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# Unravelling the Genetic Variability in rice germplasm under temperate conditions of Kashmir valley



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### ABSTRACT

The present investigation was undertaken to generate information on variability, character association in 247 genotypes including 242 test germplasm accessions (comprising local landraces a well as accessions procured from national and international gene banks) and five checks namely Shalimar Rice-1, Shalimar Rice-2, Shalimar Rice-3, Shalimar Rice-4 and Shalimar Rice-5. The analysis of variance under augmented block design revealed that the mean sum of squares for blocks ignoring treatments showed significant results for characters like plant height, number of grains per panicle, 1000 seed weight and yield per plant, while blocks eliminating treatments showed significant results for all the characters except, number of effective tillers per plant and number of grains per panicle. Both treatments when ignoring blocks and treatments eliminating blocks showed significant results for all the characters except for number of efffective tillers per plant. The mean sum of squares was significant for all traits in test entries except number of efffective tillers per plant. For checks, the mean sum of squares showed significance for all the characters. The mean sum of squares for checks vs entries also were significant for all the traits. The magnitude of phenotypic coefficient of variation was recorded to be moderate for plant height, number of effective tillers per plant, panicle length, 1000 seed weight and high for number of grains per panicleand for yield per plant. Also the magnitude of genotypic coefficient of variation was recorded to be low for Number of effective tillers per plant while as it was moderate for plant height, panicle length, 1000 seed weight and high for both number of grains per panicle and yield per plant. High heritability (> 70 %) was shown by grain yield per plant, , test weight, plant height, , test weight. Number of effective tillers per plant exhibited significant positive correlation with panicle length, and 1000 seed weight and was found to be highly significant with grain yield.

Keywords: Genetic variability, Rice, correlation coefficinets, germpalsm and temperate Region

#### Introduction

RICE (*Oryza sativa* L.) also known as 'Millennium Crop' is an indispensable crop for food security in the world and a staple source of food for more than half of the world's population. The demand for food is increasing with the increase in worlds population. Therefore, there is need for increase in the productivity of rice. To sustain the high productivity level of rice, genetic variability existing in nature or created through crop breeding is of immense value. Genetic uniformity within a crop is readily brought about by using the same gene or gene complexes during breeding programs. When uniformity becomes the cause of genetic vulnerability, genetic diversity is the only insurance against it.

\*Corresponding Author: Anand Kumar and Shabir H. Wani DOI: https://doi.org/10.21276/AATCCReview.2025.13.02.171 © 2025 by the authors. The license of AATCC Review. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (http://creativecommons.org/licenses/by/4.0/). To overcome the menace of this uniformity, it is essential that genetic variability, present in both the cultivated and wild species, is systematically exploited and used to generate new gene complexes for higher grain yield and tolerance to biotic and abiotic stresses. The effectiveness of selection depends upon the range of genetic variability already existing in the population in respect of important economic characters. The progress of breeding in such a population is primarily conditioned by the magnitude, nature and inter relationship of genetic variation for various plant characters. It is important to assess the relative magnitude of variability in order to use such information together with other selective parameters for the improvement of plant type through the adoption of effective breeding methods (Williams, 1964; Briggs and Knowles, 1967). Genetic variability (GCV) helps to choose a particular genotype whereas heritability (h<sup>2</sup>) along with the genetic advance (percent of mean) is more useful in predicting the resultant effective selection of the best genotypes. Genetic parameters, therefore, help in partitioning the overall variability into heritable and non-heritable components.

#### **Materials and Methods**

The material used in present study comprised of 247 genotypes including 242 test germplasm accessions (comprising local landraces a well as accessions procured from national and international gene banks) and five checks namely Shalimar Rice-1, Shalimar Rice-2, Shalimar Rice-3, Shalimar Rice-4, and Shalimar Rice-5. All of the check varieties are released by SKUASTKashmir. The material is the germplasm collection being maintained at MRCFC, Khudwani SKUAST-K and comprised diverse classes and growth habits.

#### **Field design**

The material was evaluated in augmented block design (Federrer, 1956). The design consisted of 11 blocks containing 27 genotypes in each with 22 test entries and five check entries. Each genotype was represented by a plot size of 2 x 2-meter dimensions with 5 lines. The plants were space planted for optimal expression of traits. Data was collected from ten randomly selected competitive plants on various morphological, yield and yield-contributing traits. In each block the checks were allotted randomly. The analysis of variance was done using R Studio. Six quantitative traits namely plant height, number of effective tillers/plant, number of grains per plant, panicle length, seeds/pod, 1000-seed weight(Test Weight) and seed yield/plant.

#### Data analysis

Data on grain yield and yield-related traits were analyzed in R software. Analysis of variance and variability was done using R software (version 4.2.0). The association between grain yield and its component traits was calculated using formulas for genotypic correlation co-efficients as suggested by Johanson *et al.*, (1955). The phenotypic and genotypic co-efficient of variation was analyzed using formulas suggested by Singhand Chaudhary (1985); heritability as suggested byJohnson *et al.*, (1955); genetic advance as given byBurton, (1952) and genetic aspercentofmeanasdescribedbySouza*et al.*, (2009)

#### **Results and Discussion**

#### Analysis of variance

In the present study a set of 247 genotypes including 242 test germplasm accessions along with five checks namely Shalimar Rice-1, Shalimar Rice-2, Shalimar Rice-3, Shalimar Rice-4 and Shalimar Rice-5 were evaluated in an augmented block design for yield and yield component traits. The analysis of variance (Table 1) revealed that the mean sum of squares for blocks ignoring treatments showed significant results for characters like plant height, number of grains per panicle, 1000 seed weight and yield per plant, while blocks eliminating treatments showed significant results for all the characters except, number of effective tillers per plantand number of grains per panicle. Both treatments when ignoring blocks and treatments eliminating blocks showed significant results for all the characters except for number of efffective tillers per plant. The mean sum of squares was significant for all traits in test entries except number of efffective tillers per plant. For checks, the mean sum of squares showed significance for all the characters. The mean sum of squares for checks vs entries also were significant for all the traits. This suggested the availability of an appreciable amount of variability in the germplasm lines studied. Pratap et al., 2012 stressed the importance of genetic variability in the original breeding materials in increasing the likelihood of creating desired recombinants for crop improvement.

The standard errors of difference (Table 2) were computed for all traits for comparison of adjusted means of test entries in same block, test entries in different block, checks, test entries and checks.

# Estimation of mean, range, phenotypic and genotypic coefficient of variation, heritability (broad-sense) and expected genetic Advance (% of mean)

The mean values (Table 3) of plant height (cm), number of effective tillers per plant, number of grains per panicle, panicle length (cm),1000 seed weight (g) and seed yield per plant (g) were 128.08+1.43, 10.86+0.13, 126.17+1.80, 19.23+0.19, 27.32+0.23, 22.38+0.43, respectively. Plant height and number of effective tillers per plant ranged from 66.87 to 186.29 cm and 5.04 to 17.68 respectively. The number of grains per panicle, panicle length (cm),1000 seed weight (g) and seed yield per plant (g) ranged from 55.81 to 207.21, 10.42 to 26.82, 18.59 to 40.79 and 9.75 to 52.15.

The magnitude of phenotypic coefficient of variation (Table-4 fig 1) for, was recorded to be moderate(10-20%) for plant height (cm)(17.54), number of effective tillers per plant(16.90) , panicle length (cm)(12.80),1000 seed weight (g) (12.39) and high ((>20%)) for Number of grains per panicle(22.44) and for yield per plant(29.32). Also the magnitude of genotypic coefficient of variation was recorded to be low (<10%) for Number of effective tillers per plant (8.60) while as it was moderate(10-20%) for plant height (cm)(17.54), , panicle length (cm)( 10.22),1000 seed weight (g) (10.63) and high (>20%) for both Number of grains per panicle (21.92) and yield per plant (28.03). In this study least difference was observed between GCV and PCV in traits Number of grains per panicle, plant height and grain yield explaining the minimal influence of the environment on yield and yield-related traits (Beena et al., 2021). Thus selection based on these traits will be useful.

## Estimates of heritability (broad sense) and genetic Advance (% of mean at 5%)

Estimation of heritability (bs) was high (>70%) for all the traits and ranged from 63.77-95.42per cent except for Number of effective tillers per plant where it was low 25.91 per cent (Table-4). High heritability (> 70%) was shown by grain yield per plant, , test weight, plant height, , test weight,. These results were consistent with findings of Bastia et al., (2008) and Zhang et al., (2005) for 100 grains weight, Akinwale et al., (2011) plant height, 100 grains weight and yield per plant and ElMalky et al., (2008) test weight in rice.. Genetic advance over mean was high for Plant height (34.21), number of grains per panicle (44.11), Grain yield per plant (55.20), Medium for Panicle length (16.81) and 1000-grain weight( 18.82) Table 5. High heritability coupled with high GAM was recorded for Plant height, number of grains per panicle and Grain yield per plant. Similar results were observed by Sharma et al., (2004); Manjunath et al., (2012); Shet et al., (2012); Kiran et al., (2013); Sadimantara et al., (2014) for productive tillers per plant in rice. High heritability coupled with moderate GAM was recorded for panicle length and 1000grain weight. These characters were not much influenced by environmental factors. So, these traits were mostly controlled by additive and /or additive × additive gene interactions and may respond to direct selection for trait improvement.

#### Estimates of Genotypic Correlation Coefficients.

Yield is a complex polygenic character and is influenced by genetic constitution of the genotypes and its interplay with the environment. It is, therefore, essential to estimate the total genetic makeup of the yield contributing components and their correlation and causation factors. Indirect selection based on one or more grain yield components have been considered to be more effective than the direct selection for grain yield. Correlation at the genotypic level was estimated among the traits (Table 5 Fig.2). Number of effective tillers per plant exhibited significant positive correlation with panicle length, and 1000seed weight and was found to be highly significant with grain yield. (Lakshmi *et al.*, 2020; Srivastava *et al.*, 2017; Sudeepthi *et al.*, 2020 also reported a positive and significant correlation of number of effective tillers with grain yield per plant. The number of grains per panicle also showed a significant correlation with grain yield.Panicle length and 1000 seed weight was also recorded to be positively correlated.

#### Table 1: ANOVA for Augmented Block Design

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Source	Df	РН	NOT	NGPP	PL	1000 SW	YIELD
Treatment (ignoring Blocks)	246	554.12**	3.75 ns	908.64**	10.84**	13.98**	54.33**
Treatment (eliminating Blocks)	246	530.83**	3.77 <sup>ns</sup>	889.23**	11.07**	13.89**	43.85**
Block(eliminating Treatments)	10	31.04**	4.45 <sup>ns</sup>	14.34 <sup>ns</sup>	10.06**	8.96**	4.50*
Block(ignoring Treatments)	10	593.87**	3.88 <sup>ns</sup>	491.92**	4.43 ns	11.17**	259.42**
Checks	4	3009.88**	15.53**	7564.36**	237.47**	20.44**	276.27**
Testentries vs. Checks	1	2602.60**	47.06**	71.19**	257.94**	594.29**	1878.87**
Test entries	241	504.86**	3.37 ns	801.65**	6.06**	11.46**	43.08**
Error	40	26.88	2.50	36.66	2.19	3.03	3 71

Table 2: Standard Error of mean

Comparison	NGPP	NOT	РН	PL	TW	Yield
A Test Treatment and a Control Treatment	2.95	1.81	3.00	1.69	1.99	0.96
Control Treatment Means	1.10	0.67	1.12	0.63	0.74	0.36
Comparison	NGPP	NOT	РН	PL	TW	Yield
Two Test Treatments (Different Blocks)	4.00	2.45	4.06	2.29	2.70	1.30
Two Test Treatments (Same Block)	3.65	2.23	3.71	2.09	2.46	1.19

#### Table 3: Descriptive statistics of agromorphological traits

Trait	Mean	Std.Error	Std.Deviation	Min	Max
Plant height	128.08	1.43	22.47	66.87	186.29
Number of effective tillers per plant	10.86	10.86 0.13 2.10		5.04	17.68
Number of grains per panicle	126.17	1.80	28.32	55.81	207.21
Panicle length	19.23	0.19	3.05	10.42	26.82
1000-grain weight	27.32	0.23	3.69	18.59	40.79
Grain yield per plant	22.38	0.43	6.72	9.75	52.15

 $Table \ 4: Phenotypic \ and \ Genotypic \ coefficient \ of \ variation, heritability \ (broad-sense) \ and \ Expected \ genetic \ Advance \ (\% \ of \ mean)$ 

Parameters	Phenotypic variance $(\hat{\sigma}^2 p)$	Genotypic variance $(\hat{\sigma}^2 g)$	Phenotypic coefficient of variation (PCV)	Genotypic co-efficient of variation (GCV)	Heritability (%)	hBS.category	Genetic Advance over mean	GAM.category
Plant height	504.86	477.98	17.54	17.07	94.67	High	34.21	High
Number of effective tillers per plant	3.37	0.87	16.90	8.60	25.91	Low	9.03	Low
Number of grains per panicle	801.65	764.99	22.44	21.92	95.42	High	44.11	High
Panicle length	6.06	3.86	12.80	10.22	63.77	High	16.81	Medium
1000-grain weight	11.46	8.43	12.39	10.63	73.59	High	18.82	Medium
Grain yield per plant	43.08	39.37	29.32	28.03	91.38	High	55.20	High

#### Table 5: Correlation coefficients for various morphological traits

	NGPP	NOT	PH	PL	TW	Yield
NGPP	1.00000	0.0234	0.08736	0.00308	0.0651	0.1307
NOT		1.00000	0.04183	0.14781	0.1470	0.2599
PH			1.00000	-0.00792	0.0209	-0.0344
PL				1.00000	0.1499	0.1087
TW					1.00000	0.1031
Yield						1.00000

NGPP: Number of grains per panicle, NOT: Number of effective tillers per plant, PH: Plant Height, PL: Panicle length, TW: 1000 seed weight, Yield: grain yield



Fig 1:Phenotypic and Genotypic coefficient of variation



#### Fig 2:Correlation coefficients for various morphological traits

#### References

- 1. Akinwale, M.G., Gregorio, G., Nwilene, F., Akinyele, B.O., Ogunbayo, S.A. and Odiyi, A.C. 2011. Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *African Journal of plant science*, 5(3): 207-212.
- 2. Bastia, D., Mishra, T.K. and Das, S.R. 2008. Genetic variability and selection indices for grain yield in upland rice. *ORYZA-An International Journal on Rice*, 45(1): 72-75.
- Briggs, F.N. and Knowles, P.F.1967. Introduction to plantbreeding. Reinhold Publishing Corporation, NewYork/London, pp. 401-411
- Burton, G.W. 1952. Quantitative inheritance in grasses. In: Proceeding of 6th International Grassland Congress, United States: Pennsylvania State College, pp. 277-283.
- 5. El-Malky, M.M., El-Habashy, M.M. and Abdelkhalik, A.F. 2008. Rice germplasm evaluation for agronomic traits and their influence on stem borer (*Chiloagamemnon*Bles.) resistance. *Journal of Agricultural Research*,46(3): 206
- 6. Federer, W.T. 1956. Augmented designs. *Hawaiian Planters Record*, 55: 191-208.
- 7. Johanson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Estimates of genetic and environmental variability in Soyabean. *Agronomy Journal*, 47(7): 314-315.

- 8. Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955.Estimates of genetic and environmental variability insoyabeans. Agronomy Journey, 47:314-318.
- 9. Kiran, T.V., Rao, Y.V., Subrahmanyam, D., Rani, N.S., Bhadana, V.P., Rao, P.R. and Voleti, S.R. 2013. Variation in leaf photosynthetic characteristics in wild rice species. *Photosynthetica*, 51:350-358.
- Lakshmi, V.I., Sreedhar, M., Gireesh, C. and Vanisri, S. 2020. Genetic variability, correlation and path analysis studies for yield and yield attributes in African rice (*Oryza glaberrima*) germplasm. *Electronic Journal of Plant Breeding*, 11(02): 399-404.
- 11. Manjunath, B.L., Verma, R.R., Ramesh, R. and Singh, N.P. 2012. Evaluation of varieties and local manurial sources for organic rice (*Oryza sativa*) production. *Indian Journal of Agronomy*, 57(3):241-244.
- 12. Pratap, A., Gupta, D.S. and Rajan, N. 2012. Breeding Indian Field Crops. *Agro bios Publishers*, New Delhi, India. p 208-227.
- 13. Sadimantara, G.R. and Cahyono, E. 2014. Genetic analysis on some agro-morphological characters of hybrid progenies from cultivated paddy rice and local upland rice. *Advanced Studies in Biology*, 6(1): 7-18.
- 14. Sharma, R.P., Pathak, S.K., Haque, M. and Raman, K.R. 2004. Diversification of traditional rice (*Oryza sativa*)-based cropping system for sustainable production in South Bihar alluvial plains. *Indian journal of agronomy*, 49(4): .218-222.
- 15. Shet, R.M., Rajanna, M.P., Ramesh, S., Sheshshayee, M.S. and Mahadevu, P.2012. Genetic variability, correlation and path coefficient studies in F2 generation of aerobic rice (*Orzya sativa* L.). *Electronic Journal of Plant Breeding*, 3(3): 925-931.
- Singh RK, Choudhury BD 1985. Biometricalmethod inquantitative genetic analysis.Kalyani Publishers, Ludhiana, New Delhi,pp.54-57
- 17. Souza, A.R.R., Miranda, G.V., Pereira, M.G. and Souza, L.V.D. 2009. Predicting the genetic gain in the Brazilian white maize landrace. *Ciência Rural*, 39: 19-24.
- Srivastava, A.K., Zhang, C., Caine, R.S., Gray, J. and Sadanandom, A. 2017. Rice SUMO protease Overly Tolerant to Salt 1 targets the transcription factor, Osb ZIP 23 to promote drought tolerance in rice. *The Plant Journal*, 92(6): 1031-1043.
- 19. Sudeepthi, K., Srinivas, T.V.S.R., Kumar, B.R., Jyothula, D.P.B. and Umar, S.N. 2020. Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 11(01): 144-148.
- 20. Williams, W. 1964. Genetic Principals and Plant Breeding.Blackwell Scientific Publication, Oxford London, pp.209-220.
- 21. Zhang, X., Wang, D., Fang, F., Zhen, Y. and Liao, X. 2005.Food safety and rice production in China. *Research of Agricultural Modernization*,26:85-88