“Assessment of genetic variability for yield & its contributing traits in rice (*Oryza sativa* L.)”

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ABSTRACT

The entitled research work “Assessment of genetic variability for yield & its contributing traits in rice (*Oryza sativa* L.)” 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.

INTRODUCTION

Rice belongs to family Poaceae andit 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. (Anonymous, 2022). 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.

MATERIAL 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, 2021with 20x15cm spacing. The experimental material was planted intwo replication in RBD design.

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RESULTS AND DISCUSSION

The analysis of variance for yield and its contributing traits is shown in the table 1.1. 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.

Table1.1Analysis of Variance (ANOVA) for yield and its contributing traits

S.	Source of variance	Mean Sum of Squares

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No.		Replication	Treatment	Error
		d. f. (1)	d. f. (49)	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
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

Estimation of genotypic and phenotypic coefficient of variation:

Yield & 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.* (2013), Chamar *et al.* (2021),Noatia*et al.* (2021) and Singh *et al.* (2021).

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 (2021).

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.* (2021) and Sudeepthi*et al.* (2020) for the panicle length, days to 50 % flowering, by Donkor*et al.* (2020) for days to 50 % flowering and plant height.

4.2.3. Estimation of heritability and genetic advance as % of mean:

Yield & 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 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).

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Table 1.2 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 to50% 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**-HarvestIndexindex.

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SUMMARY AND CONCLUSIONS

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.

Conclusion:

- 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.

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