

## **Genetic Variability Assessment in Lowland Rice Cultivars of Bihar, India**

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### **Authors' contributions**

*This work was carried out in collaboration among all authors. Authors NK carried out on field research work and took observation and authors DS, TAM, NS, RC assisted during observations and data recording. Authors Ravi Kant, Rajesh Kumar and Nilanjaya outlined the research plan with author NK and supervised the work during the entire crop season and also helped in collection of review. All authors read and approved the final manuscript.*

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### **ABSTRACT**

The present investigation for various genetic parameters was done for twenty-two lowland rice genotypes in R.C.B.D. with three replications at Rice Breeding Section, Pusa Farm, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar. Analysis of variance revealed significant differences ( $P$ -value =0.01) among genotypes for all the characters. Brasali was the highest yielder suggesting that it can be used for crossing programme for improvement in yield. The phenotypic variance was higher than corresponding genotypic variances for all the characters studied. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were highest for grain yield per plant followed by 1000 grain weight, plant height, number of panicles, root volume, leaf length and days to 50 % flowering revealing that sufficient variability was present in the gene pool for these characters. Thus, there is ample scope for genetic improvement of these traits

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through selection. The broad sense heritability ranged from 23 % (panicle length of main axis) to 97% (1000 grain weight). High heritability was obtained for most of the characters except for panicle length of main axis and kernel width. High heritability accompanied with high genetic advance as percent of mean was recorded for days to 50% flowering, plant height, root volume, number of panicles, 1000 grain weight, leaf length and grain yield per plant. High values of GCV, PCV, heritability and genetic advance as percent of mean observed for various characters indicate that these traits can be used as selection indices for yield improvement.

**Keywords:** GCV; PCV; heritability; genetic advance; R.C.B.D.

## 1. INTRODUCTION

Rice is the world's most important food crop and a primary food source for more than one third of world's population [1]. Over 90 percent of the world's rice is produced and consumed in the Asia-Pacific Region. It belongs to the family *Poaceae* and sub family *Oryzoidea* and tribe *Oryzeae* [2]. This genus comprises more than 22 species distributed through the Tropical and Sub-tropical regions of Asia, Africa, central and south America and Australia, of which, there are only two cultivated species; *Oryza glaberrima* (Steud.) and *Oryza sativa* L [3]. The estimated world rice production for the year 2019-20 is 496.67 million metric tons [4].

Rice possess tremendous variability therefore it has crossed all the latitudinal boundaries, growing equally well in tropical, sub-tropical as well as in temperate regions. Being a diverse crop and with adaption in various ecological conditions, it is important to have knowledge of genetic variability that can be exploited in a breeding programme. The knowledge of genetic variability present in a given crop species is of paramount importance for the success of any plant breeding programme. The scope of improvement depends upon the extent of genotypic and phenotypic variability present in the crop species. The ratio of genotypic variance and phenotypic variance gives the estimates of heritability which gives the idea of environmental effects on a genotype and reliability of a character [5]. Johnson, et al. [6] suggested that heritability and the genetic advance when calculated together would prove more useful in predicting the resultant effect of selection of phenotypic expression, without genetic advance the estimates of heritability will not be of practical value and emphasised the concurrent use of genetic advance along with heritability.

Bihar is one of the recurrent flood prone area of India, so it's a treasure house of rice cultivars and landraces having very useful genes and gene combinations required to thrive flood

situation. So, variability in the existing germplasm need to be studied, which may be exploited in future breeding programmes to develop new varieties adapted to local ecological conditions. Present investigation was carried out seeking the problem as stated.

## 2. MATERIALS AND METHODS

The present research work was conducted at Rice Breeding Section, Pusa Farm, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar during *kharif* 2018, from June, 26 to December 28. Geographically university farm is situated between 25.98°N latitude and 85.67°E longitudes at 51.8 above mean sea level. Twenty-two lowland rice cultivars were taken for current investigation. The experimental design adopted was R.C.B.D., with three replications. Firstly, the rice seedlings were raised in nursery seedbeds for 25 days and then the seedlings were transplanted manually in the puddled plots prepared for sowing. Standard spacing of 20 x 15 cm was maintained and all the recommended package of practices were followed during growth period. Observations were taken randomly from five plants within each replication. Data were recorded for fifteen traits viz. grain length (mm), grain width (mm), kernel length (mm), days to 50% flowering, plant height (cm), root volume (mm<sup>3</sup>), panicle length of main axis' (cm), leaf length (cm), leaf width (cm), no. of panicle per hill, days to maturity, stem thickness (mm), 1000 grain weight, kernel width (mm), grain yield per plant (g).

Mean performance of the genotypes and genetic parameters such as genetic coefficient of variation, heritability, and genetic advance were calculated for all fifteen characters using following formulas.

### 2.1 Mean

The mean value of each character was worked out by dividing the totals by the corresponding number of observations

$$\text{Mean} = \frac{\sum X}{N}$$

Where,

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

## 2.2 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

## 2.3 Component of Variance

### 2.3.1 Genotypic variance

The genotypic variance ( $V_G$  or  $\sigma_g^2$ ) is the variance due to the genotypes present in the population. The formula used for calculation of genotypic variance was as follows

$$\text{Genotypic variance } (\sigma_g^2) = \frac{Mst - EMS}{\text{Number of replication } (r)}$$

### 2.3.2 Environmental or error variance

The environmental variance ( $V_E$  or  $\sigma_e^2$ ) is the variance due to environmental deviation.

$$\sigma_e^2 = EMS$$

### 2.3.3 Phenotypic variance

Phenotypic variance ( $V_P$  or  $\sigma_p^2$ ) denotes the total variance present in a population for particular character and is calculated by following formula

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Where,

$\sigma_g^2$  = Genotypic variance  
 $\sigma_e^2$  = Error variance

### 2.3.4 Standard error of mean

Standard error of means was calculated by following formula

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

### 2.3.5 Critical difference

Critical difference was calculated by following formula

$$CD = \sqrt{\frac{2EMS}{r}} \text{ t value}$$

Where,

EMS = error mean sum of squares  
 r = number of replications  
 t-value = Table value of error difference at 5% level of significance

Significant "F" value indicates that, there is significant difference among the treatments. But to compare any two particular treatments, it is tested against CD value.

## 2.4 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.

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

In the present investigation three types of coefficient 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 [7]

$$(i) \text{ PCV } (\%) = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100 = \frac{\sigma_p^2}{\bar{x}} \times 100$$

$$(ii) \text{ GCV } (\%) = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100 = \frac{\sigma_g^2}{\bar{x}} \times 100$$

$$(iii) \text{ ECV } (\%) = \frac{\text{Error standard deviation}}{\text{Mean}} \times 100 = \frac{\sigma_e^2}{\bar{x}} \times 100$$

Where,

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

## 2.5 Standard Deviation

It is the square root of the variance

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

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

## 2.6 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 [8], [6] and [9].

$$GA = K \cdot \sigma_p \cdot h^2$$

$$= K \cdot \sigma_p \cdot \frac{\sigma_g^2}{\sigma_p^2}$$

Where,

K = Selection differential at 5% level intensity, i.e. 2.06 which is constant  
 $\sigma_p$  = Phenotypic standard deviation  
 $h^2$  = Heritability in broad sense

Genetic advance as percent of mean (GA%)

$$GA (\%) = \frac{GA}{\bar{x}} \times 100$$

The range of genetic advance is classified as suggested by [6].

Low: Less than 10%  
 Moderate: 10-20%  
 Higher: More than 20%

## 2.7 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 [6].

$$h^2 (\text{broad sense}) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

$\sigma_g^2$  = Genotypic variance  
 $\sigma_p^2$  = 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

## 3. RESULTS AND DISCUSSION

### 3.1 Analysis of Variance

The Analysis of variance revealed that the 22 genotypes were significantly different ( $P$  value= 0.01) for all the quantitative characters studied, except leaf length (Table 1). The other characters included leaf width, days to 50 % flowering, days to maturity, plant height, panicle length of main axis, number of panicles per plant, kernel length, kernel width, grain length, grain width, root volume, stem thickness, 1000 seed weight and grain yield per plant. In any plant breeding programme variability and selection are indispensable. Success of plant breeding programme depends on extent of variability present in the material under study. The more the variability the better is the chance of selection. In the present study, wide range of variability was observed among the genotypes for all characters. Genotype Brasali exhibited highest mean value (Table 2) for grain yield per plant followed by Sagar Samba. Brasali(64.60), Sagar Samba(49.70), Radha(35.24) and Kishori(33.17) were found superior over check Swarna for trait grain yield per plant. The results were in accordance with the findings of [10], [11].

### 3.2 Genotypic and Phenotypic Variances

In the present investigation, the phenotypic variance was higher than corresponding genotypic variances for all the characters studied (Table 3). However, the difference between genotypic and phenotypic variance was quite low indicating that the variability obtained was mostly due to genotypic constitution of the genotypes

and the effect of external factors was less. The genotypic and phenotypic variances for the different characters under study were highest for root volume, followed by plant height, days to 50% flowering, days to maturity and grain yield per plant [12] and [13] had similar types of findings.

**Table 1. List of Genotypes**

SI no	Genotypes	Sources
1	Santosh	R.P.C.A.U., Pusa
2	Kanak	R.P.C.A.U., Pusa
3	Radha	R.P.C.A.U., Pusa
4	Pankaj	O.U.A.T., Orissa
5	Satyam	R.P.C.A.U., Pusa
6	Rajshree	R.P.C.A.U., Pusa
7	Swarna	N.R.R.I, Cuttack
8	Sudha	R.P.C.A.U., Pusa
9	Vaidehi	R.P.C.A.U., Pusa
10	Janaki	R.P.C.A.U., Pusa
11	Barogar	R.P.C.A.U., Pusa
12	Madhukar	N.D.U.A.T, U.P.
13	Singhara	R.P.C.A.U., Pusa
14	Ujaladhusarisa	Landrace, BIHAR
15	Sagar samba	O.U.A.T., Orissa
16	Jagannath ballava	O.U.A.T., Orissa
17	Brasali	N.D.U.A.T, U.P.
18	Meghnad	N.D.U.A.T, U.P.
19	Silhat	N.D.U.A.T, U.P.

### 3.3 Genotypic and Phenotypic Coefficient of Variation

Phenotypic coefficient of variation was higher than their corresponding genotypic coefficient variation for all the characters (Table 3). The relative difference between phenotypic coefficient of variation and genotypic coefficient of variation was narrow for some characters such as grain length, days to 50% flowering, and kernel length suggesting that there was less environmental effect on the expression of phenotype of such characters. Hence selection for these traits may be effective on their phenotypic values. On the other hand, the gap was wide for some characters such as panicle length of main axis and grain yield per plant suggesting role of environment in expression of these characters. In the present investigation, phenotypic coefficient of variation higher than the genotypic coefficient of variation was in accordance with [14] and [10].

Genotypic coefficient of variation and phenotypic coefficient of variation was found highest for grain yield per plant, 1000 grain weight, plant height, number of panicles, root volume, leaf length and days to 50 % flowering revealing that sufficient variability was present in the gene pool for these characters. Thus, there is ample scope for genetic improvement of these traits through selection. The high magnitude of genotypic coefficient of variation for grain yield was also obtained by [15] and [16].

**Table 2. Analysis of variance for 15 quantitative characters in 22 lowland genotypes of rice**

SI no.	Characters	Source of variation		
		Replication	Genotype	Error
1	Grain length (mm)	0.03	2.07**	0.04
2	Grain width (mm)	0.03	0.29**	0.04
3	Kernel length (mm)	0.08	1.04**	0.29
4	Days to 50% flowering	96.92	777.49**	13.27
5	Plant height (cm)	148.46	3554.52**	76.57
6	Root volume (mm <sup>3</sup> )	1400622.00	20914257.40**	3164946.15
7	Panicle length of main axis (cm)	1.37	8.03**	4.21
8	Leaf width (cm)	0.03	0.06**	0.02
9	Number of panicles	1.21	21.23**	3.90
10	Days to maturity	223.20	482.90**	56.30
11	Stem thickness (mm)	0.05	0.418**	0.06
12	1000 grain weight (g.)	5.31	82.39**	0.92
13	Kernel width (mm)	0.11	0.09**	0.036
14	Leaf length (cm)	5.6	190.56**	13.86
15	Grain yield per plant (g.)	11.34	444.53**	32.34

**Table 3. Mean performance of 22 genotypes of rice for fifteen characters**

Character	GL	GW	KL	DFL	PLH	RV	PLMA	LW	NP	DTM	ST	TW	KW	LL	YLD
<b>Genotype</b>															
SANTOSH	9.20	2.42	7.13	98.67	142.40	17000.65	25.17	1.37	17.78	149.67	4.30	22.37	1.83	50.30	23.20
KANAK	8.73	2.67	6.73	100.67	98.70	20333.88	24.53	1.27	16.10	148.33	3.83	22.42	2.40	52.40	28.17
RADHA	7.87	2.67	6.10	97.33	142.93	17334.18	26.17	1.37	11.55	141.33	3.87	22.60	2.07	52.06	35.24
PANKAJ	7.67	2.83	5.93	119.33	104.87	21833.97	24.57	1.57	14.00	142.00	3.73	16.65	2.00	46.43	29.74
SATYAM	9.20	2.92	7.33	121.67	102.87	21000.58	22.93	1.03	15.88	143.67	4.43	21.28	1.93	45.90	16.68
RAJSHREE	7.20	2.75	5.70	104.00	138.33	17717.27	23.23	1.20	13.75	130.00	3.77	19.36	1.93	56.27	20.73
SWARNA (C)	7.93	2.83	6.07	108.33	98.80	21667.19	23.50	1.07	14.55	138.00	4.20	27.56	2.08	45.73	18.10
SUDHA	9.73	2.58	6.93	120.67	162.00	14834.05	22.50	1.10	15.22	150.00	4.67	25.88	2.17	65.07	21.30
VAIDEHI	9.27	2.23	6.50	118.33	159.70	16000.82	21.60	1.07	18.11	151.33	4.40	25.46	2.20	61.10	26.57
JANAKI	8.93	2.92	6.73	121.33	180.97	14167.06	21.73	1.13	11.55	148.00	4.27	29.19	2.17	59.10	28.31
BAROGAR	7.67	3.17	5.67	119.67	184.60	14833.88	23.90	1.53	16.42	145.67	4.27	21.60	1.85	59.40	14.13
MADHUKAR	8.80	2.57	6.53	120.00	126.17	19000.46	24.97	1.30	18.30	139.00	4.20	21.75	2.00	63.97	28.40
SINGHARA	6.73	2.37	5.47	144.33	226.53	16367.39	23.43	1.30	11.83	172.00	4.23	19.23	1.97	56.43	8.20
UJALA DHUSARISA	8.80	2.64	6.87	122.67	165.13	15300.56	22.17	1.20	15.50	149.33	4.67	27.97	2.00	66.00	22.67
SAGAR SAMBA	9.07	2.42	6.13	110.33	121.13	20333.79	27.83	1.30	23.65	138.00	4.77	16.65	1.75	66.13	49.70
JAGANNATH BALLAVA	7.60	2.42	5.67	155.67	151.67	14567.22	22.37	1.03	16.42	170.33	4.53	12.44	1.75	64.50	15.90
BRASALI	8.73	2.25	5.87	145.67	160.03	17400.58	26.57	1.23	16.07	169.67	3.30	19.50	2.00	64.73	64.60
MEGHNAD	8.17	2.60	5.93	120.33	185.67	14867.34	22.47	1.30	15.77	150.33	3.70	23.52	1.83	63.50	33.43
SILHAT	9.33	2.58	6.67	119.00	155.87	16000.98	23.07	1.27	16.87	145.67	3.77	25.64	2.13	62.63	20.43
SHYAMALA	8.77	2.30	6.60	149.33	185.37	13667.28	23.93	1.30	18.17	181.67	4.27	26.55	1.93	65.83	20.53
BPT-5204-SUB 1	7.17	1.70	5.07	125.00	102.07	20137.33	24.00	1.20	16.22	142.33	3.97	9.47	1.67	40.70	23.80
KISHORI	9.07	2.83	6.73	136.00	126.30	20000.46	25.67	1.27	17.53	149.33	3.93	13.29	2.08	50.43	33.17
MEAN	8.44	2.58	6.29	121.74	146.46	17471.22	23.92	1.25	15.97	149.80	4.14	21.38	1.99	57.21	26.50
C.D.	0.31	0.34	0.28	6.00	14.42	2931.42	3.38	0.21	3.26	12.36	0.41	1.58	0.31	6.13	9.37

GL= Grain length, GW= Grain width, KL= Kernel length, DFL= Days to 50% flowering, RV= Root volume, PLMA= Panicle length of main axis, LW= Leaf width, NP= number of panicles per hill, DTM= Days to maturity, ST= Stem thickness, TW=1000 grain weight, KW= Kernel width, LL= Leaf length, YLD= Grain yield per plant

**Table 4. Genetic parameters of 15 quantitative characters in 22 lowland rice genotypes**

Sl. no	Characters	$\Sigma^2_g$	$\Sigma^2_p$	GCV	PCV	H <sup>2</sup> (Broad sense) %	Genetic advance as % of mean
1	Grain length (mm)	0.68	0.71	9.77	10.02	0.95	19.62
2	Grain width (mm)	0.08	0.13	11.10	13.73	0.65	18.47
3	Kernel length (mm)	0.34	0.37	9.26	9.64	0.92	18.33
4	Days to 50% flowering	254.74	268.01	13.11	13.45	0.95	26.33
5	Plant height (cm)	1159.31	1235.89	23.25	24.00	0.94	46.38
6	Root volume (mm <sup>3</sup> )	5916437.00	9081383.00	13.92	17.25	0.65	23.15
7	Panicle length of main axis (cm)	1.27	5.487	4.72	9.79	0.23	4.68
8	Leaf width (cm)	0.02	0.03	9.86	14.06	0.49	14.24
9	Number of panicles	5.78	9.68	15.05	19.49	0.60	23.95
10	Days to maturity	142.20	198.51	7.96	9.41	0.72	13.88
11	Stem thickness (mm)	0.12	0.18	8.33	10.27	0.66	13.93
12	1000 grain weight (g.)	27.16	28.08	24.37	24.78	0.97	59.38
13	Kernel width (mm)	0.02	0.05	6.61	11.65	0.32	7.73
14	Leaf length (cm)	58.89	72.76	13.41	14.91	0.81	24.86
15	Grain yield per plant (g.)	137.40	169.74	44.23	49.16	0.81	81.98

### 3.4 Heritability and Genetic Advance as Per Cent of Mean

The broad sense heritability ranged from 23% (panicle length of main axis) to 97% (1000 grain weight) (Table 4). High heritability was obtained for most of the characters except for panicle length of main axis and kernel width. Similar results were found in the result of [17].

Genetic advance was highest for grain yield per plant followed by 1000 grain weight and plant height. It was lowest for panicle length of main axis and kernel width, whereas moderate estimates were observed for some characters such as days to 50 % flowering, leaf length, number of panicles, root volume, grain length, grain width and kernel length. High heritability accompanied with high genetic advance as percent of mean was recorded for days to 50 % flowering, plant height, root volume, number of panicles, 1000grain weight, leaf length and grain yield per plant. This suggests that subjecting these characters to any selection scheme for exploiting fixable genetic variance is highly effective and desirable. Above findings followed the findings of [18] and [19].

## 4. CONCLUSION

Genotype Brasali exhibited highest mean value for grain yield per plant followed by Sagar Samba Brasali, Sagar Samba, Radha and Kishori were superior over the check, Swarna for trait grain

yield per plant. Analysis of variance revealed significant differences among genotypes for all the characters.

For all the fifteen quantitative characters, phenotypic variance was higher than its corresponding genotypic variance but difference was quite low, showing that contribution of genotype was substantially less influenced by the environment. High values of GCV, PCV, heritability and genetic advance as percent of mean were observed for grain yield per plant, 1000 grain weight and plant height indicating that these traits can be used as selection indices for yield improvement.

High heritability accompanied with high genetic advance as percent of mean was recorded for days to 50 % flowering, plant height, root volume, number of panicles, 1000grain weight, leaf length and grain yield per plant, suggesting that these characters can be subjected to any selection scheme for exploiting fixable genetic variance.

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## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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