

Genetic Variability Studies for Yield, Nutritional and Cooking Quality Characters in Coloured Rice (*Oryza sativa* L.)

Billa Satish Chandra, T Haritha, B Krishnaveni, M Swapna and M Tushara
Department of Genetics and Plant breeding, ANGRAU Agricultural College, Bapatla

ABSTRACT

In the present study 35 coloured rice genotypes along with three checks were evaluated in randomized complete block design (RBD) for yield, nutritional and cooking quality traits to estimate the extent of genetic variability, heritability (broad sense) and genetic advance as per cent of mean. The analysis of variance revealed significant variability for all the characters studied. Among the traits studied, high phenotypic and genotypic coefficients of variation were recorded for the traits *viz.*, for yield traits like number of filled grains per panicle, grain yield/plant(g) and quality like alkali spreading value and nutritional traits like total phenol content(mg/100g), flavonoid content(mgQE/100g) and anthocyanin content(mg/100g) indicating large amount of variation among the genotypes included in the study. High heritability coupled with high genetic advance as per cent of mean was recorded for plant height (cm), ear bearing tillers per plant, panicle length (cm), test weight (g), number of filled grains per panicle, water uptake, alkali spreading value, protein content (%), Zn content (ppm), Fe content (ppm), total phenol content (mg/100g), antioxidant activity (mgAAE/100g), flavonoid content (mgQE/100g), anthocyanin content (mg/100g) and grain yield per plant (g) indicating that these traits were governed by additive gene effects and hence direct phenotypic selection may be rewarding for improvement of these traits in rice.

Keywords: Genetic advance, GCV, Heritability, PCV and Variability

Rice (*Oryza sativa* L.) is the predominant staple food crop for more than half of the world's population and is playing a pivotal role in providing human nutrition, energy supply and food security. It is not only the major source of carbohydrates, but also source of essential micronutrients. It is the only cereal, cooked and consumed as a whole grain. Hence quality considerations are much more important in rice than for any other food crops (Hossain *et al.*, 2009). India is the second largest producer of rice but pigmented rice is restricted to some parts of Northeast and in Western Uttar Pradesh, Punjab, and Gujarat *etc.* India produces majorly 3 different pigmented rice – black rice, red rice and purple rice. All three are unique in their functional properties. Eleven different colours of rice varieties are known to exist ranging from the commonly seen white to dark purple or black coloured rice. (Richa Sati and Shweta Singh, 2019). Recently, rice consumers are showing great interest for colored rice varieties due to their potential health benefits. The success of any crop improvement programme relies upon the nature and magnitude of

genetic variability. The efficiency of selection relies upon the degree of genetic variability present in the plant population. Characters like yield and its components being polygenic in nature, the breeder has to select desired genotypes from the knowledge of components of variation. For this the basis is to partition the total variation into phenotypic and genotypic components and to study the extent of these components for various traits which measure aids to type of gene action and helps in deciding breeding procedure for the genetic improvement of particular trait. The nature and extent of variability is the basis for all crop improvement programmes. According to Allard (1960), yield is polygenically controlled quantitative character and is highly influenced by environment. Partitioning of observed variability into heritable and non-heritable components is very much essential to get a true indication of the genetic coefficient of variability as a useful measure of the magnitude of genetic variance present in the population. Assessment of variability for morphological and yield related traits is essential in

planning of appropriate breeding strategy for genetic improvement of the crop. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm.

MATERIAL AND METHODS

The present investigation was carried out using 35 coloured rice genotypes grown in randomized complete block design with two replications during *Kharif*, 2022 at Agricultural College Farm, Bapatla. Each genotype was grown in a five rows of 3.0 m length with a spacing of 20 cm between rows and 15 cm between plants, within the row. The data was recorded on ten competitive plants taken from each replication on days to 50 per cent flowering, plant height (cm), ear bearing tillers per plant, panicle length (cm), test weight (g), number of filled grains per panicle, grain yield/plant (g), L/B ratio, water uptake, alkali spreading value, amylose content (%), protein content (%), Zn content (ppm), Fe content (ppm), total phenol content (mg/100g), antioxidant activity (mgAAE/100g), flavonoid content (mgQE/100g) and anthocyanin content (mg/100g). Analysis of variance was worked out by the method suggested by Panse and Sukhatme (1961) and the genotypic and phenotypic coefficient of variations were estimated by the method suggested by Burton (1952). The data analysis was carried out with INDOSTAT software. The GCV and PCV are classified as low (< 10%), moderate (10-20%) and high (> 20%) as suggested by Sivasubramanian and Madhavamenon (1973). Heritability was estimated by the formula given by Johnson *et al.* (1955) and they classified the heritability as low (below 30%), moderate (30- 60%) and high (above 60%). The range of genetic advance as per cent of mean was classified as low (< 10%), moderate (10-20%) and high (> 20%) as suggested by Johnson *et al.* (1955). Heritability estimates along with genetic advance are more helpful in predicting the genetic gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will always exhibit high genetic advance. Heritability provides information on magnitude of inheritance of quantitative characters while genetic advance helps in formulating suitable selection procedure.

RESULTS AND DISCUSSION

Analysis of variance for 18 characters, revealed significant differences among the genotypes for all the characters included under study indicating the presence of greater variability among the genotypes. (Table 1). Low GCV and PCV (<10%) values were recorded for the traits *viz.*, days to 50% flowering and amylose content (%) indicating that the variability for these characters among the genotypes was meagre. Similar findings were reported for these characters by Devi *et al.* (2022) and Nirmaladevi *et al.* (2015).

Moderate GCV and PCV (10-20%) values were recorded for the traits *viz.*, Plant height (cm), ear bearing tillers per plant, panicle length (cm), test weight (g), L/B ratio, water uptake, protein content (%), Zn content (ppm), Fe content (ppm) and antioxidant activity (mgAAE/100g). These results are in agreement with the earlier reports for these characters of Nath and Kole (2021), Manivelan *et al.* (2022), Dhavaleshvar *et al.* (2019), Kumar *et al.* (2020), Devi *et al.* (2022) and Pathak *et al.* (2017).

The characters, number of filled grains per panicle, alkali spreading value, total phenol content (mg/100g), grain yield/plant (g), anthocyanin content (mg/100g) and flavonoid content (mgQE/100g) registered higher GCV and PCV (>20%) values indicating that large amount of variation is present among the genotypes for these characters similar results were obtained by Devi *et al.* (2022), Singh *et al.* (2020), Sanghamitra *et al.* (2018), Sridevi (2018) and Devi *et al.* (2022). High heritability coupled with high genetic advance as per cent of mean (Table 2 and Figure 1) was reported for plant height (cm), ear bearing tillers per plant, panicle length (cm), test weight (g), number of filled grains per panicle, water uptake, alkali spreading value, protein content (%), Zn content (ppm), anthocyanin content (mg/100g), Fe content (ppm), antioxidant activity (mgAAE/100g), flavonoid content (mgQE/100g), total phenol content (mg/100g) and grain yield/plant (g) indicating that these traits were mostly under the control of additive gene action and hence direct phenotypic selection of these traits would be effective for crop improvement. Similar findings were earlier reported for these characters by Singh *et al.* (2020) for plant height, panicle length, alkali spreading value, Zn content, Fe content, antioxidant activity and test weight; Rao *et al.* (2020) for ear bearing tillers per

plant; Devi *et al.* (2022) for grain yield per plant, number of filled grains per panicle and water uptake; Sanghamitra *et al.* (2018) for protein content and total phenol content. High heritability coupled with moderate genetic advance as per cent of mean was observed for the traits *viz.*, days to 50% flowering, L/B ratio and amylose content (%) indicating the presence of both additive and non-additive genetic effects and genetic improvement of these characters can be exploited through heterosis breeding. Similar findings were earlier reported by Manivelan *et al.* (2022) for days to 50% flowering, Devi *et al.* (2020) for L/B ratio and Singh *et al.* (2020) for amylose content.

High PCV and GCV were recorded for the traits *viz.*, number of filled grains per panicle, alkali spreading value, total phenol content, flavonoid content, anthocyanin content and grain yield/plant indicating large amount of variation included in study among the genotypes. High heritability coupled with high genetic advance as per cent of mean is recorded for some yield contributing traits, like plant height, ear bearing tillers per plant panicle length, test weight, number of filled grains per panicle and nutritional and quality traits like water uptake, alkali spreading value, protein content, Zn content, Fe content, total phenol content, antioxidant activity, flavonoid content, anthocyanin content and grain yield/plant indicating that these traits were under the control of additive gene action and hence direct phenotypic selection of these traits would be effective for crop improvement.

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Table1. Analysis of variance for yield, nutritional and cooking quality traits in rice (*Oryza sativa* L.)

Source	Degrees of freedom	Days to 50 per cent flowering	Plant height (cm)	Ear bearing tillers per plant	Panicle length (cm)	Test weight (g)	Number of filled grains per panicle	L/B ratio	Water uptake	Alkali spreading value	Amylose content (%)
Mean sum of squares											
Replication	1	20.629	19.663	0.825	4.889	4.177	160.514	0.005	2.8	0.082	0.196
Treatments	34	112.487**	816.526**	4.817**	13.414**	24.39**	1674.951**	0.156**	192.464**	3.46**	4.669**
Error	34	26.746	68.083	0.983	1.951	1.804	86.514	0.034	5.506	0.035	0.5
Source	Protein content (%)	Zn content (ppm)	Fe content (ppm)	Total phenol content (mg/100g)	Antioxidant activity (mgAAE/100g)	Flavonoid content (mgQE/100g)	Anthocyanin content (mg/100g)	Grain yield / plant (g)			
Mean sum of squares											
Replication	0.448	3.432	0.129	0.089	3.657	2.161	12.943	0.082			
Treatments	5.234**	24.293**	9.522**	1070.103**	404.392**	40577.161**	6420.849**	77.217**			
Error	0.188	1.084	0.184	24.648	10.458	185.495	22.046	5.554			

*Significant at 5 per cent level of probability

** Significant at 1 per cent level of probability

Table 2: Estimates of genetic parameters for grain yield and biochemical characters in rice (*Oryza sativa* L.)

S.No.	Characters	Mean	Range		GCV (%)	PCV (%)	Genetic Advance	Heritability (Broad Sense) (%)	Genetic Advance as % of Mean
			Minimum	Maximum					
1	Days to 50 per cent flowering	84.8	78	110	7.72	9.83	10.58	61.58	12.47
2	Plant height (cm)	129.5	88.6	167.1	14.94	16.24	36.66	84.61	28.3
3	Ear bearing tillers per plant	10.9	8	14	12.65	15.56	2.32	66.11	21.19
4	Panicle length (cm)	21.1	16.1	27.5	11.3	13.08	4.26	74.6	20.11
5	Test weight (g)	21.6	11.2	26.2	15.54	16.74	6.43	86.23	29.73
6	Number of filled grains per panicle	112.2	88	223	25.11	26.44	55.13	90.18	49.12
7	L/B ratio	2.4	1.7	3.1	10.09	12.61	0.41	63.98	16.62
8	Water uptake	63.6	50	85	15.19	15.63	19.36	94.44	30.41
9	Alkali spreading value	3.1	1.5	7	42.06	42.48	2.67	98.01	85.77
10	Amylose content (%)	23.4	19.3	25.8	6.17	6.87	2.67	80.66	11.41
11	Protein content (%)	10.5	8.3	15	15.03	15.58	3.16	93.08	29.86
12	Zn content (ppm)	21.9	13.8	28.7	15.51	16.21	6.71	91.46	30.55
13	Fe content (ppm)	12.7	9.4	17.4	16.98	17.32	4.37	96.21	34.32
14	Total phenol content(mg/100g)	82.5	53.6	143.2	27.71	28.35	46.03	95.5	55.78
15	Antioxidant activity(mgAAE/100g)	94.7	29.1	111.7	14.81	15.2	28.17	94.96	29.73
16	Flavonoid content(mgQE/100g)	376.6	178.6	710.3	37.73	37.91	291.42	99.09	77.37
17	Anthocyanin content(mg/100g)	108.1	49.8	242.7	52.3	52.48	116.12	99.32	107.36
18	Grain yield per plant (g)	24.8	14.1	41.7	24.08	25.88	11.47	86.58	46.16

PCV-Phenotypic Coefficient of Variation; GCV-Genotypic Coefficient of Variation

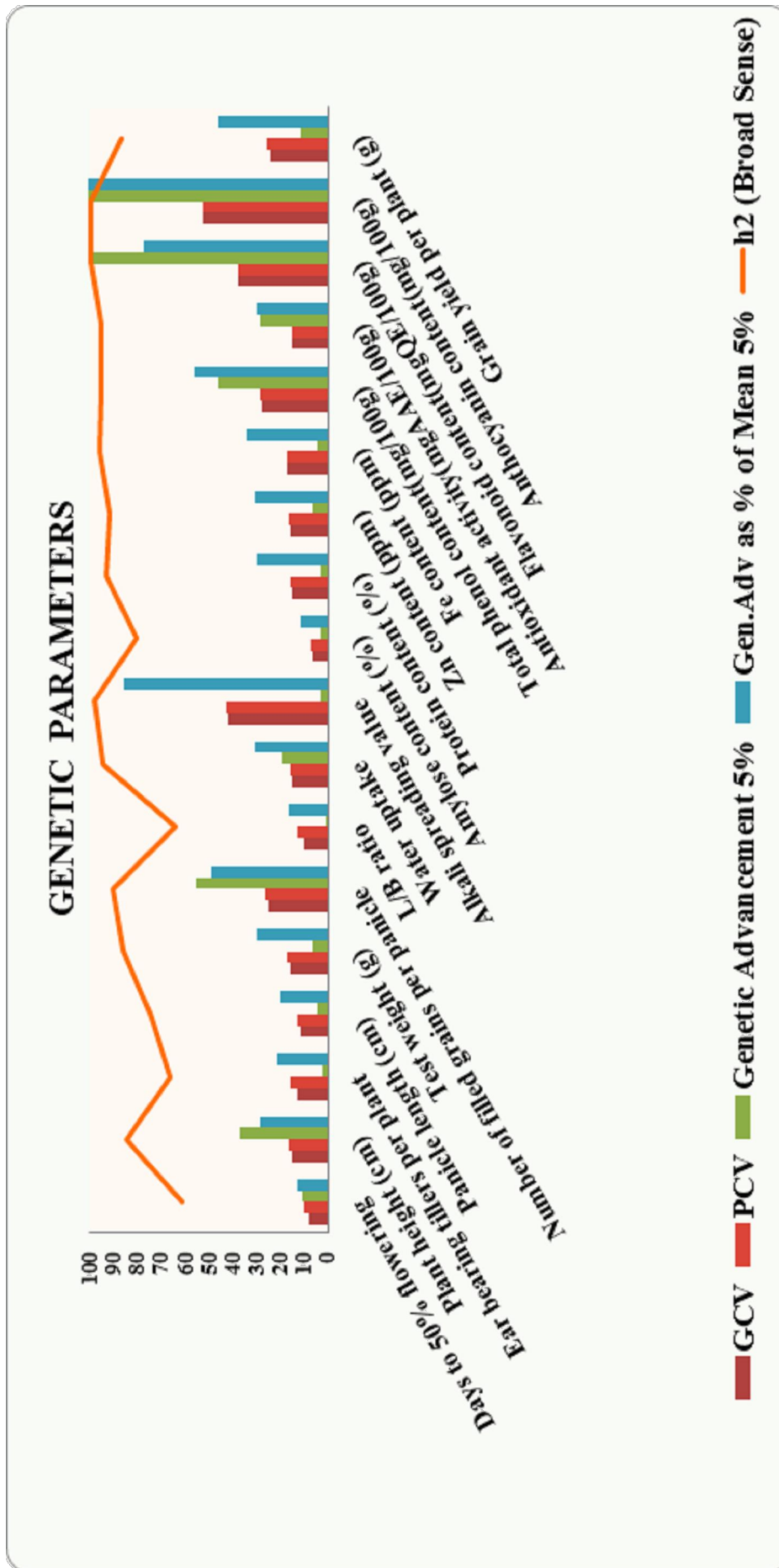


Figure 1: Pattern of GCV, PCV, heritability and genetic advance as percent of mean for 18 traits in 35 genotypes of rice (*Oryza sativa* L.)

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