

Results and Discussions

Analysis of Variance

For all the yield and quality traits studied, the analysis of variance revealed highly significant differences among all the 33 advanced breeding lines considered under the investigation, indicating substantial genetic variation within the material. The results of analysis of variance for yield and quality traits are provided in Table 1. The F-test for all yield and quality traits showed that the mean sum of squares was highly significant at the 1% level of significance. Significant genetic variability for various yield and quality related traits in rice was also documented by Dhanwani *et al*. (2013), Ketan and Sarkar (2014), Abebe *et al*. (2017), Gupta *et al*. (2021) and Parihar *et al* (2023).

Table 1: Analysis of variance for yield attributing and grain quality traits in advanced breeding lines of rice

S. No	**Sources of variance**	**Mean sum of squares**		
		Replication (df=1)	**Genotypes (df=32)**	**Error (df=32)**
1.	Days to 50% flowering	0.5455	25.0568**	2.4830
2.	Plant height (cm)	68.0558	132.3867**	17.7355
3.	Number of effective tillers per plant	0.0183	3.6670**	0.5561
4.	Panicle length (cm)	2.0599	3.7437**	0.5456
5.	Length of flag leaf (cm)	12.4976	12.8907**	3.8351
6.	Breadth of flag leaf (cm)	0.0070	0.0506**	0.0018
7.	Spikelet fertility percent	9.5076	132.0401**	9.0414
8.	100 seed weight (g)	0.0932	0.4858**	0.0350
9.	Biological yield per plant (g)	16.0728	88.9665**	10.8658
10.	Harvest Index (%)	2.1456	26.5379**	8.8395
11.	Grain yield per plant (g)	5.2137	24.0553**	2.3682
12.	Hulling percentage	0.2293	3.6906**	0.6402
13.	Milling percentage	9.8909	6.7981**	2.4311
14.	Paddy length (mm)	0.0024	1.1671**	0.0112
15.	Paddy breadth (mm)	0.0014	0.0904**	0.0057
16.	Paddy L/B ratio	0.0024	0.2091**	0.0093
17.	Brown rice length (mm)	0.0006	0.6878**	0.0119

18.	Brown rice breadth (mm)	0.0074	0.0351**	0.0049
19.	Brown rice L/B ratio	0.0070	0.1386**	0.0105
20.	Kernel length (mm)	0.0606	0.5419**	0.0162
21.	Kernel breadth(mm)	0.0055	0.0408**	0.0017
22.	Kernel L/B ratio	0.00002	0.1246**	0.0037
23.	Kernel length after cooking (mm)	0.0218	1.8609**	0.0071
24.	Kernel breadth after cooking (mm)	0.0014	0.0720**	0.0045
25.	Cooked rice L/B ratio	0.00001	0.1809**	0.0056
26.	Elongation ratio	0.0014	0.0533**	0.0012
27.	Gel consistency	0.9697	1307.599**	0.2666
28.	Alkali spreading value	0.0152	1.4669**	0.1089
29.	Amylose percentage	0.3068	165.9233**	0.0743
30.	Head rice recovery (%)	19.0517	119.1791**	9.8395

**Significance at 1% level of probability

Assessment of Genetic variability

Various genetic parameters such as range, mean, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance as % of mean for various yield attributing and quality traits were presented in Table 2. Phenotypic Coefficient of Variation (PCV) was consistently higher than the Genotypic Coefficient of Variation (GCV) for all traits, indicating that environmental conditions are masking the full expression of genetic variability. These results are in agreement with the findings of Subbaiah *et al.* (2011), Patel *et al.* (2014) and Allam *et al.* (2015).

Higher values of GCV and PCV were observed for the gel consistency, alkali spreading value, amylose percentage. Comparable results were obtained by Veerabadhiran *et al.* (2009) for gel consistency, Umarani *et al.* (2017) for amylose percentage and Kurumanchali *et al.* (2019) for alkali spreading value. Traits showing moderate GCV and PCV values were the number of effective tillers per plant, breadth of flag leaf (cm), 100 seed weight (g), biological yield per plant (g), grain yield per plant (g), elongation ratio and head rice recovery (%). These results align with those documented by Raju *et al.* (2004) for number of effective tillers, Umadevi *et al.* (2009) for grain yield, breadth of flag leaf, Nirmaladevi *et al.* (2015) for elongation ratio, Rukmini *et al.* (2016) for head rice recovery (%), Gupta *et al.* (2022) for 100 seed weight and Yadav *et al*. (2022) for biological yield. Traits exhibiting low PCV and GCV values included days to 50% flowering, plant height (cm), panicle length (cm), length of flag leaf (cm), spikelet fertility percent, harvest index (%), hulling percentage, milling percentage, paddy length (mm), paddy breadth (mm), paddy L/B ratio, brown rice length (mm), brown rice breadth (mm), brown rice L/B ratio, kernel length (mm), kernel breadth(mm), kernel L/B ratio, kernel length after cooking (mm), kernel breadth after cooking (mm), cooked rice L/B ratio. Similar observations were reported by Singh *et al*. (2005) for kernel length, kernel breadth, kernel L/B ratio, Mamatha *et al*. (2007) for days to 50% flowering, Veerabadhiran *et al*. (2009) for kernel length after cooking, Dhanwani *et al*. (2013) for paddy length, paddy breadth, brown rice breadth, Ekka *et al*. (2015) for brown rice breadth, Nirmala *et al*. (2015) for hulling percentage, Rukmini *et al*. (2016) for panicle length and milling percentage, Rajendra *et al*. (2017) for days to 50% flowering and panicle length, Umarani *et al*. (2017) for spikelet fertility percent, Kumar *et al*. (2018) for plant height, Singh *et al*. (2020) for length of flag leaf and Yadav *et al*. (2022) for harvest index.

Traits showing high heritability values included days to 50% flowering, plant height, number of effective tillers per plant, panicle length, breadth of flag leaf, spikelet fertility percent, 100 seed weight, biological yield per plant, grain yield per plant, hulling percentage, paddy length, paddy breadth, paddy L/B ratio, brown rice length, brown rice breadth, brown rice L/B ratio, kernel length, kernel breadth, kernel L/B ratio, kernel length after cooking, kernel breadth after cooking, cooked rice L/B ratio, elongation ratio, gel consistency, alkali spreading value, amylose percentage and head rice recovery. Comparable findings were highlighted in the work of Sankar *et al*. (2006) for days to 50% flowering, plant height, panicle length, Veerabadhiran *et al*. (2009) for hulling, kernel breadth after cooking, cooked rice L/B ratio, gel consistency, Umadevi *et al*. (2009) for breadth of flag leaf, Dhanwni *et al*. (2013) for paddy length, paddy breadth, paddy L/B ratio, brown rice breadth, Ketan and Sarkar (2014) for spikelet fertility percent, Allam *et al*. (2015) for test weight, brown rice length, brown rice L/B ratio, kernel length, kernel breadth, kernel L/B ratio, kernel length after cooking, elongation ratio, alkali spread value and amylose content, Limbani *et al*. (2017) for head rice recovery, grain yield, amylose percentage, Yadav *et al*. (2017) for biological yield per plant and Sandeep *et al*. (2018) for panicle length, number of effective tillers. Moderate heritability was observed for characters such as length of flag leaf, harvest index and milling percentage. These outcomes correspond to those identified by Kumar and Ramesh (2008) for harvest index, Mahesh *et al*. (2022) for milling percentage.

High levels of genetic advance as percentage of the mean were noted for the number of effective tillers per plant, breadth of flag leaf, 100 seed weight, biological yield per plant, grain yield per plant, gel consistency, alkali spreading value, amylose percentage and head rice recovery. These observations are in agreement with the findings of Karthikeyan *et al*. (2009) for total biological yield per plant, Umadevi *et al*. (2009) for breadth of flag leaf, 100 seed weight, Allam *et al*. (2015) for alkali spreading value, grain yield per plant, Nirmaladevi *et al*. (2015) for head rice recovery, gel consistency, amylose percentage and Sandeep *et al*. (2018) for number of effective tillers grain yield per plant. Moderate genetic advances as % of the mean were found in traits such as plant height, length of flag leaf, spikelet fertility percent, paddy length, paddy breadth, paddy L/B ratio, brown rice length, brown rice L/B ratio, kernel length, kernel breadth, kernel L/B ratio, kernel length after cooking, kernel breadth after cooking, cooked rice L/B ratio and elongation ratio. Comparable findings were highlighted in the work of Dhanwni *et al*. (2013) for paddy length, paddy breadth, Allam *et al*. (2015) for kernel breadth, Ekka *et al*. (2015) for brown rice length, kernel length, Nirmaladevi *et al*. (2015) for kernel length after cooking, elongation ratio, Kumar and Deo (2016) for spikelet fertility percent and Rahangdale *et al*. (2019) for length of flag leaf. Traits with low genetic advance as percentage of the mean included days to 50% flowering, panicle length, harvest index, hulling percentage, milling percentage and brown rice breadth. Similar pattern of results was obtained by Ketan and Sarkar (2014) for days to 50% flowering, panicle length, Allam *et al*. (2015) for brown rice breadth and Ashok *et al*. (2016) for milling.

The traits that exhibited both high heritability and high genetic advance as % of mean were number of effective tillers per plant, panicle length (cm), breadth of flag leaf (cm), 100 seed weight (g), biological yield per plant (g), grain yield per plant (g), gel consistency, alkali spreading value, amylose percentage and head rice recovery (%). These traits were influenced by additive genetic effects, making them suitable for selection and improvement. These findings were consistent with the results reported by Singh *et al*. (2005) for number of effective tillers per plant, Veerabadhiran *et al*. (2009) for gel consistency, amylose percentage, Devi *et al*. (2019) for breadth of flag leaf, Dhurai *et al*. (2014) for 100 seed weight, number of effective tillers, grain yield per plant, Allam *et al*. (2015) for alkali spread value, panicle length, Sandeep *et al*. (2018) for panicle length and Yadav *et al*. (2022) for biological yield.

The traits that exhibited high heritability and moderate genetic advance as % of mean were plant height (cm), spikelet fertility percent, paddy length (mm), paddy breadth (mm), paddy L/B ratio, brown rice length (mm), brown rice L/B ratio, kernel length (mm), kernel breadth (mm), kernel L/B ratio, kernel length after cooking (mm), kernel breadth after cooking (mm), cooked rice L/B ratio and elongation ratio. These traits were influenced by both additive and non-additive genetic effects, hence simple selection may be effective. These results were in consonance with the findings of Dhanwni *et al*. (2013) for paddy length, paddy breadth, Allam *et al*. (2015) for kernel breadth, Ekka *et al*. (2015) for brown rice length, Nirmaladevi *et al*. (2015) for elongation ratio, Rukmini *et al*. (2016) for kernel length, kernel breadth, kernel length after cooking, Limbani *et al*. (2017) plant height, Kumar *et al*. (2020) for spikelet fertility

The traits that exhibited high heritability and low genetic advance as % of mean were days to 50% flowering, panicle length (cm), hulling percentage and brown rice breadth (mm). Low genetic advance as % of mean implies non-additive gene action and high heritability of such traits is due to favourable influence of the environment rather than genotype and selection in such cases is ineffective but heterosis breeding may be useful for improvement of such traits. Similar observations were reported in their studies by Veerabadhiran *et al*. (2009) for hulling percentage, Ketan and Sarkar (2014) for panicle length and Rajendra *et al*. (2017) for days to 50% flowering.

The trait that exhibited moderate heritability and moderate genetic advance as % of mean was length of flag leaf (cm). Similar result was obtained by Rahangdale *et al*. (2019) for length of flag leaf.

The traits that exhibited moderate heritability and low genetic advance as % of mean were harvest index (%) and milling percentage. The parallel trend was observed in the research conducted by Yadav *et al*. (2017) for harvest index and Mahesh *et al*. (2022) for milling percentage.

Figure 1: Diagrammatic representation of genetic parameters (GCV, PCV, heritability and genetic advance as % of mean)

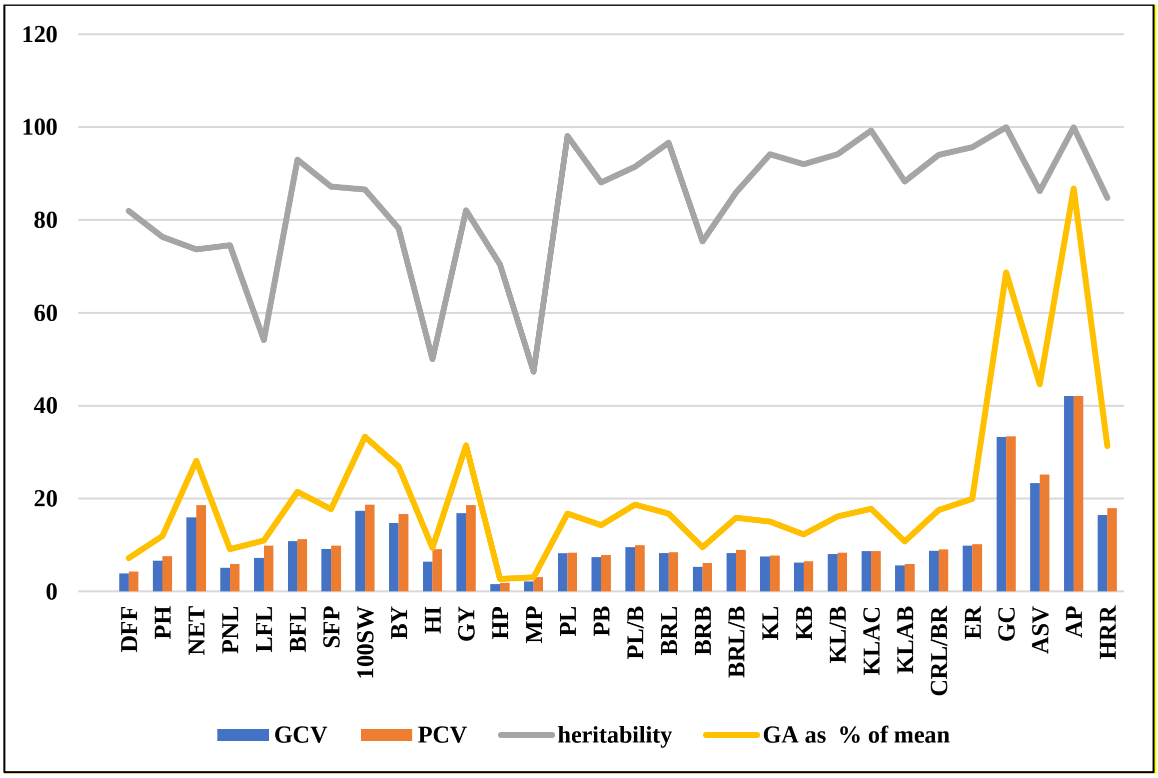

Table 2: Genetic parameters for various yield attributing and quality traits

S. No	Traits	Mean	Range		Coefficient of Variation		h^2 %	GA as % of mean
			Max	Min	GCV	PCV		
1.	Days to 50% flowering	98.97	104.00	94.00	3.85	4.25	81.97	7.18
2.	Plant height (cm)	114.95	133.37	99.32	6.63	7.58	76.37	11.93
3.	Number of effective tillers per plant	7.93	11.00	6.20	15.90	18.53	73.66	28.12
4.	Panicle length (cm)	24.78	27.35	22.24	5.12	5.93	74.56	9.11
5.	Length of flag leaf (cm)	29.20	36.32	24.72	7.23	9.83	54.14	10.96
6.	Breadth of flag leaf (cm)	1.45	1.91	1.19	10.81	11.21	92.98	21.47
7.	Spikelet fertility percent	85.02	94.73	62.19	9.20	9.86	87.18	17.71
8.	100 seed weight (g)	2.76	3.58	1.62	17.39	18.70	86.56	33.34
9.	Biological yield per plant (g)	43.02	64.19	32.40	14.75	16.67	78.23	26.88
10.	Harvest Index (%)	46.16	52.22	39.05	6.43	9.10	50.03	9.38
11.	Grain yield per plant (g)	19.81	30.84	13.59	16.84	18.59	82.07	31.44
12.	Hulling percentage	79.38	81.68	76.63	1.55	1.85	70.44	2.68
13.	Milling percentage	68.77	72.74	65.09	2.14	3.12	47.32	3.04
14.	Paddy length (mm)	9.23	10.60	8.15	8.23	8.31	98.10	16.79
15.	Paddy breadth (mm)	2.79	3.20	2.25	7.38	7.86	88.06	14.27

16.	**Paddy L/B ratio**	3.33	4.18	2.72	9.49	9.93	91.44	18.70
17.	**Brown rice length (mm)**	7.01	7.95	6.10	8.29	8.43	96.61	16.78
18.	**Brown rice breadth (mm)**	2.30	2.65	2.00	5.33	6.13	75.40	9.53
19.	**Brown rice L/B ratio**	3.05	3.62	2.63	8.29	8.95	85.92	15.84
20.	**Kernel length (mm)**	6.83	7.65	5.90	7.50	7.73	94.18	15.00
21.	**Kernel breadth(mm)**	2.25	2.60	1.90	6.20	6.47	91.98	12.26
22.	**Kernel L/B ratio**	3.04	3.55	2.65	8.08	8.32	94.17	16.15
23.	**Kernel length after cooking (mm)**	11.10	14.00	9.00	8.67	8.70	99.24	17.80
24.	**Kernel breadth after cooking (mm)**	3.30	3.95	2.95	5.57	5.92	88.27	10.78
25.	**Cooked rice L/B ratio**	3.37	4.38	2.81	8.78	9.06	94.02	17.54
26.	**Elongation ratio**	1.63	1.99	1.36	9.88	10.11	95.65	19.92
27.	**Gel Consistency**	76.67	99.25	31.50	33.34	33.35	99.96	68.68
28.	**Alkali spreading value**	3.53	6.50	3.00	23.34	25.14	86.18	44.63
29.	**Amylose percentage**	21.61	51.34	1.74	42.14	42.16	99.91	86.77
30.	**Head rice recovery (%)**	44.83	62.59	23.42	16.49	17.91	84.75	31.28

Max= Maximum, **Min**= Minimum, **GCV**= Genotypic Coefficient of Variation, **PCV**= Phenotypic Coefficient of Variation, **h^2**= Heritability in Broadsense, **GA as % of mean**= Genetic Advance as percent of mean.

Genetic Diversity

Based on genetic dissimilarities the genotypes were grouped in to five distinct clusters according to agglomerative hierarchical analysis. The Euclidean distance matrix of 528 pair of genotypes estimated from different yield attributing and quality traits were used to construct dendrogram based on the Unweighted Pair-group Methods with Arithmetic Means (UPGMA). The advanced breeding lines were tabulated beside their respective clusters and presented in Table 3. This indicates the presence of significant genetic diversity among the advanced breeding lines studied. The genotypes grouped under same cluster had similarity for many traits but dissimilarity to other genotypes in other clusters with one or more traits. Similarly, Garg *et al*. (2011) grouped 48 diverse rice genotypes into 5 clusters, Majumder *et al*. (2015) grouped 30 rice genotypes into 5 clusters and Sree *et al*. (2023) grouped 40 diverse rice genotypes into 5 distinct clusters. The dendrogram representing thirty three advanced breeding lines distributed into five major clusters and distinguished by different colours was shown in Figure 2.

Table 3: Clustering pattern among 33 advance breeding lines of rice for both yield and quality traits

Cluster Number	No. of genotypes	Percent of genotypes	Advanced breeding lines
I	6	18.18%	R 2370-96-2-9-1 **[1]**, R 2496-483-1-582-1 **[15]**, R2757-4-1 **[24]**, R2737-54-1 **[29]**, R2757-55-1 **[30]**, Karma Mahsuri (C) **[32]**
II	19	57.57%	R 2546-C5-3-472-1 **[2]**, R 2406-184-2-112-1 **[4]**, R 2404-164-2-87-1 **[5]**, R 2698-150-1 **[6]**, R 2542-C1-8-442-1 **[7]**, R 2296-31-1 **[8]**, R 2550-C9-3-500-1 **[11]**, R 2699-19-1 **[12]**, R 2701-45-1 **[13]**, R 2697-169-1 **[16]**, R 2406-182-1-106-1 **[17]**, R 2296-30-1 **[18]**, R 2697-140-1 **[19]**, R 2406-182-2-107-1 **[20]**, R2737-98-1 **[22]**, R2737-3-1 **[26]**, R2737-25-1 **[27]**, R2737-26-1 **[28]**, IGKV R 1244 (C) **[33]**
III	2	6.06%	R 2506-485-1-584-1 **[3]**, IR17A2192 **[14]**
IV	5	15.15%	R 2405-171-91-1 **[9]**, R 2326-108-1-61-1 **[21]**, R2764-25-1 **[23]**, R2764-35-1 **[25]**, Narendra 359 (C) **[31]**
V	1	3.03%	R 2545-C4-6-468-1 **[10]**

The average intra and inter-cluster distances among five clusters were tabulated and presented in Table 4. Highest inter-cluster distance was observed between Clusters

I and V (76.364) followed by Clusters I and II (63.178), III and V (56.890) and Clusters IV and V (55.025) suggesting wide diversity between these clusters. The least inter-cluster distance was observed between Clusters III and IV (25.812) followed by Clusters I and III (31.773), I and IV (33.236) and Clusters II and V (34.866) indicating close relationship between the genotypes of these clusters. The genotypes within each cluster were closer to each other than the genotypes in different clusters. The intra-cluster distances were lesser than the inter-cluster distances, which was implying that the genotypes within a cluster tend to diverse less from each other. The intra-cluster distance was ranged from 9.739 in Cluster III to 18.381 in Cluster IV.

Figure 2: The dendrogram based on UPGMA clustering method showing genetic relationships among 33 rice genotypes for all traits

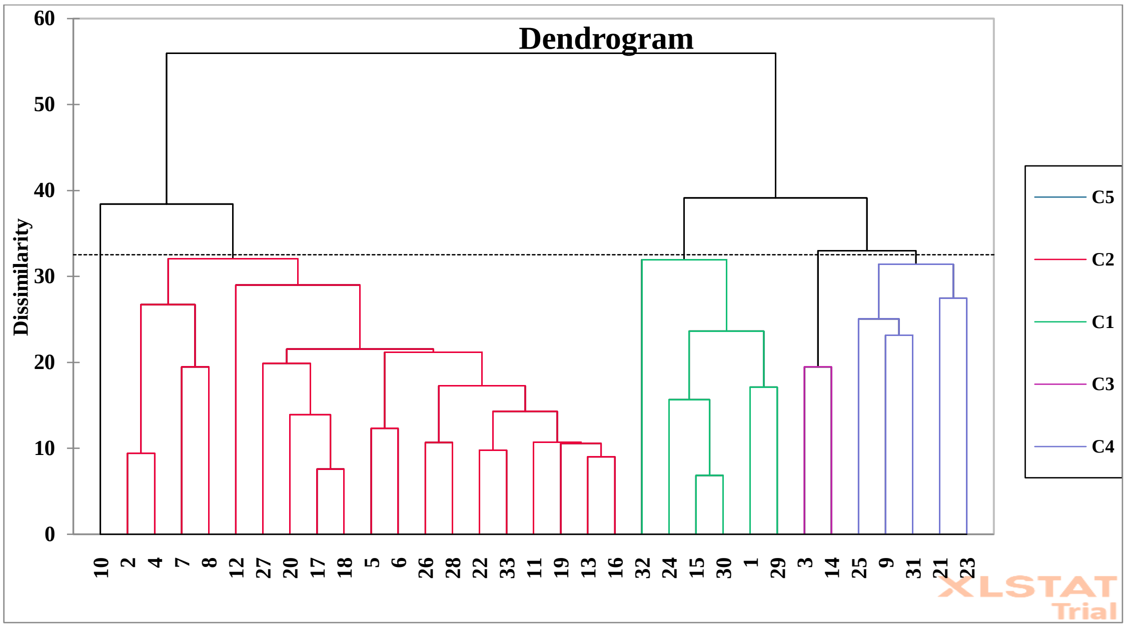

Table 4: Average intra-cluster (diagonal) and inter-cluster distance values

Cluster Number	I	II	III	IV	V
I	**15.649**	63.178	31.773	33.236	76.364
II		**16.480**	43.779	36.519	34.866
III			**9.739**	25.812	56.890
IV				**18.381**	55.025
V					**0**

The cluster mean values of all the traits assessed were shown in Table 5 along with percent contribution towards genetic diversity. Cluster I did not show highest mean for any trait, whereas, Cluster II showed highest means for traits paddy length (9.445mm), brown rice length (7.176mm), brown rice L/B ratio (3.061) and kernel length (6.974mm). Cluster III manifested maximum number of highest cluster means for various characters including grain yield per plant (22.820g) such as number of effective tillers per plant (9.100), panicle length (26.265cm), breadth of flag leaf (1.550cm), spikelet fertility percent (87.065%), 100 seed weight (3.070g), biological yield (4.930g), kernel length after cooking (11.475mm), cooked rice L/B ratio (3.475) and elongation ratio (1.725). Cluster IV and V exhibited same number of highest cluster mean for various characters**.** Traits with highest cluster mean under Cluster IV were days to 50% flowering (100.20), length of flag leaf (29.578cm), harvest index (48.198%), hulling percentage (80.430%), milling percentage (70.186%), paddy L/B ratio (3.642), kernel L/B ratio (3.284) and head rice recovery (52.900%). Traits with highest cluster mean under Cluster V were plant height (129.670cm), paddy breadth (2.900mm), kernel breadth (2.400mm), brown rice breadth (2.350mm), kernel breadth after cooking (3.400mm), gel consistency (97.250), alkali spreading value (4.500) and amylose percentage (51.340). Cluster III had maximum number of highest desirable cluster means including grain yield and hence, could be directly selected and utilized in breeding programmes. Similar findings were observed by Devi (2016), Solanki *et al*. (2019) and Bekis *et al*. (2021) under cluster mean analysis.

Among all the traits under study, gel consistency (53.08%) showed maximum contribution towards diversity followed by amylose percentage (25.08%), brown rice length (3.87%), kernel breadth after cooking (2.58%), brown rice breadth (2.31%), brown rice L/B ratio (1.79%), kernel breadth (1.22%), grain yield per plant (1.22%), harvest index (1.06%) and the least contribution was observed by spikelet fertility percent (0.01%) followed by number of effective tillers per plant (0.03%), length of flag leaf (0.03%) and milling percentage (0.04%).

Table 5: Average performance of advanced breeding lines for each cluster for different characters along with percent contribution of traits

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Percentage contribution
Days to 50% flowering	100.17	98.42	98.00	**100.20**	98.00	0.1%
Plant height (cm)	106.75	116.02	127.77	112.61	**129.67**	0.16%
Number of effective tillers per plant	8.33	7.95	**9.10**	7.07	7.10	0.03%
Panicle length (cm)	24.15	25.07	**26.26**	24.11	23.11	0.09%
Length of flag leaf (cm)	28.78	29.45	27.69	**29.57**	27.86	0.03%
Breadth of flag leaf (cm)	1.40	1.50	**1.55**	1.32	1.25	1.01%
Spikelet fertility percent	84.00	85.46	**87.06**	84.90	79.12	0.01%
100 seed weight (g)	2.84	2.85	**3.07**	2.32	2.06	0.15%
Biological yield per plant (g)	40.96	45.30	**49.93**	35.47	35.91	0.57%
Harvest Index (%)	48.15	45.18	45.51	**48.19**	43.87	1.06%
Grain yield per plant (g)	19.63	20.50	**22.82**	17.03	15.75	1.22%
Hulling percentage	78.72	79.22	79.7	**80.43**	80.35	0.1%
Milling percentage	68.68	68.50	68.95	**70.18**	66.99	0.04%
Paddy length (mm)	8.46	**9.44**	9.07	9.41	9.25	0.37%
Paddy breadth (mm)	2.75	2.85	2.65	2.61	**2.90**	0.71%
Paddy L/B ratio	3.08	3.32	3.42	**3.64**	3.19	0.33%
Brown rice length (mm)	6.44	**7.17**	6.82	7.13	7.10	3.87%
Brown rice breadth (mm)	2.28	**2.35**	2.25	2.17	**2.35**	2.31%

Brown rice L/B ratio	2.82	**3.06**	3.04	3.29	3.02	1.79%
Kernel length (mm)	6.32	**6.97**	6.72	6.92	6.90	1.03%
Kernel breadth(mm)	2.21	2.28	2.30	2.11	**2.40**	1.22%
Kernel L/B ratio	2.85	3.05	2.92	**3.28**	2.88	0.61%
Kernel length after cooking (mm)	10.80	11.18	**11.47**	11.04	10.65	0.04%
Kernel breadth after cooking (mm)	3.25	3.33	3.30	3.21	**3.40**	2.58%
Cooked rice L/B ratio	3.32	3.37	**3.47**	3.43	3.14	0.68%
Elongation ratio	1.71	1.61	**1.72**	1.59	1.54	0.71%
Gel consistency	33.54	95.34	53.75	62.50	**97.25**	53.08%
Alkali spreading value	4.25	3.23	3.75	3.50	**4.50**	0.75%
Amylose percentage	17.98	22.77	21.02	15.81	**51.34**	25.08%
Head rice recovery (%)	39.69	44.53	45.50	**52.90**	39.56	0.28%

Note: Bold digits represent highest mean values for the particular traits.

Conclusion

Highly significant genetic variation was observed among genotypes for all traits studied, indicating a strong potential for selecting superior genotypes for yield and quality improvement. Higher PCV values than GCV in most of the characters indicates masking effect of the environment on the expression of genetic variability. Traits such as number of effective tillers per plant, panicle length (cm), breadth of flag leaf (cm), 100 seed weight (g), biological yield per plant (g), grain yield per plant (g), gel consistency, alkali spreading value, amylose percentage and head rice recovery (%) displayed high heritability and high genetic advance as % of mean implying that additive genetic effects influenced the inheritance of traits, making them suitable for direct selection. Cluster II with maximum genotypes and intra-cluster distance, suitable for within-cluster hybridization, while inter-cluster crosses between Cluster I and V, Cluster I and II were likely to produce broader genetic recombination because of their maximum genetic divergence. Cluster III exhibited maximum number of highest cluster mean values including grain yield per plant (g). Therefore, the genotypes R 2506-485-1-584-1 and IR17A2192 under Cluster III could be directly utilised in hybrid breeding programmes for obtaining improved grain yield and quality.

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