Genetic Variability, Heritability and Genetic Advance Studies in 3K Rice(*Oryza sativa* L.)Genome Subset Panel

Abstract

The presence of genetic variability for a specific trait in the population is very crucial for the development of a crop improvement programme and for adopting appropriate techniques for selection. An experiment was carried out to determine the extent of genetic variability present in fifty genotypes of rice during *Rabi* 2021. Analysis of variance revealed presence of highly significant differences for all the 12 characters under study, indicating the existence of genetic variability among the genotypes. The magnitude of PCV was slightly greater than GCV for 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, indicating that the traits under study are less influenced by environmental factors. So there is possibility for genetic improvement for these traits through direct selection. The estimates of PCV and GCV were moderate for the traits *viz.*, days to 50% flowering, plant height, panicle length, spikelet fertility and test weight, indicating that there is influence of environmental factors rather than the genotype alone. The heritability and genetic advance estimates were high for all the other 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. This indicated the greater influence of additive gene action and such selection would likely to be effective for improvement of thesecharacters under study.

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Keywords: Rice, variability, heritability, genetic advance

Comment [A2]: Use words that are not in the title

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 tonnes 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 tonnes by the year 2030 (CRRI, 2013). Grain yield is a complex character which is highly influenced by many quantitative traits which are governed by polygenes. Although average rice yield rose, evidence is accumulating to suggest that the impressive rates of yield growth achieved earlier are no longer being sustained. Hence there is a need to improve productivity by utilizing the existing genetic variation in rice germplasm. A comprehensive knowledge of genetic variability present in the crop species for the trait under improvement is of outmost important for the success of any plant breeding programme. Genetic variation along with heritability estimates would give a good idea about the efficiency of selection (Burton, 1952).

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Heritability and genetic advance are considered as important selection parameters. Heritability is referred as the ratio of genotypic variance to the total variance or phenotypic variance.It is the measure of transmission of characters from one generation to another generation. Heritability estimates will be of immense help to the plant breeder in selecting superior individuals for a desired character under study for successful utilization in the plant breeding programme. Genetic advance refers to the improvement in the mean genotypic value of the selected plants over the parental or base population**.** It is the measure of genetic gain under selection. According to Allard (1960), the success of genetic advance under selection depends on three factors *viz.*, genetic variability, heritability and selection intensity. Estimates of broad sense heritability, genetic advance (GA), genetic advance as % of the mean (GAM), provide genetic information which indicate the possible progress that can be made through selection. Keeping in view the above perspectives, the present study was taken up with the objective of estimating the genetic variability heritability and genetic advance for yield and yield related traits in 3k rice genome subset panel, which could be useful in selection and further improvement of ricegenotypes.

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Materials and methods

The experimental material comprised of 50 genetically diverse genotypes of rice (*Oryzasativa*L.)belongingto3k rice genome subset panel.The investigation was carried out at

Indian council of agricultural research (ICAR)-Indian Institute of Rice Research, Rajendranagar, Hyderabad, during *Rabi* 2021. Theexperimentaltrialwaslaidoutin E8 plot in ICAR-IIRR field in completely randomized block design with two replications. Thirty daysold seedlings were transplanted in the main field. Each entry was represented by four rows of 3 m length with a spacing of 20 cm between rows and 15 cm between hills. Recommended agronomic and plant protection measures were followed for raising a healthy nursery and main crop during the experiment.

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Replication-wise data was taken on the basis of five randomlyselected plants in each genotype and observations were recorded for twelve quantitative traits *viz.*, 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).The mean of five plants for each metric trait was considered for statistical analysis using SAS software version 9.2. The analysis of variance (ANOVA) was carried out on the basis of model described by Cochran and Cox (1957) for completely randomized block design. The genotypic and phenotype variances were calculated as per the formulae given by Burton and Devane, 1953.

Comment [A10]: The method of measuring attributes should be included with the reference

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

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

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

$$h^2 B = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where:

$h^2 B$ = Heritability in broad sense

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 g$ = Genotypic variance

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

$$GA = \frac{K \times \sqrt{\sigma^2 p} \times \sigma^2 g}{\sigma^2 p}$$

Where:

GA = Expected genetic advance

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

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 g$ = Genotypic variance

Figure-1: Collection and observation of physiological and morphological data of experimental crop.

Results and Discussion

Analysis of variance revealed presence of highly significant differences among the 50 genotypes for all the 12 characters *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 adequate amount of genetic variability among the genotypes under study and the details are presented in table 1. Analysis of variance also indicates the representativeness of the 3k rice genome subset panel capturing maximum variability available among sub species of *O. sativa*. The phenotypic and genotypic coefficients of variation, heritability and genetic advance as per cent of mean were estimated for fifty genotypes and the details are furnished in table 2.

Comment [A11]: The scientific reasons for the results should be clearly stated

The present study revealed that the estimates of PCV were slightly higher than GCV for all the traits indicating that the traits under study are less influenced by environmental factors. As the expression of characters was less influenced by the environment, these traits can be utilized for selection. The magnitude of PCV and GCV estimates were moderate 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, which indicates that the selection could be postponed for these traits until advanced generations to enhance the gene flow and to fix favourable alleles or the base or parental population could be improved through intermating followed by recurrent selection.

High estimates of GCV and PCV were recorded 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.* (2020) 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*. (2020) 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. In similar to our findings, the above reported observations for high PCV and GCV estimates in several genotypes for important yield and yield related traits, does indicate that genetic improvement could be made through direct selection for these traits.

Comment [A12]: The scientific reasons for the results should be clearly stated

Heritability refers to the ratio of genotypic variance to the total variance or phenotypic variance. According to Falconer (1989) heritability is a good index of transmission of characters from parents to their offspring. The outstanding function of heritability lies in expressing the phenotypic value reliability for a trait as a guide to the breeding value for that trait in a population (Falconer, 1960). In its broader sense it specifies the proportion of the total phenotypic variability that is due to genetic causes. Traits with high heritability % are least affected by the environment in their expression. Quantitative traits due to their sensitivity to the environment usually have low heritability estimates (Allard, 1960). Heritability estimates can be used for prediction of genetic gain, which indicates the genetic improvement as a result of selection of best individuals.

Genetic advance is regarded as the improvement in the mean genotypic value of the selected plants over the parental population**.** It is the measure of genetic gain under selection.Estimates of broad sense heritability, genetic advance (GA), genetic advance as % of the mean (GAM) helps to find out the genetic gain expected from selection than heritability estimatesalone.

High heritability (H) coupled with high genetic advance (GA) estimates were 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%). 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 andLakshmi *et al.* (2017) for panicle length andBeena *et al*. (2021), Nihad *et al.* (2021), Keerthiraj *et al.* (2020), Gour *et al.* (2017), Devi *et al.* (2016) for test weight.

Comment [A13]: The scientific reasons for the results should be clearly stated

Similar results were obtained by Bhargava *et al.* (2021), Beena *et al.* (2021), Kumar *et al.*

(2020), 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 expression of these characters is influenced to less extent by environmental factors and hence one can adopt selection.

Comment [A14]: The relationship between grain yield and other traits should be presented with stepwise regression

Conclusion

The genetic architecture of grain yield is based on the overall net effect produced by various yield components interacting with one another. The present study revealed that there is presence of adequate genetic variability in the material under investigation. 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 the presence of considerable amount of variation and additive gene action. Hence, phenotypic selection would be effective for the improvement of these characters.

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Comment [A15]: be updated

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

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

*Significance at 5% level

DFF- Days to 50% flowering, PH- Plant height, NT- 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.

Table 2. Variability parameters 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 5%)
				PCV (%)	GCV (%)		
1	Days to 50% flowering	100.36	69-128	13.79	13.62	97.6	27.73
2	Plant height (cm)	138.88	69-185.5	19.73	19.26	95.3	38.74
3	Panicle length	26.31	17.5-35.5	11.72	10.81	85.04	20.54
4	No. of tillers	11.96	6-21	30.08	25.38	71.18	44.11
5	No. of productive tillers	10.4	5-19	28.30	23.43	68.53	39.96
6	Panicle weight (g)	3.39	0.9-7.6	38.90	35.26	78.1	64.21
7	No. of filled grains	127.01	42-97	35.32	29.86	71.48	52.02
8	No. of unfilled grains	38.44	1-101	71.63	64.53	81.14	119.75
9	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