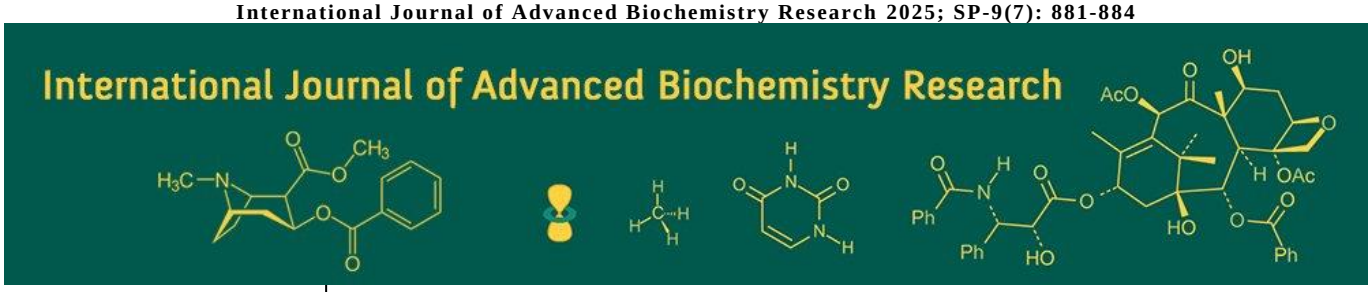

ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2025): 5.29
IJABR 2025; SP-9(7): 881-884
www.biochemjournal.com
Received: 01-04-2025
Accepted: 05-05-2025

Kuldeep Kumar Patel
M.Sc. (Ag), Department of Genetics and Plant Breeding, Institute of Agriculture and Natural Sciences, Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur, Uttar Pradesh, India

Dr. Pandurang B Arsode
Department of Genetics and Plant Breeding, Banaras Hindu University, Varanasi, Uttar Pradesh, India

Dr. Noopur Singh
Assistant Professor, Department of Genetics and Plant Breeding, Institute of Agriculture and Natural Sciences, Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur, Uttar Pradesh, India

Eisha Singh
M.Sc. (Ag), Department of Entomology, Institute of Agriculture and Natural Sciences, Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur, Uttar Pradesh, India

Yuvraj Kumawat
M.Sc. (Ag), Department of Genetics and Plant Breeding, Institute of Agriculture and Natural Sciences, Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur, Uttar Pradesh, India

Alka Yadav
M.Sc. (Ag), Department of Genetics and Plant Breeding, Institute of Agriculture and Natural Sciences, Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur, Uttar Pradesh, India

Corresponding Author:
Kuldeep Kumar Patel
M.Sc. (Ag), Department of Genetics and Plant Breeding, Institute of Agriculture and Natural Sciences, Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur, Uttar Pradesh, India

Assessment of genetic variability, correlation association in different genotypes of rice (*Oryza sativa* L.)

Kuldeep Kumar Patel, Pandurang B Arsode, Noopur Singh, Eisha Singh, Yuvraj Kumawat and Alka Yadav

DOI: https://www.doi.org/10.33545/26174693.2025.v9.i7Sl.5008

Abstract
The present study investigates the genetic variability, heritability, and correlation of yield and yield-attributing traits in 13 rice (*Oryza sativa* L.) genotypes. Analysis of variance revealed significant differences among genotypes for all 13 traits, including days to 50% flowering, days to maturity, plant height, flag leaf length, flag leaf width, panicle length, number of effective tillers, number of grains per panicle, test weight, spikelet fertility, kernel length, kernel breadth, and yield per plant. The highest genotypic coefficient of variation (GCV) was observed for flag leaf width (55.82%) and yield per plant (53.30%), indicating substantial genetic variability for these traits. Moderate GCV values were recorded for number of effective tillers (28.94%), number of grains per panicle (22.33%), days to 50% flowering (17.07%), plant height (16.41%), test weight (15.07%), panicle length (12.88%), flag leaf length (12.54%), kernel length (11.73%), days to maturity (8.42%), spikelet fertility percentage (8.04%), and kernel breadth (6.07%). The phenotypic coefficient of variation (PCV) was highest for flag leaf width (85.64%) and yield per plant (57.09%), with moderate PCV observed for number of effective tillers (31.86%) and number of grains per panicle (23.23%). Correlation analysis revealed significant positive phenotypic and genotypic correlations between yield per plant and traits such as panicle length, plant height, number of grains per panicle, and days to maturity, suggesting these traits as potential selection criteria for yield improvement. The study underscores the importance of considering both genetic and environmental factors in breeding programs aimed at enhancing rice yield and its components.

Keywords: Rice (*Oryza sativa* L.), correlation coefficients, variability, agro-morphological traits

Introduction
A significant cereal crop, rice (*Oryza sativa* L.) Chromosome no. 2n=24 (reported by Mr. Kuwada in 1910) is a member of the Oryzoidea subfamily of the Poaceae family. The "Global Grain" gets its name from the fact that it is a staple in more than 100 nations. In Asia, 50% of the world's population depends on rice for their sustenance, and 90% of the world's rice is cultivated and consumed (Yugandhar *et al.*, 2018) [12]. Rice is a staple food for almost half of the global population. More than half of the world's population relies on Asian farmed rice (*Oryza sativa* L.) for sustenance (Khush 2005) [8]. Rice, a model organism and one of the oldest domesticated crops, has been extensively explored in terms of its phylogenetic and geographic origins (Molina *et al.* 2011; Gross and Zhao 2014; Gutaker *et al.* 2020) [9, 7, 6].

Variability results when there is a difference in genetic makeup of individuals of a plant population or due to the change in environment. When there is considerable degree of genetic variation among individuals of breeding material, selection is effective (Sumanth *et al.*, 2017) [11]. Correlation is a measure of the mutual relationship between two variables. Correlation analysis can help plant breeders understand how improving one characteristic leads to synchronous improvements in others. The relationship between yield and its component features is better understood through studies of the relationship between yield and its components. Phenotypic correlation indicates the degree to which the two factors are linked and is influenced by genetic and environmental connections. Meanwhile, genotypic correlation plays a crucial role in designing effective breeding strategies. Studies on the association between yield-related traits consistently showed a positive relationship between grain yield.

Materials and Methods

The current experimental inquiry was carried out at the Institute of Agriculture and Natural Sciences, Deen Dayal Upadhyaya Gorakhpur University, during the 2024 *kharif season*. Gorakhpur. Geographically, Agricultural Research Farm, Hirapuri Farm, DDUGU, Gorakhpur is located 83 meters above mean sea level and between latitudes 26.75°N and longitudes 83.38'E. Gorakhpur's subtropical climate is characterized by a wet season that usually lasts from mid-June to early October because of the monsoon. In Gorakhpur, the relative humidity varies from around 38% in May, when it's summer, to 84% during the monsoon season in August. with almost 68% on average. The temperature in average varies up to 10 °C to 35 °C.During summer season temperature varies up to 25 °C to 35 °C, In monsoon season 24 °C to 30 °C and in winter season temperature varies up to 23 °C to °C. Rainfall in this area is 112 cm annually. The majority of the soil in this region is alluvial soil, which has a pH between 6.5 and 7.9. Plants of each genotype were spaced 40 cm, spacing between row is 20 cm, apart from one another and 15 cm, plot size area is 1 × 3 meter. Ploughing depth was 12-15 cm and spacing between replications is 60 cm. The phenotypic data was recorded for the 13 yield contributing traits from 5 plants per replication per genotype. Days to 50% flowering (DTF), Days to maturity (DTM), Plant Height (PH), Panicle Length (PL), Flag leaf Length (FLL), Flag leaf Width (FLW), No. of Effective Bearing Tillers (NET), No. of Grains per Panicle (NGPP), Kernel Length (KL), Kernel Breadth (KB), Spikelet fertility % (SPF%), Test weight (TW), Yield per Plant (YPP) were evaluated. For each trait, means of the replicates were used in the data analyses.

Results and Discussion

1. Analysis of Variances: This analysis of variance showed a significant difference between 13 genotypes of rice for 13 characteristics (Table no. 1), including Days to 50% flowering, Days to maturity, Plant height, Flag leaf length, Flag leaf Width, Panicle length, No. of effective tillers. of grain per panicle, test weight, Spikelet Fertility, Kernel length, Kernel breadth and Yield per plant.

2. Genetic Variability: The highest GCV was observed for Flag leaf width (55.82), Yield per plant (53.30) and moderate GPV was observed for No. of effective tiller (28.94), No. of grain per panicle (22.33), Days to 50% flowering (17.07), Plant height (16.41), Test weight (15.07), Panicle length (12.88), Flag leaf length (12.54), Kernel length (11.73), Days to maturity (8.42), Spikelet fertility% (8.04), Kernel length (6.07). Babu *et al.* (2024) [2] and Yadav and Pith (2022) [13].

The highest PCV was recorded for Flag leaf Width (85.64), Yield per plant (57.09), No. of effective tillers (31.86) and moderate PVC was observed for No. of grain per panicle (23.23), Plant height (17.31), Panicle length (17.22), Days to 50% flowering (17.08, Flag leaf length (16.72), test weight (16.08), Kernel length(12.17), Spikelet Fertility (9.37), Days to maturity (8.47) and Kernel breadth (6.84). These findings were like results obtained by Dhanwani *et al.* (2013) [5], Ashish *et al.* (2016) [1], B Demeke *et al.* (2023) [4].

3. Correlation Coefficient estimation: The phenotypic and genotypic correlation have particular significance in breeding programme. The phenotypic correlation coefficient aids in determining the selection index, while the genotypic correlation coefficient offers a close, major of association between character and gives an indication of character that may be useful for overall crop improvement. They may also aid in identifying characteristics that have little of no importance in the selection programme information regarding the relationship between the yield and yield component facilities the choice of suitable breeding method to be applied and selecting the parent for improving the crop. The analysis of correlation coefficient prevalent the degree of association between yield and component given the mutual relationship between the yield component. The correlation of different traits with grain yield was examine both at phenotypic and genotypic level. The present analysis revealed that the Phenotypic correlation coefficient for all the characters is Higher than genotypic correlation coefficient indicating strong association between characters genetically. The traits panicle length, plant height, No. of grain per panicle, Days to maturity were positively and higher significantly correlation with Yield per plant at phenotypic level. At phenotypic level highly significant positive correlation with grain yield was observed with Panicle length, Flag leaf width and plant height. Zhang, Y. (2018) [3], M. A. (2018).

Table 1: Analysis of variance of 13 rice genotypes

Source			Replication	Genotypes	Residual
Degree of Freedom			2	12	24
01	Days to 50% Flowering	DTF	82.69	841.51**	0.39
02	Days to maturity	DTM	56.10	393.33**	1.52
03	Plant Height	PH	206.80	1241.92**	44.93
04	Flag Leaf Length	FLL	0.84	77.401**	15.95
05	Flag leaf Width	FLW	2.27	6.13**	1.91
06	Panicle Length	PL	21.85	42.87**	8.90
07	No. of Effective Tillers	NET	6.23	12.3269**	0.81
08	No. of Grain per panicle	NGPP	232.70	7270.3**	194.60
09	Test Weight	TW	0.02	31.841**	1.40
10	Spikelet Fertility	SPF	56.21	137.13**	14.65
11	Kernel Length	KL	0.13	3.03797**	0.08
12	Kernel Breadth	KB	0.00	0.037627**	0.00
13	Yield per Plant	YPP	42.03	182.456**	8.53

Table 2: Mean performance of 13 rice genotypes

Genotype	DTF	DTM	PH	FLL	FLW	PL	NPP	NET	NGPP	TW	SPF	KL	KB	YPP
CRDDHAN5	73.67	133.67	89.50	41.66	1.55	25.11	6.67	6.50	141.00	13.53	72.22	7.99	1.50	4.81
CRDDHAN 802	78.67	141.33	124.75	35.83	6.86	29.61	12.00	12.00	283.50	19.43	87.26	7.34	1.72	35.60
PB1692	87.33	124.33	131.31	34.83	1.73	28.23	7.67	7.50	196.50	24.84	78.05	9.87	1.78	16.24
RANJEETSUB1	125.00	150.00	112.75	29.29	1.63	16.58	8.00	8.00	263.00	19.14	82.94	7.79	1.81	18.96
CRDDHAN 801	109.67	144.33	120.30	29.51	1.96	26.58	7.67	7.50	255.50	19.36	77.86	7.52	1.78	12.93
SABOURMOTI	86.67	124.33	101.82	31.16	1.91	23.41	5.00	5.00	179.16	20.34	81.22	8.58	1.70	7.98
CR1009SUB 1	124.33	152.33	110.08	37.57	1.63	24.91	7.67	7.50	218.99	22.24	65.14	7.31	1.99	15.14
DRRDHAN 39	97.33	124.67	120.48	35.13	1.91	32.31	4.50	4.50	192.83	24.45	76.26	9.64	1.85	10.16
CRDDHAN8	86.00	125.67	137.66	42.33	1.71	28.00	5.50	5.50	201.83	24.30	82.28	9.12	1.77	11.06
BVSD1	88.00	125.00	169.99	45.96	1.79	25.24	4.50	4.50	236.96	23.72	75.92	9.23	1.83	10.55
PRR121	96.33	124.33	108.59	34.49	1.60	24.13	5.00	5.00	138.50	24.15	76.52	10.11	1.76	7.07
CRDDHAN 800	108.33	144.67	113.66	32.49	1.83	26.66	7.00	7.00	225.80	18.50	88.34	7.79	1.79	16.49
RAJENDRAMANSURI	113.67	149.00	141.50	38.94	1.53	28.74	7.50	7.50	294.33	20.78	89.06	7.81	1.67	18.70

Table 3: Genetic Variability, Heritability, and Genetic advance

Traits	Minimum	Maximum	Mean	SE	CD at 5%	Genotypic Variance	Phenotypic Variance	GCV	PCV	Heritability (%)	GA	GAas % of mean
DTF	73.67	125.00	98.24	0.36	1.05	280.37	280.76	17.07	17.08	95.51	34.47	35.15
DTM	124.33	152.33	136.02	0.71	2.08	130.60	132.12	8.42	8.47	91.96	23.41	17.25
PH	89.50	169.99	122.79	3.87	11.30	399.00	443.93	16.41	17.31	90.89	39.01	32.05
FLL	29.29	45.96	36.30	2.31	6.73	20.48	36.43	12.54	16.72	87.90	6.99	19.37
FLW	1.53	6.86	2.40	0.80	2.33	1.41	3.32	55.82	85.64	92.81	1.59	74.95
PL	16.58	32.31	25.89	1.72	5.03	11.32	20.22	12.88	17.22	59.02	5.19	19.86
NPP	4.50	12.00	7.01	0.53	1.54	3.89	4.72	28.92	31.87	89.17	3.69	54.07
NET	4.50	12.00	6.97	0.52	1.52	3.84	4.65	28.94	31.86	45.04	3.67	54.15
NGPP	138.50	294.33	217.38	8.05	23.51	2358.57	2553.14	22.33	23.23	92.12	96.16	44.20
TW	13.53	24.84	20.88	0.68	1.99	10.15	11.55	15.07	16.08	60.91	6.15	29.10
SPF	65.14	89.06	79.15	2.21	6.45	40.83	55.48	8.04	9.37	77.77	11.29	14.21
KL	7.31	10.11	8.50	0.16	0.46	0.99	1.06	11.73	12.17	77.51	1.97	23.29
KB	1.50	1.99	1.76	0.03	0.09	0.01	0.01	6.07	6.84	40.19	0.20	11.10
YPP	4.81	35.60	15.07	1.69	4.92	57.97	66.51	53.30	57.09	79.69	14.64	102.52

Table 4: Correlation Coefficient estimation

Traits	DTF	DTM	PH	FLL	FLW	PL	NPP	NET	NGPP	TW	SPF	KL	KB	YPP
DTF	1**	0.7218**	-0.0344	-0.3649*	-0.2793	-0.3171*	0.0837	0.083	0.4302**	0.0553	-0.02	-0.3825*	0.5462**	0.113
DTM		1**	-0.1565	-0.2375	0.084	-0.214	0.5753**	0.5737**	0.6335**	-0.4493**	0.1405NS	-0.8579**	0.1595 NS	0.4752**
PH			1**	0.4465**	0.0308	0.1929	-0.0981	-0.088	0.4823**	0.5419**	0.1264	0.2549	0.1916	0.2187
FLL				1**	-0.176	0.2978	-0.1441	-0.1426	-0.1161	0.0997	-0.2484	0.1423	-0.1157	-0.1351
FLW					1**	0.1872	0.4404**	0.4496**	0.3494*	-0.026	0.325*	-0.257	-0.0848	0.5025**
PL						1**	0.0365	0.0363	-0.0308	0.2493	0.1337	0.1444	-0.0842	0.0703
NET								1**	0.569**	-0.4038*	0.2499	-0.6013**	-0.0356	0.8743**
NGPP									1**	-0.0616	0.4608**	-0.5709**	0.195	0.7262**
TW										1**	-0.09	0.6552**	0.5235**	-0.0944
SPF											1**	-0.1845	-0.1881	0.407*
KL												1**	0.0207	-0.4464**
KB													1**	0.1416
YPP														1**

Conclusion

Present investigation experimental material consisting of 13 genotypes was studied to know that genetic variability for 13 characters. The presence of genetic variability was confirmed by major variation for several features using ANOVA and Genotypic coefficient of variation. Furthermore, it is observed that a majority of the characteristics had high heritability estimates, and several traits had significant genetic progress. As a result, the material has a high degree of genetic variety for the selection process. The correlation coefficient study revealed that grain yield per plant high significant positive correlation with Panicle length, Flag leaf width, and Plant height. it shows that these traits should be considered during the selection of plant.

References

1. Ashish G, Sabagh AE, Ghareb A, Rewainy IEL. Evaluation of promising lines in rice (*Oryza sativa* L.) to agronomic and genetic performance under Egyptian conditions. International Journal of Agro and Agricultural Research. 2016;8(3):52-57.
2. Babu H, Thouseem N. Genetic variability, correlation and path analysis of yield and its attributing traits in rice (*Oryza sativa* L.). International Journal of Plant & Soil Science. 2024;36(8):1029-1043. https://doi.org/10.9734/ijpss/2024/v36i84936
3. Chen JY, Zhang HW, Zhang HL, *et al*. Natural variation at qHd1 affects heading date acceleration at high temperatures with pleiotropism for yield traits in rice. 2018.

4. Demeke B, Dejene T, Abebe D. Genetic variability, heritability, and genetic advance of morphological, yield related and quality traits in upland rice (*Oryza sativa* L.) genotypes at Pawe, northwestern Ethiopia. Cogent Food & Agriculture. 2023;9(1):2157099.
5. Dhanwani RK, Sarawgi AK, Solanki A, Tiwari JK. Genetic variability analysis for various yield attributing and quality traits in rice (*Oryza sativa* L.). The Bioscan. 2013;8(4):1403-1407.
6. Gutaker RM, Groen SC, Bellis ES, *et al.* Genomic history and ecology of the geographic spread of rice. Nature Plants. 2020;6:492-502.
7. Gross BL, Zhao Z. Archaeological and genetic insights into the origins of domesticated rice. Proceedings of the National Academy of Sciences. 2014;111:6190-6197.
8. Khush GS. What it will take to feed 5.0 billion rice consumers in 2030. Plant Molecular Biology. 2005;59:1-6.
9. Molina J, Sikora M, Garud N, *et al.* Molecular evidence for a single evolutionary origin of domesticated rice. Proceedings of the National Academy of Sciences. 2011;108:8351-8356.
10. Ogunniya MI. Genetic variability, heritability and genetic advance for yield and its related traits in rainfed lowland rice (*Oryza sativa* L.) genotypes at Fogera and Pawe, Ethiopia. Advances in Crop Science and Technology. 2017;5(2):Article 272.
11. Sumanth V, Suresh BG, Ram BJ, Srujana G. Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (*Oryza sativa* L.). Journal of Pharmacognosy and Phytochemistry. 2017;6(4):1437-1439.
12. Yugandhar RP, Kota S, Kiran UB, Shridhar M. Principal component analysis for agro-morphological and quality characters in germplasm of rice (*Oryza sativa* L.). International Journal of Advanced Biological Research. 2018;8(2):268-273.
13. Yadav EK, Pitha CC. Studies on genetic variability, divergence and characters associated with yield components in rice. International Journal of Environment and Climate Change. 2022;12(11):2105-2115. https://doi.org/10.9734/ijecc/2022/v12i1131200