Indian Journal of Agricultural Sciences **94** (7): 786–790, July 2024/Short Communication
https://doi.org/10.56093/ijas.v94i7.146835

Genetic variability, association and diversity analysis of yield and its component traits in rice (*Oryza sativa*) germplasm

VAIBHAV PATHAK[1], C H PRASUNA[1], B UMAKANTH[1], K SUREKHA[1], L V SUBBARAO[1] and G PADMAVATHI[1]*

ICAR-Indian Institute of Rice Research, Hyderabad, Telangana 500 030, India

Received: 27 December 2023; Accepted: 13 May 2024

Keywords: Correlation, Genetic divergence, Genetic variability, Heritability, Rice

Rice (*Oryza sativa* L.) is the third largest cereal grown in 162 Mha with 755 Mt global production (FAO 2022). India ranks first in the area (44.8 Mha) and second in production (130 Mt) in the world (https://pib.gov.in 2023). During the last five decades, more than six-fold increase in rice production (20.58–130.29 Mt) (https://agricoop.gov.in) was achieved, which underpinned the country's self-sufficiency and rice export. Rice genetic resources are bestowed with enormous genetic diversity which serves as potential sources for generating elite lines as they display wider adaptability across environments (Brar and Khush 2002). Therefore, the present study was carried out to evaluate extent of genetic variability, heritability, diversity and the relationship between yield and its component traits in a collection of 60 rice germplasm accessions.

An experiment was conducted during winter (*rabi*) season of 2022 at ICAR-Indian Institute of Rice Research, Hyderabad, Telangana. A set of 60 rice germplasm was grown in five-row plots measuring 5 m in length, with a spacing of 20 cm × 15 cm using a randomized block design (RBD) in three replications. The prescribed set of farming practices was followed and the data were collected from 5 randomly selected plants. The statistical analysis involved testing the significance of each character using the methodology proposed by Panse and Sukhatme (1985). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated using the formula recommended by Burton (1952). The heritability in the broad sense and the genetic advance were estimated as suggested by Allard (1960) and Johnson *et al.* (1955), respectively. Nitrogen concentration in grain was determined by micro-Kjeldahl method (Jackson 1991). The protein content was determined by multiplying nitrogen content with a 5.95 factor (Huang *et al.* 2019). Correlation analysis was performed using the R programme (R Development Core Team 2020). The degree of genetic divergence was assessed using Mahalanobis's D^2 statistic (Mahalanobis 1936). The genotypes were classified into distinct clusters utilizing Tocher's method (Rao 1952).

Genetic variability: The analysis of variance revealed statistically significant differences (P<0.01) for all 10 traits examined, suggesting genetic variation among the genotypes (Fig. 1, Table 1). The highest yield (22.76 g) was recorded in IC458483 and 100-grain weight was found to be maximum in IC75919 (2.92 g). Genotype IC210775 registered the longest panicle length (31 cm). Total and effective tillers were maximum for IC210760 (22) and IC75980 (19), respectively. The genotype IC 210767 was found to be the earliest genotype with 107 days duration. High protein content was found in IC75965 (9.8%) (Supplementary Table 1). The observed higher genotypic variance compared to environmental variance in most traits except panicle length and maturity duration indicated that the diversity observed in the test material primarily resulted from genetic factors rather than environmental factors (Boranayaka *et al.* 2020). Hence, selection and hybridization will possibly facilitate the genetic improvement of the crop.

The values of GCV and PCV were high for total tiller number (24.8 and 28.3%), effective tiller number (25.9 and 30.3%) and grain yield (23.2 and 27.1%), respectively (Table 1). The high estimates of GCV and PCV together with moderate to high heritability (45–90%) except for days to maturity (29%) and grain width (39%) suggested a scope for improving individual traits through simple selection.

Heritability and genetic advance: Genetic gain under selection can be more accurately predicted by combining heritability estimates with genetic advance. Analysis revealed high heritability (>60%) with high GAM (>20%) for plant height (90 and 41.3%), total tillers (77 and 57.6%) and effective tillers (73 and 58.3%), grain yield (70 and 51.1%), 100-grain weight (96 and 32.6%) and grain length

[1]ICAR-Indian Institute of Rice Research, Hyderabad, Telangana. *Corrresponding author email: padmaguntupalli6@gmail.com

Table 1 Genetic parameters of variability for agronomic traits in rice germplasm

	PH	TTN	ETN	PL	DM	GY	HGW	GL	GW	P
Range	70.9–133	8–22	6–19	18.2–31	107–164	7.55–22.76	1.58–2.92	6.7–10.4	1.1–2.0	6.6–9.8
Mean	95.1	12.6	10.3	24.8	137	17.1	2.35	8.36	1.7	8.68
ECV	5.5	13.5	15.8	9.37	12.16	15.3	2.43	3.5	9.55	7.06
Vg	247	9.9	7.2	3.85	111.4	15.7	0.09	0.71	0.02	0.31
Vp	275	12.8	9.9	9.26	389.4	22.6	0.09	0.79	0.04	0.69
Ve	28	2.9	2.7	5.41	277.9	6.8	0	0.09	0.03	0.38
GCV	16.5	24.8	25.9	7.91	7.7	23.2	12.6	10	7.57	6.44
PCV	17.4	28.3	30.3	12.27	14.4	27.1	12.8	10.6	12.18	9.56
h^2b	90	77	73	42	29	70	96	89	39	45
GA	39.3	7.3	6	3.34	14.91	8.7	0.77	2.1	0.21	0.99
GAM	41.3	57.6	58.3	13.47	10.88	51.1	32.6	25	12.41	11.46

PH, Plant height (cm); TTN, Total tiller number; ETN, Effective tiller number; PL, Panicle length (cm); DM, Days to maturity (Days); GY, Grain yield (g); HGW, 100-grain weight (g); GL, Grain length (mm); GW, Grain width (mm); P, Protein percentage (%); Vg, Genotypic variance; Vp, Phenotypic variance; Ve, Environmental variance; GCV, Genotypic coefficient of variation; PCV, Phenotypic coefficient of variation; h^2b, Broad sense per cent (%); GA, Genetic advance; GAM, Genetic advance over mean (%).

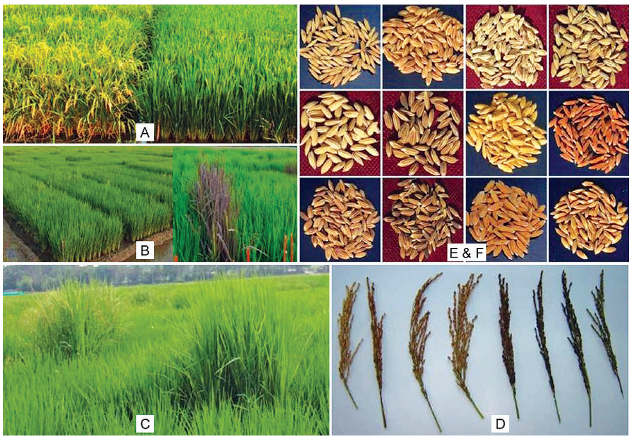

Fig. 1 Genetic diversity in rice germplasm accessions (A) Maturity duration; (B) Pigmentation of plants; (C) Plant height; (D) Panicle length; (E) Grain type; and (F) Grain colour.

(89 and 25%). This indicates additive gene action and the potency of selection for these attributes (Srujana *et al.* 2017, Yadav *et al.* 2017, Bhargavi *et al.* 2021).

Correlation analysis: The correlation between the yield and yield components is important for devising strategies for selection of plants. In this study, GY was positively correlated with PH (r = 0.17), TTN (r = 0.21), ETN (r = 0.11), PL (r = 0.25), DM (r = 0.15), HGW (r = 0.01) and GL (r = 0.29) while negatively correlated with GW (r = -0.14) and P% (r = -0.18) (Fig. 2). These findings suggest that selecting for ETN, PL, DM and 100 GW traits could enhance yield (Kritika *et al.* 2021). The observed significant genotypic association of these traits can be attributed to the pleiotropic effect between genes governing various traits. A significant positive correlation at 0.0001 was registered between PH and PL (r = 0.51) and also between TTN and ETN (r = 0.93). PH displayed a positive significant correlation at 0.001 with TTN (r = 0.47) while HGW with GW (r = 0.42). HGW was positively correlated with grain width (r = 0.42) and grain length (r = 0.32) and a similar association was noticed between 100 GW and kernel breadth by Venkata Lakshmi *et al.* (2014).

Genetic divergence analysis: Genetic divergence studies revealed the categorization of germplasm accessions into 8 clusters based on their D2 values, implying a high diversity in the rice genotypes. Maximum accessions (18) were observed in clusters I followed by cluster II (12), cluster III (12), cluster V (9) and VI (6), while clusters IV, VII and VIII consisted of 1 accession each (Fig. 3). The higher inter cluster distance observed for all traits reflected substantial genetic diversity among the genotypes (Table 2). The inter-cluster distance estimates showed that clusters VI and VII diverged the most (480.68), followed by V and VI (385.04), VI and VIII (384.05), and IV and VI (313.16). Cluster VI has the greatest intra-cluster distance (D2 = 80.12), followed by cluster V (D2 = 62.18). Choosing genotypes from distant clusters for hybridization is expected to execute maximum heterosis among the segregants and eventually, useful recombinants would be recovered (Kiran *et al.* 2023).

Cluster-wise mean values of 10 different traits were estimated to assess the superiority of clusters in the improvement of various characters. Further, it was noticed that variation among maximum cluster means existed for different characters supporting the observed diversity (Table 3). No cluster was found with genotypes possessing all favourable traits and therefore, recombination breeding between genotypes of different clusters would be promising (Banumati *et al.* 2010).

In view of the intrinsic performance of the superior genotypes within the clusters, the germplasm IC458483, IC210775, IC75919, IC75980 and IC75965 from clusters VIII, I, IV, VII and V, respectively could be directly selected as they displayed the best agronomic traits such as grain yield, panicle length, 100-grain weight, effective tillers and proteins, respectively. It was noticed that the high heterotic progeny with high yield, more productive

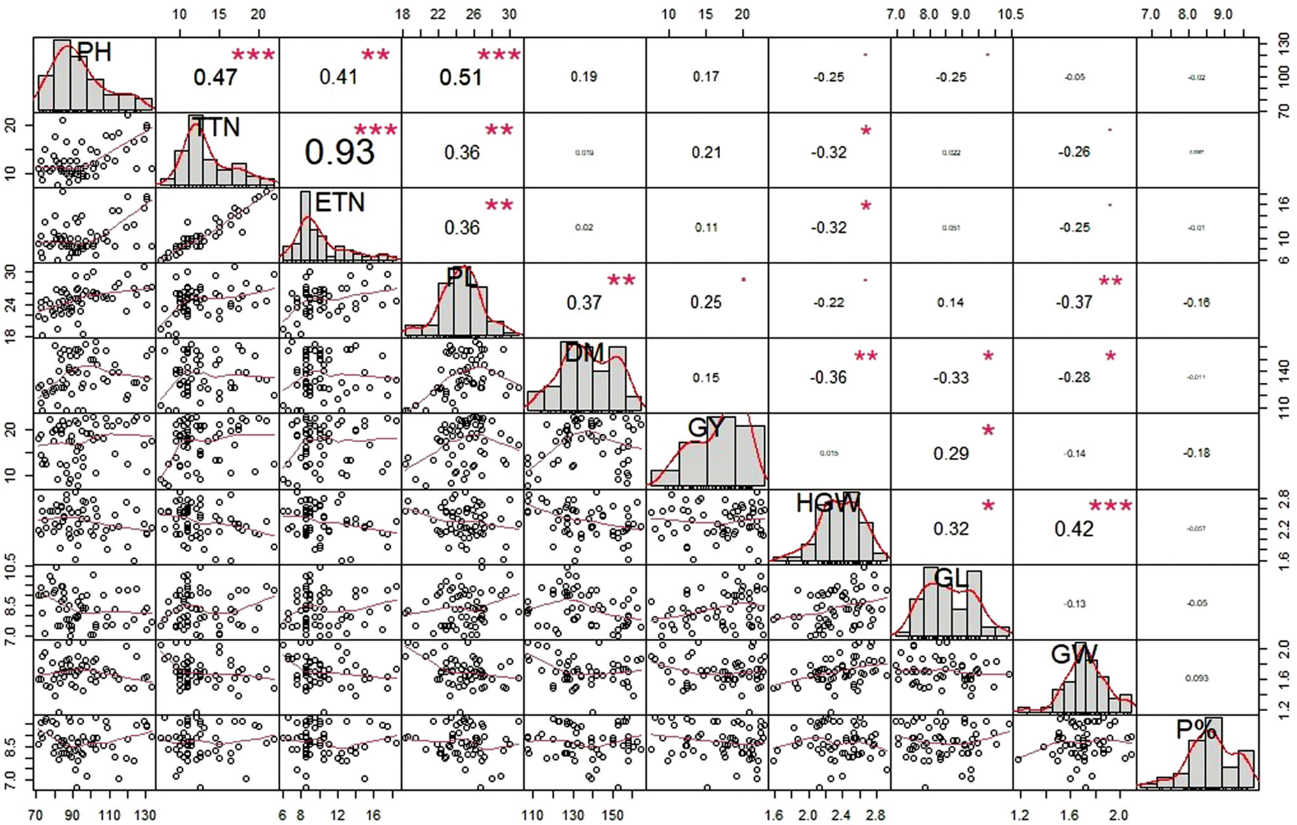

Fig. 2 Genotypic correlation coefficients of yield and its associated traits in germplasm.
PH, Plant height; TTN, Total tiller number; ETN, Effective tiller number; PL, Panicle length; DM, Days to maturity; GY, Grain yield; HGW, 100-grain weight; GL Grain length; GW, Grain weight; P%, Protein percentage.

Table 2 Mean inter and intra-cluster (diagonal) distances for yield traits in rice germplasm lines

Clusters	I	II	III	IV	V	VI	VII	VIII
I	39.41	107.12	127.81	60.66	65.84	278.21	143.97	110.61
II		50.58	129.87	148.70	166.17	121.53	310.67	245.27
III			55.09	98.14	192.03	173.45	145.10	106.97
IV				30.12	80.98	313.16	62.60	81.89
V					62.18	385.04	156.61	153.90
VI						80.13	480.68	384.05
VII							36.01	43.89
VIII								0.60

Table 3 Cluster means of yield traits and their contribution to total divergence in rice germplasm lines

Cluster	Plant height (cm)	Tillers/ plant	Effective tillers/ plant	Panicle length (cm)	Days to maturity	Grain yield (g)	100-grain weight (g)	Grain length (mm)	Grain width (mm)	Protein (%)
Cluster I	87.4	12.2	10.1	24.42	134.7	19.1	2.49	8.8	1.67	8.53
Cluster II	85.4	11.2	9.5	23.85	139.9	15.0	2.15	8.3	1.68	8.78
Cluster III	114.6	15.2*	12	26.37	147.6*	18.2	2.25	7.7	1.6	8.85
Cluster IV	92.7	11.0	9	25.10	139.5	21.2	2.55	6.7	1.7	8.74
Cluster V	86.8	10.6	8.6	23.65	123.4	14.1	2.71	8.6	1.8	8.52
Cluster VI	102.3	14.9	12	26.41*	141.3	14.96	1.79	7.9	1.5	8.74
Cluster VII	119.3	15.0	12.1*	22.70	117.0	21.0	2.73*	7.5	2.0*	7.95
Cluster VIII	124.5*	11.0	8.5	25.80	130.5	22.7*	2.56	9.30	1.9	9.43*
Contribution (%)	4	8	9	0	18	44	10	04	0	3

*Maximum

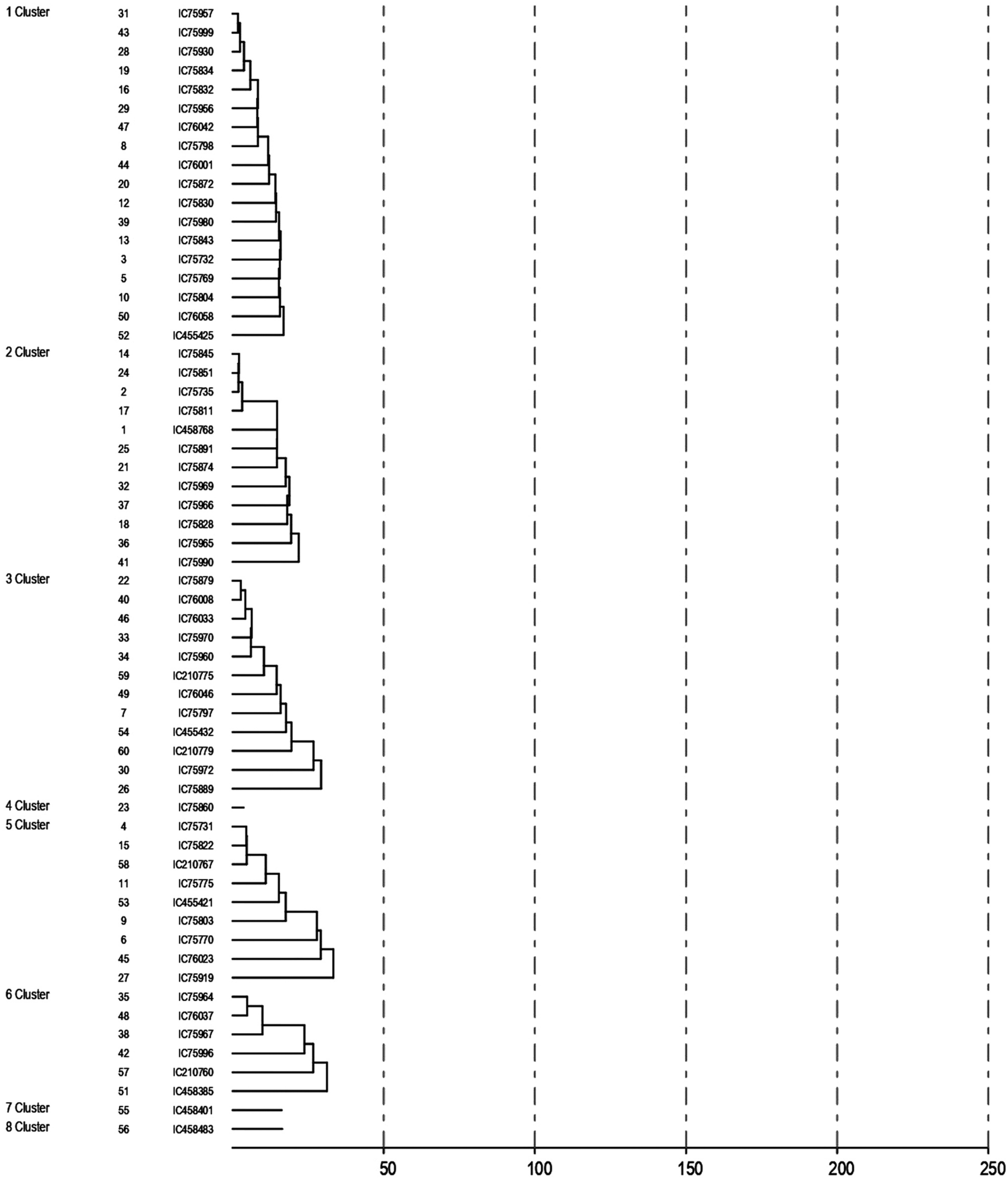

Fig. 3 Clustering of rice genotypes using Tocher's method.

tillers and long panicles would possibly be recovered in the segregating generations by crossing genetically dissimilar parents of the most diverse clusters, i.e. VIII, VII and VI. In this context, the genotypes of cluster VIII (IC76023, IC455432, IC458401, IC458483 and cluster VII (IC75732, IC75769, IC75804, IC75832, IC75872, IC75860, IC75889, IC75980, IC76001, IC76042, IC76046, IC76058) and cluster VI (IC75972, IC75996, IC458385, IC210760) could be chosen as parents in a breeding effort aimed at increasing crop production. The germplasm from clusters I, II, IV, V and VI displayed low plant height (<110 cm) and hence, it is possible to recover semi-dwarf segregants in breeding programmes. The germplasm of clusters III, VI and IV exploited as potential parents for developing late duration breeding material, while cluster VII could generate early duration material. It is interesting to note that the germplasm of cluster VIII is a good source for breeding high yielding as well as protein rich genotypes because they are superior in grain yield and protein content.

Among all traits, grain yield accounted significant genetic divergence (44%), followed by days to maturity (18%), 100-grain weight (10%), and effective tillers (9%) (Table 3). These traits contributed >80% towards total divergence, so they should be given priority in crossing programs and selection of segregants in succeeding segregating generations (Krishnaveni and Rani 2015, Supriya *et al.* 2017) for test weight and grain yield.

SUMMARY

An experiment was conducted during winter (*rabi*) season of 2022 at ICAR-Indian Institute of Rice Research, Hyderabad, Telangana to evaluate extent of genetic variability, heritability, diversity and the relationship between yield and its component traits in a collection of 60 rice germplasm accessions. Results showed that germplasm accessions exhibited ample genetic variability and diversity for yield traits. Based on per se performance, inter crosses between the genotypes IC458483 with high grain yield, IC210775 with more panicle length, IC75919 with high 100-grain weight, IC75980 with more productive tillers and IC75965 with high protein content could produce positive transgressive segregants for improving respective traits. Plant height, total and effective tillers, grain yield and 100-grain weight traits which exhibited the highest heritability and genetic advance could be vital for selection in hybridization programmes. Crossing among genotypes of diverse clusters specifically VI, VII and VIII is suggested as this could create a broad variation useful for selecting genotypes with both high yield and long panicles.

REFERENCES

Allard R W. 1960. *Principles of Plant Breeding*, 1st edn. John Wiley and sons Inc, New York, USA.

Banumati S, Manimaran R, Sheeba A, Manivannan N, Ramya B, Kumar D and Ramasubramanian G V. 2010. Genetic diversity analysis of rice germplasm lines for yield attributing traits. *Electronic Journal of Plant Breeding* **1**(4): 500–04.

Bhargavi M, Shanthi P, Reddy V L N, Mohan Reddy D and Ravindra Reddy B. 2021. Estimates of genetic variability, heritability, and genetic advance for grain yield and other yield attributing traits in rice (*Oryza sativa* L.). *The Pharma Innovation Journal* **10**(5): 507–11.

Boranayaka M B, Lokesha R, Latha H C and Mahanth Shivayogayya K. 2020. Genetic variability, character association, frequency and normality distribution studies for F2 population of BPT-5204 × WAB-450 cross in rice (*Oryza sativa* L.) *International Journal of Current Microbiology and Applied Science* **9**(5): 278–95.

Brar D S and Khush G S. 2002. Transfering genes from wild species into rice. *Quantitative Genetics, Genomics and Plant Breeding,* pp. 197–217. M S Kang (Ed). A CABI Publication, Wallingford, UK.

Burton G W. 1952. Quantitative inheritance in grasses. *(In) Proceedings of International Grassland Congress* **1**: 277–83.

FAO. 2022. Food Inspection. Food safety and quality. FAO, Rome, Italy.

Huang M, Zhang H, Zhao C, Chen G and Zou Y. 2019. Amino acid content in rice grains is affected by high temperature during the early grain-filling period. *Scientific Reporter* **9**(1): 2700.

Jackson P E, Krol J, Heckenberg A L, Mientijes M and Staal W. 1991. Determination of total nitrogen in food, environmental and other samples by ion chromatography after kjeldahl digestion. *Journal of Chromatography* **546**: 405–10.

Johnson H N, Robinson H F and Comstock R E. 1955. Estimates of genetic and environmental variability in soybean. *Agronomy Journal* **27**: 314–18.

Kiran A, Sharma D J, Subbarao L V, Gireesh C and Agrawal A P. 2023. Correlation coefficient and path coefficient analysis for yield, yield attributing traits and nutritional traits in rice genotypes. *The Pharma Innovation Journal* **12**(2): 1978–83.

Krishnaveni B and Rani N S. 2015. Association of grain yield with quality characteristics and other yield components in rice. *Oryza* **43**(4): 320–22.

Kritika Williams, Aman Mishra, Akansha Verma, B G Suresh and Lavanya G R. 2021. Genetic variability and correlation studies for yield and yield related traits in rice (*Oryza sativa* L.) genotypes. *International Journal of Current Microbiology and Applied Science* **10**(1): 752–64.

Mahalanobis P C. 1936. On the generalized distance in statistics. *Proceedings of the National Institute of Sciences of India* **2**: 49–55.

Panse V G and Sukhatme P V. 1985. *Statistical Methods for Agricultural Workers*. ICAR, New Delhi.

R Development Core Team. 2020. R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing. Available at: http://www.R-project.org

Rao C R. 1952. *Advanced Statistical Methods in Biometrical Research*. John Wiley and Sons, New York, USA.

Srujana G, Suresh B G, Lavanya G R, Jalandhar Ram B and Sumanth V. 2017. Studies on genetic variability, heritability and genetic advance for yield and quality components in rice *(Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry* **6**(4): 564–66.

Supriya K, Vanisri S, Jagadeeswar R and M Sreedhar. 2017. Genetic diversity for yield: Its contributing characters in rice (*Oryza sativa*). *International Journal of Current Microbiology and Applied Sciences* **6**(10): 2424–28.

Venkata Lakshmi M, Suneetha Y, Yugandhar G and Venkata Lakshmi N. 2014. Correlation studies in rice (*Oryza sativa* L.). *International Journal of Genetic Engineering and Biotechnology* **5**(2): 121–26.

Yadav R, Rajpoot P, Verma O P, Singh P K, Singh P and Pathak V. 2017. Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) for grain yield and its contributing attributes under sodic soil. *Journal of Pharmacognosy and Phytochemistry* **6**(5): 1294–96.