Original Research Article

Studies on Genetic Variability for Yield and Related Traits of Breeding Linesof Cross RNR15048 × Tunga.

.

ABSTRACT

Aims: The improvement of crop yields depends on the extent of genetic diversity present in breeding materials**.**An experiment was carried out for forty five breeding lines of rice to assess variability for 12 quantitative and 2 qualitative traits*viz*, days to 50 per cent flowering, days to maturity, plant height (cm), number of tillers per plant, number of productive tillers plant, panicle length(cm), number of grains per panicle, number of filled grains per panicle, spikelet fertility (%), test weight (g), length to Breadth (L/B) ratio, Protein Content(g/100g), Carbohydrate content(g/100g), grain yield per plant(g).

Study design: The experiment was carried out inRandomised Complete Block Design with two replications.

Place and Duration of Study: During kharif 2023 atAgricultural and Horticultural Research Station, Kathalagere,Davangere.

Methodology: The research utilized 45 breeding lines resulting from the cross RNR15048 × Tunga, sourced from the Department of Genetics and Plant Breeding at the College of Agriculture in Shimoga, along with 5 checks. Data was recorded and analyzed statistically using R software.

Results: The analysis of variance indicated significant differences among the breeding lines for all traits examined. High to moderate values of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and high heritabilityalong with a high genetic advance as a percent of the meanwere observed for the following traits: plant height, number of tillers per plant, number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, test weight, protein content, and grain yield.

Conclusion: This study indicates that yield improvement programs should focus on traits such as plant height, number of tillers per plant, number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, test weight, protein contentand grain yield.

Keywords: Rice, GCV, PCV, Heritability, Genetic advance as per cent of mean

1. INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important cereal crops globally, feeding nearly half of the world's population, earning the title "Global Grain." Its critical role in food security is especially relevant in countries like India, where rice production needs to increase to meet future demands. By 2050, rice yields must reach 121 million tons, requiring an annual increase of about two million tons [1]. Belonging to the Poaceae family with a chromosome number of 24, rice includes 24 species, of which two *Oryza sativa* and *Oryza* *glaberrima* are cultivated. Its global importance was highlighted by the 2004 International year of rice.

Rice is the staple food of Asia, providing 80% of the energy needs for over two billion people in the region. Nutritionally, it contains about 80% carbohydrates, 7-8% protein, 3% fiber, and 3% fat [2] Although the protein content is relatively low, it is of high nutritional value [3] and rice also contains essential vitamins and minerals like thiamine, niacin, zinc, and phosphorus [4].

Genetic variability is key to rice breeding programs aimed at improving yield and quality parameters. The phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic gain help identify suitable genetic material for breeding [5]. The natural genetic diversity found in rice populations is crucial for developing new, high-yielding varieties [6]. This variability enables breeders to select desirable traits and improve rice varieties for the future [7].

2. MATERIAL AND METHODS

The experiment was conducted during kharif 2023 at Agricultural and Horticultural Research Station, Kathalagere. Forty five breeding lines of rice of cross RNR-15048 × Tunga with five checks *viz*., RNR-15048, Tunga, BPT-5204, Sahyadri Kempumukthi and KPR-1 were used to evaluate genetic variability. Applying a 20 cm row to row and 15 cm plant to plant spacing,twentyone days old seedlings were manually transplanted to the main field at a rate of one seedling per hill in Randomised Complete Block Design with two replications.

Five plants were chosen at random from each line and used for taking the observations on 12 quantitative and 2 qualitative traits *viz,* days to 50 per cent flowering, days to maturity, plant height (cm), number of tillers per plant, number of productive tillers plant, panicle length(cm), number of grains per panicle, number of filled grains per panicle, spikelet fertility (%), test weight (g), length Breadth (L/B) ratio, grain yield per plant(g), protein Content(g/100g), carbohydrate content(g/100g).Quality analysis for protein and carbohydrate was done by Lowry's and Anthrone method respectively.The average of observations recorded on the five plants was considered for statistical analysis.Variability analysis was performed using R software.PCV and GCV were calculated by the formula suggested by Burton and De Vane[8].Heritability in broad sense was calculated by the formula suggested by Lush [9]. Genetic advance was studied by the formula suggest by Johnson et al. [10].

3. RESULTS AND DISCUSSION

3.1 Analysis of variance

Analysis of variance indicated significant genetic differences were seen across breeding lines of rice for a variety of attributes *viz.,* days to 50 per cent flowering, days to maturity, plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of grains per panicle, number of filled grains per panicle, spikelet fertility, test weight, length to Breadth ratio, protein content, carbohydrate content and grain yield per plant, indicating that selection will be successful (Table 1). Manjunatha et al.[11] and Sudeepthi et al.[12] cited the same outcomes.

3.2 Phenotypic and Genotypic Coefficient of Variation

According to Shivasubramanian and Menon [13], they classified PCV and GCV value as high (>20%), medium (10-20%) and low (<10%). On the basis of this, in the present study indicated that Low PCV and GCV (< 10%) recorded for days to 50 per cent flowering(7.73% and 7.49%),days to maturity(6.14% and 5.90%), spikelet fertility(2.96% and 2.44%) and carbohydrate content(2.04% and 1.94%) which are in line with the results of

Sudeepthi et al [14],Murali et al.[15]. The presence of low values for phenotypic and genotypic coefficients of variation suggests that selecting these traits for crop improvement programs may not be effective.High and moderate was observed for traits numberof grains per panicle(20.50% and 16.67%), number of filled grains per panicle (20.53% and 16.43%) and grain yield per plant (23.83% and 19.58%) aligning with the results of Ram et al.[16], Nath and Kole [6] and Tiwari et al. [17].Moderate values of PCV and GCV were found for plant height(12.59% and 11.28%), number of tillers per plant(18.02% and 14.86%), test weight(14.36% and 12.26%), and productive tillers per plant (18.74% and 15.39%)consistent with Demeke *et al*. [18], Gour et al.[19], and Edukondalu et al.[20]. These findings indicate good potential for improving crop yield through selective breeding of these traits (Table 2).

3.3 Heritability (h^2) and Genetic advance as percent of mean (GAM)

Johnsonet al.[10] classified heritability values as high (>60%), moderate (30-60%) and values less than 10% low and genetic advance as *per cent* of mean as low (0-10%), medium (10 - 20%) and high (20% and above).High heritability coupled with high genetic advance as per cent mean (GAM) was recorded for traits *viz.,* plant height(80.24% and 20.82%), number of tillers per plant(68.04% and 25.25%), number of productive tillers per plant(67.43% and 26.03%), number of grains per panicle(66.09% and 27.91%), number of filled grains per panicle(64.04%and 27.08%), test weight(72.89% and 21.56%), protein(90.51% and 20.36%) and grain yield per plant(67.54% and 33.16%) which are in conformity with the findings by Sravan et al. [21], Edukondalu et al.[20] and Anyaoha et al.[22].Such high heritability and genetic advance as per cent of mean is mainly because of additive gene action which indicates that the selection will be effective (Figure 1).

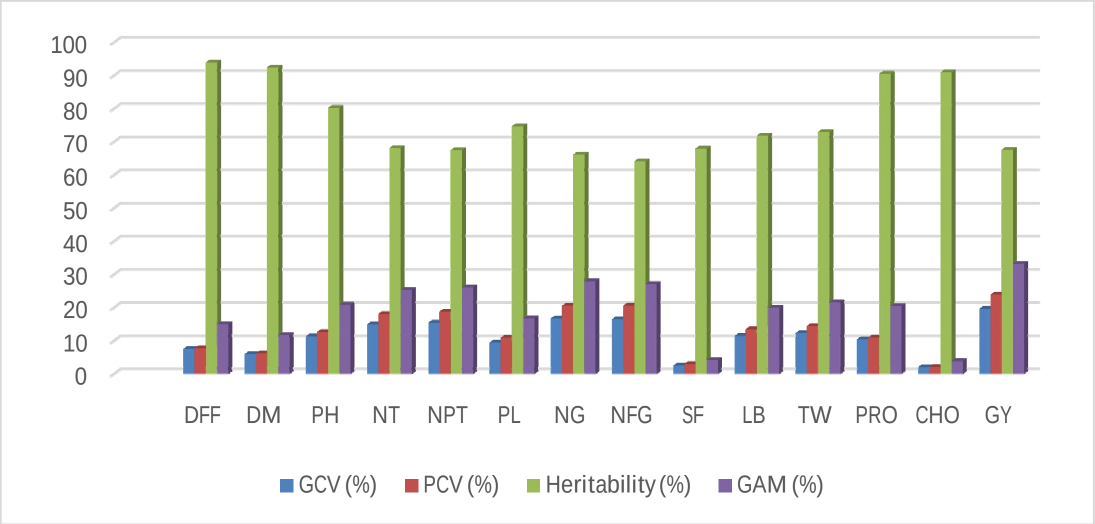

Figure 1: pattern of GCV, PCV, heritability and genetic advance as percent of mean for various traits in breeding lines of rice.

DFF- Days to 50 per cent flowering, DM- Days to maturity, PH- Plant height (cm), NT- Number of tillers per plant, NPT- Number of productive tillers per plant, PL- Panicle length (cm), NG- Number of grains per panicle, NFG- Number of filled grains per panicle, SF- Spikelet fertility, LB- Length breadth ratio (%), TW- Test weight (g), PRO – Protein content (g per100g), CHO – Carbhohydrate content (g per100g), GY- Grain yield per plant (g).

Table 1 Analysis of variance for yield and related traits in breeding lines of rice

Source of variation	Degrees of freedom	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of tillers perplant	Number of productive tillers per plant	Panicle length (cm)	Number of grains
Replication	1	6.76	7.84	0.04	2.1	1.36	0.66	73.1
Genotype	49	121.78**	127.01**	719.584**	11.54**	12.17**	9.27**	4881.53**
Error	49	3.84	5.04	78.87	2.19	2.37	1.35	996.62

Source of variation	Degrees of freedom	Number of filled grains per panicle	Spikelet fertility (%)	Length breadth ratio	Test weight (g)	Protein (g/100g)	CHO (g/100g)	Grain yield perplant (g)
Replication	1	0.42	6.031	0.063	9.88	0.05	0.56	0.26
Genotype	49	4065.62**	13.64**	0.346**	23.35**	2.06 **	4.04**	142.64**
Error	49	891.35	2.606	0.06	3.66	0.10	0.192	27.64

*** - Significant at 1% level*

Table 2 Genetic variability parameters for yield and related traits in breeding lines of rice

Sl. No.	Traits	Mean	Range		GCV (%)	PCV (%)	Heritability (%)	GAM (%)
			Min	Max				
1	DFF	102.58	87.00	124.50	7.49	7.73	93.88	14.94
2	DM	132.34	117.00	154.50	5.90	6.14	92.36	11.68
3	PH	158.64	98.50	181.45	11.28	12.59	80.24	20.82
4	NT	14.54	9.90	22.50	14.86	18.02	68.04	25.25
5	NPT	14.39	10.00	21.35	15.39	18.74	67.43	26.03
6	PL	21.19	16.55	24.15	9.39	10.87	74.61	16.71
7	NG	264.45	166.90	370.15	16.67	20.50	66.09	27.91
8	NFG	242.49	133.70	332.80	16.43	20.53	64.04	27.08
9	SF	96.42	86.75	98.42	2.44	2.96	67.91	4.14
10	LB	3.34	2.44	4.56	11.38	13.43	71.83	19.88
11	TW	25.59	12.25	35.50	12.26	14.36	72.89	21.56
12	PRO	9.52	7.18	11.14	10.39	10.92	90.51	20.36
13	CHO	71.31	67.40	73.94	1.94	2.04	90.94	3.82
14	GY	38.72	25.15	58.00	19.58	23.83	67.54	33.16

DFF- Days to 50 per cent flowering, DM- Days to maturity, PH- Plant height (cm), NT- Number of tillers per plant,NPT- Number of productive tillers per plant, PL- Panicle length (cm), NG- Number of grains per panicle, NFG- Number of filled grains per panicle, SF- Spikelet fertility, LB- Length breadth ratio (%), TW- Test weight (g), PRO – Protein content (g per100g), CHO – Carbhohydrate content (g per100g), GY- Grain yield per plant (g).

4. CONCLUSION

In the present study, traits such as plant height, number of tillers per plant, number of productive tillers per plant number of grains per panicle, number of filled grains per panicle, test weight and grain yield per plant showed high genetic advance as a per cent of the meancombined with high heritability and moderate to high GCV and PCV values. This suggests that these traits suitable for use in crop improvement programs through effective selection processes.The breeding lines, R×T-9-1-14 and R×T-8-9-21 performed better compared to checks in respect to grain yield

REFERENCES

1. Buelah J, Reddy VR, Srinivas B, Balram N, Correlation and path analysis for yield and quality traits in hybrid rice (*Oryza sativa* L.). Int J Environ Clim. 2022;12(10):723-728.
2. Juliano BO,Factors affecting nutritional properties of rice protein. Trans Natl Acad Sci Technol. 1985; 7:205-16.
3. Chaudhari PR, Tamrakar N, Singh L, Tandon A, Sharma D. Rice nutritional and medicinal properties. J Pharmacogn Phytochem. 2018;7(2):150-6.
4. Bagchi TB, Ghosh A, Kumar U, Chattopadhyay K, Sanghamitra P, Ray S, Adak T, Sharma S. Comparison of nutritional and physicochemical quality of rice under organic and standard production systems. Cereal Chem. 2016;93(5):435-43.
5. Kishore NS, Srinivas T, Nagabhushanam U, Pallavi M, Sameera SK. Genetic variability, correlation and path analysis for yield and yield components in promising rice (*Oryza sativa* L.) genotypes. SAARC J Agric. 2015;13(1):99-108.
6. Nath S, Kole PC. Genetic variability and yield analysis in rice. Electron J of Plant Breed. 2021;12(1):253-8.
7. Awad-Allah MM, Mohamed AH, El-Bana MA, El-Okkiah SA, Abdelkader MF, Mahmoud MH, El-Diasty MZ, Said MM, Shamseldin SA, Abdein MA. Assessment of genetic variability

and bran oil characters of new developed restorer lines of rice (*Oryza sativa* L.). Gene. 2022;13(3):509.

8. Burton GW, Devane EW. Estimating heritability in tall fescue (*Festuca arundiraceae*) from replicated clonal material. Agron. J. 1953; 45: 478-481.

9. Lush JL. Heritability of quantitative characters in farm animals.Genet Heriditas.1949*;*35:356-375.

10. Johnson HW, Robinson HF, Comstock RE. Estimation of genetics and environmental variability in soybean. *Agron. J*. 1955; 47: 477-483.

11. Manjunatha B, Kumara BN. Genetic variability analysis for quantitative traits in rice (*Oryza sativa* L.). J Exp Agric Int. 2019:1-4.

12. Sudeepthi K, Srinivas TV, Kumar BR, Jyothula DP, 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):144-8.

13.Sivasubramaniam S, Madhava Menon P. Heterosis and inbreeding depression in rice.Madras Agric. J.1973; 60(2):1134-1144.

14. Sudeepthi K, Srinivas TV, Kumar BR, Jyothula DP, 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):144-8.

15. Murali S, Ram M, Kumar AS, Lanka C, Gurjar D. Exploring the role of genetic variability in rice yield stability and production efficiency. Pharma Innov J. 2023;12(6):2726-8.

16. Ram BJ, Babu GS, Lavanya GR, Kumar KM, Spandana B. Genetic variability for yield attributing traits of elite rice germplasm (*Oryza sativa* L.). J Pharmacog Phytochem. 2017;6(3):832-4.

17. Tiwari DN, Tripathi SR, Tripathi MP, Khatri N, Bastola BR. Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. Adv Agric. 2019;2019(1):5975901.

18. Demeke B, Dejene T, Abebe D. Genetic variability, heritability, and genetic advance of morphological, yield related and quality traits in upland rice (*Oryza Sativa* L.) genotypes at pawe, northwestern Ethiopia. Cogent Food & Agric. 2023;9(1):2157099.

19.Gour L, Koutu GK, Singh SK, Patel DD, Shrivastava A, Singh Y. Genetic variability, correlation and path analyses for selection in elite breeding materials of rice (*Oryza sativa* L.) genotypes in Madhya Pradesh.Pharma Innovation. 2017;6(11):693-6.

20. Edukondalu B, Reddy VR, Rani TS, Kumari CA, Soundharya B. Studies on variability, heritability, correlation and path analysis for yield, yield attributes in rice (*Oryza sativa L*.). IJCMAS. 2017;6(10):2369-76.

21.Sravan T, Rangare NR, Suresh BG, Kumar SR. Genetic variability and character association in rainfed upland rice (*Oryza sativa* L.). Journal of Rice Research. 2012;5(1):2.

22. Anyaoha C, Adegbehingbe F, Uba U, Popoola B, Gracen V, Mande S, Onotugoma E, Fofana M. Genetic diversity of selected upland rice genotypes (*Oryza sativa* L.) for grain yield and related traits. IJPS. 2018.