

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 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).
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 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.

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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 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

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