



Assessment of Genetic Variability for Yield & Its Contributing Traits in Rice (*Oryza sativa* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The research work was executed Research cum Instructional Farm, Genetics and Plant Breeding department of IGKV Raipur (C.G.) during *kharif* 2021. The research material under research comprised of 50 rice germplasm lines including two checks namely Mahamaya and Rajeshwari, which were tested in RBD with two replications. The observation of research investigation were recorded for total eight characters *viz.* Days to 50% flowering, Number of tillers per plant, Panicle length(cm), Plant height(cm), 1000seed weight(g), Grain yield per plant(g), Biological yield per plant(g), Harvest index(%). The analysis of variance showed that there was a highly significant variation in genotypes for all of the studied characters. A small difference between PCV and GCV suggests that the environment has little impact on the concerning traits. The number of tillers per plant, 1000 seed weight, grain yield per plant, biological yield per plant and harvest index had high heritability along with high genetic advance as a percent of mean indicates that the heritability is most likely caused by additive gene action and selection may be effective.

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1. INTRODUCTION

Rice belongs to family Poaceae and it is believed to be originated in South East Asia. "Rice is Life", the famous motto of the International Rice Year 2004, emphasised the importance of rice as a food and commerce commodity. India has the largest rice-growing area in the world, ranks second in production, with about 127.93 million tonnes in 2021-2022, after China [1]. In rice breeding programmes, yield increase is the primary breeding goal and recognizing of the type and degree of genetic variation influencing the inheritance of quantitative features like yield and yield components is critical for successful genetic improvement. Plant breeders frequently choose yield components that tangentially increase yield. A trait's heritability (h^2) is crucial in determining how it will react to selection. It has been established that in order to plan a successful breeding programme and genetic improvement of plants for quantitative traits requires accurate estimates of heritability.

2. MATERIALS AND METHODS

The experimental material included 50 rice genotypes including 48 germplasm and two checks namely Mahamaya and IGKVR1 (Rajeshwari). The experimental materials were received from germplasm section, Department of Genetics and Plant Breeding, IGKV, Raipur (C.G.). Genotypes of rice were evaluated at the Research cum Instructional Farm, Department Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur. The plant material of rice direct sowing on June 22, 2021 with 20x15cm spacing. The experimental material was planted into two replication in RBD design.

3. RESULTS AND DISCUSSION

The analysis of variance for yield and its contributing traits is shown in the Table 1. The analysis of variance of all the quantitative characters except panicle length showed that

there is highly significant variation found among the genotypes. Panicle length (cm) also showed significant difference.

3.1 Estimation of Genotypic and Phenotypic Coefficient of Variation

3.1.1 Yield and yield contributing traits

The high value of GCV and PCV was recorded only for grain yield per plant 24.49 and 25.96, respectively. These results are in agreement with the findings of Dhanwani et al. [2], Chamar et al. [3], Noatia et al. [4] and Singh et al. [5].

Moderate genotypic and phenotypic coefficient variation were recorded in number of tillers per plant (GCV 16.22, PCV 18.95), 1000 seed weight (GCV 15.38, PCV 16.31), biological yield per plant (GCV 18.93, PCV 20.57) and harvest index (GCV 18.59, PCV 19.07). Similar findings were also reported by Sonwani [6].

The low estimates of GCV and PCV were reported in days to 50% flowering (GCV 4.89, PCV 5.23), plant height (GCV 7.19, PCV 8.76) and panicle length (GCV 4.17, PCV 7.74). Similar findings have been reported by Noatia et al. [4] and Sudeepthi et al. [7] for the panicle length, days to 50 % flowering, by Donkor et al. [8] for days to 50% flowering and plant height.

3.2 Estimation of Heritability and Genetic Advance as % of Mean

3.2.1 Yield and yield contributing traits

High heritability estimates was recorded for days to 50 % flowering (87.24%), number of tillers per plant (73.27%), plant height (67.37%), 1000 seed weight (88.92%), grain yield per plant (88.99 %), biological yield per plant (84.75%) and harvest index (95.00%). Low heritability estimate was recorded panicle length (29.04%) only. High genetic advance as % of mean was

Table 1. Analysis of Variance (ANOVA) for yield and its contributing traits

S. No.	Source of variance	Mean Sum of Squares		
		Replication d. f. (1)	Treatment d. f. (49)	Error d. f. (49)
1.	Days to 50% flowering	13.69	61.62**	4.20
2.	Number of tillers per plant	0.04	0.79**	0.12
3.	Plant height (cm)	4.51	314.13**	61.24
4.	Panicle length (cm)	0.50	4.80*	2.64

S. No.	Source of variance	Mean Sum of Squares		
		Replication	Treatment	Error
		d. f. (1)	d. f. (49)	d. f. (49)
5.	1000 seed weight (g)	2.23	28.72**	1.68
6.	Grain yield per plant (g)	1.29	11.72**	0.68
7.	Biological yield per plant(g)	5.98	31.79**	2.62
8.	Harvest index (%)	0.06	161.79**	4.14

** Significant at 1 % level, * Significant at 5 % level, d. f. Degree of freedom

Table 2. Estimates genetic variability of various yield and its contributing traits

S. N.	Characters	Mean	Range		PCV (%)	GCV (%)	h ² (bs)	GA as % of mean
			Min.	Max.				
1	DTFF	109.65	96.50	120.00	5.23	4.89	87.24	9.40
2	NTPP	3.56	2.50	5.00	18.95	16.22	73.27	28.60
3	PH	156.39	128.89	176.75	8.76	7.19	67.37	12.16
4	PLN	24.91	21.79	28.35	7.74	4.17	29.04	4.63
5	TSW	23.90	11.33	32.05	16.31	15.38	88.92	29.88
6	GYPP	9.59	3.19	15.65	25.96	24.49	88.99	47.60
7	BYPP	20.17	10.59	26.56	20.57	18.93	84.75	35.90
8	HI	47.76	27.08	64.31	19.07	18.59	95.00	37.31

DTFF- Days to 50% flowering, **NTPP-** Number of tillers per plant, **PLN-** Panicle length, **PH -** Plant height, **TSW-** 1000 seed weight, **- GYPP** Grain yield per plant, **BYPP-** Biological yield per plant, **HI-** Harvest Index index.

recorded for number of tillers per plant (28.60), 1000 seed weight (29.88), grain yield per plant (47.60), biological yield per plant (35.90), harvest index (37.31). Moderate genetic advance as % of mean was recorded for plant height only, while low genetic advance as % of mean was recorded for days to 50% flowering (9.40) and panicle length (4.63).

4. SUMMARY

According to the analysis of variance, there were highly significant differences for all traits under study. Analysis manifested that the mean sum of squares is highly significant for all the traits. The high PCV and GCV was estimated for grain yield per plant among all yield and its contributing traits. High heritability was recorded for harvest index, grain yield per plant, 1000 seed weight, days to 50 % flowering, biological yield per plant, number of tillers per plant and plant height among all yield and its contributing traits. Maximum genetic advance as % of mean was estimated for grain yield per plant, harvest index, biological yield per plant, 1000 seed weight and number of tillers per plant among all yield and its contributing traits.

5. CONCLUSIONS

For all of the characters studied, analysis of variance revealed that highly significant variation among genotypes. The available genetic

variability present in the material can be use for improvement of rice cultivars.

- Low difference between PCV and GCV indicate the low influence of the environment on the concerning traits.
- Yield and its contributing traits namely number of tillers per plant, 1000 seed weight, grain yield per plant, biological yield per plant, harvest index had high heritability accompanied with high genetic advance as a % of mean indicates that the most likely the heritability is due to additive gene action and selection may be effective.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Anonymous. As per 2nd Advance Estimates of production of major crops, 2021-22, Ministry of Agriculture & Farmers Welfare, Government of India; 2022.
2. 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.
3. Chamar JP, Joshi RP, Katkani D, Sahu D, Patel V. Genetic variability, heritability and

- correlation coefficient analysis in rice (*Oryza sativa* L.) germplasm J. Pharm. Innov. 2021;10(5):763-769.
4. Noatia P, Sao A, Tiwari A, Nair SK, Gautama D. Genetic Dissection of Yield determinants in advance breeding lines (ABLs) of rice (*Oryza sativa* L.) under irrigated condition of Chhattisgarh, India. Int. J. Plant Soil Sci. 2021;33(20):119-131.
 5. Singh B, Gautama D, Sao A, Nair SK. Assessment of genetic variability, heritability and genetic advance for yield and quality traits in advanced breeding lines of rice (*Oryza sativa* L.). The Pharma Innov J. 2021;10(8):1627-1630.
 6. Sonwani P. Diversity and association analysis in yield and yield attributing traits of rice germplasm (*Oryzasativa*L.). M.Sc. (Ag.) Thesis, Indira Gandhi Krishi Vishwavidyalaya, Raipur. 2021; 1-110.
 7. Sudeepthi K, Srinivas TVSR, Kumar BR, Jyothula DPB, Umar SN. Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). Electron. J. Plant Breed. 2020;11(01): 144-148.
 8. Donkor EF, Adjei RR, Boadu SE, Boateng AS, Durowaa OOA. Genetic variability, heritability and path analyses of yield and yield related traits of newly developed rice (*Oryzasativa* L.) genotypes in lowland ecology in Ghana. Journal of Innovative Agriculture. 2021;8(1):16-20.

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