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Evaluating rice germplasm for agro morphological and yield attributing characters in rice (*Oryza sativa* L.)

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Abstract

The current study evaluated 55 rice genotypes during *Kharif*, 2024 for yield and its component traits at Rice Research unit Farm, Department of Genetics and Plant Breeding, IGKV, Raipur. The experiment was conducted in Randomized Block Design with two replications to study agro morphological characterization, genetic variability parameters and genetic divergence analysis. Morphological traits are primarily governed by genetic factors, making them less susceptible to environmental influences. Considerable variation was observed in 18 agro morphological characterization recoded in yield and yield attributing traits. The variance analysis revealed significant genotypic differences across all 16 traits studied. Most of the yield attributing parameters showed differences in both PCV (Phenotypic coefficient of variation) and GCV (Genotypic coefficient of variation) values. This allows for effective selection processes to be implemented, leveraging the genotypic diversity to drive desired trait improvements. Among the studied attributes, the traits like number of unfilled grains per panicle, grain yield per plant, harvest index, number of filled grains, and number of effective tillers per plant exhibited both high phenotypic (PCV) and genotypic coefficients of variation (GCV), indicating substantial genetic variability. These values indicate the extent of genetic variation and the potential for selection and improvement in these traits. High heritability together with high genetic advance as a mean percentage for quantitative characters was plant height, number of filled grains per panicle, grain yield per plant, harvest index, number of unfilled grains per panicle, paddy breadth, brown rice length to breadth ratio, brown rice breadth, and paddy length to breadth. indicating their potential for improvement through selection. This indicates the involvement of additive gene action in the expression of these traits. Therefore, these characteristics can be effectively enhanced through mass selection and hybridization strategies focused on progeny selection. 55 rice genotypes were classified into seven distinct clusters, ensuring that genotypes within the same cluster (intra cluster) had smaller average distances compared to those in different clusters (inter cluster). Among these, Cluster I contained the majority of the genotypes (30) followed by while clusters II with 16 genotypes, cluster III with 5 genotypes. The cluster IV, cluster V, cluster VI, cluster VII, had the least number of genotypes i.e. one.

Keywords: Rice**,** agro morphological characterization, genetic variability parameters and genetic divergence analysis.

Introduction

Rice (*Oryza sativa* L. 2n = 24) belongs to the family of Poaceae. It covers 165 million hectares of land worldwide and produces 787 million tons. India is the world's second largest producer and consumer of rice with 52.47 lakh hectare of cultivated area and 117.94 million tonnes production in 2022-23 (Anonymous, 2023) [1]. The most significant grain in the world, rice provides 15% of the world's protein and 21% of its energy per person. Of the twenty two species of rice (genus *Oryza*), only two - *Oryza sativa* L. and *Oryza glaberrima* L. are domesticated. Asian rice is *Oryza sativa* L., while African rice is *Oryza glaberrima* L. As a result, *Oryza sativa* L. is the main crop grown and consumed throughout Asia, where almost 90% of the world's rice is produced. Additionally, rice is a staple food for almost 2.4 billion people in Asia, including Bangladesh, Thailand, Sri Lanka, China, Japan, and parts of India (Warusawithana *et al*., 2017) [20]. Approximately 90% of the world's rice production comes from Asia, making it the world's largest producer. Over 75% of the world's rice is consumed by people in Asian nations, making rice essential to the region's food security.

The demand for rice is anticipated to increase further due to the anticipated population expansion (Tripathi *et al*., 2011) [19]. Around the world, 165.68 million hectares of rice are farmed, yielding 514.57 million tones of rice and 4640 kg of productivity per hectare in 2022 - 2023 (Anonymous, 2024) [2]. Asia accounts about 85 percent of the world's rice land. About 90% of the rice produced worldwide is cultivated in Asian countries, where it is the primary staple crop. Biotechnology will serve as a powerful force in broadening the use of exotic germplasm in *Oryza* and related genera (Chang and Vaughan, 1991) [5]. We also need the inspired and concerted teamwork of those various sectors of society that, during the 1960s and 1970s, made the "Green Revolution" an unprecedented event in the history of agriculture. Morphological characterization forms the basis for assessing phenotypic diversity in germplasm. Smith and Smith (1989) [18], concluded that morphological traits provide preliminary but critical insights into the extent of variation among genotypes, which is essential for selection in breeding programs. The study of genetic variability is equally vital, as it determines the potential for improvement through selection. Burton (1952) [3] emphasized the importance of genetic variance as a key indicator of selection potential, where higher variability leads to better opportunities for crop enhancement. Heritability and genetic advance estimates help determine the proportion of observed variation that is heritable and can be passed on to subsequent generations. As noted by Johnson *et al*. (1955) [9], high heritability coupled with high genetic advance suggests the predominance of additive gene action, indicating that selection will be more effective. The assessment of genetic divergence is crucial for selecting genetically diverse parents for hybridization. Mahalanobis (1936) [11] introduced the D^2-statistics, later expanded by Rao (1952) [14], which has been widely adopted for grouping genotypes based on multivariate traits. Such analyses help in identifying heterotic groups and improving hybrid breeding strategies.

Materials and Methods

As biological material for the study, fifty rice accessions and five checks viz. Pusa 44, IR 64, Swarna, DRR Dhan 42 and MTU 1010 were used. These fifty rice germplasm accessions were taken from DBT Network Project. The accessions of rice were transplanted in the "field at Research Cum Instructional Farm, Department of Genetics and Plant Breeding, IGKV, Raipur during *kharif* 2024. The seeds were sown directly on July 1st, 2024, and the seedlings were later transplanted into the field following a randomized block design with two replications. Check varieties were also randomly assigned within the blocks. Days to 50 % flowering, plant height (cm), number of effective tillers per plant, panicle length (cm), number of filled grains panicle per panicle, number of unfilled grains panicle per panicle, spikelet fertility (%), 1000 grain weight (g), harvest index (%) and grain yield per plant (g) were recorded.

Results and Discussion

Genetic variation, which refers to the differences observed among individuals within a plant population, is essential for any breeding program. Without such variation, it would be impossible to enhance existing lines or create new, distinct ones. In experiment, all the treatment showed significant difference. these show adequate genetic variability present is rice accessions. Comparable observations were made by Saha *et al.* (2019) [15]. Rajesh *et al.* (2016) [12] observed significant variations in yield and its contributing traits, including days to 50% flowering, plant height, number of productive tillers per plant, panicle length, panicle weight, number of spikelet's per panicle, total filled grains per panicle and grain yield per plant.
grain yield per plant.

Range and Mean of each character

Analysis of variance revealed that mean sum of square due to treatment showed highly significant (at 1% level of significance) for all quantitative attributes. The highest mean performance was recorded for number of filled grains per panicle, reaching 1150.90. The result observed for mean performance showed that efficient amount of variability present among different genotypes. The GCV values exhibited a broad range, varying from 5.42% for spikelet fertility to 38.41% for the number of unfilled grains per panicle. The phenotypic coefficient of variation (PCV) in the present study ranged from 5.92 % spikelet fertility to 41.62% for the number of unfilled grains per panicle.

Table 1: Experimental materials used in the study

S. No.	IC No.	S. No.	IC No.
1	IC203804	29	IC465399
2	IC207827	30	IC282429
3	IC519027	31	IC134918
4	IC85876A	32	IC74859
5	IC450162	33	IC458492
6	IC132650	34	IC388272
7	IC86486	35	IC514010
8	IC278350	36	IC134244
9	IC513889	37	IC86208
10	IC460331	38	IC464954
11	IC134308	39	IC203457
12	IC134788	40	IC467021
13	IC115275	41	IC516935
14	IC145385	42	IC258944
15	IC388529	43	IC268025
16	IC435410	44	IC462155
17	IC591357	45	IC450341
18	IC124657	46	IC463946
19	IC134846	47	IC460453
20	IC386259	48	IC610265
21	IC135704	49	IC596877
22	IC455385	50	IC123977
23	IC256834	1 Check	Pusa 44
24	IC133547	2 Check	IR 64
25	IC85874	3 Check	Swarna
26	IC203779	4 Check	DRR Dhan 42
27	IC134735	5 Check	MTU 10 10
28	IC512813		

Distribution frequency of agro morphological traits in rice germplasm accessions

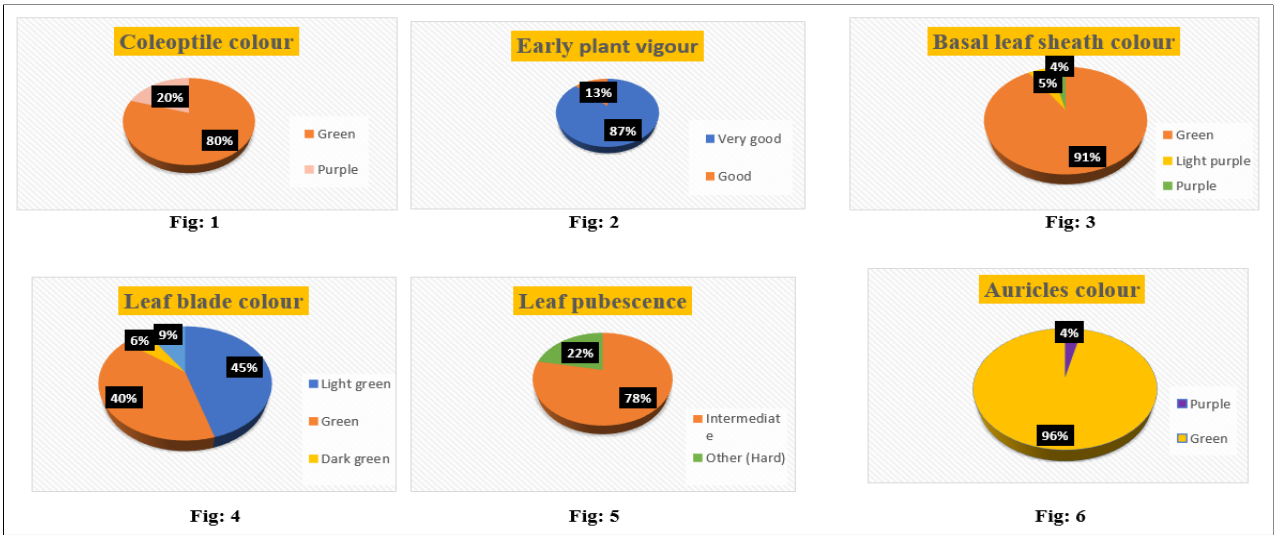

Fig: 1 Fig: 2 Fig: 3

Fig: 4 Fig: 5 Fig: 6

Fig 1a: Frequency distribution of morphological traits Coleoptile colour, Early plant vigour, Basal leaf sheath colour, Leaf blade colour, Leaf pubescence and Auricles colour in fifty-five germplasm accessions.

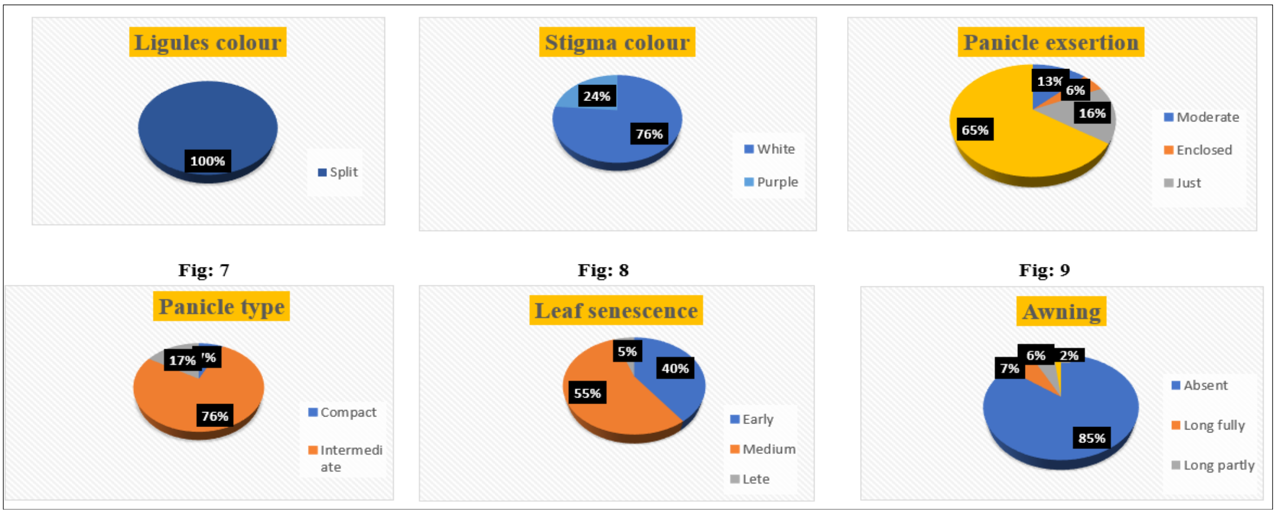

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Fig 1b: Frequency distribution of morphological traits Ligule colour, Stigma colour, Panicle exsertion, Panicle type, Leaf senescence and Awning in fifty-five germplasm accessions.

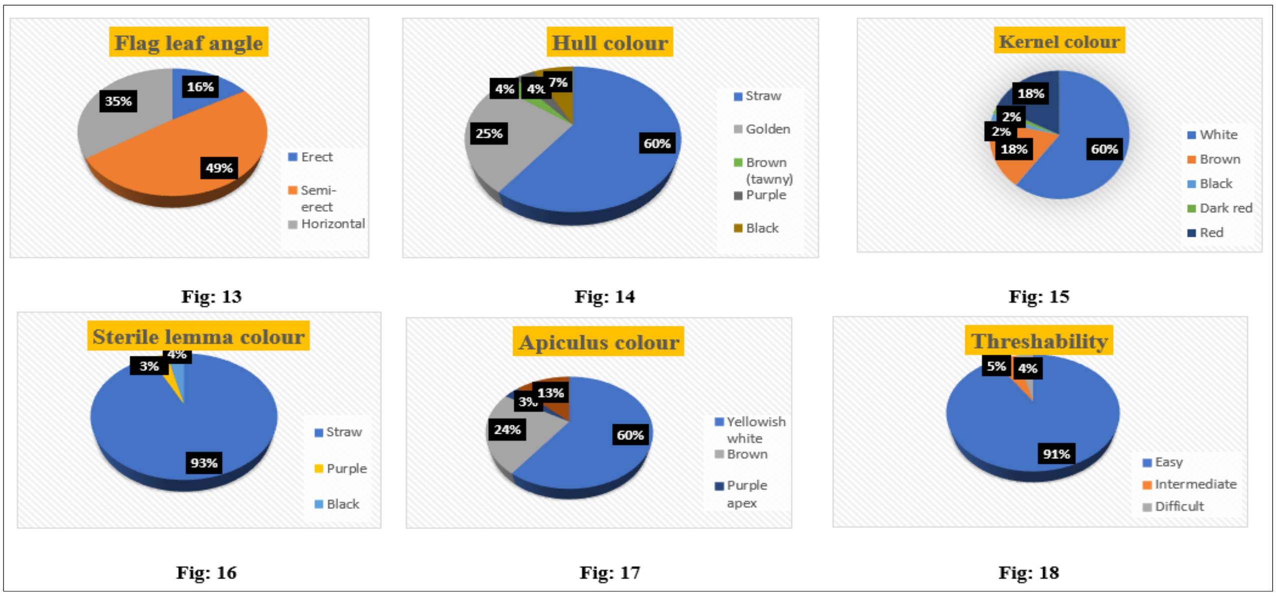

Fig: 13 Fig: 14 Fig: 15

Fig: 16 Fig: 17 Fig: 18

Fig 1c: Frequency distribution of morphological traits, Flag leaf angle, Hull colour, Kernel colour, Sterile lemma colour, Apiculus colour and Threashability in fifty-five germplasm accessions.

Table 2: Analysis of variance of yield and yield attributing traits among 50 rice genotypes including 5 checks.

S.no.	Source of variation	Mean sum of squares		
		Replication	Treatment	Error
	Degree of freedom	1	54	54
1	Days to 50% flowering	14.55	112.88**	11.92
2	Plant height (cm)	5.24	756.63**	37.96
3	Panicle length (cm)	1.00	35.86**	11.43
4	Number of effective tillers	1.33	2.42**	1.01
5	Number of filled grains per panicle	104.08	1150.90**	72.90
6	Number of unfilled grains per panicle	0.66	74.63**	5.98
7	Spikelet fertility percentage (%)	0.47	51.91**	4.54
8	Harvest index (%)	2.50	126.67**	9.35
9	100 seed weight (g)	0.03	0.29**	0.06
10	Paddy length (mm)	0.02	0.73**	0.14
11	Paddy breadth (mm)	0.10	0.26**	0.02
12	Paddy l/b ratio	0.14	0.45**	0.07
13	Brown rice length (mm)	0.10	0.52**	0.10
14	Brown rice breadth (mm)	0.02	0.10**	0.01
15	Brwon rice l/b ratio	0.23	0.42**	0.04
16	Grain yield per plant (g)	1.35	359.02**	1.77

** significant at 1% Probability level

Analysis of variance revealed highly significant differences among the lines, indicating substantial genetic variability. The mean sum of square due to genotypes was highly significant (1% level of significance) for all 55 characters. This indicates that there is a lot of variability among the 55 rice genotypes for all of the traits. Similar findings have been reported by Dhidhi, S. *et al*. (2021) [7] and Kuna, S. *et al.* (2025) [10].

Table 3: Genetic parameters of variation for yield and its contributing traits

Genetic Parameters	Grand mean	Range		GCV (%)	PCV (%)	h^2 (bs)	GA% Mean
		Max	Min				
Days to 50% flowering	87.31	115.00	72.00	8.14	9.05	80.90	15.08
Plant height (cm)	144.56	185.50	100.50	13.11	13.79	90.45	25.69
Panicle length (cm)	27.16	37.20	20.35	12.87	17.90	51.67	19.06
No. of effective tillers per plant	7.01	9.30	4.90	11.99	18.69	41.13	15.84
Number of filled grains per panicle	133.88	184.00	93.00	17.34	18.48	88.09	33.53
Number of unfilled grains per panicle	15.26	29.65	3.20	38.41	41.62	85.16	73.01
Spikelet fertility percentage (%)	89.75	98.00	71.70	5.42	5.92	83.92	10.23
Harvest index (%)	38.45	56.86	21.54	19.92	21.45	86.26	38.11
Hundred seed weight (g)	2.60	3.29	1.58	12.95	16.22	63.75	21.29
Paddy Length (mm)	8.59	10.35	7.15	6.31	7.70	67.23	10.66
Paddy Breadth (mm)	2.72	3.45	2.05	12.68	13.65	86.24	24.25
Paddy L/B ratio	3.22	4.55	2.45	13.64	15.76	74.90	24.32
Brown Rice Length (mm)	6.31	7.50	5.45	7.28	8.85	67.72	12.34
Brown Rice Breadth (mm)	2.27	2.70	1.25	9.29	10.57	77.32	16.83
Brown rice L/B ratio	2.83	5.05	2.15	15.54	16.91	84.43	29.41
Grain yield per plant (g)	41.10	65.30	26.45	32.52	32.68	87.02	44.67

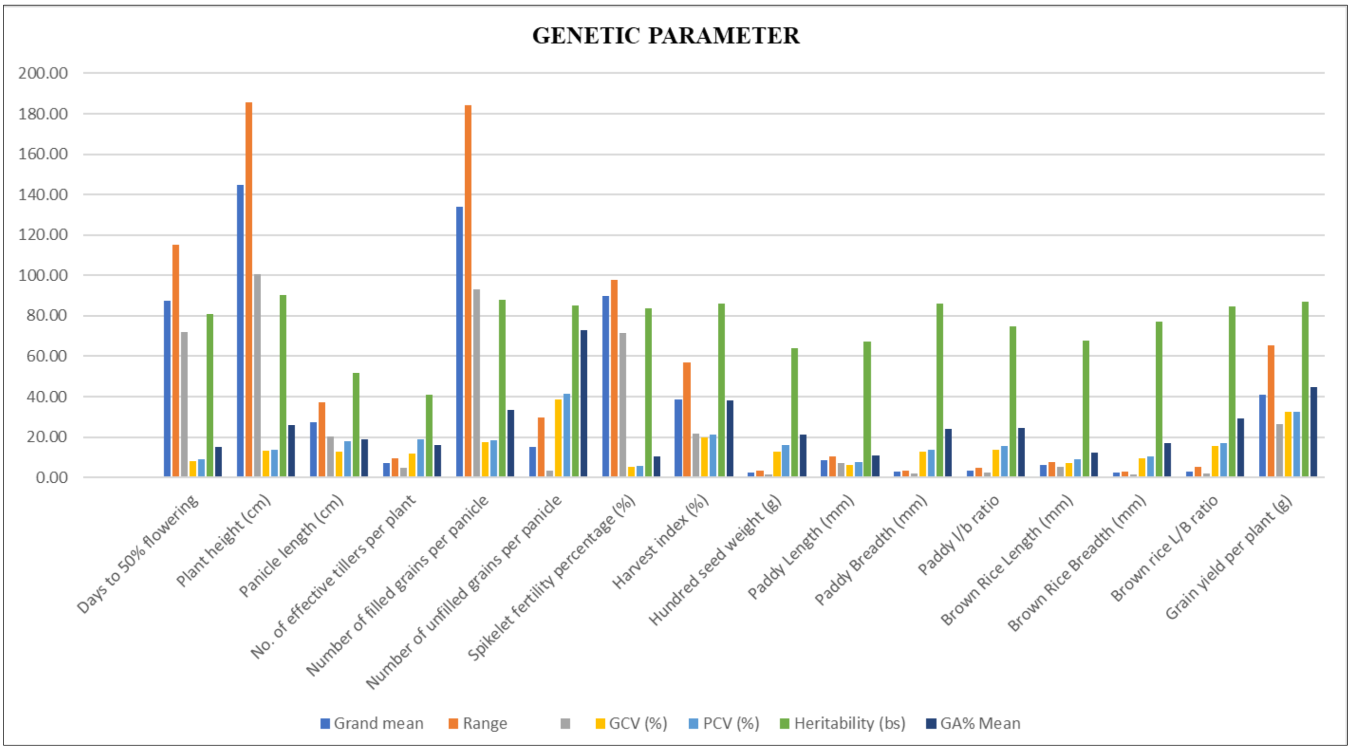

Fig 2: Estimation of variability parameters for yield and yield attributing traits in rice

Agro morphological characterization

Morphological traits are primarily governed by genetic factors, making them less susceptible to environmental influences. Considerable variation was observed in characters such as coleoptile colour, early plant vigour, basal leaf sheath colour, leaf blade colour, leaf pubescence, ligule shape, stigma colour, panicle exsertion, panicle type, flag leaf angle, presence of awns, leaf senescence, hull colour, kernel colour, sterile lemma colour, apiculus colour, and threshability. All morphological traits, except for ligule shape, coleoptile colour, and auricle colour. Similar findings have been reported by Dhruw *et. al.* (2025) [8].

Unique rice accessions were identified based on Basal leaf sheath colour (Purple IC388272), Auricle colour (Purple IC388272, IC134918), Awning (Short partly IC463946), Hull colour (Purple IC463946, IC388272, Brown (tawny) IC3134788, IC467021), Kernel colour (Dark red IC86486, Black IC134308), Sterile lemma colour (Purple IC86486, IC450341, Black IC278350, IC134308), Apiculus colour (Purple apex IC134308, IC450341) and Threashability (Late Swarna, IR 64).

Genetic variability analysis

The GCV values exhibited a broad range, varying from 5.42% for spikelet fertility to 38.41% for the number of unfilled grains per panicle. Out of all the traits studied, the highest genotypic coefficient of variation (GCV) was recorded for the number of unfilled grains per panicle (38.41%), followed by the grain yield per plant (32.52%). Traits that showed moderate GCV included harvest index (19.92%), number of filled grain per panicle (17.34), brown rice length to breadth ratio (15.54%), paddy length to breadth ratio (13.64%), plant height (13.11%), 100 seed weight (12.95%), panicle length (12.87), paddy breadth (12.68) and number of effective tillers per plant (11.99%).Traits with low GCV (less than 10%) were brown rice breadth (9.29), days to 50% flowering (8.14%), brown rice length (7.28), paddy length (6.31%) and spikelet fertility (5.42%).

The phenotypic coefficient of variation (PCV) in the present study ranged from 5.92 % spikelet fertility to 41.62% for the number of unfilled grains per panicle. A high degree of PCV was observed for the number of unfilled grains per panicle (41.62%), followed by the grains yield per plant (32.68%) and harvest index (21.45%). Moderate levels of PCV were recorded for number of filled grain per plant (18.69), number of effective tillers per plant (18.48%), panicle length (17.90), brown rice length to breadth ratio (16.91%), 100 seed weight (16.22), paddy length to breadth ratio (15.88%), plant height (13.79), paddy breadth (13.65%) and brown rice breadth (10.57%). A low degree of phenotypic variation was noted in days to 50% flowering (9.05), brown rice length (8.85%), paddy length (7.70%), and spikelet fertility (5.92%).

Traits such as the number of unfilled grains per panicle, grain yield per plant and the harvest index exhibited both high phenotypic (PCV) and genotypic coefficients of variation (GCV), indicating substantial genetic variability. Similar findings have been reported by Singh, B. *et al.* (2021), Among the traits, number of unfilled grains/panicle (58.88) had highest GCV and PCV value followed by grain yield (26.17).

The highest heritability estimates (above 60%) were recorded for several traits, including the plant height (90.45), number of filled grains per panicle (88.09%), grain yield per plant (87.02), harvest index (86.26%), followed by paddy breadth (86.24%), number of unfilled grains per panicle (85.16), brown rice length to breadth ratio (84.43%), spikelet fertility (83.92%), days to 50% flowering (80.90%), brown rice breadth (77.32%), paddy length to breadth ratio (74.90%), brown rice length (67.72%), paddy length (67.23%),100 seed weight (63.75%), panicle length (51.67%) and number of effective tillers per plant (41.13%).

The highest genetic advance as a percentage of the mean was observed for number of unfilled grains per panicle

(73.01%), grain yield per plant (44.67), followed by harvest index (38.11%), number of filled grains per panicle (33.53%), brown rice length to breadth ratio (29.41%), plant height (25.69%), paddy length to breadth ratio (24.32%), paddy breadth (24.25%) and 100 seed weight (21.29%).

Traits that exhibited a moderate level of genetic advance as a percentage of the mean included panicle length (19.06%), brown rice breadth (16.83%), number of effective tillers per plant (15.84%), days to 50% flowering (15.08%), brown rice length (12.34%), paddy length (10.66%), and spikelet fertility (10.23%).

High heritability together with high genetic advance as a mean percentage for quantitative characters was plant height, number of filled grains per panicle, grain yield per plant, harvest index, number of unfilled grains per panicle, paddy breadth, brown rice length to breadth ratio, brown rice breadth, and paddy length to breadth. indicating their potential for improvement through selection. This indicates the involvement of additive gene action in the expression of these traits. Therefore, these characteristics can be effectively enhanced through mass selection and hybridization strategies focused on progeny selection. These results are in line with the findings of Devkota *et al*. (2023) [6], suggesting the influence of additive gene action in the expression of these traits. Similarly, Sao *et al.* (2024) reported comparable results for plant height, grain yield per plant, and harvest index.

Genetic divergence analysis

Tocher's method was used to group 55 rice genotypes into seven distinct clusters. The intra cluster distances (within the same group) were found to be smaller than the inter cluster distances (between different groups), indicating meaningful genetic variation among clusters.

Cluster I contained the majority of the genotypes (30) followed by while clusters II with 16 genotypes, cluster III with 5 genotypes. The cluster IV, cluster V, cluster VI, cluster VII, had the least number of genotypes i.e. one.

Cluster IV recorded the highest mean values for a number of traits, including: plant height (182.35), panicle length (29.60), number of effective tillers per plant (7.45), harvest index (90.45), 100 seed weight (57.45) and grain yield per plant (21.40), The lowest mean value for spikelet fertility (2.71).

The inter cluster distances among the seven clusters for yield and its attributing traits are shown in Table 4.8. The greatest distance was observed between cluster II and cluster VI (887.48), followed by cluster IV and cluster VI (810.11), cluster I and cluster IV (647.60), and cluster and I cluster II (629.08). On the other hand, the smallest intra cluster distance was recorded between cluster III and cluster III (63.16), followed by cluster II and cluster II (80.30), cluster I and cluster I (96.02). Similar findings were reported by Ramteke *et al.* (2023) [13] for yield and yield attributing characters using D^2 analysis, to study the diversity pattern among the genotypes, based on the analysis. The hybridization between genetically distant cluster ensure the greater genetic variability in the progeny thereby increases the chance of obtaining superior hybrid observed by Chattar *et al.* (2025) [4].

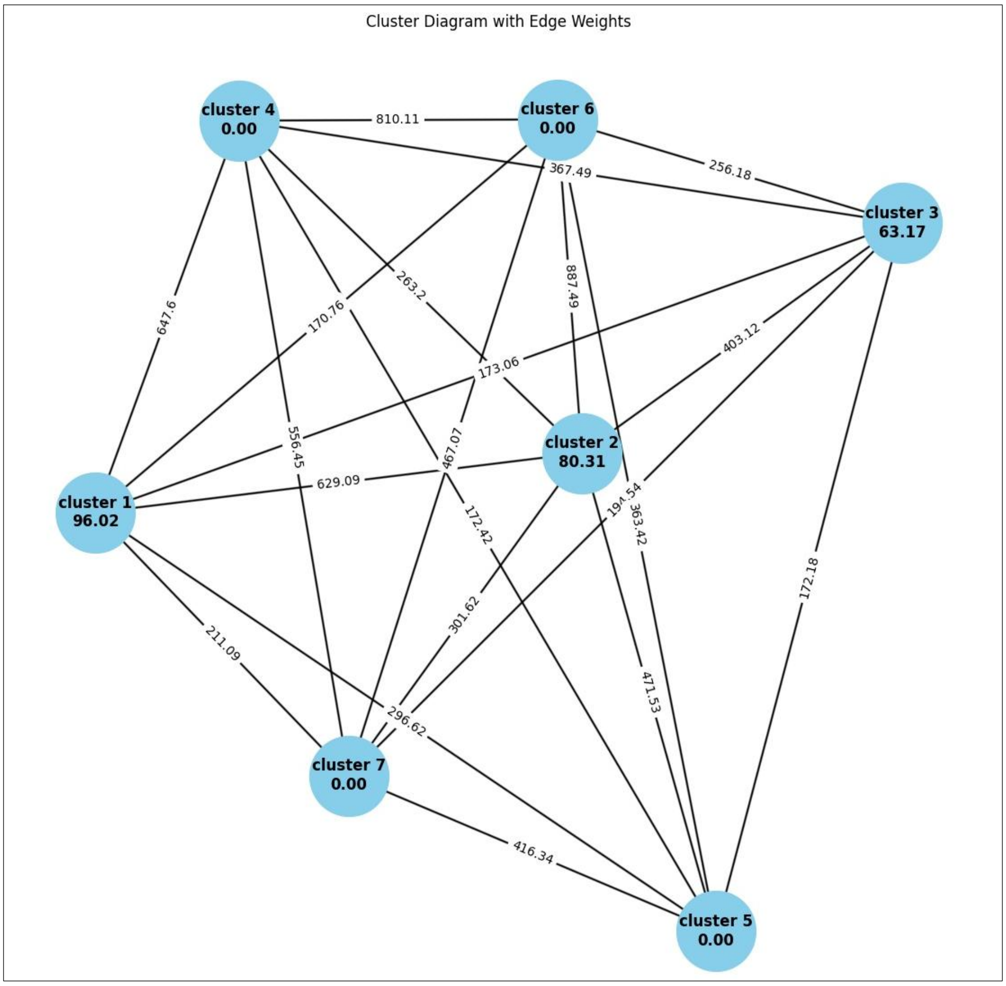

Fig 3: Cluster diagram with Intra and Inter cluster distances

Table 4: Clustering pattern of 55 rice germplasm genotypes

Cluster	Total genotypes	Name of rice accessions
Cluster I	30	IC123207, IC123693, IR 64, IRGC 1042, IRGC 1049, IRGC 1092, IRGC 113, IRGC 1237, IRGC 1238, IRGC 1277, IRGC 1364, IRGC 1365, IRGC 1411, IRGC 1455, IRGC 1500, IRGC 1621, IRGC 1642, IRGC 1676, IRGC 1800, IRGC 1936, IRGC 2000, IRGC 2019, IRGC 2040, IRGC 759, IRGC 864, IRGC 896, IRGC 927, PUSA 44, RL-12119, RL-9601
Cluster II	16	IRGC 1375, IRGC 1420, IRGC 1526, IRGC 1700, IRGC 1786, IRGC 1899, IRGC 2041, IRGC 2055, IRGC 2056, IRGC 2091, IRGC 881, IRGC 901, DRR Dhan 42, MTU 1010, RL-2583, SWARNA
Cluster III	5	IRGC 1873, IRGC 1905, IRGC 1912, IRGC 2022, IRGC 757
Cluster IV	1	RL-1972
Cluster V	1	RL-2136
Cluster VI	1	IRGC 1088
Cluster VII	1	IRGC 1488

Table 5: Mean performance of genotypes in individual clusters for yield traits Cluster/Character

Trait	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
1	114.18	113.90	96.00	117.00	118.50	109.21	81.50
2	170.46	156.06	148.20	182.35	146.30	108.89	117.30
3	28.80	25.69	26.90	29.60	25.10	25.38	25.40
4	6.97	6.02	6.60	7.45	6.80	6.95	5.30
5	113.49	113.10	72.70	111.20	122.10	114.36	83.40
6	18.47	15.54	11.50	17.90	22.30	19.03	13.30
7	3.03	3.61	3.35	2.85	2.95	2.71	2.75
8	87.26	89.29	86.25	90.45	82.70	87.04	87.75
9	22.72	30.49	22.85	57.45	13.70	25.70	17.80
10	12.37	14.68	11.90	21.40	11.80	11.57	9.05

Note- 1 = Days to 50% flowering, 2 = Plant height, 3 = Panicle length, 4 = Number of effective tillers per plant, 5 = Number of filled grain per panicle, 6 = Number of unfilled grains per panicle, 7 = Spikelet fertility, 8 = 100 seed weight, 9 = Harvest index, 10 = Grain yield per plant

Table 6: Average inter cluster mean values and intra cluster mean value for fifty-five genotypes for yield and yield attributing traits

Cluster Number	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	96.02	629.08	173.05	647.60	296.62	170.75	211.09
Cluster II		80.30	403.12	263.20	471.53	887.48	301.62
Cluster III			63.16	367.49	172.18	256.18	194.54
Cluster IV				0.00	172.42	810.11	556.45
Cluster V					0.00	363.42	416.34
Cluster VI						0.00	467.06
Cluster VII							0.00

Conclusion

Analysis of variance revealed highly significant differences among genotypes for all quantitative traits studied.

A higher degree of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for several traits, including number of unfilled grains per panicle, grain yield per plant (g), harvest index (%), number of filled grains per panicle, suggesting that the traits having sufficient variability was found thus indicated ample scope for genetic enhancement for choice for these characters.

The highest heritability estimates were observed for traits such as plant height, number of filled grains per panicle, grain yield per plant, harvest index, paddy breadth, number of unfilled grains per panicle, brown rice length to breadth ratio, spikelet fertility, days to 50% flowering, brown rice breadth, paddy length to breadth ratio, brown rice length, paddy length and 100 seed weight.

Traits such as plant height, number of filled grains per panicle, grain yield per plant, harvest index, number of unfilled grains per panicle, paddy breadth, brown rice length to breadth ratio, brown rice breadth, and paddy length to breadth ratio exhibited both high heritability and high genetic advance, indicating their potential for improvement through selection. This indicates the involvement of additive gene action in the expression of these traits. Therefore, these characteristics can be effectively enhanced through mass selection and hybridization strategies focused on progeny selection.

Using Tocher's method, the 55 rice genotypes were categorized into seven clusters, ensuring that genotypes within the same cluster (intra cluster) had smaller average distances compared to those in different clusters (inter cluster). Among these, Cluster I contained the majority of the genotypes (30) followed by while clusters II with 16 genotypes, cluster III with 5 genotypes. The cluster IV, cluster V, cluster VI, cluster VII, had the least number of genotypes i.e. one.

Acknowledgement

None

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