Genetic Variability and Correlation Studies in High-yielding Varieties of Rice (*Oryza sativa* L.)

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Abstract

Rice is the major staple food crop of India and there is an anticipated high demand due to increasing population. Information on yield contributing traits and the level of heritable variation in these traits is essential for establishing the genotype's potential for future breeding programmes. The study was conducted to evaluate the variability in yield contributing traits and their correlation in a set of released rice varieties from ICAR - Indian Institute of Rice Research, Hyderabad. The objective of the study was to estimate the genotypic and phenotypic coefficient of variation, heritability and genetic advance of yield and related traits using thirty-two rice cultivars. For all evaluated traits, the phenotypic coefficient of variation was found to be significantly higher than the genotypic coefficient of variance, implying that the expression of these traits is influenced by the environment. High heritability coupled with high genetic advance was observed for panicle weight whereas low heritability coupled with low genetic advance over per cent mean was recorded for productive tiller number. The traits *viz.,* tiller number, productive tiller number, flag leaf width, panicle weight, number of grains per panicle, number of filled grains per panicle and test weight exhibited a positive association, whereas the number of unfilled grains per panicle and plant height exhibited negative association with grain yield.

Introduction

Rice (*Oryza sativa* L.) is the principal staple food crop for human race and one of the world's foremost crops, with over a hundred nations cultivating it. Rice is grown in a variety of climatic conditions around the world, including tropical and subtropical climates. During the main crop season (*Kharif*), the principal rice ecology is found across temperatures ranging from 20-40 °C in flooded environments and with a solar radiation requirement of 25-95 per cent. Rice is grown in more than 150 million hectares around the world, with India accounting for one-third of the total (*i.e.*, 44 million hectares). However, India's rice production (122 million tonnes) is only a fifth of global rice production (503 million tonnes). India is first in the world in terms of area and second in terms of rice production. Rice is a calorie source for more than 70% of India's population and a key source of income for millions of farmers.

The global population is steadily rising, with an anticipated 9.1 billion people by 2050, but agricultural productivity is not keeping pace. By 2050, global agricultural production is expected to increase by 100-110 per cent to feed the whole population (FAO 2009). Rice production is being threatened by dwindling natural resources, socio-economic constraints, biotic and abiotic stresses and climatic uncertainty as the demand grows.

Variation is the prerequisite for every breeding programme. The range of genetic variability in selected genotypes is determined by the degree of genetic variation among genotypes, which provides more selection chances. In establishing the genotype's potential for future breeding programmes, the level of heritable variation in the attributes is particularly useful. To measure the degree of diversity in a germplasm sample, genetic parameters such as the genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV) can be considered. Estimating heritability is a useful method for proving the consistency of phenotypic value. As a result, increased heritability benefits in the character selection procedure. Heritability is a term used to describe how much genetic variation across individuals in a community causes variation in phenotypic traits. In evaluating the gain under selection, heritability estimates combined with genetic advancement are usually more informative than heritability estimates alone.

Grain yield is a multifaceted trait that is influenced by a number of various aspects, and it responds poorly to direct selection when decisions are made solely on the basis of yield. Knowledge of the relationship between grain yield and its component features will be useful in improving grain yield. As a result, correlation analysis is required to determine the relationship between yield and yield components (Akhtar *et al.*, 2011). Correlation measures the degree and direction of association between two or more variables and provides information about yield contributing characters. This information is useful to a plant breeder in the selection of elite genotypes from diverse genetic populations. On the other hand, the genotypic correlation, which represents the genetic component of the phenotypic correlation, is one of inheritable nature and is thus utilized to drive breeding programmes. In plant breeding, estimates of the correlation coefficient are useful in determining

yield components, which can be used for genetic improvement of yield.

The focus of this study is to estimate the correlation among the various quantitative traits of rice in order to understand the relationship between grain yield and its constituent features and aid the effective selection for a successful breeding program. The high-yielding varieties released from ICAR-Indian Institute of Rice Research, Hyderabad were used in this study to understand the range of available yield potential. The finding of this research will assist in the identification of suitable genetic material and for further development of high-yielding varieties in the subsequent breeding programmes to support varietal improvement.

Materials and Methods

The experiment was conducted during *kharif*, 2021 on IIRR farm located at International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad, Telangana, India. The experiment material comprises of 32 rice genotypes (DRR Cultivars) **(Table 1)** and the experiment was planned in a randomized block design. Each experimental unit consists of a plot size of 2m². All genotypes were sown separately in an experimental unit with three replications. 30 days old seedlings were transplanted with a spacing of 20 cm × 20 cm. The crop was grown with the recommended package of practices. Fertilizers were applied to the crop on a regular basis, as per conventional recommendations. Intercultural operations were carried out as per the requirement. Observations for 12 traits *viz*., plant height, tiller number, productive tiller number, flag leaf length, flag leaf width, panicle length, panicle weight, number of grains per panicle, number of filled grains per panicle, number of unfilled grains per panicle, single plant yield and test weight were recorded from three randomly selected plants in each replication. The genotypic and phenotypic coefficient of variation

was calculated as per the formula suggested by Burton and Devane (1953). Heritability in broad sense was calculated as suggested by Allard (1960). From the heritability estimates, the genetic advance (GA) was calculated as suggested by Johnson *et al.,* (1955). The correlation between characters was calculated by using the method suggested by Dewey and Lu (1959).

Table 1: List of rice genotypes used in the experiment

S. No.	Cultivars	S. No.	Cultivars	S. No.	Cultivars
1	DRR Dhan 39	12	DRR Dhan 50	23	Binadhan 17
2	DRR Dhan 40	13	DRR Dhan 51	24	Salivahana
3	DRR Dhan 41	14	DRR Dhan 54	25	RP Bio 226
4	DRR Dhan 42	15	DRR Dhan 55	26	Varadhan
5	DRR Dhan 43	16	DRR Dhan 56	27	Swarnadhan
6	DRR Dhan 44	17	DRR Dhan 62	28	Akshaydhan
7	DRR Dhan 45	18	Sugandamati	29	Jaya
8	DRR Dhan 46	19	IR 64	30	Sampada
9	DRR Dhan 47	20	Vasumati	31	Dhan rasi
10	DRR Dhan 48	21	Kasturi	32	Jarava
11	DRR Dhan 49	22	Binadhan 11		

Results and Discussion

The degree of diversity for any trait is critical for crop improvement through breeding. The estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) heritability and genetic advance for the traits under study were presented in **(Table 2)**. The extent of the differences between GCV and PCV explains the amount of the influence of the growing environment on those characteristics. The higher divergence between PCV and GCV indicates that the expression of the specific trait is heavily influenced by the environment. For all evaluated traits, the phenotypic coefficient of variation was found to be significantly higher than the genotypic coefficient of variance, implying that the expression of these traits is influenced by the environment.

The estimate of the phenotypic coefficient of variation was found to be high in the number of unfilled grains per panicle (107.46). A higher magnitude of the phenotypic coefficient of variation was recorded in panicle weight (37.57), number of grains per panicle (26.44), number of filled grains per panicle (26.25), tiller number (23.53) and productive tiller number (22.38). Jahan *et al.*, (2020) observed a similar effect in panicle weight while Chavan *et al.*, (2022)'s findings were similar to findings for number of filled grains per panicle. The traits such as flag leaf length (19.98), test weight (19.27), single plant yield (17.75) and flag leaf width (16.07) exhibited a moderate level of phenotypic coefficient of variation. Low estimates of PCV were recorded in plant height (11.31) and panicle length (10.89). Similarly, Gupta *et al.*, (2022) observed a similar effect in the case of test weight and panicle length.

Table 2: Components of genetic parameters for yield and its attributing characters in rice

Traits	Range		Mean	Heritability in broad sense (h²)	GCV	PCV	GA	GA % mean
	Min	Max						
Plant height	94.00	133.00	112.22	81.24	10.20	11.32	21.25	18.94
Tiller number	9.30	20.30	15.10	23.14	11.32	23.53	1.69	11.22
Productive tiller number	9.30	18.00	14.84	14.27	8.46	22.39	0.98	6.58
Flag leaf length	15.30	39.30	32.60	74.51	17.25	19.99	10.00	30.67
Flag leaf width	1.20	2.30	1.73	62.43	12.70	16.08	0.36	20.68
Panicle length	21.10	34.10	25.87	75.34	9.45	10.89	4.37	16.90
Panicle weight	2.10	8.10	4.17	68.89	31.19	37.58	2.23	53.32
Total number of grains per panicle	127.30	316.00	235.41	47.52	18.23	26.44	60.93	25.88
Number of filled grains per panicle	114.70	282.00	199.50	29.91	14.36	26.26	32.27	16.18
Number of unfilled grains per panicle	5.00	137.30	35.91	62.31	84.84	107.47	49.52	137.95
Single plant yield	20.00	35.30	30.08	27.61	9.33	17.75	3.04	10.10
Test weight	13.50	30.50	22.43	93.87	18.68	19.28	8.36	37.28

The high estimates of GCV were observed for traits *viz.*, number of unfilled grains per panicle (84.84) and panicle weight (31.19), whereas a low value for GCV was found in panicle length (9.45), single plant yield (9.32) and productive tiller number (8.45). A similar effect for the number of unfilled grains per panicle was observed by Gebrie *et al.*, (2022). Similarly, low estimates for productive tiller number were observed in the findings of Singh *et al.*, (2022). Test weight (18.68), number of grains per panicle (18.23), flag leaf length (17.25), number of filled grains per panicle (14.36), flag leaf width (12.7), tiller number (11.32) and plant height (10.2) showed a moderate estimate for GCV.

For panicle length and plant height, lower PCV and GCV values were observed which was previously reported by Gupta *et al.*, (2022). It indicates a limited range of total variability and a strong influence of the environment on the expression of these traits. As a result, there was not much scope for direct selection for this character.

Heritability in broad sense h²b

Heritability in a broad sense was found to be higher in test weight (93.87) followed by plant height (81.24),

panicle length (75.33), flag leaf length (74.5), panicle weight (68.88), flag leaf width (62.43) and number of unfilled grains per panicle (62.31). Low heritability estimates were found in filled grains per panicle (29.9), single plant yield (27.61), tiller number (23.14) and productive tiller number (14.26) while moderate estimates were recorded in number of grains per panicle (47.52).

Genetic advance

While the genetic advance is a valuable indicator for achieving desired results on the trait of interest after selection, as estimated heritability is not much dependable due to the inclusion of the effects of both additive and non-additive genes. In comparison to genetic advance, genetic advance as a percentage of mean provides a more precise conclusion and comparable across the traits. Genetic advance over mean exhibited higher values among the number of unfilled grains per panicle (137.95), panicle weight (53.32), test weight (37.27), flag leaf length (30.67), number of grains per panicle (25.88) and flag leaf width (20.67), while the character productive tiler number (6.57) exhibited a low value and remaining characters recorded moderate values.

Heritability estimates combined with genetic advancement are more effective than heritability estimates alone in predicting gain under selection (Johnson *et al.*, 1955). High heritability coupled with high genetic advance was observed for panicle weight and similar effect was observed by Keerthiraj *et al.,* (2020), whereas low heritability coupled with low genetic advance over per cent mean was recorded in productive tiller number which was previously reported by Singh *et al.,* (2022). It suggests that non-additive genes have a role in the inheritance of these traits, implying that heterosis breeding rather than selection could be used to improve the trait.

Correlation studies

Correlation analysis of the yield and its contributing characters indicated that the genotypic correlation coefficients were higher than the phenotypic correlation coefficients in most cases, suggesting that the association was primarily due to genetic factors (Bhattacharyya *et al.*, 2007). The correlation studies for yield and its contributing characters were presented in the **(Table 3)**.

Table 3: Coefficients of phenotypic (r_p) and genotypic (r_g) among different yield components

Characters	Correlation	PH	TN	PTN	LL	LW	PL	PW	TG	FG	UFG	SPY	TW
PH	v_p	1	-0.327	-0.328	0.121	0.21	0.576**	0.555**	0.115	0.291	-0.161	-0.177	0.179
PH	v_g	1	-0.514**	-0.604**	0.104	0.249*	0.607**	0.635**	0.14	0.42**	-0.204*	-0.257*	0.1777
TN	v_p		1	0.941**	-0.493**	-0.177	-0.2967	-0.446**	0.0077	-0.2215	0.2653	0.291	-0.0596
TN	v_g		1	0.971**	-0.714**	-0.285**	-0.419**	-0.656**	0.0456	-0.393**	0.422**	-0.1319	-0.0673
PTN	v_p			1	-0.22	-0.279	-0.289	-0.556**	-0.006	-0.287	0.318	0.213	-0.18
PTN	v_g			1	-0.364**	-0.544**	-0.504**	-0.936**	0.039	-0.586**	0.597**	-0.483**	-0.286**
LL	v_p				1	-0.045	0.118	0.014	0.07	0.081	0.012	-0.242	-0.275
LL	v_g				1	-0.059	0.131	-0.012	0.064	0.077	0.012	-0.325**	-0.29**
LW	v_p					1	-0.159	0.208	0.357*	0.368*	0.115	0.3	0.01
LW	v_g					1	-0.181	0.226*	0.438**	0.488**	0.149	0.395**	0.015
PL	v_p						1	0.697**	0.038	0.222	-0.197	-0.069	0.481**
PL	v_g						1	0.769**	-0.018	0.232*	-0.248*	-0.051	0.513**
PW	v_p							1	0.188	0.579**	-0.380*	0.083	0.503**
PW	v_g							1	0.143	0.686**	-0.445**	0.123	0.555**
TG	v_p								1	0.746**	0.648**	0.047	-0.395*
TG	v_g								1	0.708**	0.745**	0.091	-0.463**
FG	v_p									1	-0.022	0.212	-0.202
FG	v_g									1	0.044	0.381**	-0.266**
UFG	v_p										1	-0.172	-0.362*
UFG	v_g										1	-0.252*	-0.399**
SPY	v_p											1	0.0029
SPY	v_g											1	0.0238
TW	v_p												1
TW	v_g												1

Note: PH= plant height, TN= tiller number, PTN= Productive tiller number, LL (cm)= Flag leaf length, LW (cm)= Flag leaf width, PL (cm) = Panicle length, PW(g)= Panicle weight, TG= total number of grains per panicle, FG= number of filled grains per panicle, UFG= number of unfilled grains per panicle, SPY(g)= single plant yield, TW(g) = Test weight

* indicates significant at 5% level of probability

** indicates significant at 1% level of probability

At the phenotypic level, a significant positive correlation was observed for plant height with panicle length (r =0.576**) and panicle weight (r = 0.555**), whereas tiller number, productive tiller number,

single plant yield and number of unfilled grains had a negative relationship with plant height; and rest of the characters exhibited a positive relationship with plant height. Similar findings were observed for plant height with panicle length and panicle weight by Parimala *et al.*, (2020) and Rukminidevi *et al.*, (2022). At genotypic level, plant height possessed positive and highly significant correlation with panicle weight (r = 0.635**), panicle length (r = 0.607**), number of filled grains per panicle (r = 0.42**) and flag leaf width (r = 0.249*) while a negative and significant correlation was associated with number of unfilled grains per panicle (r = -0.204*), single plant yield (r = -0.258*), tiller number (r = -0.515**) and productive tiller number (r = -0.604**).

Tiller number exhibited a highly positive and significant association with productive tiller number (r = 0.941**), which was previously reported by Saha *et al.*, (2019) whereas, a negative and significant association with panicle weight (r = -0.446**) and flag leaf length (r = -0.494**), while number of grains per panicle, number of unfilled grains and single plant yield showed a positive relationship; and rest of the characters showed a negative association at the phenotypic level. At genotypic level, tiller number with productive tiller number (r = 0.971**) and number of unfilled grains per panicle (r = 0.422**) exhibited a high positive and significant association, while a negative and significant association with flag leaf width (r = -0.285**), number of filled grains per panicle (r = -0.394**), plant height (r = -0.515**), panicle weight (r = -0.657**) and flag leaf length (r = -0.714**). Number of filled grains per panicle and single plant yield exhibited positive and negative relationships respectively.

Productive tiller number had a negatively significant association with panicle weight (r = -0.556**) whereas, a positive relation was observed with number of unfilled grains per panicle and single plant yield at the phenotypic level. Productive tiller number

exhibited positive and significant association with number of unfilled grains per panicle (r = 0.597**); while, a negative and significant association was observed with test weight (r = -0.287**), flag leaf length (r = -0.365**), single plant yield (r = -0.483**), panicle length (r = -0.504**). Similar effect was observed by Lakshmi *et al.*, (2014) for flag leaf width (r = -0.544**), plant height (r = -0.604**) and panicle weight (r = -0.936**) at genotypic level.

A positive relationship was observed for flag leaf length with number of unfilled grains per panicle, panicle weight, total grains per panicle, number of filled grains per panicle and panicle length, while the rest of the characters exhibited a negative relationship at a phenotypic level while at the genotypic level, there was a negative and significant association for flag leaf length with test weight (r = -0.290**) and single plant yield (r = -0.325**). Flag leaf width and panicle weight were negatively associated, whereas the rest of the characters have a positive relationship with flag leaf length. Significant positive relationship for flag leaf width was observed with number of filled grains per panicle (r = 0.368**) and total grains per panicle (r = 0.357**) at phenotypic level. At genotypic level, flag leaf width exhibited significantly positive association with panicle weight (r = 0.226*), single plant yield (r = 0.395**), number of grains per panicle (r = 0.438**) and number of filled grains per panicle (r = 0.488**).

A significant highly positive association for panicle length was observed with panicle weight (r = 0.697**), and test weight (r = 0.481**) at the phenotypic level whereas a significantly positive association was exhibited with characters *viz.*, panicle weight (r = 0.769**), test weight (r = 0.513**) and the number of filled grains per panicle (r = 0.232*) and significantly negative association with the number of unfilled grains per panicle (r = -0.248*) at the genotypic level. Panicle weight exhibited a positive and significant association with number of filled grains per panicle (r = 0.579**)
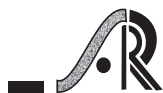
and test weight (r = 0.503**) while a negative and significant association was observed with number of unfilled grains per panicle (r = -0.380*) at phenotypic level whereas panicle weight exhibited a positively significant association with number of filled grains per panicle (r = 0.686**) and a significantly negative association with the number of unfilled grains per panicle (r = -0.445**) at genotypic level.

At both the phenotypic level and genotypic level high positive significant values were observed for number of grains per panicle with number of filled grains per panicle (r_p = 0.746**; r_g = 0.708**) and number of unfilled grains per panicle (r_p = 0.648**; r_g = 0.745**). Similar results were obtained by the study conducted by Singh *et al*., (2022) while a negative and significant association was observed with test weight (r_p = -0.395**; r_g = -0.463**).

At the genotypic level number of filled grains per panicle was observed to be negative and significantly correlated with test weight (r = -0.266**) similar results were observed by Saha *et al*., (2019).

A negative and significant association was observed for number of unfilled grains per panicle with test weight (r_p = -0.362*; r_g = -0.399**) at both phenotypic and genotypic level. A negative and significant relationship was exhibited by single plant yield (r = -0.252*) at the genotypic level.

Single plant yield exhibited a positive relationship with flag leaf width, productive tiller number, number of filled grains per panicle, panicle weight, the total number of grains per panicle and test weight whereas the rest of the characters exhibited a negative relationship at the phenotypic level **(Figure 1)**. A positive and significant association was observed with number of filled grains per panicle (r = 0.381**) and flag leaf width (r = 0.395**) while a negative and significant association was observed with number of unfilled grains per panicle (r = -0.252*), plant height (r = -0.257*), flag leaf length (r = -0.325**) and productive tiller number (r = -0.483**) at genotypic level.
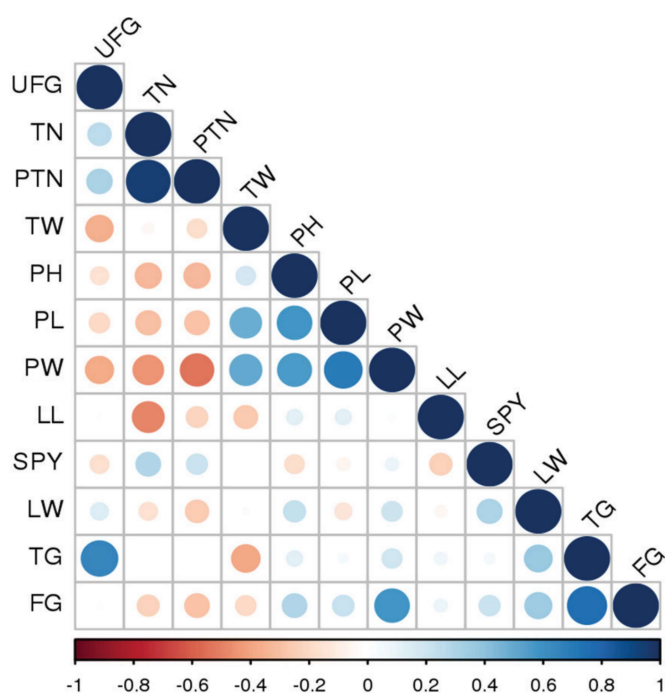

Figure 1: Correlograms showing Coefficients of phenotypic correlation among different yield components

Conclusion

The varieties under study exhibited a high variability among the traits studied. A higher estimate of the phenotypic coefficient of variation was recorded for panicle weight (37.57), the total number of grains per panicle (26.44). Low estimates of PCV were recorded in plant height (11.31) and panicle length (10.89). High GCV values were observed for traits *viz*., the number of unfilled grains per panicle (84.84) and panicle weight (31.19) whereas a low value for GCV was found in panicle length (9.45), single plant yield (9.32). Single plant yield ranged from 20g to 35.3g while the highest single plant yield was recorded in DRR Dhan 50 (35.3 g) followed by Dhanrasi (35.1 g), DRR Dhan 40 (35 g), Swarnadhan (34.7 g) and DRR Dhan 56 (34.4 g). Based on the correlation studies single plant yield exhibited a positive association with flag leaf width, productive tiller number, number of filled grains per panicle, panicle weight, the total number of grains per panicle and test weight. The variety DRR Dhan 50 was identified to have a high productive tiller number; Dhanrasi and Swarnadhan

showed a high number of filled grains per panicle; DRR Dhan 40 exhibited higher values for the number of filled grains per panicle coupled with productive tiller number which represents conclusive evidence for their high single plant yield and are potential donors for yield improvement in further breeding programmes.

Acknowledgements

References

Adhikari BN, Joshi BP, Shrestha J and Bhatta NR. 2018. Genetic variability, heritability, genetic advance and correlation among yield and yield components of rice (*Oryza sativa* L.). *Journal of Agriculture and Natural Resources*, 1(1): 149-160.

Akhtar N, Nazir MF, Rabnawaz A, Mahmood T, Safdar ME, Asif M and Rehman A. 2011. Estimation of heritability, correlation and path coefficient analysis in fine grain rice (*Oryza sativa* L.). *Journal of Animal and Plant Sciences*, 21(4): 660-664.

Bhattacharyya R, Roy B, Kabi MC and Basu AK. 2007. Character association and path analysis of seed yield and its attributes in rice as affected by bio-inoculums under tropical environment. *Tropical Agricultural Research and Extension*, 10:23-28.

Chavan BR, Dalvi VV, Kunkerkar RL, Mane AV and Gokhale NB. 2022. Studies on genetic variability for yield and yield contributing traits in aromatic rice (*Oryza sativa* L). *The Pharma Innovation Journal*, 11(2): 1732-1735.

Devi KR, Chandra BS, Hari Y, Prasad KR, Lingaiah N and Rao PJ. 2020. Genetic divergence and variability studies for yield and quality traits in elite rice (*Oryza sativa* L.) genotypes. *Current Journal of Applied Science and Technology*, 39(18): 29-43.

Devi KR, Hari Y, Chandra BS and Prasad KR. 2022. Genetic Association, Variability and Path Studies for Yield Components and Quality Traits of High Yielding Rice (*Oryza sativa* L.) Genotypes. *International Journal of Bio-Resource and Stress Management*, 13(1): 81-92, DOI:10.23910/1.2022.2297.

Dewey DR and Lu K. 1959. A correlation and path-coefficient analysis of components of crested wheatgrass seed production 1. *Agronomy Journal*, 51(9): 515-518.

FAO U. 2009. Global Agriculture Towards 2050. FAO Rome.

Gebrie GM, Abebe D, Atnaf M, Wondifraw D and Dessie A. 2022. An Investigation of Phenotypic and Genotypic Variations in 100 Upland Rice Genotypes at Pawe, North-western Ethiopia. *Journal of Genetic Resources*, 8(1): 111-116.

Gupta H, Purushottam, Gaurav Y, Yadav SK, Singh S and Kumar S. 2022. Genetic variability, heritability and genetic advance for yield and its related traits in rainfed upland rice (*Oryza sativa* L.) genotypes. *The Pharma Innovation Journal*, 11(2): 2520-2524.

Jahan N, Rahman MM, Khan NA, Hasan MM and Habib M. 2020. Genetic Variability, Heritability and Genetic Advance of Some Prominent Advanced Lines of Upland Rice (Broadcast Aus) Genotypes. *International Journal of Business, Social and Scientific Research*, 8(3): 68-73.

Johnson HW, Robinson HF and Comstock RE. 1955. Estimates of genetic and environmental variability in soybeans 1. *Agronomy Journal*, 47(7): 314-318.

Keerthiraj B and Biju S. 2020. Genetic variability, heritability and genetic advance of yield and lodging-related traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding,* 11(4): 1093-1098.

Kozak M, Singh PK, Verma MR and Hore DK. 2007. Causal mechanism for determination of grain yield and milling quality of lowland rice. *Field Crops Research,* 102(3): 178-184.

Lakshmi MV, Suneetha Y, Yugandhar G and Lakshmi NV. 2014. Correlation studies in rice (*Oryza sativa* L.). *International Journal of Genetic Engineering and Biotechnology*, 5(2): 121-126.

Parimala K, Raju CS, Prasad AH, Kumar SS and Reddy SN. 2020. Studies on genetic parameters, correlation and path analysis in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry,* 9(1): 414-417.

Saha SR, Hassan L, Haque MA, Islam MM and Rasel M. 2019. Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces: Variability and traits association in rice. *Journal of the Bangladesh Agricultural University,* 17(1): 26-32.

Singh AK, Nandan R and Singh PK. 2014. Genetic variability and association analysis in rice germplasm under rainfed conditions. *Crop Research,* 47(1-3): 7-11.

Singh VK, Wahi N, Mishra SK, Singh BD and Singh NK. 2022. Studies on Genetic variability, correlation analysis, character association and path analysis of phenotypic characteristics of twelve mega varieties of rice and its near-isogenic lines carrying high grain number per panicle QTL qGN4. 1. *Current Trends in Biotechnology and Pharmacy,* 16(1): 35-45.

Tiwari DN, Tripathi SR, Tripathi MP, Khatri N and Bastola BR. 2019. Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. *Advances in Agriculture*, 1-9. 10.1155 /2019/5975901.