Study on genetic diversity in rice (*Oryza sativa* L.) germplasm

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Abstract

In 2024, the present investigation Study on Genetic Diversity in Rice (*Oryza sativa L.*) Germplasm. Five plants selected at random from every genotype were examined for 13 yield- related traits. ANOVA results for all traits identified considerable genetic heterogeneity favourable for fostering yield improvement through breeding. These high-yielding genotypes SHUATS DHAN-1, INDRANI, AK DHAN, D DHAN-39, and JARAVA were characterized by pronounced genetic progress, elevated heritability, and pronounced variability. Their adaptation to a variety of conditions was highlighted by the clear genetic differences found in variations in phenotypic traits, including as blooming time, maturity, plant height, and yield components. Other promising lines KHAYAM DHAN, FALGUNA, KRISHNA HAMSA, and HMT displayed outstanding performance in vital yield-related traits and are therefore recommended for direct selection and incorporation into breeding programs. Cluster analysis further emphasised the genetic diversity, noting that Cluster II possesses considerable yield potential and considerable separation from other clusters most notably from Cluster VI indicating abundant opportunity for heterotic hybrid development.

Keywords: Cluster analysis, genetic diversity, grain yield, genetic advance, heritability

Introduction

Rice (*Oryza sativa* L.), a true diploid that carries 2n=24 chromosomes, has been cultivated by humankind for more than 10,000 years. Cultivated varieties are cataloged into three subspecies indica, japonica, and javanica (Vinoth *et al*. 2016) [30] and (Vivek *et al.* 2005) [31]. Indica cultivar is propagated in tropical and subtropical regions worldwide, japonica across the entire temperate zone, and javanica chiefly within Indonesia by (Veludandi Sumanth *et al.* 2017) [29] and (Singh *et al.* 2011) [22]. Rice, a day-neutral autogamous crop chiefly consumed by almost two-thirds of India's populace, plays a pivotal role in the country's economy by (Burton & Devane 1953) [5] and (Kumar *et al.* 2017) [13]. Rice's nutritional composition consists of mostly carbohydrates (80%) alongside 7-8% protein (an amino-acid spectrum revealing high concentrations of glutamic and aspartic acids, with lysine the highest quality amino acid in cereal proteins present at 3.8% (Juliano *et al*. 1985) [35].

Rice cultivation in Uttar Pradesh occupies roughly 5.9 million hectares. The cropping intensity stands at 153%. In production, the state captures the top position nationally by (Islam *et al.* 2015) [10] and (Sujitha *et al.* 2020) [27]. With production and productivity standing at respective levels of 12.27 mt and 2.7 t/ha, it becomes evident that Uttar Pradesh's rice cultivation urgently requires amplifying productivity a goal that will be fulfilled solely by cultivating high-yielding hybrid varieties (Agriculture at a Glance, 2022) [2]. India's population presently stands at 120 crores. By 2025, the population is expected to reach close to 150 crores. Accordingly, there is a necessity to create high-yielding varieties.

Materials and Methods

In 2024, the experiment was carried out during the kharif season at the Department of Genetics and Plant Breeding, Institute of Agriculture Sciences, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Naini (between 20° 33' 40" and 21° 30' N latitude, and between 73° 27' 58" and 73° 56' 36" E longitude). The climate of this area is tropical, typified by hot summers, moderately chilly winters, and a humid, warm monsoon period. The area experiences heavy rainfall, with most precipitation falling in the months of June to September. A considerable share of the rainfall arrives under the south-west monsoon, chiefly during July and August. Soil PH values lay between 7.3 and 7.6, whereas the aggregated rainfall amounted to 732.40 mm. The experiment had 3 replicates and employed a randomized block design (RBD). The amount of space between plants was measured to be 15 cm and the row spacing was 20 cm. Information was collected on a number of characteristics. Days to ripeness and 50% blooming Flag leaf width (cm), length (cm), and height (cm) of the plant Data from fifteen plants of each genotype were averaged replication-wise, and the data was used for statistical analysis. The data included a total number of tillers per hill, number of panicles per hill, panicle length (cm), spikelets per panicle, test weight (g), harvest index (%), biological yield per hill (g), and grain yield per hill (g).

Experiment Materials

In this study, the experimental material was 42 rice genotypes of the Department of Genetics and Plant Breeding, SHUATS Prayagraj.

Results and Discussion

Table 1: Analysis of Variance for 13 Quantitative Characters of rice

Summary of ANOVA				
Sr. No	**Traits**	**Mean Sum of Squares (MSS)**		
		Replications	**Genotypes**	**Error**
		(df = 2)	**(df=41)**	**(df=82)**
1	Days to 50% flowering	3.96	322.991**	1.626
2	Days to Maturity	2.055	678.254**	1.006
3	Plant Height	22.459	953.515**	9.762
4	Flag leaf length	70.199	36.345**	9.241
5	Flag leaf width	0.288	0.029**	0.007
6	Number of tillers per hill	0.207	3.116**	0.255
7	Number of panicles per hill	1.445	2.723**	0.419
8	Panicle length	16.829	13.928**	2.796
9	Number of spikelets per panicle	834.419	4238.112**	152.507
10	Biological yield per hill	38.234	222.765**	14.225
11	Harvest Index	43.303	282.035**	23.76
12	Test Weight	0.67	66.348**	0.122
13	Grain Yield Per hill	2.973	31.747**	1.205

**Significant at 0.01% level of significance, *Significant at 0.05% level of significance

Table 2: Mean performance of 42 Rice Genotypes

Sr. No	**Genotypes**	**Days to 50% flowering**	**Days to Maturity**	**Plant Height**	**Flag leaf length**	**Flag leaf width**	**Number of tillers per hill**	**Number of panicles per hill**	**Panicle length**	**Number of spikelets per panicle**	**Biological yield per hill**	**Harvest Index**	**Test Weight**	**Grain Yield per hill**
1	Indrani	109.00	132.00	107.69	31.92	1.10	5.87	5.67	26.07	168.47	36.67	48.07	24.53	17.61
2	AK Dhan	107.67	122.33	128.98	31.34	1.02	8.53	7.87	27.35	136.20	48.80	34.32	24.47	16.80
3	80 NLR 40024	108.33	125.33	102.71	23.71	1.04	7.03	6.73	20.27	195.93	37.07	32.54	16.47	12.05
4	JGL 3828	105.67	131.67	110.59	31.42	1.06	6.30	6.20	23.54	193.73	31.79	25.81	20.27	8.22
5	Bina Dhan-10	94.33	117.00	114.87	33.71	1.04	7.67	7.03	25.33	108.27	25.13	30.52	20.20	7.54
6	Lage Dhan	125.33	165.33	165.69	29.59	1.03	8.37	7.30	25.76	182.80	37.20	30.37	20.67	11.25
7	Talmunfar	122.00	158.00	161.09	36.47	0.85	9.17	8.37	25.60	144.00	40.34	21.10	12.27	8.45
8	Jarava	119.00	140.33	131.14	32.06	0.95	5.83	5.20	22.44	146.80	27.75	54.64	20.67	15.13
9	84-Nlr-3354	113.00	138.67	98.14	29.16	1.04	7.27	6.67	23.55	174.53	29.51	48.73	20.53	14.36
10	Gautam	95.33	117.67	99.07	30.57	0.86	8.53	7.03	23.14	119.87	24.87	51.90	16.73	12.60
11	Boichi	113.33	131.33	99.64	28.60	0.93	7.43	6.93	22.19	121.07	27.93	32.51	20.27	8.93
12	Vikramarya	114.00	131.67	102.89	33.71	0.98	7.87	7.03	23.05	138.93	27.48	53.94	24.67	14.39
13	DRRH-2	113.67	131.33	97.70	30.87	0.92	7.23	6.37	23.55	192.33	34.96	42.12	20.33	14.63
14	74-NLR-33359	113.33	130.00	100.45	28.19	0.93	8.93	8.43	22.60	154.80	36.67	34.30	16.73	12.47
15	81-NLR-33641	114.00	132.00	97.45	28.59	1.08	8.73	8.03	20.71	132.07	43.31	18.99	12.67	8.28
16	Lal Bhuna	115.00	135.00	118.71	27.68	0.76	8.70	8.13	21.53	203.13	41.13	25.26	16.47	10.40
17	Ranukasel	119.67	151.33	148.85	26.89	0.83	6.93	6.60	21.51	147.20	52.89	20.45	21.00	10.80
18	Sampada	115.67	143.00	99.55	27.89	0.85	6.77	6.20	22.43	123.20	28.08	34.14	12.53	9.46
19	Suraksha	114.67	146.67	107.47	30.81	0.87	5.47	5.33	23.53	135.60	26.73	33.14	20.93	8.80
20	Mandhya Vijaya	119.00	155.00	129.17	27.08	0.87	7.83	7.20	22.72	177.40	26.15	37.83	20.87	9.87
21	Signet-5455	110.33	131.33	111.55	22.53	1.12	6.50	5.93	22.21	134.20	27.49	33.21	20.60	8.88
22	Dhan-75	106.00	129.33	116.31	25.45	0.96	6.40	6.07	22.98	138.87	26.13	41.92	20.53	10.87
23	NLR	103.67	122.33	108.97	22.80	1.08	5.77	5.20	22.82	131.93	20.00	44.23	24.47	8.80
24	MTU-1035	119.00	149.33	93.03	24.54	1.16	7.50	7.07	21.39	156.53	24.93	38.95	12.33	9.67
25	79-NLR-30491	115.00	137.33	103.50	26.19	1.09	6.83	6.07	21.58	240.00	27.19	31.14	16.40	8.42
26	Kasturi	89.67	115.67	125.74	27.63	1.02	6.83	6.10	25.35	149.13	24.60	35.29	24.47	8.51
27	Dhan-38	105.00	122.00	130.17	30.40	1.14	6.63	6.20	24.69	126.20	40.33	34.77	20.40	14.05

Table 2: Contd.

Sr. No	Genotypes	Days to 50% flowering	Days to Maturity	Plant Height	Flag leaf length	Flag leaf width	Number of tillers per hill	Number of panicles per hill	Panicle length	Number of spikelets per panicle	Biological yield per hill	Harvest Index	Test Weight	Grain Yield per hill
28	Dhan-55	105.67	120.33	113.63	32.20	1.15	8.53	8.13	26.57	173.07	26.69	52.49	20.53	13.71
29	72-Dhan-59	97.00	119.00	128.44	27.09	1.11	7.53	6.80	24.31	158.67	35.47	39.51	20.73	13.92
30	NLR-34449	114.67	150.67	93.89	27.47	1.13	7.87	7.03	20.29	157.53	30.92	30.07	16.93	9.25
31	Khayam Dhan	123.33	163.67	138.26	29.25	1.02	9.00	8.30	22.53	148.13	42.45	30.89	30.60	13.03
32	MTU-1190	121.00	151.00	118.29	25.49	1.06	8.00	7.73	22.12	214.67	42.60	17.58	20.80	7.45
33	Birri Dhan-75	98.67	120.33	101.81	24.76	1.03	7.83	6.93	20.54	215.93	29.32	41.33	12.60	12.12
34	D Dhan-39	99.33	121.00	122.77	31.86	1.03	7.70	7.47	27.65	200.73	43.85	37.64	27.80	16.48
35	Sidha Sannalu	116.67	152.00	117.93	27.23	0.96	7.60	7.27	21.20	178.93	44.48	16.58	12.27	7.40
36	71-Dhan-58	115.67	148.67	92.09	22.77	1.00	7.43	6.90	21.33	114.80	33.55	33.19	13.07	11.10
37	Falguna	116.00	161.67	101.19	33.24	1.14	8.63	8.10	26.47	181.00	47.61	29.20	24.73	13.71
38	82-NLR-145	108.67	127.00	100.63	26.72	1.03	7.67	7.53	21.29	226.73	42.20	28.83	16.47	12.15
39	HMT	115.67	163.67	96.47	32.30	1.04	9.20	8.57	22.06	278.27	33.82	37.46	12.33	12.65
40	Krishna Hamsa	93.67	120.67	112.05	23.96	1.01	9.37	8.80	23.54	154.20	35.06	40.03	24.67	13.88
41	Dhan-53	118.67	159.67	88.77	25.21	0.92	8.67	8.20	22.39	211.73	38.09	22.47	12.00	8.52
42	Shuats Dhan-1 (Check)	74.00	128.33	109.30	34.25	1.10	7.97	7.56	29.33	134.87	57.60	39.39	22.60	22.36
Range	Minimum	74.00	115.67	88.77	22.53	0.76	5.47	5.20	20.27	108.27	20.00	16.58	12.00	7.40
	Maximum	125.33	165.33	165.69	36.47	1.16	9.37	8.80	29.33	278.27	57.60	54.64	30.60	22.36
Grand Mean		109.98	136.92	113.01	28.66	1.01	7.62	7.05	23.32	164.82	34.73	34.93	19.30	11.64
SEm		0.74	0.58	1.80	1.76	0.05	0.29	0.37	0.97	7.13	2.18	2.81	0.20	0.63
SEd		1.04	0.82	2.55	2.48	0.07	0.41	0.53	1.37	10.08	3.08	3.98	0.29	0.90
CD 5%		2.07	1.63	5.07	4.94	0.14	0.82	1.05	2.72	20.06	6.13	7.92	0.57	1.78
CV		1.16	0.73	2.76	10.61	8.52	6.63	9.17	7.17	7.49	10.86	13.96	1.81	9.43

Table 3: Estimation of Genetic Parameters for 42 Rice Genotypes

Sr. No	Trait	PCV	GCV	Heritability%	Genetic advance	GAM at 5%
1.	Days to 50% flowering	9.48	9.41	98.50	21.16	19.24
2.	Days to Maturity	11.00	10.97	99.56	30.88	22.56
3.	Plant Height	15.94	15.69	96.99	35.98	31.84
4.	Flag leaf length	14.92	10.49	49.44	4.35	15.19
5.	Flag leaf width	12.03	8.50	49.84	0.12	12.36
6.	Number of tillers per Hill	14.43	12.82	78.88	1.79	23.45
7.	Number of panicles per hill	15.44	12.43	64.74	1.45	20.60
8.	Panicle length	10.94	8.26	57.03	3.00	12.85
9.	Number of spikelets per panicle	23.61	22.39	89.93	72.09	43.74
10.	Biological yield per hill	26.35	24.00	83.01	15.65	45.05
11.	Harvest Index	30.01	26.57	78.37	16.92	48.45
12.	Test Weight	24.41	24.34	99.45	9.65	50.01
13.	Grain Yield Per Hill	28.98	27.41	89.42	6.22	53.39

PCV = Phenotypic coefficient of Variation, GCV = Genotypic coefficient of Variation, h^2 = Heritability in broad sense, GAM = Genetic advance in per cent of mean

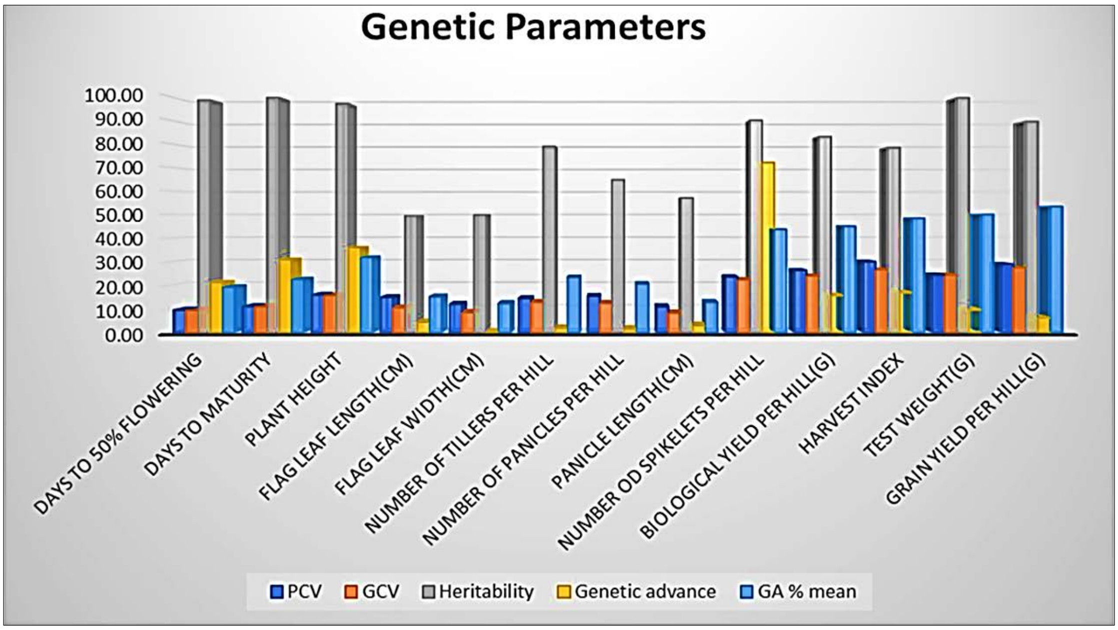

Fig 1: Histogram showing genetic parameters such as GCV, PCV, Heritability and GA

Table 4: Distribution of 42 Rice Genotypes in different Clusters using D2 statistics

Cluster	No. of Genotypes	Genotypes
I	4	Talmunfar, falguna, lage dhan, khayam dhan
II	9	Mtu-81, nlr-33641, dhan-53, mtu-1190, sidha sannalu, ranukasel, mandhya vijaya, 74-nlr-33359, lal bhuna
III	14	Dhan-75, nlr, signet-5455, suraksha, boichi, sampada, 71- dhan-58, mtu-1035, nlr-34449, birri dhan-75, 80-nlr-40024, 82- nlr-145, jgl-3828, 79-nlr-30491
IV	3	Shuats dhan-1 (check), ak dhan, ddhan-39,
V	5	Vikramarya, 84-nlr-3354, drrh-2, indrani, jaravia
VI	7	Dhan-38, 72-dhan-59, bina dhan-10, kasturi, gautam, dhan-55, krishna hamsa

Table 5: Average Intra and Inter-cluster distances of 42 Rice Genotypes

Cluster	I	II	III	IV	V	VI
I	3.007					
II	4.926	3.672				
III	3.863	6.303	3.586			
IV	3.767	4.416	3.943	3.872		
V	5.317	5.459	5.509	5.364	4.461	
VI	5.072	6.321	3.889	4.975	4.288	4.034

Diagonal bold values indicate intra-cluster analysis and off-diagonal values indicate inter- cluster distances

Table 6: Cluster Means of Different Traits in Rice

Group	Days to 50% flowering	Days to Maturity	Plant Height	Flag leaf length	Flag leaf width	Number of tillers per hill	Number of panicles per hill	Panicle length	Number of spikelets per panicle	Biological yield per hill	Harvest Index	Test Weight	Grain Yield Per hill
C I	113.73	134.8	107.51	31.54	0.996	6.81	6.19	23.73	164.21	31.28	49.5	22.15	15.23
C II	99.39	129.06	114.65	31.14	1.075	8.46	7.99	26.82	163.35	43.27	38.85	24.13	16.16
C III	101.46	123.54	118.33	27.63	1.064	6.7	6.19	23.9	142.63	28.87	35.66	21.46	10.1
C IV	120.25	153.92	137.25	28.71	0.923	8.2	7.61	22.87	174.53	40.9	25.01	19.37	9.83
C V	109.75	134.67	101.43	29.47	0.878	7.05	6.38	22.82	124.93	26.9	37.92	17.62	9.95
C VI	112.88	140.36	97.34	26.4	1.042	7.97	7.41	21.31	189.48	34.28	31.75	14.36	10.61

Table 7: Percent Contribution of 13 Characters towards Genetic Divergence

Sr. No	Characters	Percent contribution
1.	Days to 50% flowering	10.50%
2.	Days to Maturity	56.80%
3.	Plant Height	5.30%
4.	Flag leaf length	0.30%
5.	Flag leaf width	0.30%
6.	Number of tillers per hill	0.20%
7.	Number of panicles per hill	0.30%
8.	Panicle length	0.30%
9.	Number of spikelets per panicle	1.60%
10.	Biological yield per hill	1.20%
11.	Harvest Index	0.60%
12.	Test Weight	21.70%
13.	Grain Yield Per hill	0.90%

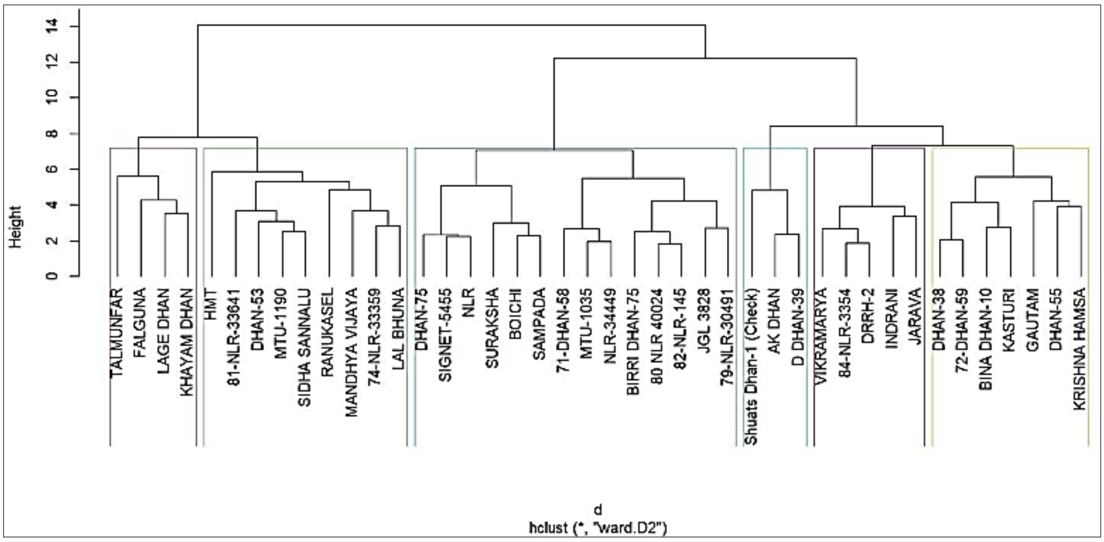

Fig 2: Cluster dendrogram showing the distribution of genotypes into different cluster

Analysis of Variance for Quantitative Characters of Rice (*Oryza sativa* L.)

Analysis of variance is shown for the different features in Table 1. The 42 distinct rice genotypes' mean sum of squares for the 13 distinct traits were highly significant at the 0.01 level of significance, suggesting that the genotypes differ greatly in terms of genetic makeup. The data in Table 1 indicates that there is enough room in the current gene pool to choose lines with promising yield and component characteristics. The results showed that there was significant genetic variation between genotypes, highlighting the importance of genotype differences in plant breeding. Because it provides a solid foundation for choosing superior genetic compositions, this variability explains upcoming efforts to create breeding material. The findings corroborate some of the research. The findings are in line with some of the earlier research by (Vinoth and colleagues 2016), (Dhanwani and colleagues 2013) [7], (Sandeep and colleagues 2018) [19], and (Satturu and colleagues 2023) [20], which revealed significant genetic variation in each of the estimated attributes described.

Table 1 displays the mean values, coefficient of variation (C.V.), standard error of the mean (SEm+), critical difference (C.D.) at 5%, and range of 42 genotypes for 13 quantitative characters. This show that all of the traits under study exhibit a wide range of variation. Based on average performance, the high-yielding rice genotypes 22.36 g in SHUATS DHAN-1, INDRANI (17.61), AK DHAN (16.80), D DHAN-39 (16.48), and JARAVA (15.13) were shown to have superior grain yields. The PCV was greater than the equivalent GCV for every characteristic that showed environmental effect. As proposed by Burton and Devane (1953), the GCV and PCV were classified as low (less than 10%), moderate (10-20%), and high (greater than 20%). GCV measures the genetic variance of a trait and ignores any environmental effect. The high GCVs reported for harvest index (26.57%), test weight (24.34%), number of spikelets per panicle (22.39%), biological yield per hill (20.00%), and grain yield per hill (27.41%) point to pronounced genetic control and substantial scope for genetic improvement via selection. GCV for plant height (15.69%), number of tillers per hill (12.82%), and number of panicles per hill (12.43%) was classified as moderate. Low genetic variation was detected in panicle length (8.26%), flag leaf length (10.49%), flag leaf width (8.50%), days to maturity (10.97%) and days to 50% flowering (9.41%).

Total trait variation, including the combined effects of genetics and environment, is captured by PCV. The present investigation identified the highest PCV for harvest index (30.01%), grain yield per hill (28.98%), biological yield per hill (26.35%), test weight (24.41%), and number of spikelets per panicle (23.61%), signaling pronounced phenotypic variability. An intermediate level of phenotypic variation was noted for plant height (15.94%), the number of panicles per hill (15.44%), the number of tillers per hill (14.43%), and flag leaf length (14.92%). Days to 50% flowering (9.48%), panicle length (10.94%), flag leaf width (12.03%), and days to maturity (11.00%) recorded the lowest PCV values. Taken together, PCV surpassed GCV for all traits, indicating only minimal environmental variation. Selection based only on phenotypic criteria is effective because of the small disparities between PCV and GCV for parameters like test weight, grain yield, and biological yield, which imply significant genetic control. Additionally, (Abigail *et al.* 2019) [1], (Rani *et al.* 2019) [17], (Sudeepthi *et al.* 2020) [26], (Guptha *et al.* 2020) [8], (Singh *et al.* 2021) [23], (Akshay *et al.* 2022) [36], and (Sravani *et al.* 2022) [24] reported similar results.

Heritability

Heritability was categorized by Johnson *et al.* as low (<30%), medium (30-60%), and high (>60%). With regard to high heritability days to maturity (99.56%), test weight (99.45%), days to 50% flowering (98.50%), and plant height (96.99%) these traits are highly amenable to early selection. Notable levels of heritability were likewise detected in spikelets per panicle (89.93%), grain yield (89.42%), and biological yield (83.01%). Values were moderate to high in number of tillers per hill (78.88%), harvest index (78.37%), and number of panicles per hill (64.74%). Moderate to low heredity for panicle length (57.03%), flag leaf width (49.84%), and flag leaf length (49.44%) points to a comparatively greater effect of environmental conditions. Similar findings are reported (Yadav *et al.* 2024) [34] and (Yadav *et al.* 2024) [35].

Genetic Advance

The greatest genetic advance (GA) was detected for spikelets per panicle (72.09), with plant height (35.98) and days to maturity (30.88) came next, followed by days to 50% flowering (21.16) and harvest index (16.92). Significant GA were likewise recorded for biological yield (15.65), test weight (9.65), and grain yield (6.22) evidence of a favourable response to selection and a predominance of additive genetic control. For panicle length (3.00), flag leaf length (4.35), number of tillers per hill (1.79), and number of panicles per hill (1.45), GA was comparatively lower, while the smallest GA was registered for flag leaf width (0.12), implying that limited selection opportunity arises from modest genetic variation or substantial environmental effects.

Genetic Advance as Percent Mean

Johnson *et al.* distinguished three categories for evaluating genetic progress as a percent mean: low (<10%), moderate (10-20%), and high (>20%).Grain yield per hill recorded the greatest GAM (53.39%), closely followed by test weight (50.01%), harvest index (48.45%), biological yield (45.05%), and spikelets per panicle (43.74%), signifying potent additive gene effects and ample prospects for selection. In addition, plant height (31.84%), number of tillers per hill (23.45%), days to maturity (22.56%), and number of panicles per hill (20.60%) show favourable GAM values. Reduced GAM for days to 50% flowering (19.24%), flag leaf length (15.19%), panicle length (12.85%), and flag leaf width (12.36%) implies a slower pace of genetic progress in those particular traits. The pronounced GAM for the primary yield-related traits verifies their potential for their deliberate selection in breeding programs to elevate grain productivity. Parallel patterns in genetic variability, heritability, and genetic advance have likewise been documented by (Kishore *et al.* 2015) [37], (Sudeepthi *et al.* 2020) [26], (Lingaiah *et al.* 2020) [38], (Bhor *et al.* 2020) [39], (Lakshmi *et al.* 2021) [40], (Akshay *et al.* 2022) [36], and (Sravani *et al.* 2022) [27] Yada24v.

Mahalanobis D2 Analysis

Observations on 13 yield and yield contributing traits for 41+1(check) rice genotypes were utilized to evaluate genetic divergence through the Mahalanobis D^2 statistic. The size of D^2 values indicated a pronounced degree of variation among the materials assayed, which consequently generated genetic diversity.

Forty-two rice genotypes were aggregated into six clusters via. Ward's (1963) hierarchical Euclidean clustering method (Table 4; Figure 2). Cluster III contained the highest number of genotypes (14), followed by Cluster II (9), Cluster VI (7), Cluster V (5), Cluster I (4), and Cluster IV (3). D^2 analyses employing thirteen traits demonstrated genetic diversity within the genotypes, thereby validating the formation of six distinct clusters with Cluster III showing the highest degree of diversity. Genotype distributions demonstrated no correlation between geographical and genetic diversity, showing that a range of forces including natural and artificial selection, breeding-material exchange, genetic drift, and environmental variation are driving diversification by Al-Jibouri *et al*. (1958) [3] and Burton (1952) [4].

Intra and Inter Cluster Average Divergence (D2)

The six rice genotype clusters' average intra and inter cluster distances (D^2) are displayed in Table 5 Cluster II and Cluster VI had the largest inter-cluster distance (6.321), followed by Cluster III and Cluster II (6.303) and Cluster V and Cluster III (5.509), suggesting that these clusters had a high level of genetic diversity. Closer genetic similarity was shown by the lowest inter-cluster distance (3.672) between Cluster II and Cluster III. Cluster I had the lowest intra-cluster distance (3.007), indicating higher genetic homogeneity, whereas Cluster III had the highest (3.586), indicating more internal variability. recommending that two parents from a more diverse parent group be chosen for the hybridization program in order to increase the capacity of the parents to combine and provide superior yield features from the diverse parents. Additionally, Shaili *et al*, (2022) [21]

Cluster mean values for quantitative characters of rice genotypes

The cluster's mean performance is the average of all correlated variables' values across all genotypes within that cluster. Genetic variability was clearly shown in analysis of 42 rice genotypes by cluster mean. The best was Cluster II with early flowering and maturity, the maximum number of tillers, panicles, panicle length, flag leaf width, biological yield, test weight, and grain yield (16.16 g), thus it is good for yield enhancement. Cluster I was the best performer in terms of harvest index (49.5%) and grain yield (15.23 g) and with efficient resource use. Cluster III was an early maturity group and the crop bred for short periods. Cluster IV possessed the tallest plants, late maturities, and largest spikelet numbers and thus was suitable for biomass or long duration yield. Clusters V and VI were intermediate with cluster VI having the highest spikelet per panicle (189.48) but low yielding. Earlier studies by (Rashid *et al.* 2017) [18], (Neeraja *et al.* 2015) [41], (Praveen *et al.* 2015) [16], (Chandramohan *et al.* 2016) [6], (Sridhar *et al.* 2016) [25], (Tejaswini *et al.* 2016) [28], (Guru *et al.* 2017) [9], (Sujitha *et al.* 2020) [27], (Kumar *et al.* 2014) [12], (Shaili *et al*, 2022) [21] and (Kumari *et al.* 2021) [15] also document.

Contribution of individual characters towards total divergence

The analysis of trait-based genetic divergence among 42 rice genotypes (Table 7; Fig 3) revealed that Days to Maturity accounted for the greatest effect (56.80%) and was thus identified as the principal driver of diversity. Test Weight added considerable influence (21.70%) to genetic divergence, with Days to 50% Flowering contributing closely behind (10.50%). Plant Height (5.30%), number of Spikelets per panicle (1.60%), and Biological Yield (1.20%) proved to have only moderate effects. Traits such as Flag Leaf Length, Flag Leaf Width, Panicle Length, Panicles, and Tillers per hill exerted only slight influences of $\leq 0.30\%$. In hybridization programmes, selecting parents that exhibit the greatest grain-yield divergence per hill tend to impart the most promising improvement traits upon progeny under selection. Earlier studies by (Rashid *et al.* 2017) [18], (Neeraja *et al.* 2015) [41], (Praveen *et al.* 2015) [16], (Chandramohan *et al.* 2016) [6], (Sridhar *et al.* 2016) [25], (Tejaswini *et al.* 2016) [28], (Guru *et al.* 2017) [9], (Sujitha *et al.* 2020) [27], (Kumar *et al.* 2014) [12], (Shaili *et al*, 2022) [21] and (Kumari *et al.* 2021) [15] also document.

Conclusion

Based on the current examination, it was determined that all of the characters had significant variation according to the analysis of variance. Due to their high heritability and genetic variability, traits including grain yield, test weight, harvest index, and biological yield identified as key markers for genetic improvement were shown to exhibit considerable genetic diversity among the rice genotypes. Marked variability in yield attributes, plant height, maturity, and flowering period all attest to the genotypes' environmental adaptability. Suggested for breeding schemes are the genotypes SHUATS DHAN-1, KHAYAM DHAN, D DHAN-39, FALGUNA, KRISHNA HAMSA, and HMT, all distinguished by their superior yield traits. Cluster II exhibited the greatest yield potential, and the cluster analysis confirmed this variety. Owing to the pronounced genetic divergence between Clusters II and VI, high-yielding hybrids may be developed. The findings furnish the genetic backbone on which climate-resilient, high-yielding rice varieties can be developed.

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