



Genetic Variability Studies for Yield Attributes in Rice (*Oryza sativa* L.) Genotypes under Late Sown Conditions

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ABSTRACT

A field experiment was conducted by using forty rice genotypes to study genetic variability, heritability and genetic advance (GA) for yield and yield associated traits in rice under late sown conditions. The experiment has revealed significant differences among the genotypes for the yield and its components. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all ten traits indicating that they all interacted with the environment to some extent. High estimates of PCV and GCV obtained for number of grains per panicle while high PCV and moderate GCV recorded for test weight and grain yield per plant. High heritability was obtained for days to 50% flowering followed by kernel length, plant height, number of grains per panicle, panicle length and days to maturity which indicates high heritable portion of variation. High genetic advance were obtained for number of grains per panicle, grain yield per plant, number of productive tillers per plant and test weight. The estimates of PCV, GCV, heritability and genetic advance as percent of mean were high for number of grains per panicle indicate the existence of high degree of variability and additive gene action in the inheritance of this trait and improvement of these characters is possible through simple selection.

Key words: *Late sown condition, Rice, Variability.*

Rice is a cereal crop belonging to genus *Oryza* of family Poaceae. Next to China, India is the second largest producer and consumer of rice. For meeting the dietary requirements of increasing population, genetic improvement of rice with higher yield, good grain quality, resistance to biotic and abiotic stresses is the most logical and promising approach. Genetic improvement mainly depends upon inclusion of genetically diverse parents having wider variability for different yield and quality characters in hybridization program. Improvement in any trait is solely depends on the amount of variability present in the base material of that trait. Heritability is the heritable portion of phenotypic variance. It is a good index of the transmission of the characters from parents to offspring (Falconer, 1981). Genetic advance it indicates the magnitude of the expected genetic gain from one cycle of selection. To increase its production a study of yield and its component characters *viz.* days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, panicle length (cm), number of grains per panicle, kernel length (mm), kernel breadth (mm), test weight (g) and grain yield per plant (g) are essential fundamental

task for making any successful breeding program (Xing and Zhang, 2010). The yield component does not act independently and in general, they are interrelated with each other that ultimately bring about the grain yield.

Thus, 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 program. Heritability and genetic advance are important selection parameters while selection is made based on yield contributing traits. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. Therefore, the objective of this study was to assess the genetic variability, heritability and genetic advance (GA) of yield and yield associated traits in some promising rice genotypes to assist the future breeding programs for yield improvement under late sown conditions.

MATERIAL AND METHODS

The experimental material used in the study comprised of 40 medium duration rice genotypes grown in different agro-ecological zones of India.

All genotypes were evaluated for grain yield and its attributing characters following randomized complete block design (RBD) with three replications during *khari* season, 2015 at Agricultural research station, Ragolu, Srikakulam, Andhra Pradesh. Transplanting was done 25 days after sowing of in a 4 m² plot. Plant to plant distance was 15 cm, row to row distance was 20 cm and the crop was raised as per recommended package of practices to ensure normal crop. Observations were recorded on 10 characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, panicle length (cm), number of grains per panicle, kernel length (mm), kernel breadth (mm), test weight (g) and grain yield per plant (g) of ten randomly selected plants in each entry in a replication. The mean of the 40 genotypes were analyzed statistically by the method outlined by Ostle (1966). The analysis of variance for different characters was carried out in order to assess the genetic variability among genotypes. Both phenotypic and genotypic coefficient of variability for all characters as estimated using the formula of Burton and De Vane (1953). The broad sense heritability (h^2) was estimated for all characters as the ratio of genotypic variance to the total or phenotypic variance as suggested by Lush (1940) and Hanson (1956). Genetic advance for each character was estimated by using the formula of Johnson et al (1955). Genetic advance as per cent mean was categorized as suggested by Johnson et al (1955).

RESULTS AND DISCUSSION

The estimates of GCV, PCV, heritability, genetic advance and genetic advance as percent of mean are presented in Table 2. A wide range of variation was observed among forty rice genotypes for nine yield contributing traits and yield as well. The perusal of ANOVA revealed that variance for all traits was highly significant. This suggested that there were inherent genetic differences among the genotypes. Phenotypic variance was higher than the genotypic variances for all the traits thus indicated the influences of environmental factor on these traits. Coefficient of variation studied indicated that estimates of phenotypic coefficient of variation (PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all the

traits indicating that they all interacted with the environment to some extent. Bhadru *et al.* (2012) also mentioned the same result in rice. The overall range of PCV found between 2.73 (for days to maturity) and 29.80 (number of grains per panicle) while the overall range of GCV was from 2.14 (for days to maturity) to 26.13 (number of grains per panicle).

The high estimates of PCV and GCV was for number of grains per panicle (29.80 and 26.13), where as traits like test weight and grain yield per plant had high PCV and moderate GCV respectively. The characters plant height, panicle length, kernel length and kernel breadth were recorded moderate PCV and low GCV respectively. However number of productive tillers per plant had moderate PCV and GCV. The characters days to 50 percent flowering and days to maturity showed low magnitude of PCV and GCV respectively. These results were in agreement with the Ramadevi *et al.* (2014) and Dhurai *et al.* (2014b) for number of grains per panicle, Chakraborty and Chakraborty (2010) for grain yield per plant and plant height, Sanghera *et al.* (2013) for panicle length.

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 trait. Heritability was classified as low (below 30%), medium (30-60%) and high (above 60%) as suggested by Johnson *et al.* (1955). The traits studied in the present investigation expressed moderate to high heritability estimates ranging from 43 to 91 percent. Among the traits, high heritability was observed for days to 50% flowering, followed by kernel length, plant height and number of grains per panicle, panicle length and days to maturity. Similar results were earlier reported by Ravi Kumar *et al.* (2015) for days to 50% flowering and days to maturity. Allam *et al.* (2015) for kernel length and plant height. Dhurai *et al.* (2014b) for number of grains per panicle and panicle length. High heritability values indicate that the traits under study are less influenced by environment in their expression. The plant breeder, therefore, may make his selection safely on the basis of phenotypic expression of these traits in the individual plant by adopting simple selection methods.

Table 1. Analysis of variance for yield and yield components among 40 genotypes of rice (*Oryza sativa* L.).

| S. No. | Source | Replication | Treatment | Error |
|---------------------|--|-------------|-------------|----------|
| | Degree of freedom | 2 | 39 | 78 |
| Mean Sum of squares | | | | |
| 1. | Days to 50 % flowering | 2.1 | 46.5974** | 1.5359 |
| 2. | Days to maturity | 3.9083 | 28.7417** | 5.0109 |
| 3. | Plant Height (cm) | 1.6353 | 391.0421** | 29.8858 |
| 4. | Number of productive tillers per plant | 1.954 | 7.3086** | 1.5766 |
| 5. | Panicle length (cm) | 4.0795 | 15.9308** | 1.8063 |
| 6. | Number of grains per panicle | 126.4364 | 8024.5752** | 731.6118 |
| 7. | Kernel Length (mm) | 0.0369 | 1.0681** | 0.0537 |
| 8. | Kernel Breadth (mm) | 0.0212 | 0.0866** | 0.0268 |
| 9. | Test weight (g) | 15.8096 | 44.3264** | 11.5515 |
| 10. | Grain yield per plant (g) | 20.351 | 33.6768** | 9.7192 |

*significant at 5% level, **significant at 1% level

Table 2. Mean, variability, heritability and genetic advance as per cent of mean for yield, yield components and grain quality parameters in rice (*Oryza sativa* L.).

| S. No. | Character | Mean | Range | | Coefficient of variation | | Heritability (%) (broad sense) | Genetic advance | Genetic advance as per cent of mean (5% level) |
|--------|-------------------------------------|--------|---------|---------|--------------------------|-------|-----------------------------------|-----------------|--|
| | | | Minimum | Maximum | PCV % | GCV % | | | |
| 1 | Days to 50 % flowering | 100.35 | 96.67 | 110.67 | 4.05 | 3.86 | 0.91 | 7.6 | 7.58 |
| 2 | Days to maturity | 131.44 | 126.67 | 138.67 | 2.73 | 2.14 | 0.61 | 4.53 | 3.45 |
| 3 | Plant Height | 117.79 | 91.47 | 140.80 | 10.41 | 9.32 | 0.80 | 20.23 | 17.18 |
| 4 | No. of productive tillers per plant | 9.88 | 7.87 | 16.83 | 18.91 | 13.99 | 0.55 | 2.11 | 21.34 |
| 5 | Panicle length (cm) | 23.81 | 17.78 | 29.08 | 10.72 | 9.11 | 0.72 | 3.8 | 15.96 |
| 6 | No. of grains per panicle | 188.70 | 100.33 | 303.13 | 29.80 | 26.13 | 0.77 | 89.05 | 47.19 |
| 7 | Kernel length (mm) | 6.09 | 4.89 | 7.61 | 10.28 | 9.55 | 0.86 | 1.11 | 18.28 |
| 8 | Kernel Breadth (mm) | 2.05 | 1.68 | 2.39 | 10.53 | 6.88 | 0.43 | 0.19 | 9.26 |
| 9 | Test Weight (g) | 23.49 | 16.97 | 32.33 | 20.18 | 14.07 | 0.49 | 4.75 | 20.21 |
| 10 | Grain Yield per plant | 17.68 | 10.32 | 24.79 | 23.80 | 15.98 | 0.45 | 3.91 | 22.12 |

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

The high genetic advance revealed by characters number of grains per panicle (89.05) and plant height (20.23) while other yield attributed traits exhibited low GA values. The values of genetic advance as per cent of mean (GAM) were high (> 20%) for characters number of grains per panicle, grain yield per plant, number of productive tillers per plant, test weight, while moderate GAM (10-

20%) for characters kernel length, plant height and panicle length. However low GAM (<10%) were revealed by kernel breadth, days to 50 % flowering and days to maturity.

Heritability should be considered along with genetic advance as per cent of mean, however it is not necessary that character showing high heritability will also exhibit high genetic advance (Johnson *et*

al., 1955). High heritability coupled with high GAM was observed with number of grains per panicle is controlled by additive type of gene action. Therefore response to selection could be anticipated in improving yield. The results are in conformity with the earlier findings of Dhurai *et al.* (2014b).

High heritability coupled with moderate GAM was observed for characters kernel length, plant height and panicle length suggesting both additive and non additive gene action. The results are in accordance with the earlier findings of Ravi Kumar *et al.* (2015) for plant height and panicle length. Ramadevi *et al.* (2014), Dhurai *et al.* (2014) for kernel length.

High heritability coupled with low GAM is observed for the character days to 50% flowering and days to maturity indicating non-additive gene action, high heritability is exhibited due to favorable influence of environment rather than genotype and selection of such traits may not be rewarding.

Moderate heritability coupled with high GAM is observed for grain yield per plant, number of productive tillers per plant and test weight suggesting both additive and non additive gene action. The results are in accordance with the earlier findings of Sanghera *et al.* (2013), Ketan and Sarkar (2014) for grain yield per plant, Sudharani *et al.* (2014) for number of productive tillers per plant.

Moderate heritability coupled with low GAM is observed for kernel breadth indicating the preponderance of non additive gene action in inheritance of this character, environment plays major role. Improvement of these characters is complicated and it might be possible through heterosis breeding. Hence selection is not effective in early segregating generations and has to be carried in later generations.

From the present findings it is evident that the estimates of phenotypic and genotypic coefficient of variation, heritability and genetic advance as percent of mean were high for number of grains per panicle indicate the existence of high degree of variability and additive gene action in the material under study, therefore selection for this trait would be more effective. High heritability coupled with moderate GAM was observed for characters kernel length, plant height and panicle

length and Moderate heritability coupled with high GAM is observed for grain yield per plant, number of productive tillers per plant and test weight suggesting both additive and non additive gene action.

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