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ASSESSMENT OF GENETIC DIVERSITY, CORRELATION, AND PATH COEFFICIENT ANALYSIS AMONG RICE (*Oryza sativa* L.) GENOTYPES

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ABSTRACT

This study was carried out at the Rice Research Farm, Prof. Rajendra Singh (Rajju Bhaiya) University, Naini, Prayagraj, Department of Genetics and Plant Breeding, to assess genetic variability, trait association, path coefficient, and genetic divergence among 14 rice genotypes during the *Kharif* season, 2025–2026. To investigate yield and associated characteristics, the experiment was set up in a randomized block design with three replications. All fourteen characters had extremely significant genotype differences according to analysis of variance, suggesting that there was enough diversity for efficient selection. For every trait, the phenotypic coefficient of variation (PCV) was marginally larger than the genotypic coefficient of variation (GCV), indicating a small environmental impact on their expression. Flag leaf area, number of spikelet's per panicle, test weight, grain yield per plant, and grain production per hectare all showed higher GCV and PCV values, indicating greater genetic diversity for these traits. Grain yield per plant, number of spikelet's per panicle, test weight, flag leaf area, and grain output per hectare all showed high heritability and high genetic advancement, suggesting the dominance of additive gene action and improved response to selection. Grain yield was found to be positively and significantly correlated with flag leaf area, number of spikelet's per panicle, harvest index, and grain yield per plant at both the genotypic and phenotypic levels. These characteristics are crucial selection criteria for yield improvement since the path coefficient study further demonstrated that they had favourable direct effects on grain production. Genetic divergence analysis grouped the 14 genotypes into three clusters. Cluster I contained the maximum number (10 genotypes), followed by Cluster II (3 genotypes) and Cluster III (1 genotype). The highest inter-cluster distance occurred between Clusters II and III, suggesting that crosses between genotypes from these clusters could be valuable for future breeding programs.

Keywords: Rice, variability, heritability, correlation, path analysis, genetic divergence.

Introduction

The most significant cereal crop and staple meal for Asian and African nations is rice (*Oryza sativa* L.). With chromosome number $2n=24$ and a genomic size of 430 MB, rice, which is a member of the Poaceae family (commonly known as the grass family), is classified in this way. Rice is thought to be the primary source of daily calories for 3.5 billion people worldwide (Li *et al.*, 2018). There are 24 species in the genus *Oryza*, 22 of which are wild and two of which are cultivated (*Oryza sativa* and *Oryza glaberrima*) (Atwell *et al.*, 2014). According to Verma and Shukla

et al. (2011), (Fresco, 2005). Rice is an enormous nutrient supplement for those living in poverty since it contains carbs, which provide energy, along with other essential elements including thiamine (B1), riboflavin (B2), niacin, phosphorus, and potassium.

Over 90% of the world's rice is grown and consumed in Asia, which is referred to as the "rice bowl" of the world. The United Nations General Assembly recognised the importance of rice and declared 2004 to be the "International Year of Rice" with the theme "Rice is Life". The initiative's goal was to increase public awareness of rice's critical role in

ensuring global food security while highlighting the need to increase rice production and productivity. In 2023, Vimal *et al.* defined the term "Global Grain" to refer to rice, which is the most common staple grain diet across Asia, Latin America, and Africa (Bhargavi *et al.*, 2023).

It provides the majority of the calories consumed by more than half of the world's population. It is rich in protein (6–10%), carbohydrates (70–80%), minerals (1.22%), and vitamins (1.22%), including riboflavin, thiamine, niacin, and vitamin E (FAO, 2020). Pigmented rice, which ranges in colour from red to dark purple, has a high content of phenolics and anthocyanins in its pericarp. Anthocyanins are well recognised as useful functional food ingredients due to their anti-inflammatory, anti-cancer, antioxidant, and cholesterol-lowering properties (Ullaha *et al.*, 2023).

Combining route analysis with correlation in grouping may lead to a clearer comprehension of the cause-and-effect linkages between different character pairings (Debnath *et al.*, 2015). Our understanding of the connections between different variables and grain production is enhanced when path analysis and correlation research are combined. The 1000-seed weight, grain yield, and the number of grains per spike were found to be strongly positively correlated. Through other associated qualities, path coefficient analysis, which divides the correlation coefficient, aids in distinguishing between direct and indirect impacts (Dinkar *et al.*, 2023).

Using Mahalanobis D2 statistics and taking into account 17 quantitative features, the type and extent of genetic divergence in 24 rice genotypes were evaluated. ANOVA showed that there was a significant degree of variation between the genotypes. Mahalanobis's D2 statistics have proven to be an effective method for assessing genetic divergence within a specific population. Prior to commencing hybridization programs, D2 statistics can be utilized to select parent combinations without the need for actual crosses. The stability of D2 statistics across multiple environments determines their utility Chhodavadiya *et al.* (2023).

Recent rice improvement programs use sophisticated statistical tools, especially Principal Component Analysis (PCA), to analyses complex trait variation, identify key traits that contribute to genetic differentiation, and select superior genotypes that combine high yield potential with increased micronutrient content (Paramanik *et al.*, 2025).

Material and Methods

The experimental material for the present investigation consisted of 13 rice genotypes along with one check variety (Sampurna). The experiment was conducted under puddle field conditions during *Kharif*, 2025–26 at the Main Experiment Station, Prof. Rajendra Singh (Rajju Bhaiya) University, Prayagraj. The trial was laid out in a Randomized Block Design (RBD) with three replications. Each replication consisted of 14 Genotypes, including 13 test genotypes and one check variety. Seeds of all genotypes were sown in well-prepared nursery beds during the *Kharif* season, and 20 to 25 days old healthy seedlings were transplanted into the main field following a spacing of 20 cm × 20 cm. Each plot measured 3 m × 2 m and consisted of seven rows of 3 m length. Recommended agronomic and plant protection measures were adopted uniformly for all treatments to raise a healthy crop. Fertilizers were applied at the recommended dose of 120:60:60 kg N: P: K/ha. Observations was recorded on five randomly selected plants from each plot for all characters except days to 50 per cent flowering, which was recorded on plot basis. Data were collected for days to 50% flowering, plant height at maturity (cm), flag leaf area (cm²), number of tillers per plant, panicle length (cm), non panicle bearing tillers per plant, number of spikelet's per panicle, biological yield per plant (g), spikelet fertility (%), L/B ratio, test weight (1000 grain weight, g), harvest index (%), grain yield per plant (g), and grain yield (q/ha).

Table 1 : List of genotypes:

Variety Notation	Experimental material	Source (Material received)
V1	Bina Dhan- 17	IIRRI , Varanasi
V2	BRRI-84	IIRRI , Varanasi
V3	BRRI -75	IIRRI , Varanasi
V4	PR-126	IIRRI , Varanasi
V5	Swarna shakti	IIRRI , Varanasi
V6	Tripura Hakachuk-2	IIRRI , Varanasi
V7	DRR-48	IIRRI , Varanasi
V8	Samba mahsuri sub-1	IIRRI , Varanasi
V9	CSR-46	IIRRI , Varanasi
V10	DRR -63	IIRRI , Varanasi
V11	DRR -50	IIRRI , Varanasi
V12	Ratnagiri -8	IIRRI , Varanasi
V13	NDR -356	IIRRI , Varanasi
Check	Sampurna	Lokal Prayagraj

Statistical Analysis

1. Analysis of variance for 14 different parameter of rice genotype
2. Mean performance of genotypes

3. Genetic variability, heritability, genetic advance and coefficient of variance analysis
4. Correlation coefficient analysis
5. Path coefficient analysis of different parameters
6. Genetic divergence analysis

Result and Discussion

Analysis of variance among the rice genotypes revealed significant variation across all studied traits. Days to 50% flowering ranged from 53.33 to 83.67 days (mean: 72.50 days), reflecting a broad spectrum of earliness and lateness. Plant height at maturity varied from 115.87 to 157.53 cm (mean: 132.06 cm). Flag leaf area showed substantial variation, ranging from 36.42 to 79.98 cm² (mean: 59.96 cm²). At maturity, each plant had an average of 22.47 tillers, ranging from 19.27 to 25.33. The main axis panicle length ranged from 23.47 to 32.93 cm, with a mean of 28.51 cm. With a mean of 2.00 and a range of 1.07 to

3.07 Non panicle-bearing tillers per plant, genotype variability was moderate. With a mean of 269.80, the number of spikelet's per panicle ranged widely from 181.20 to 379.87. The average biological yield was 60.81 g, with a range of 46.87 g to 71.07 g. With a mean of 88.12% and a range of 83.51% to 90.63%, the spikelet fertility percentage showed rather constant fertility among genotypes. The L/B ratio had a mean of 2.92 and ranged from 2.33 to 3.69. The average test weight (1000-seed weight) was 19.64 g, with a range of 13.63 g to 29.05 g. The harvest index had a mean of 37.97% and varied from 29.79% to 43.39%. Grain production per hectare varied from 39.47 q/ha to 71.13 q/ha with an average of 51.74 q/ha, suggesting significant yield variability across the genotypes under study. Grain yield per plant ranged from 16.33 g to 29.00 g with a mean of 23.36 g. Present in Table- 1.

Table 1 : Range and Mean Performance of Genotypes:

Genotypes	Day to 50% flowering	Plant Height (cm) at Maturity Time	Flag Leaf Area (cm ²)	Number of Tillers /Plant at Maturity Time	Panicle Length Main Axis at Maturity Time	Non Panicle Bearing Tillers /Plant at Maturity Time	Number of Spikelet per Panicle	Biological Yield (gm.)	Spikelet Fertility %	L/B Ratio	Test Weight (gm.) 1000 Seed	Harvest Index %	Grain Yield / Plant (gm.)	Grain Yield (q/ha)
V1	62.67	125.73	78.84	24.27	27.33	1.53	265.27	58.067	87.52	3.45	22.00	40.15	23.33	58.13
V2	53.33	122.53	41.14	22.13	28.87	1.73	210.07	69.33	90.63	3.16	20.25	38.94	27.00	44.37
V3	69.33	116.80	79.98	23.20	28.87	2.60	318.07	71.07	89.65	2.99	20.27	40.78	29.00	71.13
V4	67.67	115.87	75.65	21.47	27.67	1.07	290.93	63.33	90.26	3.69	20.49	43.11	27.33	60.54
V5	66.33	157.53	68.59	21.53	32.93	1.13	296.33	60.00	87.43	2.57	24.92	43.39	26.00	39.47
V6	64.00	144.00	67.76	22.80	32.87	1.53	283.60	57.13	87.45	2.58	20.36	40.81	23.33	47.71
V7	81.67	121.60	43.42	21.67	27.07	2.27	181.20	48.53	83.51	2.70	13.63	33.60	16.33	40.73
V8	83.33	122.20	40.84	23.27	28.27	2.47	241.00	65.33	88.70	2.76	13.88	29.79	22.67	49.04
V9	77.00	153.33	61.65	19.47	29.33	1.33	187.07	69.33	85.18	2.97	29.05	35.53	24.67	57.28
V10	77.00	140.73	52.42	19.27	23.47	2.40	335.93	46.87	88.76	2.33	15.84	36.76	17.33	57.09
V11	83.67	124.07	36.42	21.87	27.20	1.60	207.47	52.80	88.33	2.81	14.48	35.16	18.67	46.70
V12	78.00	142.27	55.40	23.00	27.87	2.73	283.93	62.73	90.00	2.79	16.56	38.31	23.33	39.97
V13	77.00	138.40	66.26	25.33	29.13	3.07	296.40	69.67	87.18	3.17	26.36	32.48	22.67	47.15
Check	74.00	123.80	71.02	25.27	28.33	2.47	379.87	57.13	89.10	2.92	16.89	42.80	25.33	65.03
Mean	72.5	132.06	59.96	22.47	28.51	2	269.8	60.81	88.12	2.92	19.64	37.97	23.36	51.74
SE	0.90	1.89	5.61	1.42	0.21	0.44	11.62	1.74	1.13	0.04	0.54	1.57	1.37	4.16
CD 5%	2.61	5.48	16.29	4.11	0.62	1.27	33.78	5.09	3.28	0.11	1.56	4.60	3.95	12.10
C.V. (%)	2.15	2.47	16.19	10.91	1.30	37.81	7.46	4.95	2.22	2.17	4.72	7.18	10.15	13.93
Min.	53.33	115.87	36.42	19.27	23.47	1.07	181.2	46.87	83.51	2.33	13.63	29.79	16.33	39.47
Max.	83.67	157.53	79.98	25.33	32.93	3.07	379.87	71.07	90.63	3.69	29.05	43.39	25.33	71.13

Table 2 : Analysis of variance for 14 different parameter of rice genotype

Genotypes	Mean sum of squares		
	Replications	Treatment	Error
	(d.f=2)	(d.f=13)	(d.f=26)
Day to 50% flowering	11.143	237.012**	2.425
Plant Height (cm) at Maturity Time	2.190	560.362**	10.680
Flag Leaf Area (cm ²)	31.430	675.908**	94.258
Number of Tillers /Plant at Maturity Time	10.487	9.944*	6.011
Panicle Length Main Axis at Maturity Time	2.103	16.546**	0.136
Non Panicle Bearing Tillers /Plant at Maturity Time	0.350	1.254*	0.569
Number of Spikelet per Panicle	376.104	10168.757**	405.067

Biological Yield (gm)	8.37	185.53**	9.80
Spikelet Fertility %	1.422	11.673**	3.818
L/B Ratio	0.002	0.388**	0.004
Test Weight (gm.) 1000 Seed	1.045	68.422**	0.859
Harvest Index %	4.57	53.61**	7.44
Grain Yield / Plant (gm.)	9.50	42.20**	5.63
Grain Yield (q/ha)	9.734	291.934**	51.960

* significant at 0.05 and ** significant at 0.01 probability level

Table 3 : Genetic variability parameters for fourteen yield attributing traits

Genotypes	Gv	Pv	Ev	GCV	PCV	ECV	Heritability	GA	GA AS%
Day to 50% flowering	78.20	80.62	2.42	12.20	12.38	2.15	0.97	17.94	24.75
Plant Height (cm) at Maturity Time	183.23	193.91	10.68	10.25	10.54	2.47	0.94	27.11	20.53
Flag Leaf Area (cm ²)	193.88	288.14	94.26	23.22	28.31	16.19	0.67	23.53	39.24
Number of Tillers /Plant at Maturity Time	1.31	7.32	6.01	5.10	12.04	10.91	0.18	1.00	4.44
Panicle Length Main Axis at Maturity Time	5.47	5.61	0.14	8.20	8.30	1.30	0.98	4.76	16.69
Non Panicle Bearing Tillers /Plant at Maturity Time	0.23	0.80	0.57	23.95	44.76	37.81	0.29	0.53	26.41
Number of Spikelet per Panicle	3254.56	3659.63	405.07	21.15	22.42	7.46	0.89	110.83	41.08
Biological Yield (gm.)	63.68	66.71	3.03	13.10	13.41	2.86	0.95	16.07	26.43
Spikelet Fertility %	2.62	6.44	3.82	1.84	2.88	2.22	0.41	2.13	2.41
L/B Ratio	0.13	0.13	0.00	12.25	12.44	2.17	0.97	0.73	24.85
Test Weight (gm.) 1000 Seed	22.52	23.38	0.86	24.16	24.62	4.72	0.96	9.59	48.85
Harvest Index %	17.08	24.52	7.44	10.88	13.04	7.18	0.69	7.12	18.75
Grain Yield / Plant (gm.)	14.83	20.45	5.62	16.52	19.36	10.15	0.72	6.75	28.90
Grain Yield (q/ha)	79.99	131.95	51.96	17.29	22.20	13.93	0.61	14.35	27.73

Genetic variability analysis

Important yield and yield-related traits, such as the number of spikelet's per panicle (PCV 22.42%, GCV 21.15%), test weight (PCV 24.62%, GCV 24.16%), flag leaf area (PCV 28.31%, GCV 23.22%), non panicle bearing tillers per plant (PCV 44.76%, GCV 23.95%), and grain yield per plant (PCV 19.36%, GCV 16.52%), showed high variability. Conversely, characteristics such as the number of tillers per plant (PCV 12.04%, GCV 5.10%) and spikelet fertility (PCV 2.88%, GCV 1.84%) demonstrated comparatively less variability. Strong genetic control and improved response to selection were indicated by the very high heritability found for panicle length (0.98), days to 50% flowering (0.97), L/B ratio (0.97), test weight (0.96), plant height (0.94), and number of spikelet's per panicle (0.89). Flag leaf area (0.67), harvest index (0.69), grain yield per plant (0.72), and grain yield (0.61) all showed moderate heritability, whereas spikelet fertility (0.41), non panicle bearing tillers (0.29), and number of tillers per plant (0.18) showed low heritability, indicating a stronger environmental influence on these traits. Test weight had the highest genetic advance as a percentage of mean (48.85%), followed by number of spikelet's per panicle (41.08%),

flag leaf area (39.24%), grain yield per plant (28.90%), and grain yield (q/ha) (27.73%). Table-3 present the analysis variance. These results suggest that these traits can effectively respond to selection because of additive gene effects. strong genetic advancement and strong heritability were only seen in the percentage of mean for 1000 seed weight. It makes it abundantly evident that selection may be successful and that the heritability is most likely caused by additive gene effects. Jadhav *et al.* (2020) discovered a similar outcome Gupta *et al.* (2021), Dhidhi *et al.* (2021), Moderate heritability for these qualities was also reported by Manju *et al.* (2021), Noatia *et al.* (2021), Demeke *et al.* (2023), Kumar *et al.* (2023), and Kerketta *et al.* (2024).

Heritability and Genetic Advance

Table-3 present the Estimates of heritability combined with genetic advancement offer a trustworthy way to evaluate the efficiency of selection for various quantitative features. Days to 50% blooming (0.97), plant height (0.94), flag leaf area (0.67), panicle length (0.98), number of spikelet's per panicle (0.89), biological yield (0.95), L/B ratio (0.97), and test weight (0.96) all showed strong broad-sense heritability (h^2_b) in the current study. Days to 50%

flowering, plant height, panicle length, biological yield, L/B ratio, and test weight all showed moderate to high genetic advance as present of mean (GAM), indicating the predominance of additive gene action and implying that direct selection for these traits would be successful for genetic improvement. On the other hand, low to moderate heritability was shown by the number of tillers per plant ($h^2_b = 0.18$), non panicle-bearing tillers (0.29), spikelet fertility (0.41), harvest index (0.69), grain yield per plant (0.72), and grain yield per hectare (0.61), in addition to low to moderate GA and GAM. This suggests that simple selection may not be very efficient for these traits due to the increased environmental influence and inclusion of non-additive gene action. Strong additive gene control and great selection efficiency were shown by the high heritability (0.89) of the number of spikelets per panicle with high GA (110.83) and GAM (41.08). In a similar vein, test weight also demonstrated substantial heritability with a very high GAM (48.85), indicating good potential for selection-based improvement. Heritability suggests that a person's character is largely determined by their genetic makeup rather than their surroundings. Days to 50% blooming had moderate GA and GAM and the highest h^2_b value (98.5%). Additionally, plant height demonstrated high H^2_B with the highest GA and high GAM. Similar results were documented. Sudeepthi *et al.* (2020). Low H^2_B , GA, and GAM were shown by the characters' number of tillers and number of panicles, suggesting that selection for these traits will not be successful. With low GA (4.0) and moderate GAM (18.09) values, the panicle length h^2_b value was high (89.95). Singh *et al.* (2023) reported similar outcomes. Both GAM and wide sense heritability were shown to be high in the character single plant yield. These findings are consistent with those of Singh *et al.* (2023) and Mandal *et al.*

(2023). Traits such as days to 50% flowering, panicle length, 1000 grain weight, grain breadth, kernel length, L/B ratio, fertility percentage, and harvest index showed high heritability and moderate genetic advancement, indicating both additive and non-additive gene action in the expression of the characters. This was consistent with the findings of Bhargava *et al.* (2021) regarding panicle length, fertility percentage, and 1000 grain weight; Gayathridevi *et al.* (2023) regarding days to 50% flowering; Lakshmi *et al.* (2022) regarding panicle length; Manivelan *et al.* (2022) regarding days to 50% flowering, panicle length, kernel length, and L/B ratio; Nithya *et al.* (2020) regarding 1000 grain weight and fertility percentage; Priyanga *et al.* (2022) regarding panicle length; and Sudeepthi *et al.* (2020).

Correlation coefficient:

The number of spikelet's per panicle, biological yield, harvest index, and grain output per plant all demonstrated a strong positive genotypic and phenotypic connection with grain yield in the current study, suggesting their direct contribution to yield improvement. At both levels, flag leaf area showed a strong positive correlation with yield characteristics, harvest index, and spikelet's per panicle. Plant height may play an indirect role in increasing yield, as seen by the positive association it demonstrated with panicle length and test weight. Non Panicle-bearing tillers and spikelet characteristics were strongly correlated with the number of tillers. Days to 50% flowering was positively correlated with non panicle-bearing tillers at the genotypic level but primarily negatively correlated with yield attributes. In general, features like biological yield and the number of spikelets per panicle, harvest index and flag leaf area. can be chosen to increase yield.

Table 4 : Genotypic correlation coefficient

Genotypes	Day to 50% flowering	Plant Height (cm) at Maturity Time	Flag Leaf Area (cm ²)	Number of Tillers /Plant at Maturity Time	Panicle Length Main Axis at Maturity Time	Non Panicle Bearing Tillers /Plant at Maturity Time	Number of Spikelet per Panicle	Biological Yield (gm.)	Spikelet Fertility %	L/B Ratio	Test Weight (gm.) 1000 Seed	Harvest Index %	Grain Yield / Plant (gm.)	Grain Yield (q/ha)
Day to 50% flowering	1.000	0.018	-0.442	-0.149	-0.397	0.585*	-0.132	-0.143	-0.428	-0.380	-0.400	-0.325	-0.178	-0.113
Plant Height (cm) at Maturity Time		1.000	0.086	-0.497	0.434	-0.224	0.027	-0.096	-0.387	-0.501	0.553*	0.088	-0.022	-0.423
Flag Leaf Area (cm ²)			1.000	0.547*	0.335	-0.103	0.6544*	0.372	0.075	0.455	0.607*	0.8323**	0.783**	0.702**
Number of Tillers /Plant at Maturity Time				1.000	0.366	0.562*	0.601*	1.097**	0.612*	0.586*	-0.070	-0.058	0.6159*	0.015
Panicle Length Main Axis at Maturity Time					1.000	-0.463	-0.030	-0.210	-0.164	-0.042	0.511	0.024	-0.162	-0.287
Non Panicle Bearing Tillers /Plant at Maturity Time						1.000	0.472	0.447	0.233	-0.290	-0.450	-0.386	0.023	-0.047

Number of Spikelet per Panicle							1.000	0.520	0.562*	-0.060	-0.009	0.574*	0.678**	0.5446*
Biological Yield (gm.)								1.000	0.528	0.405	0.116	0.211	0.777**	0.375
Spikelet Fertility %									1.000	0.334	-0.216	0.420	0.419	0.342
L/B Ratio										1.000	0.340	0.278	0.394	0.406
Test Weight (gm.) 1000 Seed											1.000	0.336	0.207	0.139
Harvest Index %												1.000	0.783**	0.580*
Grain Yield / Plant (gm.)													1.000	0.610*
Grain Yield (q/ha)														1.000

Table 5 : Phenotypic correlation coefficient:

Genotypes	Day to 50% flowering	Plant Height (cm) at Maturity Time	Flag Leaf Area (cm ²)	Number of Tillers /Plant at Maturity Time	Panicle Length Main Axis at Maturity Time	Non Panicle Bearing Tillers /Plant at Maturity Time	Number of Spikelet per Panicle	Biological Yield (gm.)	Spikelet Fertility %	L/B Ratio	Test Weight (gm.) 1000 Seed	Harvest Index %	Grain Yield / Plant (gm.)	Grain Yield (q/ha)
Day to 50% flowering	1	0.018	0.364*	0.058	-0.391*	0.3317*	-0.128	-0.089	-0.3121*	-0.371	0.3986**	-0.297	-0.149	-0.092
Plant Height (cm) at Maturity Time		1.000	0.094	0.258	0.41**	-0.151	0.030	-0.076	-0.269	-0.472	0.523**	0.084	-0.019	-0.344
Flag Leaf Area (cm ²)			1.000	0.180	0.266	-0.170	0.5242*	0.277	0.142	0.366*	0.4603**	0.6599*	0.628**	0.453**
Number of Tillers /Plant at Maturity Time				1.000	0.146	0.427*	0.253	0.393**	-0.017	0.184	-0.011	-0.023	0.235	0.162
Panicle Length Main Axis at Maturity Time					1.000	-0.257	-0.003	-0.180	-0.064	-0.047	0.496**	0.026	-0.140	-0.233
Non Panicle Bearing Tillers /Plant at Maturity Time						1.000	0.197	0.205	-0.012	-0.197	-0.222	-0.155	0.011	0.126
Number of Spikelet per Panicle							1.000	0.384*	0.4031*	-0.073	-0.003	0.516**	0.581**	0.392 *
Biological Yield (gm.)								1.000	0.160	0.3371*	0.076	0.161	0.659**	0.122
Spikelet Fertility %									1.000	0.182	-0.160	0.3051*	0.292	0.197
L/B Ratio										1.000	0.328*	0.259	0.3743*	0.291
Test Weight (gm.) 1000 Seed											1.000	0.302	0.168	0.083
Harvest Index %												1.000	0.771**	0.408**
Grain Yield / Plant (gm.)													1.000	0.393**
Grain Yield (q/ha)														1.000

Table 6 : Genotypic path

Genotypes	Day to 50% flowering	Plant Height (cm) at Maturity Time	Flag Leaf Area (cm ²)	Number of Tillers /Plant at Maturity Time	Panicle Length Main Axis at Maturity Time	Non Panicle Bearing Tillers /Plant at Maturity Time	Number of Spikelet per Panicle	Biological Yield (gm.)	Spikelet Fertility %	L/B Ratio	Test Weight (gm.) 1000 Seed	Harvest Index %	Grain Yield / Plant (gm.)	Grain Yield (q/ha)
Day to 50% flowering	-1.4758	0.0369	-1.4547	-0.0354	0.1004	2.1735	0.6412	-0.0117	-0.2170	-0.1749	1.0564	-1.0296	0.2779	-0.1130
Plant Height (cm) at Maturity Time	-0.0260	2.0919	0.2823	-0.1186	-0.1097	-0.8309	-0.1287	-0.0078	-0.1965	-0.2308	-1.4603	0.2776	0.0348	-0.4227
Flag Leaf Area (cm ²)	0.6519	0.1793	3.2933	0.1307	-0.0847	-0.3820	-3.1728	0.0304	0.0382	0.2094	-1.6047	2.6337	-1.2200	0.7027**
Number of Tillers /Plant at Maturity Time	0.2193	-1.0395	1.8037	0.2386	-0.0926	2.0884	-2.9150	0.0899	0.3107	0.2697	0.1841	-0.1830	-0.9595	0.0147
Panicle Length Main Axis at Maturity Time	0.5853	0.9070	1.1024	0.0874	-0.2530	-1.7170	0.1437	-0.0172	-0.0830	-0.0193	-1.3497	0.0747	0.2521	-0.2866
Non Panicle	-0.8647	-0.4686	-0.3391	0.1343	0.1171	3.7097	-2.2862	0.0366	0.1185	-0.1334	1.1868	-1.2221	-0.0357	-0.0466

Bearing Tillers /Plant at Maturity Time														
Number of Spikelet per Panicle	0.1952	0.0555	2.1551	0.1434	0.0075	1.7493	-4.8485	0.0426	0.2856	-0.0276	0.0247	1.8187	-1.0570	0.5446*
Biological Yield (gm.)	0.2105	-0.2003	1.2238	0.2617	0.0531	1.6591	-2.5192	0.0819	0.2679	0.1865	-0.3069	0.6687	-1.2120	0.3747
Spikelet Fertility %	0.6311	-0.8100	0.2480	0.1461	0.0414	0.8658	-2.7284	0.0432	0.5076	0.1535	0.5687	1.3275	-0.6523	0.3421
L/B Ratio	0.5607	-1.0487	1.4979	0.1398	0.0106	-1.0749	0.2908	0.0332	0.1693	0.4603	-0.8984	0.8799	-0.6142	0.4063
Test Weight (gm.) 1000 Seed	0.5906	1.1573	2.0021	-0.0166	-0.1294	-1.6679	0.0453	0.0095	-0.1094	0.1566	-2.6397	1.0632	-0.3229	0.1387
Harvest Index %	0.4802	0.1835	2.7409	-0.0138	-0.0060	-1.4327	-2.7866	0.0173	0.2129	0.1280	-0.8869	3.1645	-1.2204	0.5809*
Grain Yield / Plant (gm.)	0.2632	-0.0467	2.5789	0.1470	0.0409	0.0850	-3.2895	0.0637	0.2125	0.1815	-0.5471	2.4790	-1.5579	0.6106*

Table 7 : Phenotypic path

GeGen Genotypes	Day to 50% flowering	Plant Height (cm) at Maturity Time	Flag Leaf Area (cm ²)	Number of Tillers /Plant at Maturity Time	Panicle Length Main Axis at Maturity Time	Non Panicle Bearing Tillers /Plant at Maturity Time	Number of Spikelet per Panicle	Biological Yield (gm)	Spikelet Fertility %	L/B Ratio	Test Weight (gm.) 1000 Seed	Harvest Index %	Grain Yield / Plant (gm.)	Grain Yield (q/ha)
Day to 50% flowering	0.0239	-0.0137	-0.1128	0.0002	0.1254	0.0131	-0.0243	0.0294	-0.0065	0.1459	-0.2657	0.0568	-0.0636	-0.0919
Plant Height (cm) at Maturity Time	0.0004	-0.7728	0.0290	0.0010	-0.1315	-0.0060	0.0057	0.0254	-0.0056	0.1854	0.3489	-0.0160	-0.0081	-0.3442*
Flag Leaf Area (cm ²)	-0.0087	-0.0723	0.3099	-0.0007	-0.0854	-0.0067	0.0998	-0.0920	0.0030	-0.1437	0.3068	-0.1261	0.2690	0.453**
Number of Tillers /Plant at Maturity Time	-0.0014	0.1991	0.0558	-0.0038	-0.0469	0.0168	0.0481	-0.1306	-0.0003	-0.0723	-0.0070	0.0043	0.1005	0.1623
Panicle Length Main Axis at Maturity Time	-0.0094	-0.3169	0.0825	-0.0006	-0.3208	-0.0101	-0.0006	0.0597	-0.0013	0.0183	0.3310	-0.0050	-0.0600	-0.2331
Non Panicle Bearing Tillers /Plant at Maturity Time	0.0079	0.1169	-0.0525	-0.0016	0.0825	0.0394	0.0374	-0.0679	-0.0002	0.0774	-0.1479	0.0295	0.0048	0.1257
Number of Spikelet per Panicle	-0.0031	-0.0230	0.1625	-0.0010	0.0010	0.0077	0.1905	-0.1277	0.0084	0.0286	-0.0021	-0.0987	0.2489	0.392*
Biological Yield (gm)	-0.0021	0.0590	0.0859	-0.0015	0.0577	0.0081	0.0733	-0.3319	0.0033	-0.1324	0.0506	-0.0308	0.2827	0.1218
Spikelet Fertility %	-0.0075	0.2077	0.0439	0.0001	0.0204	-0.0005	0.0768	-0.0532	0.0208	-0.0715	-0.1068	-0.0583	0.1252	0.1971
L/B Ratio	-0.0089	0.3650	0.1135	-0.0007	0.0149	-0.0078	-0.0139	-0.1119	0.0038	-0.3926	0.2189	-0.0495	0.1603	0.2911
Test Weight (gm) 1000 Seed	-0.0095	-0.4046	0.1427	0.0000	-0.1593	-0.0087	-0.0006	-0.0252	-0.0033	-0.1289	0.6665	-0.0577	0.0719	0.0832
Harvest Index %	-0.0071	-0.0648	0.2045	0.0001	-0.0084	-0.0061	0.0984	-0.0535	0.0063	-0.1018	0.2012	-0.1911	0.3305	0.4082**
Grain Yield / Plant (gm)	-0.0036	0.0145	0.1947	-0.0009	0.0449	0.0004	0.1107	-0.2190	0.0061	-0.1470	0.1118	-0.1474	0.4283	0.3936**

Path Analysis

Table-6 & 7 present The direct and indirect effects of several features on rice grain yield were shown via

path coefficient analysis. Flag leaf area, number of spikelet's per panicle, harvest index, and grain yield per plant all show positive direct effects on grain yield

at the genotypic level, showing their significant contribution to yield improvement. Through indirect impacts, biological yield, spikelet fertility, and the L/B ratio all made favourable contributions. Grain yield per plant, harvest index, number of spikelet's per panicle, and flag leaf area all showed favourable direct effects on grain yield at the phenotypic level. While their indirect effects through other features varied, plant height and panicle length demonstrated unfavourable direct consequences. Grain yield was negatively correlated with days to 50% blooming as well. Therefore, selection based on flag leaf area, spikelets per panicle, harvest index and grain yield per plant would be effective for improving grain yield in rice.

Cluster Analysis

Table 8: Clustering pattern

Cluster	No. of Genotypes	Genotypes
I	10	T1, T12, T13, T3, T4, T5, T6, T7, T8, T9
II	3	T10, T11, T14
III	1	T2

Table 9: Estimation of average intra and inter cluster distance

Cluster	I	II	III
I	366.24		
II	711.89	336.23	
III	888.61	1634.76	0.00

Table 10: Cluster mean for different character

Cluster		Day to 50% flowering	Plant Height (cm) at Maturity Time	Flag Leaf Area (cm ²)	Number of Tillers Plant at Maturity Time	Panicle Length Main Axis at Maturity Time	Non Panicle Bearing Tillers /Plant at Maturity Time	Number of Spikelet per Panicle	Biological Yield (gm)	Spikelet Fertility %	L/B Ratio	Test Weight (gm) 1000 Seed	Harvest Index %	Grain Yield / Plant (gm)	Grain Yield (q/ha)
I	Mean	73.07	125.33	58.90	23.15	28.06	2.15	267.42	673.67	88.49	3.04	18.48	39.48	264.07	52.28
	SE±	2.50	3.71	5.02	0.83	0.63	0.23	15.84	23.87	0.92	0.10	1.29	1.36	12.26	2.33
II	Mean	69.11	151.62	66.00	21.27	31.71	1.33	255.67	596.78	86.69	2.71	24.77	40.62	241.22	48.15
	SE±	2.42	3.54	4.54	0.65	0.64	0.23	17.72	25.88	0.59	0.08	1.34	1.33	16.65	3.36
III	Mean	77.00	140.73	52.42	19.27	23.47	2.40	335.93	641.00	88.76	2.34	15.84	42.49	272.33	57.09
	SE±	2.27	3.90	3.99	0.68	0.63	0.25	14.81	25.25	0.42	0.11	1.25	1.44	15.45	3.39

Genetic divergence analysis:

The fourteen rice genotypes were divided into three separate clusters using cluster analysis, demonstrating the genotypes' significant genetic variability. With ten genotypes, Cluster I was the largest cluster, followed by Cluster II with three, and Cluster III with just one. Cluster I had the largest intra-cluster distance (366.24), suggesting greater genetic variability within this cluster. Cluster II and Cluster III had the largest inter-cluster distance (1634.76), followed by Cluster I and Cluster III (888.61), indicating greater genetic divergence and more opportunities for hybridization. Days to 50% flowering, number of spikelet's per panicle, non panicle-bearing tillers, harvest index, grain yield per plant, and grain output per hectare all showed higher mean values in Cluster III. In terms of plant height, flag leaf area, panicle length, and test weight, Cluster II performed better on average. Cluster II and Cluster III genotypes can therefore be used in breeding programs to produce desired transgressedseargeants and increase productivity.

Conclusion

The genotypes for every character under investigation showed variation, according to the current study's assessment and partitioning of genetic variability. Correlation coefficient analysis, path coefficient analysis, genetic divergence analysis, high PCV, GCV, high heritability, and genetic advancement was noted for the following characteristics: flag leaf length, leaf area, number of filled grains per panicle, total number of grains per panicle, and single plant yield, indicating the significance of these characteristics in selection. Days to 50% flowering, number of filled grains per panicle, total grains per panicle, and harvest index all showed significant positive associations with single plant yield. Days to 50% flowering, plant height, tiller count, number of panicles, flag leaf length, flag leaf width, leaf area, panicle length, total grains per panicle, 1000 grain weight, grain length, grain breadth, kernel length, kernel breadth, L/B ratio, and harvest index all demonstrated positive direct effects at either the phenotypic or genotypic level. Based on the total

results, the traits under study should be prioritized in order to choose the optimal genotypes. When selecting for grain yield, characteristics such as the number of panicles, panicle length, flag leaf length, leaf area, total number of grains per panicle, number of filled grains per panicle, 1000 grain weight, and harvest index are given weight. As a result, it is discovered that the genotypes under investigation can be utilized in rice breeding programs for additional grain yield selection.

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Author contribution

Contributed to the conception and design of the analysis paper. Contributed to the data collection. Data and analysis tools were used to write the analysed paper. Also evaluated the paper and then suggested publishing it in this journal.

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