Research Article

Evaluation of Genetic Variability for Yield and Associated Traits in Breeding Lines Derived from the Cross RNR-15048 × Tunga.

ABSTRACT

Aims: To evaluate the genetic variability of 45 rice breeding lines for 12 quantitative and 2 qualitative traits, aiming to identify and enhance traits that contribute to improved crop yield and nutritional quality in rice.

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,College of Agriculture Shimoga, along with 5 checks. Data was recorded and analyzed statistically using R software.

Results: The significant differences among the breeding lines identified through the analysis of variance highlight the potential for selecting superior genotypes within the studied rice breeding lines. High to moderate values of the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) suggest that there is substantial genetic diversity for the traits evaluated, indicating a promising opportunity for genetic improvement through selective breeding.

Conclusion: The findings of this study highlight the importance of focusing yield improvement programs on specific traits, including plant height, number of tillers per plant, productive tillers per plant, grains per panicle, filled grains per panicle, test weight, protein content, and overall grain yield. Emphasizing these traits is essential for enhancing the productivity and nutritional value of rice, ultimately supporting food security efforts.

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. According to [1], rice production must increase to meet future demands, reaching 121 million tons by 2050.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].

Yield and nutitional quality enhancement is the major breeding objective in rice breeding programmes and knowledge on the nature and magnitude of the genetic variation governing the inheritance of quantitative characters like yield and its components is essential for effective genetic improvement. A critical analysis of the genetic variability parameters, namely, Genotypic Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV), heritability and genetic advance for different traits of economic importance is a major pre-requisite[5].

2. MATERIAL AND METHODS

2.1 Location

The experiment was conducted during kharif 2023 at Agricultural and Horticultural Research Station, Kathalagere.

2.2 Planting material

Forty five breeding lines (F_6 generation) of rice of cross RNR-15048 × Tunga with five checks*viz.*,RNR-15048, Tunga, BPT-5204, Sahyadri Kempumukthi and KPR-1.

2.3 Experimenta design

Randomised Complete Block Design with two replications

2.4 Planting and management

Applying a 20 cm row to row and 15 cm plant to plant spacing, twenty one day 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 to assess genetic variability.

2.5 Trait evaluation

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% 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.

2.6 Statistical analysis

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 DeVane[6]. Heritability in broad sense was calculated by the formula suggested by Lush [7]. Genetic advance was studied by the formula suggest by Johnson et al. [8].

3. RESULTS AND DISCUSSION

3.1 Analysis of variance

The analysis of variance (ANOVA) revealed significant genetic differences among the rice breeding lines for various traits, including days to 50% 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. These results indicate that selection for these traits will be successful (Table 1). Similar findings were reported by Manjunatha et al. [9] and Sudeepthi et al. [10], confirming the importance of genetic variability in rice breeding.

3.2 Phenotypic and Genotypic Coefficient of Variation

According to Shivasubramanian and Menon [11], 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 fordays to 50%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 [12],Murali et al.[13]. 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 PCV and GCV 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.[14], Nath and Kole [15] and Tiwari et al. [16].The presence of ample amount of variation reveals the effectiveness of selection.

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 number of productive tillers per plant (18.74% and 15.39%)consistent with Demeke *et al*. [17], Gour et al.[18],Paramanik 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)

Genotypic coefficient of variation measures the extent of genetic variability per cent for a trait but does not assess the amount of genetic variation which is heritable. Heritability estimates were high for all the characters. The heritability estimates along with genetic advance can be useful to predict the effect of selection in selection programmes.

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 Anyaohaet al.[22].Such high heritability and genetic advance as per cent of mean suggest a predominance of additive gene action which indicate that selection for these traits are rewarding.(Figure 1).

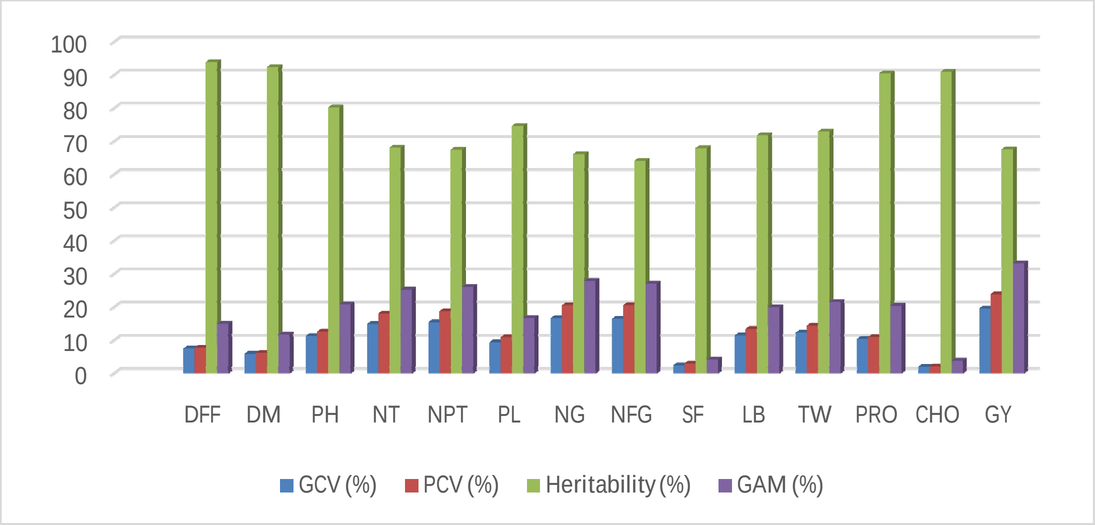

Figure 1: pattern of GCV, PCV, heritability and genetic advance as percent of mean for various traits in breeding lines of rice.

DFF- Days to 50%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%flowering	Days to maturity	Plant height (cm)	Number of tillers perplant	Number of productive tillers per plant	Panicle length (cm)	Number of grains
Mean sum of squares								
Replication	1	6.76	7.84	0.04	2.10	1.36	0.66	73.1
Genotype	49	121.78**	127.01**	719.58**	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)
Mean sum of squares								
Replication	1	0.42	6.03	0.06	9.88	0.05	0.56	0.26
Genotype	49	4065.62**	13.64**	0.34**	23.35**	2.06 **	4.04**	142.64**
Error	49	891.35	2.60	0.06	3.66	0.10	0.19	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%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

The breeding lines in this study exhibited significant variation in yield and associated traits. 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 to moderate GCV, PCV, heritability, and genetic advance, indicating strong variation and selection potential.The breeding lines, R×T-9-1-14 and R×T-8-9-21 performed better compared to checks in respect to grain yieldwhile the lines R×T-8-9-21 and R×T-9-1-12 performed well with respect to yield and protein content. The line R×T-8-9-21 showed moderate carbohydrate content with good yield. Therefore, the above mentioned lines can be further used in crop improvement programme.

Disclaimer (Artificial intelligence)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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