

# 1                    **Estimation of genetic variability for** 2                    **quantitative traits in Rice (*Oryza sativa* L.)** 3 4 5

## 6                    **Abstract:**

7                    An experiment was conducted in Agricultural and Horticultural Research Station,  
8                    Kathalagere, University of Agricultural and Horticultural Sciences, Shivamogga. The  
9                    experiment was composed of 64 rice genotypes laid in 8x8 simple lattice design conducted  
10                    experiment in *kharif* 2015. The traits panicles per square metre and yield kg/ha had higher  
11                    GCV and PCV as well as high genetic variability and phenotypic variability. Yield kg/ha had  
12                    high heritability coupled with GCV and PCV.

13                    **Key words:** Rice, Variability, Genotypes  
14

## 15                    **Introduction**

16                    The genus *Oryza* includes a total of 25 recognized species out of which 23 are wild  
17                    species and two, *Oryza sativa* and *Oryza glaberrima* are cultivated (Brar 2003). It can survive  
18                    as a perennial crop and can produce a ratoon crop for up to 30 years but cultivated as annual  
19                    crop and grown in tropical and temperate countries over a wide range of soil and climatic  
20                    condition. Rice and agriculture are still fundamental to the economic development of most of  
21                    the Asian countries. In much of Asia, rice plays a central role in politics, society and culture,  
22                    directly or indirectly employs more people than any other sector. A healthy rice industry,  
23                    especially in Asia's poorer countries, is crucial to the livelihoods of rice producers and  
24                    consumers alike. Farmers need to achieve good yields without harming the environment so  
25                    that they can make a good living while providing the rice-eating people with a high-quality,  
26                    affordable staple. Underpinning this, a strong rice research sector can help to reduce costs,  
27                    improve production and ensure environmental sustainability. Indeed, rice research has been a  
28                    key to productivity and livelihood.

29                    Yield enhancement is the major breeding objective in rice breeding programmes and  
30                    knowledge on the nature and magnitude of the genetic variation governing the inheritance of  
31                    quantitative characters like yield and its components is essential for effective genetic  
32                    improvement. A critical analysis of the genetic variability parameters, namely, Genotypic

33 Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV), heritability  
34 and genetic advance for different traits of economic importance is a major pre-requisite for  
35 any plant breeder to work with crop improvement programs. The present investigation was  
36 undertaken in this context to elucidate information on variability, heritability, genetic  
37 advance in promising rice genotypes. A good knowledge of genetic resources might also help  
38 in identifying desirable genotypes for future hybridization program.

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

#### 44 **Material and Methods:**

45 The experiment was carried out during *khariif*, 2015 at Agricultural and Horticultural  
46 Research Station, Kathalagere. The material comprised of 58 elite rice genotypes sown in a  
47 simple lattice design with two replications with spacing of 20 x 15 cm. Data were recorded  
48 on five randomly selected plants in each entry in each replications for the traits days to 50%  
49 flowering, Plant height (cm), number of panicles per square metre, except yield which  
50 recorded in kg/plot converted into kg/ha. The data subjected to INDOSTAT software to  
51 estimate Genetic coefficient of variation (%), phenotypic coefficient of variation (%),  
52 Heritability (%) (Broad sense), Genetic Advance and Genetic Advance as percent of mean.  
53 The estimates for variability treated as per the categorization proposed by Siva Subramanian  
54 and Madhavamenon (4), heritability and genetic advance as percent of mean estimates  
55 according to criteria proposed by Johnson *et al.* (2).

#### 56 **Results and discussion:**

57 In the present study analysis of variance revealed the existence of significant  
58 differences among genotypes for all traits studied. The mean, variability estimates *i.e.*,  
59 Genetic coefficient of variation (%), phenotypic coefficient of variation (%), Heritability (%)  
60 (Broad sense), Genetic Advance as percent of mean are presented in Table 1. All traits under  
61 studied have higher phenotypic coefficient of variation than genotypic coefficient of  
62 variation. The magnitude of phenotypic coefficient of variation and genotypic coefficient of  
63 variation was moderate to high for the traits panicles per square metre and yield (Roy *et al.*  
64 2001). The high PCV observed for yield per hectare (Roy, 2001). The high GCV obtained for

65 number of panicles per square metre indicating the improvement is possible through  
66 selection. Genotypic coefficient of variation measures the extent of genetic variability percent  
67 for a trait but does not assess the amount of genetic variation which is heritable. Heritability  
68 estimates were high for all the characters. The heritability estimates along with genetic  
69 advance can be useful to predict effect of selection in selection programmes. The traits like  
70 days to fifty percent flowering, yield (Thirumala rao *et al.* 2014) and plant height exhibited  
71 high magnitude of genetic advance as percent of mean. The traits plant height, days to fifty  
72 percent flowering, panicles per square metre and yield have high heritability along with  
73 genetic advance as percent of mean indicate that these characters attributable to additive gene  
74 effects which are fixable revealing that improvement in these characters would be possible  
75 through direct selection.

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

97 **Conclusion:**

98 Fifty eight rice genotypes along with one standard checks were evaluated for four yield  
99 and yield attributing traits. Results of the present investigation on variability, heritability and  
100 genetic advance indicated a scope for improvement of grain yield through selection.

101 **References:**

- 102 i. Brar DS, Khush GS (2003) Utilization of wild species of genus *Oryzae* in rice  
103 improvement. In: J S Nanda, Sharma SD Monograph on Genus *Oryzae* 283309.
- 104 ii. Garrett, K. A., Dendy, S. P., Frank, E. E., Rouse, M. N., and Travers, S. E. (2006).  
105 Climate change effects on plant disease: genomes to ecosystems. *Annu. Rev.*  
106 *Phytopathol.* 44, 489–509. doi: 10.1146/annurev.phyto.44.070505.143420.
- 107 iii. Ghazanfar, M.U., A. Habib and S.T. Sahi, 2009. Screening of rice  
108 germplasm against *Pyricularia oryzae* the cause of rice blast disease. *Pak. J.*  
109 *Phytopathol.*, 21: 41-44.
- 110 iv. Hedden, P. (2003). The genes of the green revolution. *Trends Genet.* 19, 5–9. doi:  
111 10.1016/S0168-9525(02)00009-4.
- 112 v. Hoisington, D., Khairallah, M., Reeves, T., Ribaut, J. M., Skovmand, B., Taba, S., et  
113 al. (1999). Plant genetic resources: what can they contribute toward increased crop  
114 productivity?. *Proc. Natl. Acad. Sci. U.S.A.* 96, 5937–5943. doi:  
115 10.1073/pnas.96.11.5937
- 116 vi. Johnson, H.W. Robinson, H.F. and Costock, R.E., Estimates of genetic and  
117 environmental variability in Soyabean. *Agronomy Journal*, **47(7)**: 314-318 (1955).
- 118 vii. Khush, G. S. (1997). Origin, dispersal, cultivation and variation of rice. *Plant Mol.*
- 119 viii. Milus, E. A., Kristensen, K., and Hovmoller, M. S. (2009). Evidence for increased  
120 aggressiveness in a recent widespread strain of *Puccinia striiformis f. sp tritici*  
121 causing stripe rust of wheat. *Phytopathology* 99, 89–94. doi: 10.1094/PHYTO99-1-  
122 0089.
- 123 ix. Ram, T., Majumder, N. D., Mishra, B., Ansari, M. M., and Padmavathi, G. (2007).  
124 Introgression of broad-spectrum blast resistance gene(s) into cultivated rice (*Oryza*  
125 *sativa ssp indica*) from wild rice *O. rufipogon*. *Curr. Sci.* 92, 225–230.
- 126 x. Roy, B. Hossain, M. and Hossain, F., Genetic variability in yield components of rice  
127 (*Oryza sativa* L.). *Environment and Ecology*. **19(1)**: 186-189 (2001).
- 128 xi. Singh S. K., Bhati P. K., Sharma A, Sahu V (2015) Super hybrid rice in China and  
129 India: current status and future prospects. *Int J Agric and Biol* 17: 221-232.1. Genetic

- 130 variability and association analysis in rice. *International Journal of Applied Biology*  
 131 *and Pharmaceutical Technology*. **5(2)**: 63-65.
- 132 xii. Siva Subramanian, S. and Madhavamenon, P., Combining ability in rice. *Madras*  
 133 *Agricultural Journal*. **60**: 419-421 (1973)
- 134 xiii. Tanksley, S. D., and McCouch, S. R. (1997). Seed banks and molecular maps:  
 135 unlocking genetic potential from the wild. *Science* **277**, 1063–1066. doi:  
 136 10.1126/science.277.5329.1063.
- 137 xiv. Thirumala Rao, V. Chandra Mohan, Y. Bhadr, D. Bharathi, D. and Venkanna,. V.  
 138 (2014). Genetic variability and Association analysis of Rice. *International Journal of*  
 139 *applied biology and Pharmaceutical Technology*. **5(2)** : 63-65
- 140 xv. Vaithiyalingan, M. and Nadarajan, N., Genetic variability, heritability and genetic  
 141 advance in F<sub>1</sub> population of inter sub-specific crosses of rice. *Crop Research*. **31(3)**:  
 142 476-477 (2006).
- 143 xvi. Venkanna, V., Lingaiah, N., Raju, Ch and Rao, V.T., Genetic studies for quality traits  
 144 of F population of rice (*Oryza sativa* L.). *International Journal of Applied Biology*  
 145 *and Pharmaceutical Technology*. **5(2)**: 125-127 (2014).

146

147 **Table 1: Rice genotypes, Grain type and blast disease reaction during the experiment**  
 148 **in research station.**

Traits Parameters	Days to fifty percent flowering	Plant height (cm)	Panicles per m <sup>2</sup>	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

149