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Estimation of Genetic Variability Parameters in Germplasm Accessions of Rice (*Oryza sativa* L.)

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ABSTRACT

In the present investigation, forty four germplasm accessions of rice including two checks were evaluated to estimate the genetic parameters in the experimental material for selection of the diverse parents for yield and its component traits. The experiment was laid out in an augmented design with four blocks at National Seed Project, UAS, GKVK, Bengaluru. Analysis of variance indicated the existence of significant genotypic differences among the genotypes for the yield and its component traits. The low PCV and GCV were observed for days to 50 per cent flowering, days to physiological maturity, days to harvestable maturity and thousand seed weight. However high GCV and PCV was noticed for tillers per plant, productive tillers per plant, stem length, number of seeds per panicle, panicle weight and seed yield per plant. The heritability estimates were high for days to 50 per cent flowering, days to physiological maturity, days to harvestable maturity, plant height, total number of tillers, productive tillers per plant, stem length, panicle weight, seed yield per plant and thousand seed weight. Hence, simple selection can be practiced to improve these characters in the selected genotypes.

Keywords : Rice, Standardized range, Genetic variability, GCV, PCV, Heritability

RICE (*Oryza sativa* L.) belongs to the family graminae, recognized as 'Millennium Crop' expected to contribute towards food security in the world, as it is one of the staple cereal crops and a primary source of food for more than half of the world's population. With an alarming increase in the population throughout the world, the demand for rice will continue to increase in near future. Therefore, rice breeders across the world aim at increasing the productivity. A better understanding of the relationship between grain yield and its component traits becomes necessary for making an efficient selection for the development of new varieties with improved economically important traits. The knowledge of genetic variability and heritability is a prerequisite for carrying out selection-based improvement. The information about these help in the breeding programmes by broadening the gene pool of rice and gives an indication about the efficiency of transformation of characters into future generations respectively. In any crop species setting the breeding objective to improve the crop yield is of prime importance. Understanding the nature and magnitude of genetic variation governing the inheritance of quantitative traits like yield and attributing traits are essential. Plant breeder has to analyse genetic variability parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and heritability of various economically important quantitative traits to plan future crop improvement programmes. Genetic variability plays an important role in study and identification of promising rice genotypes.

MATERIAL AND METHODS

Present investigation was conducted at the National Seed Project, University of Agricultural Sciences, GKVK, Bengaluru, Karnataka. The experiment consists of 44 accessions including two checks laid out in an augmented design with four blocks. Twenty two days old seedlings were transplanted at the rate of one seedling per hill in two rows of four meters length with plant to plant distance of 10 cm and row to row distance of 30 cm. The standard cultivation practices prescribed for rice under irrigated conditions were followed precisely. List of genotypes studied are

TABLE 1
List of genotypes studied

Sl No.	Accessions	Sl No.	Accessions
1	ARC 18112	24	PAUNDRI
2	CHANDINA	25	SRAU THMOR
3	4NCS 194	26	DILBAKSH
4	SUWEON 311	27	E ZI 32
5	TSAO SHENG LI 1	28	KABERI
6	WI BIR SHUN	29	KHAO' SIM
7	A NONG ZAO 4	30	N'YA NOFF
8	78 XUAN WU	31	QUN XUAN ZAO
9	AIJIAONANTE		
10	ANADI WHITE	32	ROJON'NY NTAOLO
11	AN NAN ZAO		
12	AR 133	33	VARY LAVA DE BOLOGNE
13	ARC 10894	34	ARC 15505
14	ATH HAGARI JARAHAN PADDY	35	KOLUBA
15	DAWK PUT	36	AZUCENA
16	E ZI 100	37	LI JIANG XIN TUAN HEI GU
17	HEGAR MANAH	38	M202
18	JIE CAO ZHAN	39	MOROBEREKAN
19	KONAMANI	40	POKKALI
20	LIU HE XI HE	41	TAINUNG 67
21	LUA DUC	42	ZHENSHAN 97 B
22	MAN TIAN QING	43	THANU
23	NS 199	44	BR 2655

mentioned in Table 1. Data were recorded on five randomly selected plants in each entry such as days to 50 per cent flowering, days to physiological maturity, days to harvestable maturity, plant height(cm), total number of tillers, productive tillers/plant, stem length (cm), panicle length(cm), panicle weight (g), number of seeds/panicle, 1000 seed weight (g) and yield. The data was subjected to statistical analysis of genotypic coefficient of variation (%), phenotypic coefficient of variation (%) and heritability in broad sense (%).

Descriptive Statistics to Assess Genetic Variability

The mean and variance of randomly chosen plants were calculated for the quantitative traits and used for statistical analysis.

Mean

Mean of each trait was computed on the basis of observation, recorded on five randomly selected plants. It is calculated by dividing the sum of all observations in a sample by their number. Thus,

$$\text{Mean} = \frac{\text{Sum of observation of all the selected plants}}{\text{Number of plants}}$$

Range

It is the difference between the lowest and the highest mean values for each character. Absolute range and standardized range were calculated by using following formulae.

$$\text{Absolute range (R)} = \text{(Highest-Lowest)}$$

$$\text{Standardized range (SR)} = \frac{\text{Highest-Lowest}}{\text{General mean}}$$

Standard Error

$$\text{S.E.} = \frac{\sigma}{\sqrt{n}}$$

Where,

σ = Population standard deviation, n = sample size

Estimation of Genetic Parameters

The co-efficient of variation for all characters at both phenotypic and genotypic levels was calculated by adopting the formula as suggested by Burton and Devane (1953).

Genotypic coefficient of variation

$$\text{GCV (\%)} = \frac{\sigma_g}{X} \times 100$$

Phenotypic coefficient of Variation (PCV)

$$\text{PCV (\%)} = \frac{\sigma_p}{X} \times 100$$

Where,

$\bar{X}$ = General mean

σ_p = Phenotypic standard deviation

σ_g = Genotypic standard deviation

GCV and PCV were categorized as proposed by Robinson *et al.* (1949) as low (0-10%), moderate (10.1% -20%) and high (> 20%).

Heritability (Broad sense)

Broad sense heritability estimates were calculated for all characters according to the formula proposed by Lush (1945).

$$h^2 \text{ (broad sense)} = \frac{Vg}{Vp}$$

Where,

h^2 = heritability (Broad sense)

Vg = Genotypic variance of population

Vp = Phenotypic variance of population

Heritability was categorized as low (0-30%), moderate (30.1-60%) and high (>60%) as proposed by Robinson *et al.* (1949).

RESULTS AND DISCUSSION

Genetic variability in any crop is prerequisite for selection of superior genotypes over the existing cultivars. The mean values for twelve yield components are given Table 2. The analysis of variance depicting the mean sum of squares for all the twelve quantitative traits under study, are summarised in table 3 and significance of mean sum of squares for yield and yield attributes indicates existence of considerable degree of variability among the germplasm accessions. The results revealed that the paddy germplasm accessions differ significantly for the characters such as days to 50 per cent flowering, days to physiological maturity, days to harvest, stem length, plant height, tillers per plant, productive tillers per plant and panicle weight per plant. The paddy germplasm accessions and checks were differed

TABLE 2

Per se performance of 44 genotypes of rice for growth, seed yield and its components traits

Genotypes	DFF	DPM	DHM	PH	TNT	PTP	SL	PL	PW	NOS	PLP	TSW
ARC 18112	87.0	130.0	142.0	108.5	37.8	30.2	85.2	23.3	15.8	70.2	6.1	22.6
CHANDINA	90.0	133.0	145.0	55.4	44.4	34.2	37.3	18.2	11.4	56.2	2.7	20.4
4NCS 194	88.0	130.0	143.0	105.0	24.8	14.8	86.5	18.5	8.1	43.0	4.4	18.9
SUWEON 311	65.0	105.0	120.0	51.0	13.4	6.0	32.3	18.7	5.5	25.8	0.6	21.6
TSAO SHENG LI 1	90.0	141.0	145.0	120.0	21.2	16.8	97.9	22.1	31.2	120.2	7.7	26.0
WI BIR SHUN	104.0	145.0	159.0	104.2	30.4	19.2	86.0	18.2	11.9	56.8	8.3	21.1
A NONG ZAO 4	82.0	124.0	137.0	53.5	25.2	16.2	36.2	17.3	10.6	38.8	3.0	27.4
78 XUAN WU	82.0	124.0	137.0	67.9	18.2	12.0	46.3	21.6	18.2	83.0	1.7	22.0
AIJIAONANTE	90.0	143.0	145.0	41.8	35.8	26.4	25.1	16.7	14.5	67.8	0.7	21.4
ANADI WHITE	73.0	116.0	128.0	107.8	48.8	38.8	87.8	20.0	18.1	79.6	4.7	22.8
AN NAN ZAO	79.0	121.0	134.0	100.4	34.4	23.4	79.8	20.6	19.9	81.8	2.2	24.4
AR 133	95.0	136.0	150.0	99.6	43.2	31.8	97.8	21.1	21.5	97.8	2.0	23.2
ARC 10894	98.0	137.0	153.0	121.0	15.0	11.0	82.1	23.2	16.7	74.8	1.9	22.0
ATH HAGARI JARAHAN PADDY	80.0	123.0	135.0	102.6	26.8	31.8	78.5	20.5	13.3	57.6	1.9	22.4

Genotypes	DFF	DPM	DHM	PH	TNT	PTP	SL	PL	PW	NOS	PLP	TSW
DAWK PUT	88.0	130.0	143.0	102.4	24.8	16.6	80.8	21.6	20.6	96.0	4.9	21.5
E ZI 100	89.0	130.0	144.0	81.4	23.4	13.2	60.1	21.3	12.5	49.0	0.9	25.6
HEGAR MANAH	98.0	149.0	153.0	107.2	21.8	14.6	85.3	21.9	17.4	69.6	3.4	25.0
JIE CAO ZHAN	90.0	133.0	147.0	113.1	23.6	17.4	90.0	23.1	13.2	56.2	5.0	23.5
KONAMANI	92.0	133.0	147.0	98.9	37.6	25.2	75.8	23.1	24.9	106.8	6.2	23.4
LIU HE XI HE	91.0	133.0	147.0	104.5	26.6	18.8	83.2	21.3	18.1	63.6	3.5	24.3
LUA DUC	78.0	120.0	133.0	103.0	24.0	18.0	82.4	20.6	15.4	58.6	0.9	19.1
MAN TIAN QING	90.0	133.0	145.0	116.3	37.2	31.0	97.5	18.8	11.1	108.0	7.6	23.5
NS 199	111.0	149.0	165.0	103.1	18.0	12.0	82.6	20.5	25.3	46.6	1.5	19.9
PAUNDRI	95.0	135.0	150.0	96.7	23.4	14.2	75.1	21.6	9.2	138.2	4.2	25.3
SRAU THMOR	110.0	148.0	165.0	93.5	41.4	32.4	74.1	19.4	34.9	90.6	2.1	18.0
DILBAKSH	104.0	145.0	159.0	99.1	32.6	21.4	77.7	21.4	16.3	82.8	2.6	22.7
E ZI 32	103.0	146.0	158.0	51.1	20.4	13.4	33.3	17.8	18.7	20.6	1.4	27.0
KABERI	92.0	132.0	147.0	50.5	45.4	28.8	31.9	18.6	5.5	77.2	3.2	19.4
KHAO' SIM	106.0	144.0	161.0	85.9	25.8	16.0	63.4	22.5	14.9	80.0	2.2	23.9
N'YA NOFF	110.0	149.0	165.0	104.5	41.2	31.4	84.0	20.5	19.1	83.0	4.1	25.7
QUN XUAN ZAO	83.0	126.0	138.0	59.1	16.4	8.4	38.3	20.8	21.3	20.2	0.5	22.2
ROJON'NY NTAOLO	97.0	118.0	132.0	115.2	26.0	17.2	90.8	24.4	4.4	115.4	2.3	23.1
VARY LAVA DE BOLOGNE	94.0	105.0	149.0	97.7	12.6	9.2	76.8	20.9	26.6	84.2	3.9	24.2
ARC 15505	77.0	119.0	132.0	98.6	25.8	18.2	75.6	23.0	9.2	128.0	0.8	22.8
KOLUBA	102.0	142.0	157.0	152.4	12.4	11.2	123.6	30.5	20.3	158.8	6.1	26.5
AZUCENA	101.0	141.0	156.0	140.7	8.4	8.4	112.6	28.1	29.1	107.8	4.4	25.3
LI JIANG XIN TUAN HEI GU	78.0	120.0	133.0	78.2	24.4	17.8	65.4	12.8	42.0	28.0	3.1	18.6
M202	72.0	113.0	127.0	64.4	20.8	13.4	47.8	16.6	27.2	44.8	2.1	24.9
MOROBEREKAN	117.0	155.0	172.0	115.2	7.0	6.0	89.7	25.5	5.2	109.4	2.8	25.8
POKKALI	91.0	132.0	146.0	99.0	54.0	43.0	79.4	19.6	11.1	68.0	2.3	21.5
TAINUNG 67	98.0	138.0	153.0	90.7	16.8	10.6	70.3	20.4	28.2	93.0	4.3	22.1
ZHENSHAN 97 B	109.0	149.0	164.0	45.8	22.6	14.2	26.8	19.0	14.6	68.6	2.2	21.9
THANU	64.5	104.0	120.0	75.3	16.3	13.3	55.8	19.3	20.5	104.5	12.0	15.7
BR 2655	67.3	108.0	122.0	91.1	22.5	18.3	62.9	28.5	15.0	140.0	16.1	18.1

DFF: Days to 50% flowering, DPM: Days to physiological maturity, DHM: Days to harvest maturity, PH: Plant height(cm), TNT: Total number of tillers, PTP: Productive tillers/plant, SL: Stem length (cm), PL: Panicle length(cm), PW: Panicle weight (g), NOS: Number of seeds/panicle, YPP: Yield per plant(g), TSW: Test weight(g).

TABLE 3

Analysis of variance (mean sum of squares) for 12 quantitative traits in rice germplasm accessions

Source	D.f	Days to 50% flowering	Days to physiological maturity	Days to harvest	Stem length (cm)	Plant height (cm)	Tillers / plant	Productive tillers/ plant	Panicle length (cm)	Number of seeds/ panicle	Panicle weight / plant	Test weight (g)	Yield/ plant (g)
Entries (A+C)	43	239.40	257.20	238.40	569.40	660.50	130.10	80.80	14.32	1340	69.20	10.40	22.53
Block	3	0.50	0.10	0.70	2.30	0.30	0.10	0.10	0.13	24.00	0.50	0.01	0.01
Accessions	41	137.90 ***	150.70 **	141.60 **	567.60 *	664.70 *	125.10 *	81.70 *	9.48	998.00	67.50 *	5.53	4.00
Checks	1	15.10 *	28.10 *	8.00	100.10	496.10 *	78.10	55.10	164.70 **	2521.00 *	125.10	4.50	30.80 **
Interaction (AXC)	1	4628.40 ***	4849.30 ***	4435.20 ***	111.50 *	651.70 *	390.20 **	71.10	62.40 **	14162.00 **	84.20 *	218.40 ***	773.30 ***
Error	3	0.80	2.10	3.30	53.70	82.20	10.50	7.10	3.34	236.00	13.20	0.74	0.67

*Significant @ P=0.05 level ; **Significant@ P=0.01 level ; *** Significant @ P=0.001 level

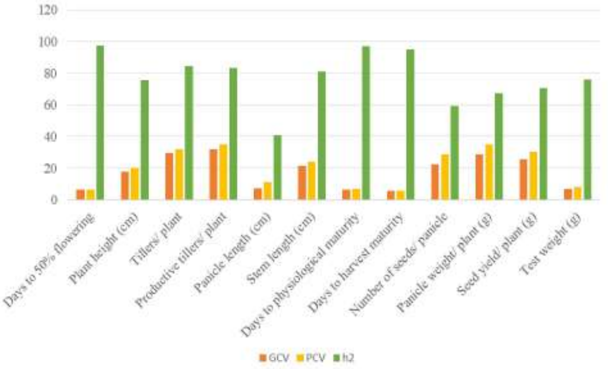

Fig.1 : Variability and heritability as per cent of mean in germplasm accessions of rice

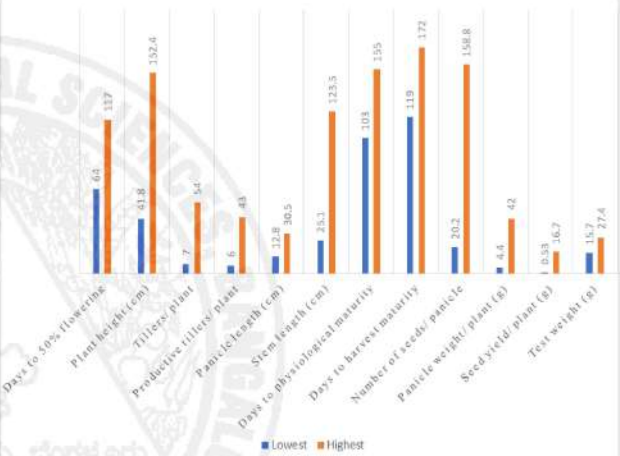

Fig.2 : Lowest and highest value of growth and yield component of germplasm accessions of rice

significantly for most of the characters studied indicating appreciable amount of genetic variability among the genotypes tested in the present study. A wide range of variance was observed for all the characters studied. Phenotypic variance was higher than genotypic variance for all the yield and its contributing characters. However narrow difference between GCV and PCV, significantly the high heritability for the characters and less influence of environment on the expression traits was observed.

The mean performance of the accessions along with estimates of range, standardized range provides the information about the presence of accessions with variable expression of the trait. The variability parameters for grain yield and its components traits are presented in Table 4.

TABLE4

Mean performance and genetic variability of accessions of rice for yield and yield components

Traits	Mean ± SE	Range		Standardized Range	GCV	PCV	h^2
		Lowest	Highest				
Days to 50% flowering	87.9 ± 2.1	64.00	117.00	0.60	6.20	6.28	97.41
Plant height (cm)	91.4 ± 3.6	41.80	152.40	1.20	17.56	20.17	75.82
Tillers/ plant	25.7 ± 1.6	7.00	54.00	1.80	29.4	32.03	84.51
Productive tillers / plant	18.6 ± 1.2	6.00	43.00	1.90	31.8	34.89	83.09
Panicle length (cm)	21.3 ± 0.5	12.80	30.50	0.80	7.11	11.14	40.72
Stem length (cm)	70.1 ± 3.3	25.10	123.50	1.40	21.61	24.01	81.04
Days to physiological maturity	128.4 ± 2.2	103.00	155.00	0.40	6.56	6.66	97.10
Days to harvest maturity	142.5 ± 2.1	119	172.00	2.10	5.55	5.70	94.95
Number of seeds / panicle	83.6 ± 5.2	20.20	158.80	1.60	22.20	28.79	59.44
Panicle weight / plant (g)	18.2 ± 1.1	4.40	42.00	2.00	28.62	34.90	67.28
Test weight (g)	22 ± 0.4	15.70	27.40	0.50	6.91	7.93	75.89
Seed yield / plant (g)	4.9 ± 0.6	0.53	16.70	3.20	25.55	30.43	70.48

Days to 50 per cent flowering ranged from 64 to 117 days with a general mean of 87.92 days and the standardized range for the trait is 0.6. The range for the plant height was recorded from 41.8 cm to 152.40 cm with a general mean of 91.44 cm and the standardized range for the trait was 1.20. The mean values for number of tillers per plant ranged from 7 to 54 with a general mean of 25.70 tillers per plant and the standardized range for the trait was 1.80. The mean values for productive tillers per plant ranged from 6 to 43 tillers with a general mean of 18.60 tillers per plant and the standardized range for the trait was 1.9. The mean values for panicle length ranged from 12.8 cm to 30.5 cm with a general mean of 21.30 cm and the standardized range for the trait was 0.8. Stem length ranged from 25.10 cm to 123.50 cm with a general mean of 70.10 cm and the standardized range for the trait is 1.40. The mean values for days to physiological maturity ranged from 103 days to 155 days with a general mean of 128.44 days and the standardized range for the trait is 0.4 days to maturity had mean value ranging from 119 days to 172 days with a general mean of 142.5 days, and the standardized range for the trait is 2.1.

The mean value for number of seeds per panicle ranged from 20.20 to 158.80 with general mean of 83.60. and the standardized range for the trait was 1.6. The panicle weight per plant with general of 18.20 g was observed for the trait with range from 4.40 g to 42.00 g with the standardized range for the trait being 2.0. The general mean of 1000 grain weight was 22.00 g with a range from 15.70 g to 27.40 g and the standardized range for the trait was 0.50. The mean seed yield per plant was ranged from 0.53 g to 16.70 g and the general mean value being 4.9 g and the standardized range for the trait was 3.2.

Estimation of Genetic Parameters

In the present investigation, the genotypic and phenotypic coefficients of variation are presented in Table 4. Low PCV and GCV for days to fifty per cent flowering, days to physiological maturity, days to harvestable maturity and thousand seed weight were recorded. Similar results were reported by Bhimnath *et al.* (2018), Pragnya *et al.* (2018), Sandeep *et al.* (2018) and Srujana *et al.* (2017). High genotypic and phenotypic coefficients of variation for tillers per plant, productive tillers per plant, stem length, number of seeds per panicle, panicle weight, seed yield per plant were recorded. Similar findings were reported by Yadav *et al.* (2011), Sandeep *et al.* (2018) and Shivani *et al.* (2018). Panicle length recorded medium PCV and the results were in conformity with Pragnya *et al.* (2018) and Yadav *et al.* (2011). Medium GCV for plant height was recorded which was similar to the findings of Sandeep *et al.* (2018), Pragnya *et al.* (2018) and Yadav *et al.* (2011). Low GCV for panicle length was reported by Bhimnath *et al.* (2018) and Srujana *et al.* (2018).

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character based on the phenotype.

The heritability estimates were high for all the traits *viz.,* days to 50 per cent flowering, days to physiological maturity, days to harvestable maturity, plant height (cm), total number of tillers, productive tillers per plant, stem length (cm), panicle weight, seed yield per plant and thousand seed weight are in conformity with the findings of Yadav *et al.* (2011), Pragnya *et al.* (2018), Shivani *et al.* (2018), Sandeep *et al.* (2018) and Bhimnath *et al.* (2018). Number of seeds per panicle and panicle length had medium heritability is similar to the findings of Bhimnath *et al.* (2018), Shivani *et al.* (2018) and Yadav *et al.* (2011).

In the present investigation, analysis of variance indicated highly significant differences among the genotypes for all the traits under study. The high standardized range for tillers per plant (1.80), productivity tillers per plant (1.90), days to harvest maturity (2.10), number of seeds per panicle (1.60), panicle weight per plant (2.00) and seed yield per plant (3.20) suggest that considerable magnitude of variability exists in germplasm accessions. A perusal of genetic variability parameters revealed that moderate to high genotypic co-efficient of variability (GCV), phenotypic co-efficient of variability (PCV) and high heritability for tillers per plant, productive tillers per plant, stem length, panicle weight per plant and seed yield per plant indicates ample scope for improvement of yield through selection of these traits. High estimates of PCV and GCV coupled with high heritability suggested that the traits can be improved through simple selection.

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