

Genetic Variability for Yield, Its Contributing Characters in Rice (*Oryza sativa* L.)

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ABSTRACT

Forty eight rice (*Oryza sativa* L.) genotypes were evaluated during kharif 2015 to estimate the genetic variability, heritability, correlation coefficients and path coefficient for 11 yield traits. The experiment was conducted in an alpha lattice design with 2 replications. Among the traits, high GCV and PCV values were observed for plant height, number of productive tillers per plant, grain yield per plant. High heritability coupled with high genetic advance as per cent of mean was observed for days to 50 per cent flowering, plant height, number of filled grains per panicle, kernel breadth, L/B ratio. This indicated that these traits were controlled by additive gene action. The remaining traits were mostly under the influence of non-additive gene effects as they recorded low to moderate estimates of genetic advance.

Key words: Genetic variability, Heritability, Genetic advance

INTRODUCTION

Rice is a main staple food for most people in the world and it is a crop with the longest history of cultivation. More than 90% of the world's rice is produced in Asia and for more than three billion people it is the staple food that accounts for 35-75% of the calorie intake⁵. Rice occupies an important position in the agricultural development, history and civilization of Asian nations. Genetic improvement mainly depends on the amount of genetic variability present in the population

which is a ubiquitous property of all species in nature. The measurement of genetic variation and understanding of mode of inheritance of quantitative traits, therefore, are essential steps in any crop improvement programme. Heritability estimates provide authentic information about a particular genetic attribute which will be transmitted to the successive generations. Grain yield is a complex trait and is dependent on many component characters and it responds poorly to the direct selection.

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For the improvement of grain yield, the knowledge on the association between grain yield and its component characters will be helpful. A wide range of genetic variability has been reported for yield traits in the past, but still there exists untapped genetic variability in germplasm which is of paramount importance in selecting the potential parents so as to get maximum heterosis and superior recombinants with respect to yield components. Genetic parameters such as genotypic coefficient of variation and phenotypic coefficient of variation are useful in detecting the amount of variability present in the germplasm. Heritability coupled with high genetic advance helps in determining the influence environment on the expression the genotypic and reliability of characters. Present investigate the genetic variability among 48 rice germplasm and to study the interrelationship among the characters with seed yield.

MATERIAL AND METHODS

The experimental material for the study comprised of 48 genotypes laid in alpha lattice design (ALD) with two replications at the Rice Research Center, Agricultural Research Institute (ARI), Rajendranagar, Hyderabad, Telangana during *Kharif*, 2015. The seedlings were transplanted to main field 15cm apart between rows and 10cm within the row. Standard agronomic practices and plant protection measures were taken as per schedule. Observations were recorded on five randomly selected plants per replication for plant height (cm), number of tillers per plant, panicle length (cm), number of filled grains per panicle, 1000 grain weight (g), grain yield per plant (g), grain length (mm), grain breadth (mm), L/B ratio and days to 50 per cent flowering, days to maturity were recorded plot basis. The analysis of variance was carried out for all the characters, the genotypic and phenotypic coefficients of variation were calculated according to the formula given by Falconer³ 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 Allard¹, Johnson *et al.*⁴ and Genetic advance refers to the expected gain or improvement in the next generation by selecting the superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by Burton².

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant differences for all the traits studied indicating the presence of sufficient amount of genetic variability among the germplasm studied. The estimates of genotypic variation (σ^2_g), phenotypic variation (σ^2_p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance (GA) for different characters have been presented in (Table 1) High estimates of variability were recorded for grain yield per plant followed by number of productive tillers per plant, plant height. In contrast, low variability was noticed for days to maturity, panicle length, kernel length, days to 50% flowering, kernel breadth, 1000 seed weight, L/B ratio, number of filled grains per panicle. High heritability coupled with high genetic advance as percent of mean was observed for days to 50% flowering, plant height, number of filled grains per panicle, 1000 seed weight, grain yield per plant, kernel breadth and L/B ratio indicating the influence of additive gene action and simple selection would be effective for improvement of these traits. Although heritability estimates are high, days to maturity and kernel length has shown low variability and moderate genetic advance as percent of mean and number of productive tillers per plant recorded moderate variability and high genetic advance as percent of mean indicating the presence of non-additive gene action. Hence, selection is not effective for these characters and further improvement is possible by intermating of superior genotypes of segregating population from recombination breeding. This finding is comparable with the results previously published by Kumar *et al.*⁶, Rajkumar *et al.*⁷, Sameera *et al.*⁹ and Sahu *et*

al⁸. Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all traits indicating less influence of environment on the traits. The estimates of heritability acts 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. All quality characters also exhibited high degree of broad-sense heritability, indicating the 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 recorded high heritability and high genetic advance indicate the control of additive gene action and selection may be effective for these characters. Bhubu Kangbu was high 1000 grain weight, slender type kernel, Sunebumap was low 1000 grain weight, medium type kernel and Keme Yaisha was bold type kernel (Plate 3.1)

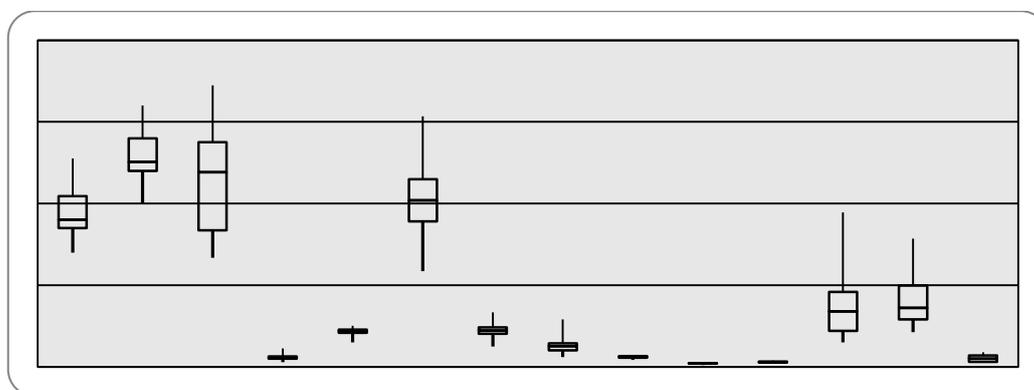
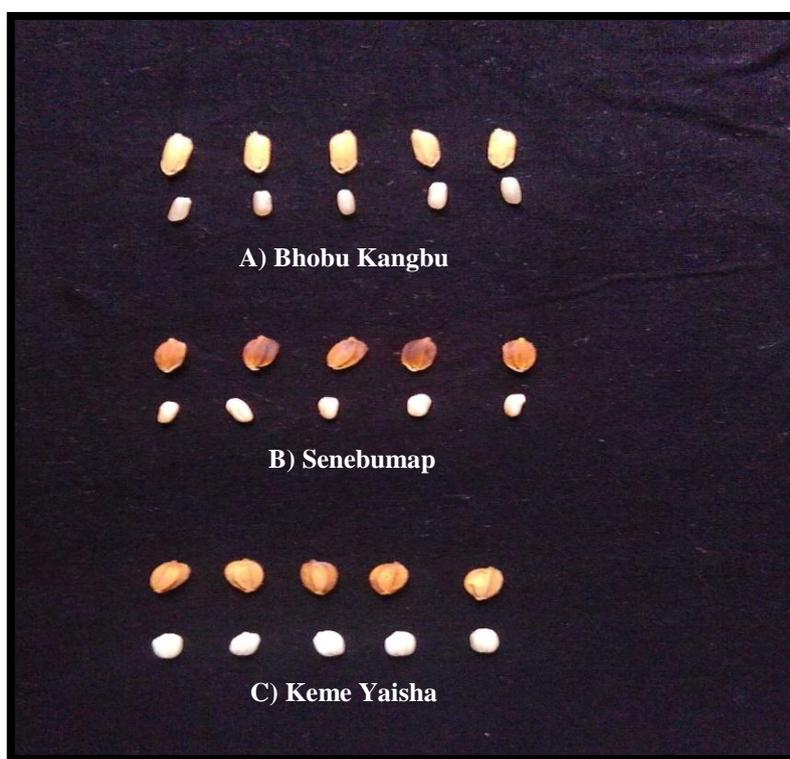


Fig. 4.3. Box plot showing quartile distribution of different characters studied and variation for each character along with the X axis

Variance and quartile distribution of quantitative, qualitative traits and sheath blight score of 48 germplasm lines were represented in box plots (Fig. 4.3). The upper, median, and lower quartiles of gray boxes represent the 75th, 50th, and 25th percentiles of the populations, respectively. The horizontal lines represent the highest and lowest variation of each trait in the population. Among the characters studied, plant height displayed the greatest **variation**, followed by number of filled grains per panicle and lesion height. Very less variation was observed in kernel length, breadth and L/B ratio followed by number of productive tillers per plant and panicle length. Distribution of variability in

number of filled grains per panicle is symmetric, where as it is skewed in plant height, days to fifty percent flowering, days to maturity, lesion height and relative lesion height. Skewness in days to fifty percent flowering and days to maturity is towards upper side representing more lines with longer duration than the median. Whereas, it is towards lower side in case of plant height indicating that, majority of the lines are below median for this character. Extreme outliers for maximum value are found in case of lesion height, relative lesion height, plant height and for maximum and minimum values in case of number of filled grains per panicle.

Table 1: Estimates of range, variability, heritability, genetic advance for grain yield and its components in rice germplasm lines

Characters	Mean	Range		Coefficient of variation		Heritability in broad sense h^2_{bs} (%)	Gen. adv. as per cent of mean (at 5%level)
		Min	Max	Phenotypic	Genotypic		
Days to 50% flowering	94.19	70.0	127	14.28	14.24	99.60	29.28
Plant height (cm)	113.13	66.8	172.3	25.83	24.07	86.80	46.20
No. of productive tillers/ plant	5.80	2.9	11.2	29.71	21.91	54.40	33.28
Panicle length(cm)	21.69	14.9	25.2	8.95	6.84	58.40	10.76
No. of filled grains per panicle	102.35	58.6	153.4	20.19	19.47	93.00	38.67
Days to maturity	128.01	100	156	8.86	8.77	98.10	17.90
1000 seed weight (g)	22.24	12.50	33.30	16.48	16.44	99.50	33.79
Grain yield for plant(g)	13.29	5.91	29.03	42.83	37.87	78.20	68.98
Kernel length(mm)	6.07	4.30	7.15	11.19	9.32	69.40	15.99
Kernel breadth(mm)	2.15	1.13	2.89	14.90	13.11	77.40	23.77
L/B ratio	2.88	1.81	3.88	17.28	16.84	95.00	33.82

CONCLUSION

High heritability coupled with high genetic advance as percent of mean was observed for days to 50% flowering, plant height, number of filled grains per panicle, 1000 seed weight, grain yield per plant, kernel breadth and L/B ratio indicating the influence of additive gene action and simple selection would be effective for improvement of these traits. Although heritability estimates are high, days to maturity and kernel length has shown low variability and moderate genetic advance as percent of mean and number of productive tillers per plant recorded moderate variability and high genetic advance as percent of mean indicating the presence of non-additive gene action. Hence, selection is not effective for these characters and further improvement is possible by intermating of superior genotypes of segregating population from recombination breeding.

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