Estimation of genetic variability for quantitative traits in Rice (*Oryzasativa*L.)

Abstract:

Abstract: The present study was conducted at Agricultural and Horticultural Research station, Kathalagere, Karnataka. Experiment was consists of sixty four rice genotypes that were evaluated to study genetic variability, heritability and genetic advance for grain yield along with four yield associated traits. The experiment was conducted using 8x8 simple lattice square design during the 2015 *kharif* main cropping season. The analysis of variance revealed statistically significant differences ($p<0.05$) indicating the existence of genetic variability among the sixty four genotypes for all the traits studied. Higher PCV and GCV values were exhibited by panicles per square meter which suggests the possibility of improving thistrait through selection. The highest heritability was recorded for days to fifty per cent flowering and plant height (cm) followed by yield kg/ha and panicles per meter square. High to medium heritability coupled with high GCV and high genetic advance as percentageof means were exhibited for plant height, panicles per square meter. Highgenetic advances as per cent of means were recorded by yield kg per hectare, panicles per square metre, Plant height (cm) and days to fifty per cent flowering.

Key words: Rice, Variability, Genotypes, Heritability, Genetic advance

Introduction

The genus*Oryza* includes a total of 25 recognized species out of which 23 are wildspecies and two, *Oryzasativa* and *Oryzaglaberrima* are cultivated (Brar 2003).It can survive as a perennial crop and can produce a ratoon crop forup to 30 years but cultivated as annual crop and grown in tropical andtemperate countries over a wide range of soil and climatic condition. Rice and agriculture are still fundamental to the economic development of most of the Asian countries. In much of Asia, riceplays a central role in politics, society and culture, directly or indirectlyemploys more people than any other sector. A healthy rice industry, especially in Asia's poorer countries, is crucial to the livelihoods of rice producers and consumers alike. Farmers need to achieve goodyields without harming the environment so that they can make agood living while providing the rice-eating people with a high-quality,affordable staple. Underpinning this, a strong rice research sector canhelp to reduce costs, improve production and ensure environmentalsustainability. Indeed, rice research has been a key to productivity andlivelihood.

Yield enhancement is the major breeding objective in rice breedingprogrammes and knowledge on the nature and magnitude of the geneticvariation governing the inheritance of quantitative characters like yieldand its components is essential for effective genetic improvement. Acritical analysis of the genetic variability parameters, namely, GenotypicCoefficient of Variability (GCV), Phenotypic Coefficient of Variability(PCV), heritability and genetic advance for different traits of economicimportance is a major pre-requisite.

Crop plant diseases caused by various pathogens such as viruses, bacteria, oomycetes and fungi pose major challenges to globalcrop production and food security. Global climate change is predictedto further increase the negative impact of biotic stresses.Higher temperatures and erratic weather pattern are likely tochange the geographical pathogen distribution.

The present investigation was undertaken in this context to elucidate information on variability, heritability, genetic advance in promising rice genotypes. A good knowledge of genetic resources might also help in identifying desirable genotypes for future hybridization program.

Material and Methods:

The experiment was carried out during *kharif,* 2015 at Agricultural and Horticultural Research Station, Kathalagere. The material comprised of sixty four rice advanced breeding lines sown in a 8x8 simple lattice design with two replications with spacing of 20 x 15 cm. Data were recorded on five randomly selected plants in each entry in each replications for the traits Days to 50% flowering, Plant height (cm), Number of panicles per square metre,except Yield which recorded in kg/plotconverted into kg/ha. The data subjected to INDOSTAT software to estimate Genetic Coefficient ofVariation (%), Phenotypic Coefficient of Variation (%), Heritability (%) (Broad sense), Genetic Advance and Genetic Advance as percent of mean. The estimates for variability treated as per the categorizationproposed by Siva Subramanian and Madhavamenon (4), heritability and genetic advance as percent of mean estimates according to criteria proposed by Johnson *et al.* (2).

Results and discussion:

In the present study analysis of variance revealed the existence of significant differences among genotypes for all traits studied. The mean, variability estimates *i.e*., Genetic coefficient of variation (%), phenotypic coefficient of variation (%), Heritability (%) (Broad sense), Genetic Advance as percentof mean are presented in Table 1. All traits under studied have higher phenotypic coefficient of variation than genotypic coefficient of variation. The magnitude ofphenotypic coefficient of variation and genotypic coefficient of variation was moderate to highfor the traits panicles per square metre and yield (Roy *et al.* 2001). The high PCV observed for panicles per square meter (33.95) (Roy, 2001). The high GCV obtained for number of panicles per square metre (33.90) indicating the improvement is possible through selection. Genotypic coefficient of variation measures the extent of genetic variability percent for a trait but does not assess the amount of genetic variation which is heritable. Heritability estimates were high for all the characters. The heritability estimates along with genetic advance can be useful to predict effect of selection in selection programmes. The traits like days to fifty percent flowering (68.07),yield kg/ha (69.33) (Thirumalarao*et al.* 2014) and plant height (69.11) exhibited high magnitude of genetic advance as percent of mean. The traits plant height, days to fifty percent flowering, panicles per square metre and yield have high heritability along with genetic advance as percent of mean indicate that these characters attributable to additive gene effects which are fixable revealing that improvement in these characters would be possible through direct selection.

Domestication and modern breeding has reduced genetic diversity of crop plants (Tanksley and McCouch, 1997) by replacing landraces and traditional farmer cultivars with modern, high yielding varieties. Although this has allowed filtering out genes that cause detrimental traits, the reduction in genetic variation now limits the options of plant breeders to develop new varieties with the existing germplasm. New varieties are constantly needed to meet consumer demands and for protection of crops against highly unpredictable biotic and abiotic stresses that are encountered in agricultural systems. Breeding of improved varieties requires the identification of novel functional genes or alleles, and this calls for making effective use of our global crop genetic resources available in seed bank collections. These seed collections represent a wide range of genetic diversity that is critical for maintaining and enhancing the yield potential and other quality traits, because they can provide new sources of resistance and tolerance to various stresses. Many of the genes for highly relevant traits in modern crop cultivars have been transferred from their wild relatives and landraces, for example the Rht and sd-1 genes that confer dwarf stature in rice and wheat, respectively (Hedden, 2003; Hoisington *et al*., 1999). In the case of rice, the six wild species *O. rufipogon,* *O. longistaminata, O. nivara, O. breviligulata, O. glumaepatula, and O. meridionalis*together with the two cultivated species *O. sativa* and *O. glaberrima* have been identified as the primary gene pool for rice cultivars because genes can be easily transferred between these species (Khush, 1997). The wild species have been used as a source of many relevant genes for rice breeding, and *O. rufipogon* has been suggested as source of broad-spectrum rice blast resistance genes (Ram *et al.*, 2007).

Conclusion:

Sixty four rice genotypes including one local check were evaluated for four yield and yield attributing traits. Results of the present investigation on variability, heritability and genetic advance indicated that the need to study the correlation between yield and other traits. Identified the two varieties performed better and shown higher variability and send them for station trial and multi season testing. High yielding and resistant varieties are selected for further crop improvement programme.

References:

1. Brar DS, Khush GS (2003) Utilization of wild species of genus Oryzae in rice improvement. In: J S Nanda, Sharma SD Monograph on Genus Oryzae 283309.
2. Hedden, P. (2003). The genes of the green revolution. Trends Genet. 19, 5–9. doi: 10.1016/S0168-9525(02)00009-4.
3. Hoisington, D., Khairallah, M., Reeves, T., Ribaut, J. M., Skovmand, B., Taba,S., et al. (1999). Plant genetic resources: what can they contribute towardincreasedcropproductivity?.Proc. Natl. Acad. Sci. U.S.A. 96, 5937–5943. doi:10.1073/pnas.96.11.5937
4. Johnson, H.W. Robinson, H.F. and Costock, R.E., Estimates of genetic and environmental variability in Soyabean. *Agronomy Journal,* **47(7)**: 314-318 (1955).
5. Khush, G. S. (1997). Origin, dispersal, cultivation and variation of rice. Plant Mol.
6. Ram, T., Majumder, N. D., Mishra, B., Ansari, M. M., and Padmavathi, G. (2007).Introgression of broad-spectrum blast resistance gene(s) into cultivated rice (*Oryzasativasspindica*) from wild rice O. rufipogon. Curr. Sci. 92, 225–230.
7. Roy, B. Hossain, M. and Hossain, F., Genetic variability in yield components of rice (*Oryzasativa*L.). *Environment and Ecology.***19(1)**: 186-189 (2001).
8. Singh S. K., Bhati P. K., Sharma A, Sahu V (2015) Super hybrid rice in China and India: current status and future prospects. *Int J Agric and Biol* 17: 221-232.1. Genetic

variability and association analysis in rice. *International Journal of Applied Biology and Pharmaceutical Technology*. **5(2)**: 63-65.

9. Siva Subramanian, S. and Madhavamenon, P., Combining ability in rice. *Madras Agricultural Journal*. **60**: 419-421 (1973)
10. Tanksley, S. D., and McCouch, S. R. (1997). Seed banks and molecular maps:unlocking genetic potential from the wild. Science 277, 1063–1066. doi:10.1126/science.277.5329.1063.
11. ThirumalaRao, V. Chandra Mohan, Y. Bhadru, D. Bharathi, D. and Venkanna,. V. (2014). Genetic variability and Association analysis of Rice. *International Journal of applied biology and Pharmaceutical Technology*. **5(2)** : 63-65
12. Kumar Vasudevan, Casiana M. Vera Cruz, Wilhelm Gruissem, and Navreet K. Bhullar (2014). Large scale germplasm screening for identification of novel rice blast resistance sources. Front Plant Sci. 2014; 5: 505.
13. Shajedur Hossain, Maksudul Haque, and Jamilur Rahman (2015). Genetic Variability, Correlation and Path Coefficient Analysis of Morphological Traits in some Extinct Local Aman Rice (Oryza sativa L). Rice Research: Open Access 2015, 4:1

Table 1: Estimates of PCV, GCV and Genetic Advance for four yield and yield component traits in sixty four advanced breeding lines of Rice.

Traits / **Parameters**	**Days to fifty percent flowering**	**Plant height (cm)**	**Panicles per m^2**	**Yield (kg/ha)**
Mean	89.25	90.18	364.64	6454.82
Genotypic variability	871.83	921.95	15279.15	4730149.00
Phenotypic variability	875.01	928.36	15328.48	4740608.00
GCV	33.08	33.66	33.90	33.69
PCV	33.14	33.78	33.95	33.73
Heritability	0.99	0.99	0.997	0.998
Genetic advance	60.71	62.33	254.22	4475.00
Genetic advance as percent mean	68.02	69.11	69.71	69.33