

Original Research Article

<https://doi.org/10.20546/ijcmas.2017.610.200>

Evaluation of Genetic Variability, Heritability and Genetic Advance for Yield and Yield Components in Rice Genotypes

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ABSTRACT

Keywords

Evaluation,
Genetic variability,
Rice, Genotype.

Article Info

Accepted:
14 September 2017
Available Online:
10 October 2017

Thirty seven rice genotypes were evaluated for their variability with regards to yield and yield components. Estimates of heritability and genetic advance in percent of mean were also obtained for the above traits. All the characters under study except days to fifty percent flowering exhibited high heritability coupled with high genetic advance as per cent of mean, which indicated that these traits were controlled by additive type of gene action in the inheritance of these characters. These characters can be further improved by following simple selection procedure. The high estimates of heritability coupled with low genetic advance as percent of mean for days to fifty percent flowering indicated the presence of non-additive gene effects, in addition to influence of environment to some extent, hence its response to selection would be poor.

Introduction

Rice (*Oryza sativa* L.) is the primary staple food for one third of the world population after maize and wheat and has been referred to as “Global Grain” (Shalini and Tulasi, 2008). It is considered a model cereal crop in the world due to its relatively small genome size, vast germplasm collection, enormous repertoire of molecular genetic resources and efficient transformation system (Paterson *et al.*, 2005).

In India, rice is cultivated in an area of nearly 43.85 million hectares with an annual production of 104.78 million tones and

productivity of 2185kg ha⁻¹, while in Telangana rice is grown in an area of 2.29 million hectares with an annual production and productivity of 6.62 million tonnes and 1334 kg ha⁻¹, respectively (Indiastat, 2014-15).

In Indian agriculture, rice plays a pivotal role, being the livelihood for 150 million rural households and accounting for 43% of National food grain production (IIRR, 2005). The area planted with rice in major production countries has been decreasing because of industrialization and urbanization.

Hence, increasing rice yields on existing land remains the primary strategy for increasing production, to meet the future demand for food, anticipated from the projected world population increase. To produce 176 million tons additional rice by 2035, the yield potential of rice needs to be increased from 10 to 12.3 tons per hectare (Khush, 2013).

Before initiating any breeding programme, the knowledge of variability and genetic diversity is a basic pre-requisite for improving the character. Similarly the additional information regarding the genetic parameters like genotypic coefficient of variation and expected genetic advance as percent of mean helps in selecting a proper breeding methodology for genetic improvement of the trait.

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 yield 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 experiment was conducted at RARS JAGTIAL, Telangana, India, during kharif 2013-14 season. The experimental material comprised of 37 rice genotypes. The experiment was laid out in a Randomized Block Design (RBD) with three replications. The nursery was sown in raised beds and healthy nursery was raised at all the locations following uniform package of practices. Thirty days old seedlings were transplanted following a spacing of 20 x 15 cm with a row length of 4.5 m for each entry.

The packages of practices as recommended by ANGRAU were adopted as per schedule throughout the crop growth period with need based plant protection measures. Fertilizers were applied at the rate of 120 kg Nitrogen, 60 kg Phosphorus and 40 kg potash ha⁻¹.

Nitrogen was applied 3 times by broadcasting at transplanting; tillering stage and panicle initiation, phosphorous and potash were applied as basal at the time of transplanting by broadcasting method. Necessary precautions were taken to maintain the crop very well. Data on days to 50% flowering (DFF), days to maturity (DM) recorded at respective stage of crop while, plant height (PH), panicle length (PL), productive tillers

per plant (PT) were recorded at harvest and number of grains per panicle (GPP), test-weight (TW), grain iron content (Fe), grain zinc content (Zn) and grain yield per plant (GY) recorded after harvest.

Estimation of iron and zinc Iron and zinc content of grain samples were estimated by Atomic Absorption Spectrophotometer [3]. One gram of seed was taken and powdered it in the grinder (nonmetallic grinder).

Powdered seed sample was digested in tri-acids (HNO₃+HCl₄+H₂SO₄) mixture (10:4:1) in micro-oven digester. The digested sample was cooled for 30 minutes and the volume was made up to 50 ml with double distilled water.

Then a known quantity of aliquot was used for subsequent analysis. A suitable blank was run simultaneously to account for the contamination from the reagents. Zinc and Iron content were estimated in the aliquot of seed extract by using Atomic Absorption Spectrophotometer (AAS) at 213.86 nm for zinc and 248.33 nm for iron.

Statistical methods for calculating the variance, heritability and genetic advance are below discussed

Variance

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

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

$$\text{Phenotypic variance } (\sigma^2_p) = (\sigma^2_g) + (\sigma^2_e)$$

$$(\sigma^2_e) = \text{Error variance}$$

Genotypic and phenotypic coefficients of variance

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

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

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

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

- <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 (h²) in the broad sense was calculated according to the formula given by Allard (1960).

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p}$$

Where

h² = heritability in broad sense

σ²_g = genotypic variance

σ²_p = phenotypic variance (σ²_g) + (σ²_e)

σ²_e = environmental variance

As suggested by Johnson *et al.*, (1955) (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).

$$GA = K \cdot h^2 (b) \cdot \sigma_p$$

Where

GA = expected genetic advance

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

σ_p = phenotypic standard deviation

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

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

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

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

Low: less than 10 %
Moderate: 10-20 %
High: more than 20 %

Results and Discussion

The results obtained from the present experimental study on evaluation of 50 rice genotypes are furnished under the Genetic variability, Heritability and genetic advance.

Genetic variability, heritability and genetic advance

The genotypic and phenotypic coefficients of variation, heritability and genetic advance as per cent of mean were estimated for 37 genotypes. Results are furnished in Table 1 for PCV, GCV and heritability, genetic advance as per cent of mean respectively.

The characters studied in the present investigation exhibited low, moderate and high PCV and GCV values.

Days to 50 per cent flowering

The genotypic and phenotypic coefficients of variation were low i.e., 10.84 and 11.312, respectively. The observed heritability estimate for this trait was high (91.9) while genetic advance as per cent of mean (21.42) were moderate. The results were conformity with Sameera *et al.*, (2015) for moderate GCV and PCV and Gampala *et al.*, (2015) for high heritability and Islam *et al.*, (2015) for moderate genetic advance as percent of mean.

Plant height (cm)

The genotypic and phenotypic coefficients of variation for this trait were moderate i.e., 19.12 and 19.41 respectively. The observed heritability estimate was high (97.0) and with high genetic advance as per cent of mean (38.81). The similar results were reported by Dhanwani *et al.*, (2013) for high GCV and PCV and Sameera *et al.*, (2015) reported high heritability coupled with high genetic advance as per cent of mean for plant height in rice.

Panicle length (cm)

The genotypic and phenotypic coefficients of variation for this trait were moderate i.e., 10.59 and 11.09 respectively.

The observed heritability estimate was high (91.1) and with moderate genetic advance as per cent of mean (20.82). The similar results were reported by Dhanwani *et al.*, (2013) for moderate GCV and PCV and Sameera *et al.*, (2015) reported high heritability coupled with high genetic advance as per cent of mean for panicle length per plant in rice.

Number of productive tillers per plant

The genotypic and phenotypic coefficients of variation for this trait were high i.e., 21.88 and 22.13 respectively. The observed heritability estimate was high (97.8) and with high genetic advance as per cent of mean (44.58). The similar results were reported by Allam *et al.*, (2015) for high PCV and Karande *et al.*, (2015) reported high heritability coupled with high genetic advance

as per cent of mean for number of productive tillers per plant in rice.

Number of grains per panicle

A high GCV (29.10) and PCV (29.19) were observed for this trait. The heritability estimate for this trait was very high (98.7) with high genetic advance as per cent of mean (59.57). The similar results were observed by Mohan *et al.*, (2015) and Sameera *et al.*, (2015) for high GCV and PCV, Karande *et al.*, (2015) for high heritability and for high genetic advance as percent of mean.

Number of filled grains per panicle

A high GCV (30.68) and PCV (30.85) were observed for this trait. The heritability estimate for this trait was very high (98.9) with high genetic advance as per cent of mean (62.84). The similar results were observed by Mohan *et al.*, (2015) and Sameera *et al.*, (2015) for high GCV and PCV, Karande *et al.*, (2015) for high heritability and for high genetic advance as percent of mean.

Table.1 Estimates of variability, heritability and genetic advance in rice genotypes

Characters	PCV (%)	GCV (%)	Heritability in broad sense(h^2) %	Gen. Adv as per cent of Mean (at 5%)
Days to 50% Flowering	11.31	10.84	0.919	21.44
Plant height	19.41	19.12	0.970	38.81
Panicle length	11.09	10.59	0.911	20.82
Productive tillers per hill	22.13	21.88	0.978	44.58
No. of grains per panicle	29.29	29.10	0.987	59.57
No. of filled grains per panicle	30.85	30.68	0.989	62.84
1000 grain weight	16.37	16.03	0.959	32.35
Grain yield per plant	41.86	41.72	0.993	85.61
Grain iron content	17.18	16.85	0.963	34.07
Grain zinc content	21.97	21.73	0.973	44.27

1000-grain weight (g)

Moderate GCV (16.03) and PCV (16.37) were recorded with high heritability estimate of (95.9) and the genetic advance as per cent of mean was high (32.35). The similar results were found by Suresh *et al.*, (2014) and Shekawat *et al.*, (2015) for moderate GCV and PCV and Gampala *et al.*, (2015) and Islam *et al.*, (2015) for high heritability coupled with high genetic advance as percent of mean.

Grain per Plant (g)

A high genotypic coefficient of variation (41.72) and phenotypic coefficient of variation (41.86) were observed for this trait. A high heritability estimate (99.3) coupled with high genetic advance as per cent of mean (85.61). The results were conformity with Allam *et al.*, (2015) and Bhati *et al.*, (2015) for high GCV and PCV and Rahman *et al.*, (2014) and Karande *et al.*, (2015) for high heritability coupled with high genetic advance as percent of mean.

Grain iron concentration (mg/kg)

The genotypic and phenotypic coefficients of variation were medium i.e., 16.85 and 17.18, respectively. The observed heritability estimate for this trait was high (96.3) while genetic advance as per cent of mean (34.07) were high. The result is conformity with Gangashetty *et al.*, (2013) for medium GCV and PCV and Sala *et al.*, (2015) for high heritability coupled with high genetic advance as percent of mean.

Grain zinc concentration (mg/kg)

The genotypic and phenotypic coefficients of variation were high i.e., 21.74 and 21.97, respectively. The observed heritability estimate for this trait was high (96.0) while

genetic advance as per cent of mean (45.98) were high. The result is conformity with Bekele *et al.*, (2013) for high GCV and PCV and Sala *et al.*, (2015) for high heritability coupled with high genetic advance as percent of mean.

The knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding programme. Information on coefficient of variation is useful in measuring the range of variability present in the characters. Heritability and genetic advance are important selection parameters. Genotypic coefficient of variation (GCV) along with heritable estimates would provide a better picture of the amount of genetic advance to be expected by phenotypic selection (Burton, 1952). It is suggested that genetic gain should be considered in conjunction with heritability estimates (Johnson *et al.*, 1955). Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone.

Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for days to 50% flowering, plant height, panicle length, number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, 1000 grain weight, grain yield per plant, grain iron concentration and zinc concentration indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits.

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.

High heritability for quantitative characters indicates the scope of genetic improvement of these characters through selection, which revealed that these characters are less influenced by environment and there could be greater correspondence between phenotypic and breeding values.

The genetic advance as percent of mean is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. The traits which are recorded showed high heritability coupled with high genetic advance. It indicates the control of additive gene and selection may be effective for these characters.

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How to cite this article:

Sriram Ajmera, S. Sudheer Kumar and Ravindrababu, V. 2017. Evaluation of Genetic Variability, Heritability and Genetic Advance for Yield and Yield Components in Rice Genotypes. *Int.J.Curr.Microbiol.App.Sci*. 6(10): 1657-1664.
doi: <https://doi.org/10.20546/ijcmas.2017.610.200>