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STUDY OF GENETIC VARIABILITY IN 23 RICE LANDRACES OF BIHAR INDIA

Nitesh Kushwaha[1*], Naincy Sinha[2], Rajesh Kumar[2], Nilanjaya[2], Ashwani Kumar[3], Digvijay Singh[4] and Tushar Arun Mohanty[5], Kanchan Kumari Gupta[6], Prem Chand Gyani[7] and Monika Gahlot[1]

[1]Division of Genetics, ICAR-Indian Agricultural Research Institute, Pusa, New Delhi, India

[2]Department of Plant Breeding and Genetics, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar, India

[3]Department of Botany, K.R. P.G. College, Mathura, U.P., India

[4]Department of Genetics and Plant Breeding, Narayan Institute of Agricultural Sciences, Gopal Narayan Singh University, Sasaram, Bihar, India

[5]Department of Genetics and Plant Breeding, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India

[6]Division of Vegetable Science, Assam Agricultural University, Jorhat, Assam, India

[7]Division of Genetics and Tree Improvement, ICFRE- Rain Forest Research Institute, Assam, India

*Corresponding author Email: farmernk.998@gmail.com

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ABSTRACT

The study evaluated 23 rice landraces along with the check variety Sugandha for 15 agronomic and yield-related traits during the kharif season of 2018 at the Rice Breeding Station, Pusa, Bihar. Analysis of variance (ANOVA) revealed highly significant mean sum of squares due to treatments for all traits, indicating substantial genetic variability among the genotypes. Days to 50% flowering ranged from 66.77 (Sathi-2) to 150.33 (Rajbhog), while days to maturity varied from 90.00 (Sathi-2) to 177.67 (Sugapankhi). Plant height ranged from 113.2 cm (Kasturi) to 214.6 cm (Karahani), with taller genotypes like Moti and Sugapankhi showing higher root volumes. Grain yield per plant varied significantly, ranging from 22.59 g (Marcha-1) to 69.28 g (Lalka Dhan), with Lalka Dhan and Sathi-2 emerging as high-yielding genotypes. CSR-30 exhibited superior grain quality, including high 1000-grain weight (31.87 g) and grain length (11.44 mm). The phenotypic coefficient of variation (PCV) was consistently higher than the genotypic coefficient of variation (GCV), but the narrow gap between them suggested a strong genetic basis for most traits. High PCV and GCV values were observed for grain yield per plant, panicle number per plant, and root volume, indicating significant genetic variability and potential for improvement. High heritability coupled with high genetic advance as a percentage of the mean was observed for most traits, suggesting the predominance of additive gene action and the effectiveness of phenotypic selection. Traits like grain yield per plant, panicle number per plant, and root volume exhibited the highest genetic advance, highlighting their potential for genetic improvement. The study identified promising genotypes such as Sathi-1, Sathi-2, CSR-30, and Lalka Dhan for early maturity, high yield, and grain quality, providing valuable insights for future rice breeding programs aimed at enhancing productivity and genetic diversity.

***Keywords*:** Genetic variability, Genetic Diversity, Rice Landraces

Introduction

Rice, scientifically known as *Oryza sativa*, holds immense cultural, historical, and economic significance, particularly in Asia, where it serves as a staple food and a symbol of identity. As a cornerstone of global food security, rice provides essential calories and nutrients to a significant portion of the world's population, with over 90% of its production and consumption concentrated in Asia. Countries like China and India play pivotal roles in its cultivation, while Africa and Latin America also contribute significantly to global rice production. In India, rice is often referred to as 'Prana,' reflecting its vital role in sustenance and culture. Globally, rice is cultivated across 167.1 million hectares, yielding 782 million tons with productivity of 4678 kg per hectare. In India alone, rice is grown on 46.15 million hectares, producing 116.47 million tons with productivity of 2638 kg per hectare (Deepika *et al*., 2023). Despite its global importance, the origins, domestication, and evolutionary genetics of rice remain complex, with the genus *Oryza* encompassing diverse wild species alongside the two cultivated ones, *Oryza sativa* and *Oryza glaberrima*. Landraces and wild relatives of rice harbor a wealth of genetic diversity, offering valuable traits such as high yield potential, improved quality, and resistance to biotic and abiotic stresses like diseases, pests, drought, and salinity. By integrating these traits into modern breeding programs, researchers can develop resilient, high-yielding rice varieties capable of addressing challenges posed by climate change, pests, and diseases. This process of genetic enhancement is crucial for ensuring food security and agricultural sustainability in the face of evolving environmental and economic pressures. The work of researchers like Saxena *et al*. (1988) underscores the importance of preserving and utilizing this genetic diversity to create innovative solutions for contemporary agricultural challenges. By harnessing the genetic potential of landraces and wild species, breeders can develop rice varieties that meet the needs of farmers and consumers while contributing to the long-term resilience and sustainability of global agricultural systems.

Rice, with its tremendous genetic variability, has successfully adapted to diverse ecological conditions, thriving in tropical, subtropical, and temperate regions across all latitudinal boundaries. This adaptability underscores its importance as a global staple crop. For effective breeding programs, understanding the genetic variability within rice is crucial, as it forms the foundation for crop improvement. The success of any plant breeding initiative depends on the extent of genotypic and phenotypic variability present in the species. The ratio of genotypic variance to phenotypic variance provides estimates of heritability, which indicates the influence of environmental factors on a genotype and the reliability of a trait for selection. Johnson et al. emphasized that heritability estimates alone are insufficient for predicting the outcomes of selection; they must be considered alongside genetic advance to assess the potential for trait improvement. Genetic advance reflects the proportion of variation attributable to additive gene action, which is crucial for effective selection. Traits with high heritability and significant genetic advance are more likely to respond positively to selection, making them ideal targets for breeding programs. Therefore, the concurrent use of heritability and genetic advance provides a more accurate and practical framework for predicting the effectiveness of selection and guiding the development of improved rice varieties with desirable traits. This approach ensures that breeding programs can harness the genetic diversity of rice to enhance productivity, resilience, and adaptability in varying environmental conditions.

Material and Methods

The present study was conducted at the Rice Breeding Station, Pusa, under Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar, during the kharif season of 2018. The research aimed to evaluate the genetic diversity among 23 rice landraces (table 1) using 15 agronomic and yield-related traits. The experiment was laid out in a Randomized Block Design (RBD) with three replications, and the landraces were planted at a standard spacing of 15 x 20 cm. All recommended agronomic practices were followed to ensure optimal growth conditions. Observations were recorded randomly from five plants within each replication for the following traits: days to 50% flowering (DFF), days to maturity (DTM), plant height (PH), stem thickness (ST), panicle length of the main axis (PLM), number of panicles per plant (PPP), length of leaf blade (LLB), width of leaf blade (WLB), 1000-grain weight (GW), grain length (GL), grain width (GWI), decorticated grain length (DGL), decorticated grain width (DGW), root volume (RV), and grain yield per plant (GY/P).

Table 1: List of Genotypes

S.NO.	GENOTYPE	SOURCE
1	PUSA SUGANDHA -2	IARI, PUSA
2	RAJBHOG	RAU, PUSA
3	KARAHANI	RAU, PUSA
4	KARIYWA	RAU, PUSA
5	DIHAWAN	RAU, PUSA
6	MOTI	RAU, PUSA
7	SUGAPANKHI	RAU, PUSA
8	JADHAN	RAU, PUSA
9	LALKA DHAN	RAU, PUSA
10	DUDHA LADU	RAU, PUSA
11	JASWA-3	IGKV,RAIPUR
12	PARWA PANKHI	IGKV,RAIPUR
13	KANKIRBI	RAU, PUSA
14	CSR-30	CSIR, KARNAL
15	SUGANDHA	RAU, PUSA
16	KASTURI	BAU, SABOUR
17	LALMATI	BAU,RANCHI

18	BASMATI-570	PAU, LUDHIANA
19	MARCHA-1	RAU, PUSA
20	MARCHA -2	RAU, PUSA
21	TARORI BASMATI	IARI,PUSA
22	SATHI-1	RAU, PUSA
23	SATHI-2	RAU, PUSA

Mean

The mean value for each of the 15 traits evaluated in the study was calculated by dividing the total sum of observations for each trait by the corresponding number of observations.

$$\text{Mean} = \Sigma x/N$$

Where,

$\sum X$ = Sum of all the observations for each character in replication

N = Corresponding number of observation.

Range

It was taken as the difference between the highest and lowest mean value for each character.

$$\text{Range} = X_n - X_t$$

Where,

X_n = Highest mean value of character

X_t = Lowest mean value of character

Component of variance

Genotypic variance

The genotypic variance (VG or σ^2_g) is the variance due to the genotypes present in the population. The formula used for calculation of genotypic variance was as follows

$$\text{Genotypic variance}\left(\sigma^2 g\right) = \frac{\text{MSt - EMS}}{\text{Number of replications (r)}}$$

Environmental or Error variance

The environmental variance (VE or σ^2_e) is the variance due to environmental deviation.

$$\sigma^2_e = \text{EMS}$$

Phenotypic variance

Phenotypic variance (VP or σ^2_p **)** denotes the total variance present in a population for particular character and is calculated by following formula

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

Where,

σ^2_g= Genotypic variance

σ^2_e= Error variance

Standard error of mean

Standard error of means was calculated by following formula

$$\text{SEm} = \sqrt{\frac{2\text{EMS}}{r}}$$

Critical Difference

Critical difference was calculated by following formula

$$\text{CD} = \sqrt{\frac{2\text{EMS}}{r}} \times \text{t value at 5\%}$$

t-value = table value of error difference at 5% level of significance

Where,

r = number of replications.

Ems = error mean sum of squares

Coefficient of Variation

It is the measure of variability evolved. Coefficient of variation is the ratio of standard deviation of a sample to its mean and expressed in percentage.

$$\text{CV}(\%) = \frac{\text{Standard deviation}}{\text{Mean}} \times 100$$

In the present investigation three types of coefficients of variations were estimated, viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and error/ environmental coefficient of variation (ECV). The formulae used to calculate PCV, GCV, ECV were given by Burton and De vane (1953).

(i) $$\text{PCV}(\%) = \frac{\text{Phenotypic standard deviation} \times 100}{\text{Mean}} = \sqrt{\frac{\sigma^2_p}{\bar{X}}} \times 100$$

(ii) $$\text{GCV}(\%) = \frac{\text{Genotypic standard deviation} \times 100}{\text{Mean}} = \sqrt{\frac{\sigma^2_g}{\bar{X}}} \times 100$$

(iii) $$\text{ECV}(\%) = \frac{\text{Error standard deviation}}{\text{Mean}} \times 100 = \sqrt{\frac{\sigma^2_e}{\bar{X}}} \times 100$$

Where,

$\sigma^2{}_p$ = Phenotypic variance
$\sigma^2{}_e$ = Environmental variance
$\sigma^2{}_g$ = Genotypic variance
X = Mean of character

Standard deviation

It is the square root of the variance

$$SD = \sqrt{\frac{\sum x^2 - \frac{(\sum x)^2}{N}}{N-1}}$$

$$\text{Variance} = \frac{\sum x^2 - \frac{(\sum x)^2}{N}}{N-1}$$

Genetic advance

Genetic advance is the improvement in mean genotypic value of selected plants over the parental population. The estimates of genetic advance were obtained by the formula given by Lush (1949) Johnson *et al.* (1955) and Allard (1960).

$$GA = K.\ \sigma_{\mathbf{p.}}\ h^2$$

$$= K.\ \sigma_{\mathbf{p}}\ \frac{\sigma_g^w}{\sigma_p^2}$$

Where,

K = Selection differential at 5% level intensity, *i.e.* 2.06 which is constant

$\sigma_{\mathbf{p}}$ = Phenotypic standard deviation

h^2 = Heritability in broad sense

Genetic advance as percent of mean (GA%)

$$GA\ (\%) = \frac{GA}{\overline{\overline{X}}} \times 100$$

The range of genetic advance is classified as suggested by Johnson *et al.* (1955)

Low: Less than 10%

Moderate: 10-20%

Higher: More than 20%

Heritability (Broad sense)

Heritability in broad sense was estimated as the ratio of genotypic to the phenotypic variance and was expressed in percentage. It was calculated by the formula given by Johnson *et al.* (1955).

$$h^2\ (\text{broad sense}) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance
$\sigma^2 p$ = Phenotypic variance
h^2 = Heritability (broad sense)

The heritability was categorized as low, moderate and high as given by Robinson *et al.* (1949).

0-30% : Low
30-60% : Moderate
60% and above : High

Results and Discussion

The analysis of variance (ANOVA) was conducted to partition the total variance observed in the study into components attributable to genotypes and other sources of variation for all 15 morphological characters (table 2). The results revealed that the mean sum of squares due to treatments was highly significant for all the traits evaluated, indicating the presence of substantial genetic variability among the rice landraces. This significant variation highlights the diverse genetic potential of the genotypes under study, which is essential for effective selection and breeding programs

Table 2: Analysis of variance for twenty-three genotypes of rice for fifteen morphological

Sl. No.	**Characters**	**Mean sum of squares**		
		Replication (d.f.=2)	**Treatments (d.f.=22)**	**Error (d.f.=44)**
1.	DAYS TO 50%FLOWERING	103.36	1,825.99**	45.94
2.	DAYS TO MATURITY	137.45	2,035.72**	62.89
3.	PLANT HEIGHT (cm)	37.39	2,836.17**	100.86
4.	STEM THICKNESS (mm)	0.60	1.35**	0.25
5.	PANICLE LENGHTH OF MAIN AXIS (cm)	12.92	152.64**	10.92
6.	PANICLE NUMBER PER PLANT	10.45	83.60**	6.19
7.	LENGTH OF LEAF BLADE (cm)	4.69	404.27**	12.73
8.	WIDTH OF LEAF BLADE(cm)	0.01	0.13**	0.03
9.	1000 GRAIN WEIGHT	1.27	86.07**	2.45
10.	GRAIN LENGTH (mm)	2.00	5.93**	0.22

11.	GRAIN WIDTH (mm)	0.07	0.78**	0.03
12.	DECORTICATED GRAIN LENGTH (mm)	0.22	4.00**	0.15
13.	DECORTICATED GRAIN WIDTH (mm)	0.01	0.52**	0.06
14.	ROOT VOLUME (mm)	31,78,751.25	36,90,34,638.12**	82,46,776.49
15.	GRAIN YIELD PER PLANT(g)	33.03	871.97**	33.30

** Significance at 1 % level *Significance at 5 % level

The study evaluated 23 genotypes for various agronomic traits, comparing them to the check variety Sugandha (table 3, 4). Days to fifty percent flowering ranged from 66.77 (Sathi-2) to 150.33 (Rajbhog), with an average of 114.06 days, while days to maturity varied from 90.00 (Sathi-2) to 177.67 (Sugapankhi), averaging 143.94 days. Sathi-1 and Sathi-2 were the earliest in both flowering and maturity, whereas Rajbhog, Karahani, and Sugapankhi were significantly late. Plant height ranged from 113.2 cm (Kasturi) to 214.6 cm (Karahani), with taller genotypes like Moti and Sugapankhi also exhibiting higher root volumes, suggesting a correlation between plant height and root development. Stem thickness was highest in Sugandha (5.067 mm), with no genotype surpassing it. Panicle length varied from 10.5 cm (Kankirbi) to 32.27 cm (Marcha-2), with Marcha-2 showing the longest panicles. Panicle number per plant ranged from 9 (Karahani) to 25 (Jadhan), with higher panicle numbers directly correlating with increased grain yield. Grain yield per plant ranged from 22.59 g (Marcha-1) to 69.28 g (Lalka Dhan), with Lalka Dhan and Sathi-2 being the highest yielders. CSR-30 stood out for superior grain quality, including 1000-grain weight (31.87 g), grain length (11.44 mm), and decorticated grain length (8.1 mm). Overall, the study identified promising genotypes like Sathi-1, Sathi-2, CSR-30, and Lalka Dhan for early maturity, high yield, and grain quality, providing valuable insights for future breeding programs.These finding was in accordance to findings of also Lingaiah *et al.,* 2015, Vanishree *et al.,* 2013.

Table 3: Mean performance of twenty-three genotypes of rice for fifteen morphological traits

Sl. No.	**Genotypes/ Characters**	**DFF**	**DTM**	**PH (cm)**	**ST (mm)**	**PLM**	**PPP**	**LLB (cm)**	**WLB (cm)**	**GW (g)**	**GL (mm)**	**GWI (mm)**	**DGL (mm)**	**DGW (mm)**	**RV (mm^3)**	**GY/P**
1	PUSA SUGANDHA-2	121.67	152.67	114.00	4.45	25.90	12.67	36.55	1.42	21.48	8.67	1.65	6.13	1.46	22667.06	43.65
2	RAJBHOG	150.33	177.00	177.00	4.45	25.38	8.67	38.67	1.05	24.50	7.53	3.61	5.43	1.63	31667.37	40.71
3	KARAHANI	141.00	175.33	214.60	4.40	24.07	9.00	22.73	1.10	22.26	7.69	2.69	5.38	2.61	35666.87	25.58
4	KARIYWA	120.67	152.67	125.58	4.04	11.22	15.67	13.57	1.41	17.97	8.07	2.16	5.99	1.89	22833.86	48.25
5	DIHAWAN	140.00	167.33	170.43	4.99	25.87	7.33	36.83	1.35	27.36	7.67	2.13	5.92	1.92	40333.65	39.00
6	MOTI	140.67	177.00	194.62	4.29	26.52	13.00	29.73	1.53	28.23	7.87	2.30	4.63	2.07	48000.34	40.56
7	SUGAPANKHI	147.33	177.67	202.68	4.60	27.55	11.67	39.75	1.27	27.58	7.63	1.76	5.33	1.67	43333.87	55.33
8	JADHAN	101.00	130.67	117.82	4.31	31.37	24.67	30.55	1.47	30.05	9.37	2.73	7.15	2.36	16700.47	59.36
9	LALKA DHAN	92.67	120.33	104.08	4.07	20.77	21.00	41.32	1.07	26.48	7.57	2.99	5.37	2.52	13000.23	69.28
10	DUDHA LADU	142.67	170.67	181.65	2.49	28.37	14.00	34.68	1.53	26.44	7.83	1.73	6.19	1.48	42667.27	47.44
11	JASWA-3	120.00	148.67	159.00	4.86	12.02	9.67	14.29	0.97	22.64	8.73	2.07	6.79	1.72	22000.50	40.07
12	PARWA PANKHI	121.67	158.00	194.73	4.51	24.57	8.67	34.85	1.23	30.10	8.35	2.27	5.33	1.73	31333.77	36.82
13	KANKIRBI	100.33	147.00	144.02	3.48	10.05	16.33	9.98	1.00	24.13	8.08	2.64	5.89	2.37	24667.07	48.40
14	CSR-30	103.00	133.00	143.30	3.79	13.02	17.67	11.56	1.00	31.87	11.44	2.32	8.10	1.73	14334.07	28.43
15	SUGANDHA	127.33	153.00	144.23	5.07	19.13	12.33	21.03	0.84	10.60	6.90	2.43	4.87	2.27	27000.33	31.12
16	KASTURI	111.67	141.67	113.20	4.53	21.37	17.00	26.17	0.93	15.90	6.13	2.27	4.27	2.16	21667.27	25.10
17	LALMATI	71.00	100.00	125.61	3.14	22.67	17.33	47.87	1.48	14.23	8.13	1.30	5.48	1.17	15667.12	30.44
18	BASMATI-570	92.00	129.33	144.65	3.90	12.43	6.67	10.97	1.01	24.07	9.47	2.41	7.04	1.84	21333.61	23.29
19	MARCHA-1	118.67	138.67	148.32	3.87	30.52	7.33	39.53	1.20	18.19	5.47	1.74	3.52	2.56	16000.47	22.59
20	MARCHA -2	118.33	147.00	157.84	3.63	32.17	12.67	39.30	1.10	20.32	5.27	1.97	3.49	1.66	19000.39	29.84
21	TARORI BASMATI	105.67	132.00	148.60	3.13	11.56	20.33	25.60	1.13	27.37	10.47	1.83	7.40	1.30	14333.73	38.20
22	SATHI-1	69.00	91.00	131.83	3.18	17.27	19.67	41.43	1.16	24.61	7.71	2.64	5.89	2.37	10100.12	36.39
23	SATHI-2	66.67	90.00	136.26	3.32	14.80	23.00	40.80	1.10	23.01	7.00	1.85	4.78	1.63	11400.10	34.15
	Mean	**114.06**	**143.94**	**151.92**	**4.02**	**21.24**	**14.19**	**29.90**	**1.19**	**23.45**	**7.96**	**2.24**	**5.67**	**1.92**	**24596.07**	**39.43**
	C.D.5%	**11.15**	**13.05**	**16.53**	**0.83**	**5.44**	**4.09**	**5.87**	**0.29**	**2.58**	**0.77**	**0.29**	**0.63**	**0.41**	**4725.51**	**9.50**
	S.E.	**3.91**	**4.58**	**5.80**	**0.29**	**1.91**	**1.44**	**2.06**	**0.10**	**0.90**	**0.27**	**0.10**	**0.22**	**0.14**	**1657.99**	**3.33**

* Superior to Sugandha (Check)

The study revealed that the phenotypic coefficient of variation (PCV) was consistently higher than the genotypic coefficient of variation (GCV) for all traits under investigation (table 5), indicating the influence of environmental factors on phenotypic expression. However, the narrow differences between PCV and GCV for most traits suggest a strong genetic basis for these characteristics. A wide range of PCV was observed across traits, with the highest values recorded for grain yield per plant (59.39), panicle number per plant (39.87), length of leaf blade (40.02), and root volume (46.09), indicating high variability influenced by both genetic and environmental factors. Traits such as days to maturity (18.65), stem thickness (19.52), and grain length (18.31) exhibited moderate PCV values. Similarly, GCV ranged from 15.21 (width of leaf blade) to 56.14 (grain yield per plant), with high GCV observed for traits like days to 50% flowering (21.36), panicle length of main axis (32.36), panicle number per plant (35.80), and root volume (45.59), highlighting significant genetic variability. Moderate GCV values were noted for traits such as days to maturity (17.81), plant height (19.88), and grain length (17.35). These findings underscore the potential for genetic improvement in traits with high GCV, while the narrow PCV-GCV gap suggests that selection based on phenotypic performance could be effective for most traits. This result followed the works of Tuhina-Khatun *et al.*, 2015, Muthuswamy *et al.*, 2006.

Table 4: Mean, range and coefficient of variance for fifteen morphological traits

Sl. No.	Characters	Mean	SE	Range	CV
1	DFF	114.06	3.91	66.67-150.33	5.94
2	DTM	143.94	4.58	90.00-177.67	5.51
3	PH (cm)	151.92	5.80	104.08-214.60	6.61
4	ST (mm)	4.02	0.29	2.49-5.07	12.47
5	PLM	21.24	1.91	10.05-32.17	15.55
6	PPP	14.19	1.44	6.67-24.67	17.54
7	LLB (cm)	29.90	2.06	9.98-47.87	11.93
8	WLB (cm)	1.19	0.10	0.84-1.53	14.66
9	GW (g)	23.45	0.90	10.60-31.87	6.68
10	GL (mm)	7.96	0.27	5.27-11.44	5.85
11	GWI (mm)	2.24	0.10	1.30-3.61	7.87
12	DGL (mm)	5.67	0.22	3.49-8.10	6.75
13	DGW (mm)	1.92	0.14	1.17-2.61	12.91
14	RV (mm^3)	24596.07	1657.99	10100.12-48000.34	11.68
15	GY/P (g)	39.43	3.33	22.59 -69.28	19.37

The study revealed that genetic advance as a percentage of the mean ranged from 23.80% (stem thickness) to 81.52% (grain yield per plant), indicating high genetic advance for all traits under investigation. This high genetic advance suggests that these traits are primarily governed by additive gene action, making them highly responsive to selection. Traits such as grain yield per plant, panicle number per plant, root volume, and days to 50% flowering exhibited particularly high genetic advance, highlighting their potential for significant improvement through selective breeding. The findings imply that phenotypic selection for these traits would be highly effective, as additive gene effects are more stable and heritable. Overall, the high genetic advance across all traits underscores the potential for genetic improvement and the effectiveness of selection-based breeding strategies for enhancing these characteristics (Anjaneyulu *et al.*, 2010; Chaudhary *et al.* 2004; Mohanty *et al.*, 2020; Kushwaha *et al.*, 2020).

Table 5: Estimates of genetic parameters for fifteen characters

Sl. No.	Characters	$\sigma^2 g$	$\sigma^2 p$	GCV	PCV	h^2 (Broad sense) (%)	Genetic Advance as per cent of Mean
1	DAYS TO 50% FLOWERING	593.4	639.3	21.4	22.2	92.8	42.4
2	DAYS TO MATURITY	657.6	720.5	17.8	18.6	91.3	35.1
3	PLANT HEIGHT (cm)	911.8	1012.6	19.9	20.9	90.0	38.9
4	STEM THICKNESS (mm)	0.4	0.6	15.0	19.5	59.2	23.8
5	PANICLE LENGHTH OF MAIN AXIS(cm)	47.2	58.2	32.4	35.9	81.2	60.1
6	PANICLE NUMBER PER PLANT	25.8	32.0	35.8	39.9	80.6	66.2
7	LENGTH OF LEAF BLADE (cm)	130.5	143.2	38.2	40.0	91.1	75.1
8	WIDTH OF LEAF BLADE (cm)	0.0	0.1	15.2	21.1	51.8	22.6
9	1000 GRAIN WEIGHT	27.9	30.3	22.5	23.5	91.9	44.5
10	GRAIN LENGTH (mm)	1.9	2.1	17.3	18.3	89.8	33.9
11	GRAIN WIDTH (mm)	0.2	0.3	22.3	23.6	88.9	43.3
12	DECORTICATED GRAIN LENGTH (mm)	1.3	1.4	20.0	21.1	89.8	39.1
13	DECORTICATED GRAIN WIDTH(mm)	0.2	0.2	20.3	24.1	71.3	35.4
14	ROOT VOLUME (mm)	120262624.0	128509400.0	44.6	46.1	93.6	88.9
15	GRAIN YIELD PER PLANT(g)	279.6	312.9	56.1	59.4	89.4	81.52

Conclusion

The analysis of variance (ANOVA) revealed that the mean sum of squares due to treatments was highly significant (at the 1% level) for all fifteen traits studied, indicating substantial genetic differences among the rice landraces. This significant variation underscores the diverse genetic potential of the materials under investigation, which is crucial for effective selection and breeding programs. The environmental influence on the expression of the quantitative traits was minimal, as evidenced by the narrow gap between the genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV). This suggests that the observed variability was primarily due to genetic factors rather than environmental conditions.

Among the traits, root volume and grain yield per plant exhibited high GCV and PCV values, highlighting their importance in the selection of landraces for future hybridization programs. These traits are likely to respond well to selection due to their high genetic variability. Additionally, all traits demonstrated high heritability coupled with high genetic advance as a percentage of the mean, indicating the predominance of fixable genetic variance. This suggests that these traits are controlled by additive gene action, making them suitable for selection and improvement. However, stem thickness and width of leaf blade were exceptions, as they did not exhibit high heritability and genetic advance.

The coefficient of variation (CV) was found to be highest for grain yield per plant, followed by the number of panicles per plant and panicle length of the main axis, indicating substantial variability in these traits. In contrast, days to maturity showed the least variability, as reflected by the minimum coefficient of variation. These findings provide valuable insights into the genetic architecture of the rice landraces and highlight the potential for improving yield and other agronomic traits through targeted breeding efforts. The high heritability and genetic advance for most traits suggest that selection based on these characteristics would be effective in developing improved rice varieties with enhanced productivity and adaptability.

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