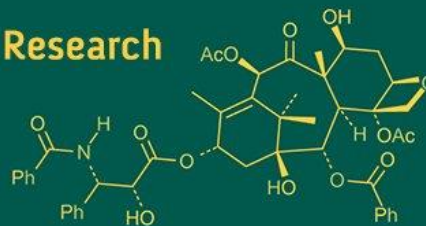


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(8): 1628-1634

www.biochemjournal.com

Received: 17-05-2026

Accepted: 20-06-2026

Chamanbharti Banjare

Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Deepak Gauraha

Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Abhinav Sao

Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Ruchi Bisen

Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Ankita Pradhan

Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Corresponding Author:

Chamanbharti Banjare

Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Assessment of genetic variability and diversity in rice (*Oryza sativa* L.)

Chamanbharti Banjare, Deepak Gauraha, Abhinav Sao, Ruchi Bisen and Ankita Pradhan

DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i8Sr.9640>

Abstract

The present investigation was conducted during *Kharif* 2025 to evaluate 55 rice genotypes at the Instructional cum Research Farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. The experiment was laid out in a Randomized Block Design (RBD) with two replications to assess agro-morphological characterization, genetic variability, character association and genetic divergence for yield and its component traits. Morphological characterization based on 18 qualitative traits revealed considerable phenotypic variation among the genotypes. Analysis of variance indicated highly significant differences for all the nine quantitative traits, confirming the presence of substantial genetic variability. The estimates of PCV were slightly higher than the corresponding GCV for all traits, indicating a limited influence of environmental factors. High GCV and PCV were observed for grain yield per plant, harvest index and plant height. High heritability coupled with high genetic advance as per cent of mean was recorded for plant height, grain yield per plant, hundred seed weight, number of filled grains per panicle and harvest index, suggesting the predominance of additive gene action and the effectiveness of direct selection. Correlation and path coefficient analyses identified harvest index, number of filled grains per panicle, panicle length and hundred seed weight as the major contributors to grain yield. Based on Mahalanobis D^2 analysis, the 55 genotypes were grouped into ten distinct clusters, Cluster I contained the maximum number of genotypes (23), followed by Cluster II (12), Cluster III (4), Cluster IV (6), Cluster V (3), Clusters VI and VII (2 each), whereas Clusters VIII, IX and X each contained one genotype with the maximum inter-cluster distance observed between Cluster III and Cluster V, indicating their potential use in hybridization programmes for developing superior recombinants.

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

Introduction

Rice (*Oryza sativa* L.; $2n = 24$) belongs to the family Poaceae and is one of the most important cereal crops in the world. It serves as the staple food for nearly half of the global population and contributes about 20% of the world's dietary energy. Among the genus *Oryza*, only two species, *Oryza sativa* L. and *Oryza glaberrima* L., are cultivated, while the remaining wild species constitute valuable genetic resources for crop improvement. Rice is widely adapted to diverse agro-climatic conditions and plays a vital role in ensuring global food and nutritional security (Kanwar *et al.*, 2017) [8]. Rice is cultivated in more than 100 countries, with Asia accounting for nearly 90% of global production. India is one of the leading rice-producing countries, cultivating rice over about 51 million hectares with a production of approximately 151 million tonnes during 2025. Chhattisgarh, popularly known as the "Rice Bowl of India," occupies about 38.99 lakh hectares under rice cultivation with a production of nearly 10.37 million tonnes, highlighting its significant contribution to the country's rice economy (Anonymous, 2025) [3]. The success of any crop improvement programme depends on the availability and efficient utilization of genetic variability. Morphological characterization provides the basis for identifying diverse genotypes, while estimates of genetic variability, heritability and genetic advance help breeders assess the effectiveness of selection for yield improvement. Since grain yield is a complex quantitative trait influenced by several interrelated characters, understanding the association among these traits is essential for developing superior genotypes (Gupta *et al.*, 2022) [7].

Grain yield is a complex quantitative trait controlled by the interaction of several component characters and is greatly influenced by environmental factors. Therefore, the study of character association and genetic diversity plays a crucial role in understanding the relationship among yield-contributing traits and identifying superior and genetically diverse parents for breeding programmes. Among the various statistical approaches, Mahalanobis D² analysis has been widely used to assess genetic divergence, classify genotypes into distinct clusters and facilitate the selection of diverse parental lines for the development of high-yielding rice cultivars (Adhikari *et al.*, 2018) ^[1].

Materials and Methods

The experimental material consisted of fifty rice germplasm accessions and five check varieties, namely IR 64, Swarna, Jaya, Dagad Desi and MTU 1010, obtained from the DBT Network Project. The experiment was conducted during *kharif* 2025 at the Research cum Instructional Farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur. The trial was laid out in a Randomized Complete Block Design (RCBD) with two replications. Seeds were sown on 7 July 2025, and the seedlings were subsequently transplanted to the

experimental field. All agronomical practices were adopted to raise crop in good condition.

Results and Discussion

Genetic variability is the foundation of any successful crop improvement programme, as it provides the basis for effective selection and the development of superior cultivars. The magnitude of variability present in a breeding population determines the scope for genetic improvement through selection. In the present study, analysis of variance revealed highly significant differences among the 55 rice genotypes for all the characters studied, indicating the presence of substantial genetic variability that can be effectively utilized in rice breeding programmes. Similar findings were reported by Saha *et al.* (2019) ^[11], who observed considerable variability among rice genotypes for important agronomic traits. Likewise, Rajesh *et al.* (2016) ^[10] also reported significant variation for key yield and yield-contributing characters, including days to 50% flowering, plant height, panicle length, number of effective tillers per plant, number of filled grains per panicle and grain yield per plant, which corroborates the results of the present investigation.

Table 1: Experimental materials used in the study

S. No.	IC No.	S. No.	IC No.
1	IC462881	29	IC464679
2	IC560793	30	IC463006
3	IC515089	31	IC465144
4	IC463883	32	IC145671
5	IC380448	33	IC455687
6	IC513073	34	IC460264X
7	IC449606X	35	IC613831
8	IC203514	36	IC462063
9	IC253455	37	IC256779
10	IC86026	38	IC464625
11	IC514106	39	IC618983
12	IC463934	40	IC86005
13	IC464016	41	IC454452
14	IC465304	42	IC513525
15	IC463152	43	IC323571
16	IC512795	44	IC466172
17	IC463241	45	IC464632
18	IC462145	46	IC277297
19	IC462975	47	IC463740
20	IC466348	48	IC610303
21	IC577101	49	IC388828
22	IC567702	50	IC596628
23	IC516708	Check 1	IR 64
24	IC466732	Check 2	Swarna
25	IC298373	Check 3	Jaya
26	IC466463	Check 4	Dagad Desi
27	IC466026	Check 5	MTU 1010
28	RL 2441		

Agro morphological characterization: Morphological traits are largely controlled by genetic factors and are therefore less influenced by environmental conditions. Substantial variation was observed for traits including early plant vigour, basal leaf sheath colour, leaf blade colour, leaf pubescence, ligule shape, stigma colour, panicle exertion, panicle type, flag leaf angle, awn presence, leaf senescence, hull colour, kernel colour, sterile lemma colour, apiculus colour, and threshability. However, no variation was

detected for ligule shape, coleoptile colour, and auricle colour. These findings are consistent with the observations reported by Dhruv *et al.* (2025) ^[6].

Distinct rice accessions were identified based on qualitative agro-morphological traits. Long partial awning was observed in IC463241. Purple hull colour was recorded in IC466026, whereas tawny hull colour was observed in IC203514 and IC512795. Light brown kernel colour was found in IC463006, while black kernel colour was recorded

in IC514106. Purple sterile lemma colour was exhibited by IC514106 and IC388828, whereas black sterile lemma colour was observed in IC203514. Purple apiculus colour (purple apex) was recorded in IC323571 and IC464632.

Difficult threshability was observed in the check varieties Swarna and IR 64. These distinct qualitative traits may serve as useful descriptors for the identification and characterization of rice germplasm.

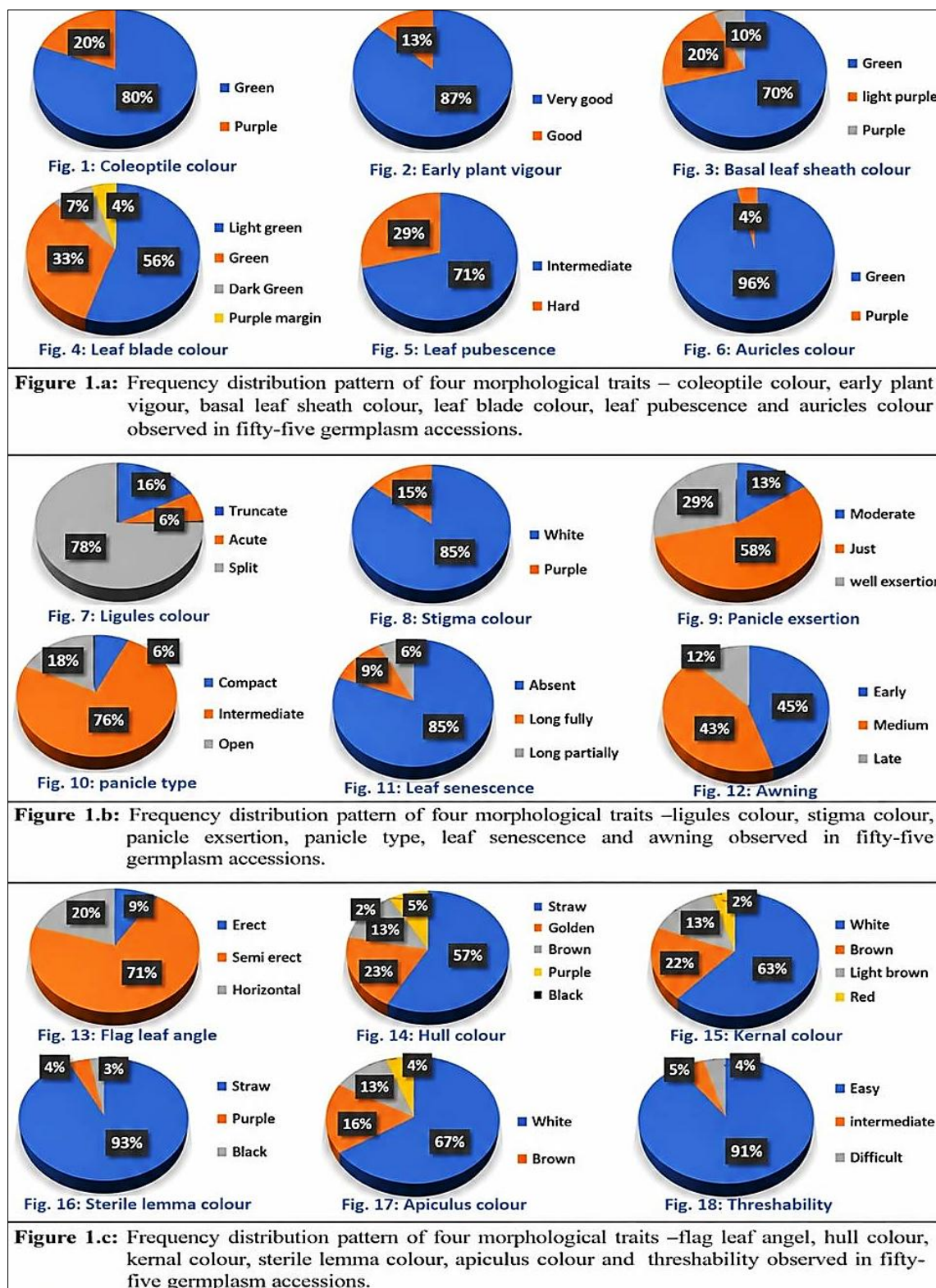


Fig 1: Distribution frequency of agro morphological traits in rice germplasm accessions

Genetic variability analysis

Substantial variation was observed among the 55 rice germplasm accessions for all the traits studied, indicating considerable genetic variability for yield and its component traits. Days to 50% flowering ranged from 74.00 to 111.00 days, plant height from 53.92 to 162.17 cm, panicle length

from 23.12 to 31.48 cm, effective tillers per plant from 5.89 to 9.50, filled grains per panicle from 98.00 to 187.17, spikelet fertility from 81.04 to 95.68%, harvest index from 24.05 to 56.36%, 100- seed weight from 1.77 to 3.25 g, and grain yield per plant from 9.00 to 22.67 g.

The PCV values were consistently higher than the corresponding GCV values for all the traits, indicating a relatively small environmental influence on trait expression. Grain yield per plant (19.25%), plant height (18.79%), and harvest index (18.51%) exhibited the highest GCV, whereas harvest index (22.49%), grain yield per plant (22.45%), and plant height (19.40%) recorded the highest PCV values. The narrow differences between PCV and GCV suggested that most of the observed variability was under genetic control. Similar findings were also reported by Kumar *et al.* (2018) [9] and Akshay *et al.* (2022) [2]. Broad-sense heritability ranged from 54.25% for spikelet fertility to 98.68% for panicle length. High heritability was recorded for panicle length, days to 50% flowering, plant height, 100-seed weight, number of filled grains per panicle,

grain yield per plant, harvest index, and number of effective tillers per plant, indicating the predominance of genetic effects on these traits.

Genetic advance as percent of mean (GAM) ranged from 4.33% to 37.50%. The highest GAM was recorded for plant height (37.50%), followed by grain yield per plant (34.21%), harvest index (31.38%), 100- seed weight (26.15%), and number of filled grains per panicle (22.07%). High heritability coupled with high GAM for plant height, grain yield per plant, 100-seed weight, and number of filled grains per panicle indicated the predominance of additive gene action, suggesting that these traits can be effectively improved through direct selection. These findings are in agreement with Chacko *et al.* (2023) [5].

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 square		
		Replication	Treatment	Error
	Degree of freedom	1	54	54
1	Days to 50% flowering	11.78	172.16**	168.22
2	Plant height (cm)	0.02	958.09**	30.57
3	Panicle length (cm)	0.23	7.75**	0.05
4	Number of effective tillers	1.11	1.38**	0.33
5	Number of filled grains per panicle	11.57	625.60**	71.82
6	Spikelet fertility percentage (%)	15.44	19.22**	5.70
7	Harvest index (%)	11.71	157.71**	30.33
8	100 seed weight (g)	0.02	0.25**	0.02
9	Grain yield per plant (g)	9.70	23.81**	2.91

** Significant at 1% Probability level

Analysis of variance revealed highly significant differences (at 1% level of significance) among the 55 rice genotypes for all the studied traits, indicating the presence of considerable genetic variability. Similar findings were

reported by Saha *et al.* (2019) [11]. Likewise, Rajesh *et al.* (2016) [10] also observed significant variation in grain yield and its associated traits among rice genotypes.

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

Genetic Parameter	Grand	Range		GCV%	PCV%	h ² (bs)	GA% Mean
	mean	Max					
Days to 50% flowering	94.26	111.00	74.00	9.75	9.93	96.44	19.72
Plant height (cm)	114.60	162.17	53.92	18.79	19.40	93.82	37.50
Panicle length (cm)	26.86	31.48	23.12	7.31	7.36	98.68	14.95
No. of effective tillers per plant	7.93	9.50	5.89	9.16	11.69	61.30	14.77
No. of filled grains per panicle	138.39	187.17	98.00	12.02	13.49	79.40	22.07
Spikelet fertility percentage (%)	91.05	95.68	81.04	2.86	3.88	54.25	4.33
Harvest index (%)	43.12	56.36	24.05	18.51	22.49	67.74	31.38
Hundred seed weight (g)	2.53	3.25	1.77	13.57	14.50	87.52	26.15
Grain yield per plant (g)	14.46	22.67	9.00	19.25	22.45	74.32	34.21

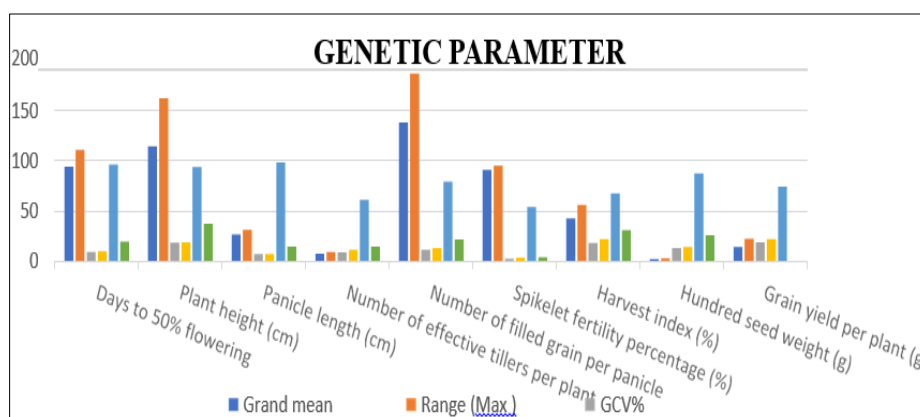


Fig 2: Estimation of variability parameters for yield and yield attributing traits in rice

Range and Mean of each character: Analysis of variance revealed highly significant differences ((at 1% level of significance) among the 55 rice genotypes for all the yield and yield-attributing traits, indicating the presence of substantial genetic variability in the experimental material. The mean performance of the evaluated traits showed considerable variation, with the highest mean value recorded for the number of filled grains per panicle (138.39), followed by plant height (cm), days to 50% flowering (94.26 days) and spikelet fertility (91.05%). The genotypic coefficient of variation (GCV) ranged from 2.86% for spikelet fertility to 19.25% for grain yield per plant, whereas the phenotypic coefficient of variation (PCV) varied from 3.88% for spikelet fertility to 22.49% for harvest index. The consistently higher PCV values than the corresponding GCV values indicated the influence of environmental factors on trait expression. However, the narrow differences between GCV and PCV for most of the characters suggested that environmental effects were relatively low and that the observed variability was predominantly under genetic control, indicating good prospects for effective selection and genetic improvement in rice.

Genetic divergence analysis

Mahalanobis D² analysis followed by Tocher's clustering grouped the 55 rice genotypes into ten distinct clusters, revealing substantial genetic diversity among the studied genotypes. The lower intra-cluster distances compared with inter-cluster distances indicated greater homogeneity within clusters and significant divergence between clusters. Cluster

I comprised the maximum number of genotypes (23), followed by clusters II (12), IV (6), III (4), V (3), VI and VII (2 each), whereas clusters VIII, IX, and X each contained a single genotype, suggesting their distinct genetic constitution. Character contribution analysis revealed that panicle length contributed the highest proportion to total genetic divergence (51.733%), followed by days to 50% flowering (18.353%), plant height (9.774%), 100- seed weight (5.086%), grain yield per plant (4.826%), number of filled grains per panicle (4.497%), harvest index (2.974%), number of effective tillers per plant (1.612%), and spikelet fertility (1.145%). Higher inter-cluster distances indicated substantial genetic divergence among the rice genotypes. The maximum inter-cluster distance was observed between clusters III and V (1481.43), whereas the minimum was recorded between clusters II and X (184.22). Cluster VII exhibited the highest intra-cluster distance (178.33), while clusters VIII, IX and X showed zero intra-cluster distance as each contained a single genotype. These results suggest that hybridization between highly divergent clusters could be useful for developing superior recombinants. Panicle length contributed the maximum to genetic divergence (51.733%), followed by days to 50% flowering (18.353%) and plant height (9.774%), indicating that these traits were the major sources of variability among the studied rice genotypes. Similar findings were reported by Bose *et al.* (2005) [4] and Zaman *et al.* (2005) [15], who also identified these traits as major contributors to genetic divergence in rice.

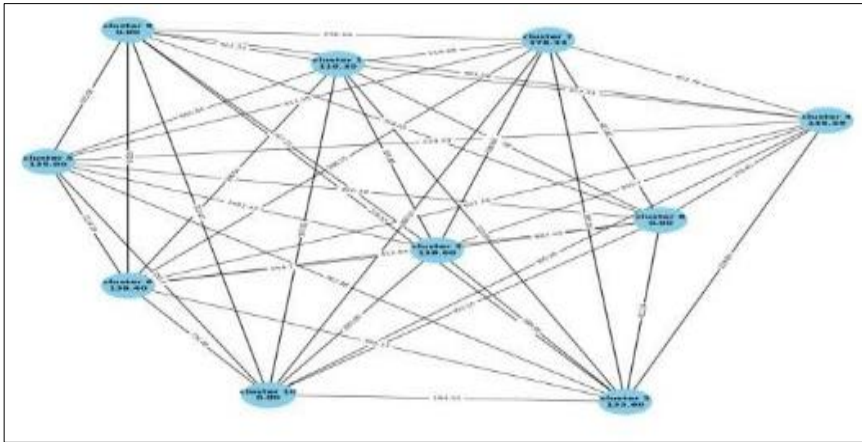


Fig 3: Cluster diagram with Intra and Inter cluster distances

Table 4: Clustering pattern of 55 rice germplasm genotypes

Cluster	Total genotype	Name of rice accessions
Cluster I	23	Dagad Desi, IC145671, IC454452, IC455687, IC460264, IC463006, IC463152, IC463241, IC463883, IC464016, IC464625, IC464679, IC465304, IC512795, IC516708, IC560793, IC567702, IC577101, IC610303, IC613831, IC86026, IR 64, Jaya
Cluster II	12	IC256779, IC323571, IC462975, IC463740, IC465144, IC466026, IC466732, IC513073, IC596628, IC618983, MTU 1010, RL 2441
Cluster III	4	IC203514, IC462145, IC466463, IC515089
Cluster IV	6	IC298373, IC462881, IC466172, IC466348, IC513525, IC86005
Cluster V	3	IC253455, IC277297, IC514106
Cluster VI	2	IC449606, IC462063
Cluster VII	2	IC380448, IC463934
Cluster VIII	1	IC464632
Cluster IX	1	IC388828
Cluster X	1	Swarna

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	Cluster VIII	Cluster IX	Cluster X
1	90.80	100.25	110.50	86.08	101.20	105.50	84.00	88.00	95.50	111.00
2	112.31	152.75	81.66	115.13	119.50	125.75	92.27	53.91	85.66	148.83
3	25.90	23.50	29.08	28.64	28.37	25.78	30.68	27.30	24.17	26.70
4	8.06	7.88	8.00	8.03	7.47	8.25	8.78	7.83	7.85	6.66
5	135.42	130.12	126.50	142.13	139.20	131.33	153.27	151.16	132.66	187.16
6	91.47	89.78	88.49	90.30	91.46	84.72	91.21	93.49	94.24	91.65
7	45.22	45.13	38.00	47.26	40.71	34.80	40.67	26.01	41.24	40.52
8	2.480	2.78	2.76	2.54	2.52	2.41	2.46	2.03	2.77	2.92
9	14.26	13.66	17.16	18.94	12.56	15.33	14.38	15.33	14	13.33

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

Table 6: Average inter cluster mean values and intra cluster mean value for yield and yield attributing traits

Cluster Number	cluster.1	cluster.2	cluster.3	cluster.4	cluster.5	cluster.6	cluster.7	cluster.8	cluster.9	cluster.10
cluster I	118.35	322.67	319.88	323.31	665.63	196.53	219.65	312.38	421.30	507.80
cluster II		133.60	699.99	239.69	362.96	595.10	295.15	411.24	218.51	184.21
cluster III			118.59	850.69	1481.43	254.70	296.65	887.59	517.22	1001.98
cluster IV				135.58	229.28	637.78	423.76	278.44	481.08	305.25
cluster V					135.00	1114.78	817.34	420.18	755.08	353.00
cluster VI						136.40	288.15	412.82	620.60	734.06
cluster VII							178.33	423.62	236.99	366.19
cluster VIII								0.00	719.04	353.23
cluster IX									0.00	312.47
cluster X										0.00

Conclusion

Analysis of variance confirmed significant genetic variability among the 55 rice germplasm accessions for all the traits studied. Higher PCV than GCV indicated a comparatively low environmental influence on trait expression. High heritability coupled with high genetic advance for plant height, grain yield per plant, harvest index, 100-seed weight, and number of filled grains per panicle suggested the predominance of additive gene action. Grain yield per plant was positively associated with harvest index, filled grains per panicle, effective tillers, spikelet fertility, panicle length, and 100-seed weight, while path analysis identified harvest index as the major positive direct contributor to grain yield. Cluster analysis revealed the highest intra-cluster distance in Cluster VII and the maximum inter-cluster distance between Cluster III and Cluster V, indicating substantial genetic divergence and suggesting that hybridization between genotypes from these clusters could be effective for developing superior rice genotypes.

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