

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 percentage of 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 for up 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 a good living while providing the rice-eating people with a high-quality,affordable staple. Underpinning this, a strong rice research sector canhelp to reduce

Comment [DGI1]: The experiment consisted of

Comment [DGI2]: days to 50% flowering

32 costs, improve production and ensure environmental sustainability. Indeed, rice research has
33 been a key to productivity and livelihood.

34 Yield enhancement is the major breeding objective in rice breeding programmes and
35 knowledge on the nature and magnitude of the genetic variation governing the inheritance of
36 quantitative characters like yield and its components is essential for effective genetic
37 improvement. A critical analysis of the genetic variability parameters, namely, Genotypic
38 Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV), heritability
39 and genetic advance for different traits of economic importance is a major pre-requisite.

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

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

49 **Material and Methods:**

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

61 **Results and discussion:**

62 In the present study analysis of variance revealed the existence of significant
63 differences among genotypes for all traits studied. The mean, variability estimates *i.e.*,
64 Genetic coefficient of variation (%), phenotypic coefficient of variation (%), Heritability (%)
65 (Broad sense), Genetic Advance as percent of mean are presented in Table 1. All traits under
66 studied have higher phenotypic coefficient of variation than genotypic coefficient of
67 variation. The magnitude of phenotypic coefficient of variation and genotypic coefficient of
68 variation was moderate to high for the traits panicles per square metre and yield (Roy *et al.*
69 2001). The high PCV observed for panicles per square meter (33.95) (Roy, 2001). The high
70 GCV obtained for number of panicles per square metre (33.90) indicating the improvement is
71 possible through selection. Genotypic coefficient of variation measures the extent of genetic
72 variability percent for a trait but does not assess the amount of genetic variation which is
73 heritable. Heritability estimates were high for all the characters. The heritability estimates
74 along with genetic advance can be useful to predict effect of selection in selection
75 programmes. The traits like days to fifty percent flowering (68.07), yield kg/ha (69.33)
76 (Thirumalarao *et al.* 2014) and plant height (69.11) exhibited high magnitude of genetic
77 advance as percent of mean. The traits plant height, days to fifty percent flowering, panicles
78 per square metre and yield have high heritability along with genetic advance as percent of
79 mean indicate that these characters attributable to additive gene effects which are fixable
80 revealing that improvement in these characters would be possible through direct selection.

81 Domestication and modern breeding has reduced genetic diversity of crop plants
82 (Tanksley and McCouch, 1997) by replacing landraces and traditional farmer cultivars with
83 modern, high yielding varieties. Although this has allowed filtering out genes that cause
84 detrimental traits, the reduction in genetic variation now limits the options of plant breeders
85 to develop new varieties with the existing germplasm. New varieties are constantly needed to
86 meet consumer demands and for protection of crops against highly unpredictable biotic and
87 abiotic stresses that are encountered in agricultural systems. Breeding of improved varieties
88 requires the identification of novel functional genes or alleles, and these calls for making
89 effective use of our global crop genetic resources available in seed bank collections. These
90 seed collections represent a wide range of genetic diversity that is critical for maintaining and
91 enhancing the yield potential and other quality traits, because they can provide new sources
92 of resistance and tolerance to various stresses. Many of the genes for highly relevant traits in
93 modern crop cultivars have been transferred from their wild relatives and landraces, for
94 example the Rht and sd-1 genes that confer dwarf stature in rice and wheat, respectively
95 (Hedden, 2003; Hoisington *et al.*, 1999). In the case of rice, the six wild species *O. rufipogon*,

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96 *O. longistaminata*, *O. nivara*, *O. breviligulata*, *O. glumaepatula*, and *O. meridionalis* together
97 with the two cultivated species *O. sativa* and *O. glaberrima* have been identified as the
98 primary gene pool for rice cultivars because genes can be easily transferred between these
99 species (Khush, 1997). The wild species have been used as a source of many relevant genes
100 for rice breeding, and *O. rufipogon* has been suggested as source of broad-spectrum rice blast
101 resistance genes (Ram *et al.*, 2007).

102 **Conclusion:**

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

109 **References:**

- 110 1. Brar DS, Khush GS (2003) Utilization of wild species of genus *Oryzae* in rice
111 improvement. In: J S Nanda, Sharma SD Monograph on Genus *Oryzae* 283309.
- 112 2. Hedden, P. (2003). The genes of the green revolution. *Trends Genet.* 19, 5–9. doi:
113 10.1016/S0168-9525(02)00009-4.
- 114 3. Hoisington, D., Khairallah, M., Reeves, T., Ribaut, J. M., Skovmand, B., Taba, S., *et al.*
115 (1999). Plant genetic resources: what can they contribute
116 toward increased crop productivity?. *Proc. Natl. Acad. Sci. U.S.A.* 96, 5937–5943.
117 doi:10.1073/pnas.96.11.5937
- 118 4. Johnson, H.W. Robinson, H.F. and Costock, R.E., Estimates of genetic and
119 environmental variability in Soyabean. *Agronomy Journal*, **47(7)**: 314-318 (1955).
- 120 5. Khush, G. S. (1997). Origin, dispersal, cultivation and variation of rice. *Plant Mol.*
- 121 6. Ram, T., Majumder, N. D., Mishra, B., Ansari, M. M., and Padmavathi, G.
122 (2007). Introgression of broad-spectrum blast resistance gene(s) into cultivated rice
123 (*Oryza sativa* ssp. *indica*) from wild rice *O. rufipogon*. *Curr. Sci.* 92, 225–230.
- 124 7. Roy, B. Hossain, M. and Hossain, F., Genetic variability in yield components of rice
125 (*Oryza sativa* L.). *Environment and Ecology*. **19(1)**: 186-189 (2001).
- 126 8. Singh S. K., Bhati P. K., Sharma A, Sahu V (2015) Super hybrid rice in China and
127 India: current status and future prospects. *Int J Agric and Biol* 17: 221-232.1. Genetic

- 128 variability and association analysis in rice. *International Journal of Applied Biology*
 129 *and Pharmaceutical Technology*. **5(2)**: 63-65.
- 130 9. Siva Subramanian, S. and Madhavamenon, P., Combining ability in rice. *Madras*
 131 *Agricultural Journal*. **60**: 419-421 (1973)
- 132 10. Tanksley, S. D., and McCouch, S. R. (1997). Seed banks and molecular
 133 maps:unlocking genetic potential from the wild. *Science* 277, 1063–1066.
 134 doi:10.1126/science.277.5329.1063.
- 135 11. ThirumalaRao, V. Chandra Mohan, Y. Bhadru, D. Bharathi, D. and Venkanna,. V.
 136 (2014). Genetic variability and Association analysis of Rice. *International Journal of*
 137 *applied biology and Pharmaceutical Technology*. **5(2)** : 63-65
- 138 12. Kumar Vasudevan, Casiana M. Vera Cruz, Wilhelm Gruissem, and Navreet K.
 139 Bhullar (2014). Large scale germplasm screening for identification of novel rice blast
 140 resistance sources. *Front Plant Sci.* 2014; 5: 505.
- 141 13. Shajedur Hossain, Maksudul Haque, and Jamilur Rahman (2015). Genetic Variability,
 142 Correlation and Path Coefficient Analysis of Morphological Traits in some Extinct
 143 Local Aman Rice (*Oryza sativa* L). *Rice Research: Open Access* 2015, 4:1
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149 **Table 1: Estimates of PCV, GCV and Genetic Advance for four yield and yield**
 150 **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