Genetic Variability, Heritability and Genetic Advance in 3K Rice (*Oryza sativa L.*) Genotypes

Abstract

The presence of genetic variation for specific traits in populations is of great importance for the development of crop improvement programs and the establishment of appropriate techniques for selection. In the winter of 2021, experiments were conducted to examine the extent of genetic variation in 50 genotypes of rice. Analysis of variance revealed the presence of highly significant differences in all 12 traits examined, indicating the presence of genetic variation between genotypes. The PCV was slightly greater than GCV for all the traits indicating the possibility for genetic improvement for these traits through direct selection. The PCV and GCV estimates were moderate for days to 50% flowering, plant height, panicle length, spikelet fertility and test weight, indicating that environmental factors are more important than genotype alone. Estimates of heritability and genetic advance were high for days to 50% flowering, plant height, number of tillers per plant, number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, total number of grains per panicle, panicle length, panicle weight, test weight, single plant yield, spikelet fertility. It is indicated that greater influence of additive gene action and it is effective for improvement of the traits in the study.

Keywords: Additive gene action, direct selection, Genotype, Phenotypic co-efficient of variation (PCV), Genotypic co-efficient of variation (GCV).

Introduction

"Rice (*Oryza sativa* L.) is an important cereal crop grown worldwide, and as a most important source of food as it accounts for 35-75% of the calorie intake of more than 3.5 billion humans" (Pathak *et al*., 2018). "The demand for rice is still increasing in Asia as the consumption rate is at least 90% and it is globally projected that the demand for rice will rise up to 650 million tons by 2050" (Chukwu *et al*., 2019). In India with increasing population, it has been estimated that rice production needs to be increased up to 121.2 million tons by the year 2030 (CRRI, 2013). Grain yield is a complex trait strongly influenced by many quantitative traits determined by polygenes. Although the average rice yield rose, there is growing evidence

that the impressive yield growth rate achieved earlier is no longer maintained. Hence there is a need to improve productivity by utilizing the existing genetic variation in rice germplasm. "A comprehensive knowledge of the genetic variability present in crop species to enhance traits is paramount to the success of any plant breeding programme. Estimates of genetic variation and heritability will give a good idea of the efficiency of selection" (Iqbal *et al*. 2018).

Heritability and genetic advance are considered important selection parameters. Heritability is referred as the ratio of genotypic variance to total variance, or phenotypic variance. This is a measure of the transmission of characters from one generation to another. Heritability estimates are very useful for plant breeders in selecting superior individuals for desired traits under study for successful use in plant breeding programs.

Genetic advance refers to improvements in the mean genotype of selected plants over the parent or baseline population. This is a measure of genetic gain under selection. According to Tiwari (2015), "the success of genetic advancement under selection depends mainly on three factors: genetic variability, heritability, and selection intensity". Broad sense heritability estimates, genetic advance (GA), and genetic advance as % of mean (GAM) provide genetic information that indicates the potential progress made possible by selection. With the above perspectives in mind, the present investigation aimed to estimate the genetic variability, heritability and genetic advance of yield and yield-related traits in 3k rice genome subset panel which could be useful in selection and further improvement of rice genotypes.

Materials and methods

The experimental material comprised of 50 genetically diverse rice genotypes (*Oryza sativa L.*) belonging to 3k rice genome subset panel. The investigation was carried out at Indian council of agricultural research (ICAR)-Indian Institute of Rice Research (IIRR), Rajendranagar, Hyderabad, during winter 2021. The experimental trial was laid out in E8 plot in ICAR-IIRR field in completely randomized block design with two replications. Thirty days old seedlings were transplanted in the main field. Each entry is represented by four rows of 3 m length, with 20 cm spacing between rows and 15 cm spacing between hills. During the experiments, recommended dose of fertilizers 100kg N, 50 kg P_2O_5, and 50 kg K_2O per hectare was applied. Nitrogen was applied in 3 split doses of 50, 25, 25 kg N/ha at the time of transplanting, 25-30 days, and 55-60 days after transplanting respectively. The entire dose of P_2O_5 and K_2O were

applied at the time of transplanting and required plant protection measures were taken to grow healthy nurseries and main crops.

Replicate data were collected based on five randomly selected plants of each genotype and observations were made for days to fifty percent flowering (DFF), plant height (PH) (cm), number of tillers per plant (TN), number of productive tillers per plant (NPT), panicle length (PL) (cm), panicle weight (PW) (g), total number of grains (TG), number of filled grains (NFG), number of unfilled grains (NUFG), 1000 grain weight (TW) (g), spikelet fertility (SPF) (%), single plant yield (SPY) (g). Statistical analysis using SAS software version 9.2 considered the average value of five plants for each metric trait. Analysis of variance (ANOVA) was performed for completely randomized block design based on a model described by Cochran and Cox (1957). Genotypic and phenotypic variances were calculated using the formula of Burton and Devane, 1953.

$$\text{Genotypic variance } (\sigma^2 g) = \frac{Mse - Mst}{r} \quad \ldots\ldots\ldots\ldots\ldots\ldots (1)$$

Phenotypic variance $(\sigma^2 p) = (\sigma^2 g + \sigma^2 e)$

Broad sense heritability (h^2) was calculated using the formula proposed by Lush, 1949 as suggested by Johnson *et al.* (1955).

$$h^2 B = \frac{\sigma^2 g}{\sigma^2 p} \times 100 \quad \ldots\ldots\ldots\ldots\ldots (2)$$

Where:

$h^2 B$ = Heritability in broad sense

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 g$ = Genotypic variance

From the estimates of heritability, the genetic advance (GA) was calculated using the formula given by Johnson *et al.* (1955).

$$GA = \frac{K \times \sqrt{\sigma^2 p} \times \sigma^2 g}{\sigma^2 p} \quad \ldots\ldots\ldots\ldots (3)$$

Where:

GA = Expected genetic advance

K = Standardized selection differential at 5% selection intensity (k = 2.063)

σ^2p = Phenotypic variance

σ^2g = Genotypic variance

Results and Discussion

Analysis of variance revealed presence of highly significant differences for all the 12 traits under study *viz.,* days to 50% flowering, plant height, number of tillers per plant, number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, total number of grains per panicle, panicle length, panicle weight, test weight, single plant yield, spikelet fertility indicating the existence of genetic variability among the genotypes and the details are presented in Table-1. Analysis of variance also demonstrates the representativeness of the 3k rice genome subset panel that captures the maximum variability available among *O. sativa* sub species. Phenotypic and genotypic coefficients of variation, heritability and genetic advance as percentage of the mean were estimated for fifty genotypes and are detailed in table 2.

Experimental field was managed to ensure uniformity and reduce experimental errors by adopting randomized block design in which the plots were divided into blocks and every treatment is replicated twice in each block. Efforts were made to increase precision of experiment by adopting the principle of local control. However, the current study revealed that the PCV (phenotypic co-efficient of variation**)** estimates was slightly higher than GCV (genotypic co-efficient of variation**)** for all the traits indicating that the traits under study are influenced by environment. PCV and GCV estimates were moderate in magnitude for five traits *viz.,* days to 50% flowering (PCV-13.79% and GCV-13.62%), plant height (PCV-19.73 and GCV-19.26), panicle length (PCV-11.72% and GCV-10.81%), spikelet fertility (PCV-18.91% and GCV-14.96%) and test weight (PCV-16.39% and GCV-15.17%). Similar such observations were made by Keerthiraj *et al*. (2020) for days to 50% flowering, Keerthiraj *et al*. (2020), Sudeepthi *et al*. (2020), Kumar *et al.* (2018) for test weight, Keerthiraj *et al*. (2020), Sudeepthi *et al*. (2020), Devi *et al*. (2016) for plant height, Keerthiraj *et al*. (2020) for panicle length, Kole *et al*. (2008) for spikelet fertility and selection for these traits suggests that they can be deferred to later generations to improve gene flow and fix for favorable alleles, or intermating followed by recurrent selection can be employed to improve baseline or parental populations.

Estimates of GCV and PCV were recorded high for number of productive tillers per plant (PCV-28.30% and GCV-23.43), number of tillers per plant (PCV-30.08% and GCV-25.38),

panicle weight (PCV-38.90% and GCV-35.26), number of unfilled grains per panicle (PCV-71.63% and GCV-64.53%), number of filled grains per panicle (PCV-35.32% and GCV-29.86%), total number of grains per panicle (PCV-34.86% and GCV-31.01%) and single plant yield (PCV-30.87% and GCV-25.05%). Results are in consistent with Nihad *et al.* (2021), Keerthiraj *et al.* (2020) for number of tillers per plant, Nihad *et al.* (2021), Keerthiraj *et al.* (2020), Kumar *et al*. (2018) for single plant yield, Nihad *et al.* (2021), Bhargava *et al*. (2021) for total number of grains per panicle, Nihad *et al.* (2021), Beena *et al*. (2021), Kumar *et al*. (2018) for the number of filled grains per panicle, Bhargava *et al*. (2021), Lakshmi *et al.* (2017) for number of productive tillers, Beena *et al*. (2021), Nihad *et al.* (2021), Saha *et al*. (2019) for number of unfilled grains, Shivani *et al.* (2018) for panicle weight. Similar to our results, the observations reported above for high PCV and GCV estimates in several genotypes of important yield and yield-related traits suggest that direct selection for these traits achieves genetic improvement. suggesting that it can be done.

High heritability (H^2) associated with high genetic advancement (GA) estimates was recorded for all the traits *viz.*, days to 50% flowering (H-97.6% and GA-27.73%), plant height (H-95.3% and GA-38.74%), number of tillers per plant (H-71.18% and GA-44.11%), number of productive tillers per plant (H-68.53% and GA-39.96%), number of unfilled grains per panicle (H-81.14% and GA-119.75%), number of filled grains per panicle (H-71.48% and GA-52.02%), total number of grains per panicle (H-79.13% and GA-56.84%), panicle length (H-85.04% and GA-20.54%), panicle weight (H-78.1% and GA-64.21%), test weight (H-85.7% and GA-28.94%), single plant yield (H-65.84% and GA-41.88%), spikelet fertility (H-62.57% and GA-24.37%) in Table-2. These results are in conformity with Beena *et al*. (2021), Keerthiraj *et al*. (2020), Manjunatha and kumara (2019), Konate *et al.* (2016), Gampala *et al.* (2015), for days to 50% flowering and Nath and Kole (2021), Shivani *et al*. (2018), Devi *et al.* (2016), Konate *et al.* (2016) for plant height and Lakshmi *et al*. (2017) for panicle length and Beena *et al*. (2021), Nihad *et al.* (2021), Keerthiraj *et al*. (2020), Gour *et al.* (2017), Devi *et al.* (2016) for test weight,. Bhargava *et al.* (2021), Beena *et al*. (2021), Bharath *et al.* (2018), Devi *et al.* (2016) for number of productive tillers, Beena *et al*. (2021), Kalaiselvan *et al.* (2019), Gour *et al.* (2017) for number of tillers, Keerthiraj *et al*. (2020), Gour *et al.* (2017) for panicle weight, Beena *et al*. (2021), Keerthiraj *et al*. (2020), Saha *et al*. (2019) for number of unfilled grains, Nihad *et al.* (2021), Beena *et al*. (2021), Gour *et al.* (2017) for number of filled grains, Bhargava *et al.*

(2021), Nihad *et al.* (2021), Beena *et al*. (2021), Devi *et al.* (2016) for total number of grains, Nihad *et al.* (2021), Bhargava *et al.* (2021), Gour *et al.* (2017), Konate *et al.* (2016) for single plant yield, Sumanth *et al.* (2017) for spikelet fertility. This indicates that there is high genetic variability and preponderance of additive gene action. Therefore these traits could be possibly improved through simple selection.

Conclusion

The genetic architecture of cereal yield is based on the net overall impact of the interactions of various yield components. The present study showed that the tested material exhibits sufficient genetic variability. All the traits *viz.*, days to 50% flowering, plant height, number of tillers per plant, number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, total number of grains per panicle, panicle length, panicle weight, test weight, single plant yield, spikelet fertility recorded high heritability coupled with high genetic advance. This indicated a significant amount of variability and the presence of additive gene action. Hence, it was showed that phenotypic selection would be effective for the improvement of various characters.

Table-1: Analysis of variance for yield and yield related traits among genotypes of rice

Parameter	Replication	Treatment	Error
Df	2	49	98
DFF	24.74	565.6*	4.58
PH	51.38	2182.9**	35.24
NT	12.6	31.4**	3.73
NPT	5.04	20.5**	2.72
PL	0.14	25.71*	1.41
PW	0.02	4.7**	0.4
TG	1786.7	8595.5**	694.2**
NFG	1354.8	4891.7**	574.1
NUFG	750.1	1989.7**	143.01
SF	122.1	483.7*	80.41
SPY	4.873	101.91**	15.02
TW	2.89	41.5**	2.18

Significance at 5% level

DFF- Days to 50% flowering, PH-plant height, NT- Number of tillers per plant, NPT-Number of productive tillers per plant, PL- Panicle length, PW- Panicle weight, TG- Total number of grains, TW-Test weight, SPY-Single plant yield, PY-Plot yield, BM-Biomass, HI- Harvest index

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Table-2: Variability parameter in rice genotypes

S.No	Characters	General mean	Range	Coefficient of variation (%)		Heritability in broad sense (h^2) %	Gen. Adv as percent of mean (at 50%)
				PCV (%)	GCV (%)		
01	Days to 50% flowering	100.36	69-128	13.79	13.62	97.6	27.73
02	Plant height (cm)	138.88	69-185.5	19.73	19.26	95.3	38.74
03	Panicle length	26.31	17.5-35.5	11.72	10.81	85.04	20.54
04	No. of tillers	11.96	6-21	30.08	25.38	71.18	44.11
05	No. of productive tilers	10.4	5-19	28.30	23.43	68.53	39.96
06	Panicle weight (g)	3.39	0.9-7.6	38.90	35.26	78.1	64.21
07	No. of filled grains	127.01	42-97	35.32	29.86	71.48	52.02
08	No. of unfilled grains	38.44	1-101	71.63	64.53	81.14	119.75
09	Total grains	165.46	63-355	34.86	31.01	79.13	56.84
10	Spikelet fertility	77.50	6-98.8	18.91	14.96	62.57	24.37
11	Test weight (g)	23.85	2-33.5	16.39	15.17	85.7	28.94
12	Single plant yield	21.47	4.9-42.7	30.87	25.05	65.84	41.88