



ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(6): 1358-1362
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www.thepharmajournal.com

Received: 16-03-2022

Accepted: 23-04-2022

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Studies on genetic variability, heritability and genetic advance for yield and its contributing traits in rice (*Oryza sativa* L.) germplasm

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Abstract

The present study was based on the germplasm evaluation experiment involving evaluation of 72 germplasm including three checks *viz.*, Shusk Samrat, NDR-359 and MTU-7029. The field experiment under present investigation was conducted in *Kharif* season 2019 at the Crop Research Station (CRS) Masodha and lab experiments was conducted in Seed Testing Laboratory, Seed Technology Section, ANDUA&T, Kumarganj, Ayodhya (UP). The experiment was conducted in Augmented Block Design with three replications. The data were recorded for 17 quantitative characters to study genetic variability, heritability and Genetic advance. Analysis of variance revealed that there is considerable variability among the genotypes. On the basis of mean performance, high seed yield per plant were exhibited by the genotypes LSD-1, MTU-7029 and NDR 359. Analysis of variance among 72 genotypes showed significant difference for all characters studied. The high estimates (>15%) of phenotypic (PCV) and genotypic (GCV) coefficients of variation were recorded in case of panicle bearing tillers per plant followed by biological yield per plant, seed yield per plant and plant height indicating that these characters could be used as selection for crop improvement. The higher estimates of heritability coupled with moderate genetic advance for plant height, days of 50% flowering, biological yield per plant, days to maturity, seedling dry weight, vigour index-II, seed yield per plant, panicle length, 1000-grain weight, seedling length, vigour index-I, grains per panicle and speed of germination, indicated that heritability of the trait is mainly due to additive effect and selection is effective for such traits.

Keywords: Rice, genetic variability, heritability and genetic advance

Introduction

Rice belongs to the family of grasses *i.e.*, *Gramineae* (*Poaceae*). Rice (*Oryza sativa*) is a diploid species having 24 chromosomes. The *Oryza sativa*, rice varieties of the world are commonly grouped into three sub-species, namely Indica, Japonica and Javanica. The cultivated rice belongs to genus *Oryza* and there are about 25 species of rice distributed in tropical, sub-tropical and warm temperate regions of the world. Out of these, most commonly cultivated species are *Oryza sativa* and *Oryza glaberrima*. The *Oryza sativa* is divided into three sub-species, namely, *Indica*, *Japonica* and *Javanica*.

Rice is the most important staple food crop of the world. Rice is the major source of calories of more than half of the global population. The importance of rice is not only as a fundamental commodity and primary food source for more than half of the world's population, but also influences issues of global concern such as food security and development. More than 90 per cent of the world's rice is grown and consumed in Asia, known as rice bowl of the world, where 60 per cent of the earth's people and two third of world's poor live (Khush and Virk, 2000) [13].

India is the second largest rice producing country the world next to China; as it is grown in almost all the state of India. From the total cultivable million ha area of 143 million ha nearly 43.79 million ha is utilized for rice cultivation with a production of 115.60 million tonnes and average productivity of 2578 kg/ha (Agricultural Statistics at a Glance, 2018). Uttar Pradesh has largest area of rice *i.e.* 5.87 million ha with production of 12.51 million tonnes. The productivity of rice in Uttar Pradesh is 2131 kg/ha. Though India ranks first in area under rice, its productivity is not even half of China.

The success of plant breeding depends on the extent of genetic variability present in a crop. Knowledge on the nature and magnitude of genetic variation governing the inheritance of quantitative characters like yield and its components is essential for genetic improvement.

A critical analysis of genetic variability present in the germplasm of a crop and its estimation is a pre-requisite for initiating any crop improvement programme as well as adopting appropriate selection techniques. It is very difficult to judge whether observed variability is heritable or not. Heritability indicates the extent of transmissibility of a character into future generations. Moreover, knowledge of heritability is also essential for selection of component traits for yield improvement. Genetic advance measures the difference between the mean genotypic values of selected population and the original population from which these were selected. Heritability estimates along with genetic advance is normally more helpful in predicting the genetic gain under selection than heritability estimates alone.

Heritability is the ratio of genotypic variance to total or phenotypic variance (Broad sense) and the ratio of additive genetic variance to phenotypic variance (Narrow sense). Genetic advance is the improvement in mean genotypic value of selected plants over the parental population. Identification of effective selection criteria for effective traits improvement. The present investigation was under taken in this context to elucidate information on variability, heritability and genetic advance in rice genotypes.

Materials and Methods

The experimental material comprised of 72 genotypes of rice collections exhibited wide spectrum of variation for various characters, were evaluated under field and lab condition during *Kharif*, 2019. The experiment was conducted in augmented design at Crop Research Station (CRS) Masodha and seed quality parameters were tested in Seed Testing Laboratory of the Seed Technology Section, Acharya Narendra Deva University of Agriculture and Technology,

Kumarganj, Ayodhya (U.P.) situated between 26.47° N latitude, 82.12° E longitude and at an altitude of 113 meters above the mean sea level. The climate of district Ayodhya is semi-arid with hot summer and cold winter. Nearly 80% of total rainfall is received during the monsoon (only up to September) with a few showers in the winter. The characters studied were days to 50% flowering, days to maturity, plant height (cm), number of tillers per plant, number of panicle bearing tillers per plant, grains per panicle, panicle length (cm), biological yield (g), harvest index, 1000-seed weight (g), speed of germination, seed germination (%), seedling length (cm), seedling dry weight (g), seed vigour index-I (VI-I), seed vigour index-II (VI-II) and seed yield per plant (g). The soil type of experimental site was sandy loam, low in organic carbon, carbon, phosphorous and rich in potash.

The variability was estimated as per procedure for analysis of variance suggested by Panse and sukhatme (1985) [16], PCV and GCV were calculated by the formula by Burton (1952) [6] heritability in broad sense (h^2) by Burton and De Vane (1953) and genetic advance i.e., the expected genetic gain were calculated by using the procedure given by Johnson *et al.* (1955) [12]. Observations were recorded and the data was subjected to statistical analysis.

The observations were recorded on five randomly selected competitive plants of a genotype in a plot in each replication for seventeen characters in the experiment. The mean values of observations recorded on five plants of each line were used for analysis. Laboratory observations were recorded as per ISTA rules.

Variance

The genotypic and phenotypic variance was calculated as per the formulae (Burton and Devane, 1953).

$$\text{Genotypic variance } (\sigma^2g) = \frac{(\text{Mean sum of squares due to treatments} - \text{Mean sum of squares due to error})}{\text{Number of replications}}$$

$$\text{Phenotypic variance } (\sigma^2p) = (\sigma^2g) + (\sigma^2e)$$

(σ^2e) = Error variance

Genotypic and phenotypic coefficients of variance

The genotypic and phenotypic coefficients of variation were calculated according to the formula given by falconer (1981) [8].

$$\text{Genotypic Coefficient of variation} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{Phenotypic Coefficient of variation} = \frac{\text{Phenotypic standard deviation}}{\text{Mcan}} \times 100$$

Categorization of the range of variation was effected as proposed by Sivasubramanian and Madhavamenon (1973) [18].

<10%: low
10-20%: moderate
>20%: high

Heritability and Genetic advance

Heritability

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total

population. Heritability (h^2) in the broad sense was calculated according to the formula given by Allard (1960) [3].

$$h^2 = \frac{\sigma^2g}{\sigma^2p}$$

Where,

h^2 = heritability in broad sense

σ^2g = genotypic variance

σ^2p = phenotypic variance (σ^2g) + (σ^2e)

σ^2e = environmental variance

As suggested by Johnson *et al.*, (1955) [12] (h^2) estimates were categorized as

Low: 0-30%

Medium: 30-60%

High: above 60%

Genetic advance

Genetic advance refers to the expected gain or improvement in the next generation by selecting superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952) [6].

$$GA = K. h^2 (b). \sigma p$$

Where

GA = Expected genetic advance

K = Selection differential, the value of which is 2.06 at 5% selection intensity

$h^2 (b)$ = Heritability in broad sense

σp = Phenotypic standard deviation

In order to visualize the relative utility of genetic advance among the characters, genetic advance as percent for mean was computed.

$$GA \text{ as percent of mean} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

The range of genetic advance as percent of mean was classified as suggested by Johnson *et al.*, (1955) [12].

Low: less than 10%

Moderate: 10-20%

High: more than 20%

Results and Discussion

Genetic variability is the raw material on which selection acts to bring improvement in genetic architecture of plants. Heritability in broad sense and genetic advance in percent of mean as direct selection parameters provide index of transmissibility of parameters, which gives indication about the effectiveness of selection in improving the characters. High heritability estimates along with high genetic advance are more useful in predicting the gain under selection than heritability estimates alone. The higher estimates of heritability (Table-1) coupled with moderate genetic advance for plant height, days of 50% flowering, biological yield per plant, days to maturity, seedling dry weight, vigour index-II, seed yield per plant, panicle length, 1000-grain weight, seedling length, vigour index-I, grains per panicle and speed of germination, indicated that heritability of the trait is mainly due to additive effect and selection is effective for such traits. The results obtained under present study are in accordance with earlier reports of Kumar *et al.* (2008) [15], Singh *et al.* (2011) [17], Kishore *et al.* (2018) [14] and Ganapati *et al.* (2020) [9].

The higher estimate of heritability accompanied with moderate to low genetic advance for germination percentage, number of tillers per plant, harvest index, panicle bearing tillers per plant, biological yield per plant, seed yield per plant, plant height, days of 50% flowering, days of maturity, grains per panicle, numbers of tillers per plant, vigour index-II, 1000-grain weight, panicle bearing tillers per plant, seedling dry weight, panicle length, harvest index, vigour index-I, seedling length, speed of germination, germination percentage is indicative of non-additive gene action suggesting limited scope for improving these characters through phenotypic selection. High heritability is being exhibited due to favorable influence of the environment rather than genotype. Also been reported earlier findings Akinwale *et al.* (2011) [2], Jain *et al.* (2013) [11] and Behera *et al.* (2018) [5].

Table 1: Analysis of variance of augmented design for 17 characters of rice germplasm

Characters	Source of Variation		
	Blocks	Entries	Error
	d. f. (7)	d. f. (72)	d. f. (14)
Day to 50% flowering	0.449	112.824**	0.429
Day to maturity	1.151	195.320**	1.147
Plant height (cm)	0.205	252.895**	0.629
No. of tillers/plant	0.506	2.872**	0.532
Panicle bearing tillers/plant	0.148	6.071**	1.217
Panicle length (cm)	0.160	3.021**	0.134
Grains/panicle	39.51	320.545**	42.056
1000-grain weight (g)	0.113	4.638**	0.190
Biological yield/plant (g)	0.560	247.172**	0.665
Harvest Index (%)	5.570	21.264*	5.296
Speed of germination	0.128	0.796**	0.087
Germination (%)	1.108	11.049**	0.723
Seedling length (cm)	0.142	3.596**	0.134
Seedling dry weight (g)	0.00003	0.001**	0.00001
Vigour Index-I	1406.14	54053.130**	1615.58
Vigour Index-II	0.245	10.933**	0.151
Seed yield/plant (g)	1.097	54.557**	1.190

Table 2: Estimates of range, grand mean, phenotypic (PCV) and genotypic (GCV) coefficients of variation and genetic advance in percent of mean (\bar{G}_a) for seventeen characters in rice

S. No.	Character	Range		Grand mean \bar{X}	PCV (%)	GCV (%)	Genetic advance in per cent of mean (\bar{G}_a %)	Heritability (h^2_b %)
		Lowest	Height					
1	Day to 50% flowering	70.79	120.21	89.66	12.08	12.06	24.80	99.63
2	Day to maturity	91.91	152.54	111.93	10.99	10.95	22.48	99.24
3	Plant height (cm)	65.61	154.01	109.00	15.35	15.33	31.55	99.78
4	No. of tillers/plant	7.78	18.33	11.41	12.55	10.80	19.15	74.07
5	Panicle bearing tillers/plant	5.33	14.64	7.74	19.05	12.65	17.29	44.06
6	Panicle length (cm)	12.46	27.64	21.08	8.01	7.82	15.73	95.28
7	Grains/panicle	79.85	180.62	153.06	11.83	11.05	21.26	87.19
8	1000-grain weight (g)	17.17	26.90	21.02	9.17	8.93	17.92	94.87
9	Biological yield/plant (g)	40.78	93.37	69.51	19.01	18.97	39.01	99.62
10	Harvest Index (%)	30.82	71.27	41.21	10.03	8.33	14.26	69.01
11	Speed of germination	15.80	19.43	17.91	4.00	3.64	6.84	83.05
12	Germination (%)	85.28	94.83	88.87	2.11	1.88	3.46	79.52
13	Seedling length (cm)	22.05	31.07	25.94	5.81	5.64	11.27	94.08
14	Seedling dry weight (g)	0.249	0.341	0.316	7.95	7.88	16.09	98.14
15	Vigour Index-I	1974.70	2823.20	2305.60	6.43	6.19	12.27	92.65
16	Vigour Index-II	22.00	28.7	28.4	9.27	9.17	18.69	97.81
17	Seed yield/plant (g)	31.37	41.85	35.41	18.17	17.75	35.75	95.53

The highest estimates of phenotypic (PCV) and as well as genotypic (GCV) coefficient of variation were observed (Table-2) for Panicle bearing tillers/plant followed by biological yield per plant, seed yield per plant, plant height. Thus, above mentioned three characters were characterized by high estimates (>15%) of PCV and GCV. The existence of high variability for above characters in rice has also been reported earlier by Kumar *et al.* (2008) ^[15], Aditya *et al.* (2013) ^[1] and Ashish *et al.* (2016) ^[4].

The Moderate estimates (<15% to >10%) of PCV and GCV were recorded in case number of tiller per plant, days of 50% flowering, Grains per panicle, days to maturity and Harvest index. Remaining traits, Vigour index-II, 1000-grain weight, panicle length, seedling dry weight, vigour index-I, seedling length, speed of germination and germination percentage possessed low (<10%) values of PCV as well as GCV.

The results of the presented study in respect of genotypic and phenotypic coefficient of variation are broadly in the findings of earlier workers Kishor *et al.* (2018) ^[14], Dubey *et al.* (2018) ^[7], Behera *et al.* (2018) ^[5] and Htwe *et al.* (2019) ^[10].

Conclusion

Wide spectrum of variation was observed for seed characters of 72 rice genotypes with 3 checks. High magnitude of genotypic and phenotypic coefficients of variation were observed for panicle bearing tillers per plant followed by biological yield per plant, seed yield per plant and plant height indicating there by, substantial scope for improving in this character after hybridization and subsequent selection. The moderate estimate of PCV and GCV were observed for number of tiller per plant, days of 50% flowering, grains per panicle, days to maturity and harvest index which suggested possibility of obtaining reasonable improvement through selection. The low estimation of PCV and GCV were observed for vigour index-II, 1000-grain weight, panicle length, seedling dry weight, vigour index-I, seedling length, speed of germination and germination percentage. Considering the overall result it is apparent that certain information obtained here will help in future for improving existing rice genotypes.

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