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# **Appraising Components of Genetic Variation and Association among Rice (*Oryza sativa* L.) Breeding Lines for Yield and Its Component Traits**

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## **Author's contribution**

*The sole author designed, analysed, interpreted and prepared the manuscript.*

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## **ABSTRACT**

The present study was undertaken to estimate components of genetic variation and to ascertain association among rice breeding lines for yield and its component traits. Sixty eight rice breeding lines along with four checks were evaluated in Augmented Block Design during *kharif* 2021. Analysis of variance indicated presence of sufficient genetic variation among the lines, while estimates of components of variation revealed maximum contribution of genotypic variance to the phenotypic variance indicating its exploitation through selection and hybridization. High heritability coupled with high genetic advance was observed for 1000 grain weight, plant height, days to 50 per cent flowering and grain yield per plant indicating that these traits can be improved through selection. Simultaneously, estimates of association revealed that grain yield was found to have significant and positive association with 1000 grain weight and grain length indicating that these traits are suitable for indirect selection whereas, it exhibited significant negative association with days to 50 per cent flowering and panicle length.

**Keywords:** *Genetic advance under selection; rice; yield and its components.*

## 1. INTRODUCTION

Rice (*Oryza sativa* L.) is a prominent cereal food crop of India and simultaneously contributes significantly in dietary requirements globally as well. India is the second largest producer of rice in the world with a production of 120.30 million tonnes and a productivity of 2.73 tonnes per hectare being cultivated over an area of 44 million hectares [1] while, in the Union Territory of Jammu and Kashmir it was cultivated over an area of 280.51 thousand hectares with production and productivity of 5874 thousand quintals and 20.94 quintals per hectare, respectively [2]. The extent of efficiently exploiting the genetic variation present in the breeding material so as to select lines having desirable component traits necessitates estimation of components of variation as well as association among them. Simultaneously, in order to exploit a breeding population for improving a trait, there is dire need to understand the magnitude of variation along with the extent to which the traits are heritable. Heritable variation is of great interest to plant breeders as it plays a vital role in implementing a successful breeding programme. Genetically diverse parents are utilized to obtain superior recombinants in segregating generations. Statistical indicator of relationship between two variables viz., correlation helps in indirect selection of complex polygenic traits, because direct selection for yield is unreliable due to environmental effects. Broad sense heritability shows the relative magnitude of genotypic and phenotypic variations for various traits and is important during selection. However, heritability is not very useful on its own as it includes both additive and non-additive variances, as a result estimation of heritability along with genetic advance is considered more accurate in estimating the genetic gain under selection. Selection is considered to be more remunerative if a trait having high genetic advance also exhibits high association with yield. In the present experiment an attempt was made to estimate components of genetic variation and also to delineate association of various traits with grain yield.

## 2. MATERIALS AND METHODS

The present study was carried out during *Kharif* 2021 at Sher-e-Kashmir University of Agricultural Sciences and Technology, Chatha, Jammu. The material for the study consisted of 68 rice breeding lines and 4 locally adapted varieties as checks. The experiment was laid out in

Augmented Block Design in four blocks with replicated checks, having plot size of 1.6 m<sup>2</sup>. Row to row and plant to plant spacing was kept 20x15 cm while, standard agronomic and plant protection practices as per package and practice were adopted to raise a good crop. Five plants per line were randomly selected and tagged to record data on grain yield and its attributing traits viz., days to 50 per cent flowering, days to maturity, plant height(cm), number of effective tillers per plant, panicle length, 1000 grain weight, grain yield per plant, kernel length, kernel breadth and length/breadth ratio. The genotypic and phenotypic variances and genotypic and phenotypic co-efficient of variation for all traits were estimated as per Cochran and Cox [3] and Burton and Devane [4], while, broad sense heritability ( $h_{bs}^2$ ) was estimated as described by Allard [5]. Genetic advance (GA) was determined as described by Johnson et al. [6] and correlation as per the formula given by Miller et al. [7]. Ten kernels from each of the five randomly chosen plants were taken and the length and breadth was measured using a digital vernier caliper and average was worked out, while length-breadth ratio was estimated by dividing kernel length by kernel breadth.

## 3. RESULTS AND DISCUSSION

Analysis of variance (Table 1) as per augmented block design revealed significant differences among the lines for all traits recorded indicating enormous amount of differences among the lines thereby, hinting sufficient scope of selection among the lines followed by hybridization. These results are in close agreement with the results of Devi et al. [8] and Choudhary et al. [9] in their respective research studies. Genetic components of variation estimated (Table 2) revealed that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV), thereby, indicating that environment has played mega role in the infestation of these traits. As regards genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) higher GCV and PCV values were recorded for length breadth ratio, number of effective/ tillers per plant, 1000 grain weight, kernel length and kernel breadth hinting that these characters can be relied upon for improving rice breeding lines. Days to 50 per cent flowering, days to maturity and panicle length were found to have moderate values of PCV and GCV suggesting that these can be improved through positive selection based on phenotypic variation.

**Table 1. Analysis of variance as per Augmented block design**

Source of variation	d.f	Days to 50% flowering (no)	Days to maturity	Plant height (cm)	Number of effective tillers per plant	Panicle length (cm)	1000 grain weight (g)	Grain yield per plant (g)	KL (mm)	KB (mm)	L/B Ratio
<b>Mean Sum of Squares (MSS)</b>											
Blocks (ignoring treatments)	3	97.82**	93.66*	502.31**	35.24**	45.78**	43.56**	25.61**	5.29**	0.21**	2.93
Treatments (ignoring blocks)	71	100.05**	47.88*	483.19**	14.64*	18.84*	16.32	25.40**	5.29**	0.99**	21.86*
Checks	3	21.27*	53.01*	597.18**	10.75*	18.26*	46.63**	17.43*	5.23**	0.69**	29.77**
Varieties	67	102.26**	48.72*	375.05**	11.99*	16.66*	49.27**	8.84*	5.11**	0.33**	19.84*
Checks vs. Varieties	1	107.81**	131.32**	698.12**	13.98*	23.44*	37.93*	6.04*	1.97**	0.81**	32.61**
Error	9	2.91	6.83	25.11	1.83	2.67	2.97	0.83	0.09	0.008	2.11

\*indicate significant at 5 % level of significance

\*\*indicate significant at 1 % level of significance

**Table 2. Estimates of components of genetic variation among yield and its attributing traits**

S. No.	Traits	Range (Min.-Max.)	Genotypic variance	Phenotypic variance	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	Heritability ( $h^2$ bs) (%)	Genetic advance (%)	GA as % of mean
1	Days to 50 per cent flowering (no)	87.00-122.00	23.91	27.04	5.80	6.08	88.42	16.02	6.93
2	Days to maturity (no)	129.00-157.00	09.05	16.57	3.43	4.15	54.61	13.71	11.74
3	Plant height (cm)	95.30-177.20	89.89	117.81	8.41	9.46	76.30	17.02	21.20
4	Number of effective tillers per plant	9.70-14.90	2.74	4.69	15.53	19.89	58.42	6.61	27.74
5	Panicle length (cm)	22.67-31.06	3.14	6.04	7.72	9.94	51.98	5.47	13.52
6	1000 grain weight (g)	19.30-28.00	10.01	13.24	15.97	17.87	75.60	21.50	25.04
7	Grain yield per plant (g)	11.14-24.17	2.32	3.40	9.37	12.47	68.23	17.31	8.72
8	Kernel length (mm)	6.17-7.5	0.87	1.07	13.35	13.74	81.30	5.32	17.53
9	Kernel breadth (mm)	1.61-1.77	0.05	0.06	12.00	13.20	83.33	1.83	42.53
10	Length/breadth ratio	4.39-5.52	3.71	5.91	40.93	49.64	62.77	1.77	45.04

**Table 3. Association among grain yield and its attributing traits**

Traits	Days to 50% Flowering (no)	Days to maturity (no)	Plant Height (cm)	Number of effective tillers per plant	Panicle length (cm)	1000 grain weight (g)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Grain yield per plant (g)
Days to 50%flowering (no)	1.00	0.77**	-0.27**	0.21*	-0.58**	-0.27**	-0.27**	0.17**	-0.27**	-0.23*
Days to maturity (no)		1.00	-0.21*	0.11	-0.37**	-0.11	-0.27**	0.10	-0.23*	-0.14
Plant height (cm)			1.00	-0.10	0.53**	-0.21*	0.23*	0.02	0.21**	0.13
Number of effective tillers per plant				1.00	-0.06	-0.04	-0.07	0.09	-0.04	0.08
Panicle length (cm)					1.00	0.47**	0.51**	-0.34**	0.57**	-0.22*
1000 grain weight (g)						1.00	0.63**	0.21*	0.29**	0.23*
Kernel length (mm)							1.00	-0.47**	0.62**	0.21*
Kernel breadth (mm)								1.00	-0.67**	-0.07
L/B ratio									1.00	0.012
Grain yield per plant (g)										1.00

\*indicate significant at 5 % level of significance

\*\*indicate significant at 1 % level of significance

Results of present study are in agreement with the results of Kumar et al. [10] and Choudhary et al. [9]. Components of variation calculated through PCV and GCV delineates limit of genetic differences in a plant population but provide no information related to genetic and environmental factors affecting selection pressure therefore, heritability estimates depicts proportion of total variation which can be inherited from generation to generation and guides breeders to develop efficient and goal oriented breeding programme. Estimates of heritability in the present study ranged from 51.98 % (panicle length) to 88.42% (days to 50 per cent flowering). Simultaneously, estimates of genetic advance reveals in build capability along with other reasons of creating variation and heritability estimates along with estimates of genetic advance helps in ascertaining the possible genetic control for a particular character. If high heritability estimates are followed with high genetic advance estimates it depicts additive gene interactions between the genes controlling the specific trait, thus selection is considered effective whereas, high heritability estimates when followed with low genetic advance depicts non-additive gene interactions between the genes controlling the specific trait. Simultaneously, when low heritability is followed with low genetic advance it indicates that there is influence of environment and selection will not be rewarding. The findings of present study confirmed that characters 1000 grain weight, plant height, days to 50 per cent flowering and grain yield per plant were found to have high genetic advance (GAM) coupled with high heritability implying that these traits efficiently inherited from generation to generation. Sandeep et al. [11], Mushtaq et al. [12] and Choudhary et al. [9] also reported similar results in their respective studies. Yield being polygenic control (Table 3) can not be selected directly as it is influenced by cumulative action of genes with unknown effects. Therefore, for maximizing yield breeders had to perform indirect selection by ascertaining the association between yield and associated traits. Association studies informs about the relationships that exist between various traits and also regarding, how a particular traits contributes to towards genetic architecture. Genotypic correlation coefficient informs internal relationship between genes influencing expression of traits while, phenotypic correlation informs strength of the observed association between two traits. Grain yield was found to have significant and positive association with 1000 grain weight and grain length indicating that these traits are suitable for

indirect selection whereas, it exhibited significant negative association with days to 50 per cent flowering and panicle length. 1000 grain weight showed highly significant positive association with grain panicle length while, it showed significant negative association with days to 50 per cent flowering and plant height. These findings were in agreement with the findings of Priya et al. [13] and Prakash et al. [14] who also reported similar results in their respective studies.

#### 4. CONCLUSION

Presence of sufficient genetic variation was observed among the lines and maximum contribution of genotypic variance to the phenotypic variance revealed that this variation can be exploited through selection and hybridization. Traits viz., 1000 grain weight, plant height, days to 50 per cent flowering and grain yield per plant exhibited high heritability coupled with high genetic advance revealing their improvement through selection. Grain yield was found to have significant and positive association with 1000 grain weight and grain length indicating their suitability for indirect selection via other component traits.

#### COMPETING INTERESTS

Author has declared that no competing interests exist.

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