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ASSESSMENT OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD AND YIELD COMPONENTS IN RED RICE (*ORYZA SATIVA* L.)

Nanda K.P.[1]*, Vavdiya P.A.[2], Asondariya K.H.[3], Jadav R.V.[1], Mungra K.S.[4] and Naghera Y.V.[5]
[1]Department of Genetics and Plant Breeding, College of Agriculture,
Junagadh Agricultural University, Junagadh 362001, Gujarat, India.
[2]Hill Millet Research Station, Navsari Agricultural University, Waghai (Dangs) 394730, Gujarat, India.
[3]Department of Genetics and Plant Breeding, N. M. college of Agriculture,
Navsari Agricultural University, Navsari 396450, Gujarat, India.
[4]Main Rice Research Centre, Navsari Agricultural University, Navsari 396450, Gujarat, India.
[5]Department of Biotechnology, College of Agriculture, Junagadh Agricultural University,
Junagadh 362001, Gujarat, India.
*Corresponding author E-mail: kunali.nanda119@gmail.com

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ABSTRACT

Red rice (*Oryza sativa* L.), a nutritionally enriched rice type, holds significant potential for yield improvement in rainfed and tribal regions. The present study evaluated 40 diverse red rice genotypes during *kharif*-2024 at Main Rice Research Centre, Navsari Agricultural University, Navsari, using a Randomized Block Design (RBD) with three replications. Significant genetic variability was observed across all sixteen agro-morphological and biochemical traits. The results revealed that Phenotypic Coefficient of Variation (PCV) values were generally higher than the corresponding Genotypic Coefficient of Variation (GCV) values for all traits studied. High GCV and PCV were observed for grain yield per plant and productive tillers per plant, while low values were noted for plant height and panicle length. The relatively narrow difference between PCV and GCV for most characters indicated minimal environmental influence and a predominance of genetic factors in trait expression. High heritability coupled with high genetic advance as percent of mean was recorded for traits like productive tillers per plant, grains per panicle, 100 grains weight, protein content and zinc content, indicating the effectiveness of simple selection. In contrast, traits such as panicle length, kernel length and Length breadth ratio (L/B ratio) showed low genetic advance, suggesting polygenic control and environmental influence. These results indicate ample scope for selection-based improvement of key yield-related and quality traits in red rice breeding programmes.

***Keywords* :** *Red rice, Genetic variability, Heritability, Genetic advance, Yield components.*

Introduction

Rice (*Oryza sativa* L.) is one of the most important staple food crops globally, particularly in Asian countries, feeding more than half of the world's population (FAO, 2023). In India, rice cultivation plays a vital role in rural livelihoods and national food security, occupying a major share of the total cultivated area (Anon., 2023). Among different types of rice, red rice holds unique importance due to its superior nutritional composition, appealing coloration and adaptation to diverse agro-ecological regions (Sahu *et al.*, 2020).

Red rice varieties are rich in micronutrients like zinc, iron, protein and anthocyanins, offering therapeutic benefits and potential in combating malnutrition (Bouis, 2003; Indrasari, 2018). As a functional food, red rice can contribute to human health by reducing risks of chronic diseases through its antioxidant properties (Oko and Ugwu, 2011). Moreover, rice is not only consumed for calories but also increasingly for its quality traits, especially in health-conscious markets.

In the context of crop improvement, genetic variability plays a crucial role in enhancing complex traits like yield and grain quality. The existence of wide variability in traditional red rice landraces provides ample scope for selection and breeding (Kumar, 2010; Sadimantara *et al.*, 2021; Shridevi *et al.*, 2025). Genetic parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability (h^2) and genetic advance (GA) help quantify this variability and predict the response to selection (Burton and De Vane, 1953; Johnson *et al.*, 1955).

High heritability coupled with high genetic advance indicates the predominance of additive gene action and suggests that improvement through selection would be effective (Miller *et al.*, 1958). These parameters are crucial in guiding breeding strategies aimed at improving yield, nutritional quality and adaptability in rice (Allard, 1960; Dabhi and Prajapati, 2025). The present investigation was therefore undertaken to evaluate the genetic variability, heritability estimates and genetic advance in red rice genotypes for both yield and nutritional traits, with the aim of identifying superior genotypes and traits suitable for selection and genetic improvement.

Table 1 : Name of the rice genotypes used in the present study

Sr. No.	Name of genotypes	Sr. No.	Name of genotypes
1	NVSR-762	21	IET-32901
2	NVSR-657	22	IET-32902
3	NVSR-658	23	IET-32903
4	NVSR-662	24	IET-32904
5	NVSR-674	25	IET-32905
6	NVSR-659	26	IET-32906
7	NVSR-651	27	IET-32907
8	NVSR-784	28	IET-32025
9	NVSR-1259	29	IET-32908
10	GNR-4	30	IET-32909
11	GR-23	31	IET-32910
12	GR-26	32	IET-32911
13	IET-3293	33	IET-28664
14	IET-3294	34	IET-32912
15	IET-3295	35	IET-32913
16	IET-3296	36	IET-32914
17	IET-3297	37	IET-32014
18	IET-3298	38	IET-32915
19	IET-32899	39	IET-32916
20	IET-32900	40	CHOHARTO

Materials and Methods

The present investigation was conducted at the Main Rice Research Centre, Navsari Agricultural University, Navsari, during the *kharif*-2024 season. The experimental site is located at 20.92° N latitude and 72.93° E longitude with an elevation of 10 meters above mean sea level. The region falls under AES-III (South Gujarat Heavy Rainfall Agro-climatic Zone) and receives an average annual rainfall of about 1500 mm. The experimental material comprised forty red rice (*Oryza sativa* L.) genotypes. The trial was laid out in a Randomized Block Design (RBD) with three replications. Each genotype was transplanted in a plot of 3 rows of 2.5 m length, spaced 20×15 cm. Standard agronomic and plant protection measures were adopted throughout the crop growth period to raise a healthy crop.

Observations were recorded on sixteen characters, encompassing both agro-morphological and biochemical traits. These traits included days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), productive tillers per plant, grains per panicle, 100 grain weight (g), grain yield per plant (g), straw yield per plant (g), harvest index (%), kernel length (mm), kernel breadth (mm), length/breadth ratio, protein content (%), amylose content (%) and zinc content (%). For the majority of traits, data were recorded by randomly selecting and tagging five competitive plants from each plot. However, observations for days to 50% flowering and days to maturity were recorded on a plot basis. The protein content was estimated by the Lowry *et al.* (1951) method using Folin-Ciocalteu reagent. The amylose content was determined by the Juliano (1971) method. The zinc content in grain samples was estimated by Atomic Absorption Spectrophotometry (AAS) after acid digestion, following standard protocols (Islam *et al.*, 2025). The list of forty genotypes of red rice shown in table-1.

Results and Discussion

The analysis of variance (Table-2) indicated that the mean sum of squares due to genotypes were highly significant ($p < .01$) for all sixteen traits: days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), productive tillers per plant, grains per panicle, 100 grains weight (g), grain yield per plant (g), straw yield per plant (g), harvest index (%), kernel length (mm), kernel breadth (mm), L/B ratio, protein content (%), amylose content (%) and zinc (Zn) content (%). This high level of variation confirms the existence of substantial genetic diversity among the red rice genotypes studied, offering ample opportunity for improvement through selection. Similar findings of high genotypic variability in rice have been reported by Ratna *et al.* (2015), Oladosu *et al.* (2018) and Hulmani *et al.* (2024).

Estimates of genotypic and phenotypic coefficients of variation (GCV and PCV), heritability (h^2bs) and genetic advance as percent of mean (GA%) are presented in Table-3. High GCV and PCV values were recorded for productive tillers per plant, grains per panicle, 100 grains weight, grain yield per plant, straw yield per plant, protein content and zinc content indicating a predominantly genetic basis for these traits with minimal environmental influence. This implies that selection for these traits would be effective and reliable. Similar high variability patterns have also been documented by Sanghera *et al.* (2013), Priyanka *et al.* (2016) and Babu *et al.* (2012).

In contrast, low to moderate GCV and PCV were observed for days to maturity, plant height, panicle length, harvest index, kernel length, kernel breadth and L/B ratio. These results suggest a stronger environmental influence on these traits, thereby limiting their immediate scope for genetic improvement through direct selection. These findings are supported by earlier work from Edukondalu *et al.* (2017) and Santipriya *et al.* (2017).

The broad-sense heritability estimates ranged from moderate to high for most characters, suggesting considerable genetic control. Traits such as days to 50%

flowering, productive tillers per plant, grains per panicle, 100 grains weight, grain yield per plant, straw yield per plant, kernel length, kernel breadth, protein content, amylose content and zinc content showed high heritability (>70%), indicating that these are primarily governed by additive gene action. These results align with those of Seyoum *et al.* (2012), Santipriya *et al.* (2017) and Priyanka *et al.* (2016).

Genetic advance as percent of mean (GA%) was also high for several traits including productive tillers per plant, grains per panicle, 100 grains weight, grain yield per plant, straw yield per plant, protein content and zinc content. The simultaneous occurrence of high heritability and high GA% suggests that these characters are under strong additive genetic control and can be improved effectively through direct selection. These trends have been similarly observed by Babu *et al.* (2012), Edukondalu *et al.* (2017) and Ratna *et al.* (2015).

However, traits such as days to 50% flowering, days to maturity, plant height, panicle length, kernel breadth and L/B ratio showed low to moderate GA% despite having moderate to high heritability. This indicates a potential role of non-additive gene effects or environmental variability, suggesting that direct selection may not be as efficient. Alternative strategies like hybrid breeding or marker-assisted selection might be more beneficial for these traits. Similar observations were made by Ratna *et al.* (2015) and Santipriya *et al.* (2017).

In conclusion, the current findings emphasize the traits - productive tillers per plant, grains per panicle, 100 grains weight, grain yield per plant, protein content and zinc content as key contributors to genetic improvement in red rice. These traits, with their high heritability and GA%, should be prioritized in future breeding efforts aimed at improving both yield and nutritional quality.

Table 2 : Analysis of variance of experimental design for yield and yield contributing characters

Source of variation	Degree of freedom	Days to 50% flowering	Days to maturity	Plant height (cm)	Panicle length (cm)	Productive tillers per plant	Grains per panicle	100 grains weight (g)	Grain yield per plant (g)
Replication	2	5.86	3.32	178.00	1.97	0.17	14.89	0.02	10.55
Treatment	39	110.67**	67.02**	336.30**	18.80**	4.45**	2456.86**	0.21**	53.44**
Error	78	4.17	13.27	135.02	4.17	0.56	39.36	0.01	5.54

Source of variation	Degree of freedom	Straw yield per plant (g)	Harvest index (%)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Protein content (%)	Amylose content (%)	Zn content (%)
Replication	2	0.69	18.01	0.09	0.01	0.26	0.07	0.43	0.77
Treatment	39	56.01**	31.20**	1.07**	0.07**	0.49**	1.97**	8.25**	25.56**
Error	78	10.12	11.22	0.15	0.01	0.09	0.08	0.5	0.37

*, ** significant at 5% and 1% levels of significance, respectively

Table 3 : Measures of variability parameters of sixteen characters

Chara-cters	Range of variation		Mean	Genotypic variance	Phenotypic variance	Environment variance	GCV (%)	PCV (%)	Heritability (h^2_{bs}) (%)	Genetic advance (% Mean)
	Min	Max								
DTF	91.00	111.00	100.98	35.55	39.71	4.16	5.90	6.24	89.51	11.50
DTM	123.33	142.33	132.35	17.91	31.18	13.26	3.19	4.21	57.46	4.99
PH	102.40	153.87	126.02	67.09	202.11	135.02	6.50	11.28	33.20	7.71
PL	16.07	27.00	22.30	4.87	9.05	4.17	9.90	13.49	53.87	14.97
PTPP	6.07	10.33	7.79	1.30	1.86	0.56	14.61	17.51	69.65	25.12
GPP	120.42	219.80	158.22	805.83	845.20	39.36	17.94	18.37	95.34	36.09
HGW	0.96	2.12	1.67	0.07	0.08	0.01	15.84	16.49	92.22	31.34
GY	13.81	27.67	21.88	15.97	21.51	5.54	18.27	21.20	74.24	32.42
SY	25.41	43.98	32.96	15.30	25.41	10.12	11.86	15.29	60.18	18.96
HI	34.01	45.42	39.67	6.66	17.88	11.22	6.51	10.66	37.25	8.18
KL	6.45	8.60	7.47	0.31	0.45	0.15	7.42	9.03	67.57	12.57
KB	1.73	2.58	1.93	0.02	0.03	0.01	7.38	9.51	60.26	11.80
L/B	2.95	4.76	3.90	0.13	0.22	0.09	9.36	11.99	61.01	15.06
PC	6.27	8.73	7.63	0.63	0.71	0.08	10.40	11.05	88.52	20.16
AC	21.49	28.80	24.66	2.58	3.08	0.50	6.52	7.12	83.72	12.29
ZC	11.73	25.13	16.47	8.40	8.77	0.37	17.60	17.98	95.74	35.47

Where, σ_g^2, σ_p^2 and σ_e^2 are the genotypic, phenotypic and environmental variance respectively. GCV% and PCV% are genotypic and phenotypic coefficient of variation respectively.

DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height (cm), PL= Panicle length (cm), PTPP= Productive tillers per plant, GPP= Grains per panicle, HGW= 100 grains weight (g), GY= Grain yield per plant (g), SY= Straw yield per plant (g), HI= Harvest index (%), KL= Kernel length (mm), KB= Kernel breadth (mm), L/B= L/B ratio, PC= Protein content (%), AC= Amylose content (%), ZC= Zn content (%)

Conclusion

The present study on forty red rice genotypes revealed substantial genetic variability for a wide range of yield and quality-related traits. Analysis of variance indicated significant differences among genotypes for all the studied traits, indicating the presence of exploitable genetic diversity. The estimates of phenotypic and genotypic coefficients of variation were moderate to high for most traits, particularly for productive tillers per plant, grains per panicle, 100 grains weight, grain yield per plant, straw yield per plant, harvest index, amylose content and zinc content suggesting ample scope for genetic improvement through selection.

High heritability estimates were observed for grains per panicle, 100 grains weight, grain yield per plant, protein content and zinc content accompanied by high genetic advance as percent of mean. This indicates the predominance of additive gene action in governing these traits and confirms their amenability to improvement through direct selection. Traits such as panicle length, straw yield per plant, kernel breadth and L/B ratio showed moderate heritability with moderate genetic advance, implying a combination of additive and non-additive gene actions and thus may require more targeted selection strategies.

Overall, the study highlights the availability of significant genetic variation in red rice genotypes for both yield and nutritional traits. This variability can be effectively utilized for developing high-yielding and nutritionally enriched cultivars of red rice through selection and breeding programs.

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