Estimation of genetic variability parameters for various yield attributing traits in germplasm collection of Rice (*Oryza sativa* L.)

ABSTRACT

Genetic variability parameters were studied in 2879 germplasm accessions of rice for 11 quantitative traits. Moderate value of genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) was observed for the traits, 100 seed weight, seedling height, L:B ratio, plant height, and number of effective tillers, whereas rest of the traits had low GCV and PCV values. High heritability was observed for all the traits except leaf length, leaf width and grain yield per plant. High heritability coupled with high genetic advance as percent of mean was observed for 100 seed weight, seedling height and L:B ratio. High heritability coupled with moderate genetic advance as percent of mean was recorded for days to 50% flowering and plant height. The presence of high heritability and high genetic advance as percent of the mean indicated the presence of additive gene effects for controlling aforesaid traits, hence selection in later generations will be rewarding in a breeding programme.

Key words: Rice germplasm, heritability, genetic advance, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV).

INTRODUCTIONS

Rice is the most consumed cereal grain in the world, constituting the dietary staple food for more than half of the planet’s human population. India being the second largest producer of rice still lags behind is productivity per unit area. The rising demand, saturation of cultivable field and low gross domestic production of rice are likely to cause a supply shortage of a crop in near future. By the year 2025, about 785 million tons of paddy, which is 70 per cent more than the current production will be needed to meet the growing demand (Manonmani and Khan, 2003). This ranks first among the three major cereals, followed by wheat and maize. It is one of the oldest cultivated sources of nutrients to flourish under a wide range of environments and it has 22 wild species in the *Oryza* genus. It may be cultivated in a variety of environments, including upland, lowland, and rain-fed. It is one among India's most important crops. Moreover, it is a nutrient-rich cereal crop that provides 20 % of the calories and 15 % of the protein consumed by the world's population.

Crop improvement is heavily dependent on understanding the genetic diversity and population structure of germplasm collections. Because rice is an important crop in the globe, there is a lot of curiosity in the origins and diversity of *Oryza sativa*. Current theories suggest that domesticated rice originated from a polyphyletic source, most likely from either an annual or perennial variety of *O. rufipogon*, through at least two separate domestication processes (Second, 1982; Cheng *et al*., 2003; Vitte *et al*., 2004).

Minerals and fibers are also present in the rice grains. Collection and classification of existing germplasm is critical not only for using appropriate attribute-based donors in breeding programmers, but also for protecting the distinctive rice for the future. In Asia, rice production contributes to almost 90 % of global output (Faysal *et al.,* 2022). Estimating genetic gain under selection will be more accurate when heritability and evolution are combined (Demeke *et al.*, 2023). To enhance rice production, many programmes and activities were developed. However, the successes continue to be up to par, which has prompted the country to shift from being a net rice producer to an import in recent years (Joshi *et al*., 2011; Bishwajit *et al.,* 2013). Crop failure in recent years has been mainly caused by climate change scenarios such as unpredictable rainfall, disease and pest attack, and genetic degradation owing to developmental activities (Ali *et al*, 2017).

The characterization and evaluation of conserved genetic resources in gene banks are very essential to document the presence of genetic variability and diversity for different important traits. Keeping in view the importance of variability, the present study has been conducted to estimate the variability parameters in large number of germplasm accessions.

MATERIALS AND METHODS

The materials for the study comprised of 2879 germplasm accessions of rice i.e. 2879 germplasm accessions received from ICAR- NBPGR (National Bureau of Plant Genetic Resources), New Delhi including 6 checks namely, Annada, IR 64, Pusa Basmati-1, Swarna, NDR-97 and Jaya of different duration groups. The experimental materials were grown in *Kharif*, 2022 in Augmented Block Design. Twenty one days old seedlings of each genotype were transplanted manually in 2 row of 2-meter length maintaining a spacing of 20 cm between rows and 15 cm between plants in each row. Observations were recorded on 3 randomly selected plants from each genotype for 11 quantitative traits viz., days to 50% flowering, no. of effective tillers, days to maturity, panicle length, plant height, 100 grain weight, seedling height, leaf length, leaf width, grain yield per plant and grain length/breadth ratio. The mean values of these were used for statistical analysis through XL Stat.

RESULTS AND DISCUSSION

The experiment was carried out in Augmented Block Design with the objective to assess the variability present in the rice accessions. In almost all the traits evaluated in the experiment, the phenotypic coefficient of variation (PCV) was greater in magnitude than the genotypic coefficient of variation (GCV). This indicated that the apparent variance is attributable not just by genes but also due to environmental effects. The mention of a slight distinction between GCV and PCV was also reported by Mustafa and Isheikh (2007), Kole *et al*. (2008) and Mulugeta Syoum *et al.* (2012). Classifying the overall variation into its constituent parts could facilitate the preservation and application of genetic resources. Also, it provides the possibility to use appropriate germplasm for crop enhancement of certain plant features (Pecetti *et al*., 1996).

The phenotypic coefficient of variation (PCV) with higher magnitude is presented in Table No.1. Higher phenotypic coefficient of variation (PCV) was recorded for the traits grain yield per plant (37.43), similar to the findings of Lingaiah *et al.,* (2014). Moderate phenotypic coefficient of variation was observed for the traits, seedling height (16.34), L/B ratio (15.65), leaf width (14.12), leaf length (13.18), plant height (12.04), 100 seed weight (19.4) and number of effective tillers (19.39) and rest of the traits had low PCV. The lowest GCV was recorded in days to 50% flowering (9.35), days to maturity (7.3) and panicle length (5.81). The results are in agreement with Bisen *et al.* (2009), Singh *et al*. (2011), Subbaiah *et al.* (2011) and Babu *et al.* (2012). Moderate GCV was recorded for 100 seed weight (17.93), seedling height (16.34), L/B ratio (14.05), plant height (10.98) and the number of effective tillers (11.27). Prajapati *et al.* (2011) and Ananadarao *et al.* (2011) also reported similar observations in their study.

The presence of higher genotypic coefficient of variation (GCV) suggests that the population has a considerable genetic diversity. The phenotypic coefficient of variation was higher than the GCV in the present research, but the difference was moderate, indicating that environment impact on traits expression was low. Similar findings has also been reported by Sarawgi *et al.* (1994), Ganesan *et al.* (1995) and Sharma and Dubey (1997).

To identify a trait's response to phenotypic selection, heritability is crucial. For a breeding programme to be successful, improving quantitative traits in plants requires accurate heritability estimation (Saidon *et al.,* 2020). The estimates of genetic advance expressed as a percentage of the mean offer greater confidence about the efficacy of selection in enhancing the traits. Genetic progress indicates the new population's genotypic value is higher than that of the original population. Heritability estimates alone are less useful in predicting the gain under selection than heritability estimates combined with significant genetic advancement.

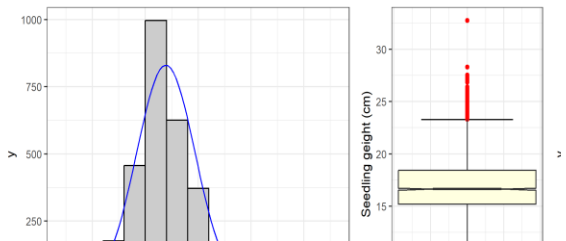
However, it's not always the case that a trait with high heritability also has strong genetic advances (Johanson *et al.,* 1955). High heritability was recorded for seedling height (100), days to 50 % flowering (100), days to maturity (100), 100 seed weight (85.45), plant height (83.23) and L/B ratio (80.68). Li-Yun *et al.* (2003) and Satyanaryan *et al*. (2005) also reported similar findings. Genetic advance as percent of mean was higher for the 100 seed weight (33.72) and L/B ratio (26.04). High heritability coupled with higher genetic advance as percent of the mean were observed for 100 seed weight, seedling height and L/B ratio. High heritability coupled with moderate genetic advance as percent of mean was recorded for plant height and days to maturity and rest of the traits are low heritability and genetic advance as percent of mean, the findings were also in agreement with Kujur *et al*. (2023). The result shows the presence of additive gene effects. Hence, selection of desirable genotype for future breeding programme will be rewarding.

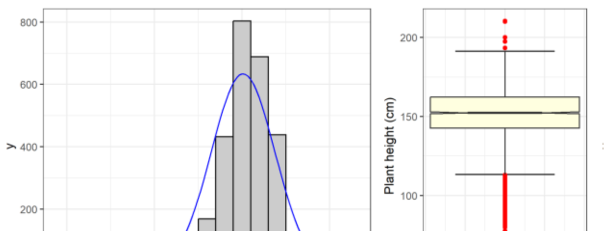
Table 1: Estimation of genetic variability parameters for quantitative traits

S.	**Traits**	**Mean**	**Range**		**GCV**	**h^2 bs**	**GAM**

No.			Min.	Max.	PCV (%)	(%)	(%)	
1.	Leaf length (cm)	55.04	27.16	2.06	13.18	12.16	85.07	23.13
2.	Leaf width (cm)	1.09	0.6	2.06	14.12	11.28	63.07	18.57
3.	Days to 50% flowering	106.59	65.00	148.00	9.35	9.35	99.79	19.29
4.	Plant height (cm)	150.48	52.00	210.33	12.04	10.98	83.23	20.67
5.	Panicle length (cm)	25.10	9.10	32.63	9.15	5.81	40.29	7.61
6.	No. of effective tillers	6.53	1.33	13.33	19.39	11.27	33.76	13.51
7.	Days to maturity	136.59	95.00	178.00	7.30	7.30	99.79	15.05
8.	L/B ratio	3.23	1.70	5.40	15.65	14.05	80.68	26.04
9.	100 seed weight (g)	2.36	0.77	4.90	19.40	17.93	85.45	34.02
10.	Grain yield per plant (g)	19.86	2.00	116.00	37.43	35.20	82.03	32.03

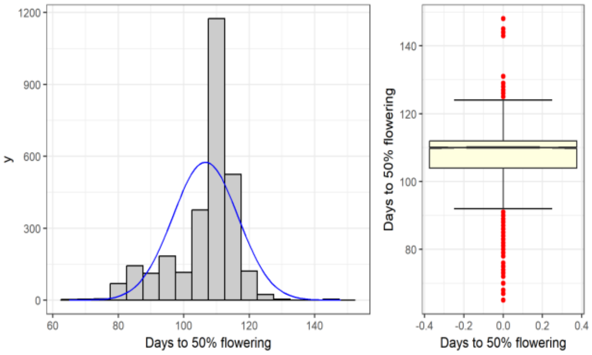
Where, Min: minimum, Max: maximum, PCV: phenotypic coefficient of variation, GCV: genotypic coefficient of variation, h^2bs: heritability (broad sense), GA: genetic advance, GAM: genetic advance as percent of mean

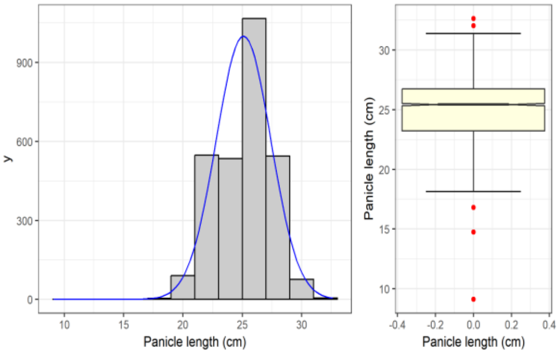




Seedling height

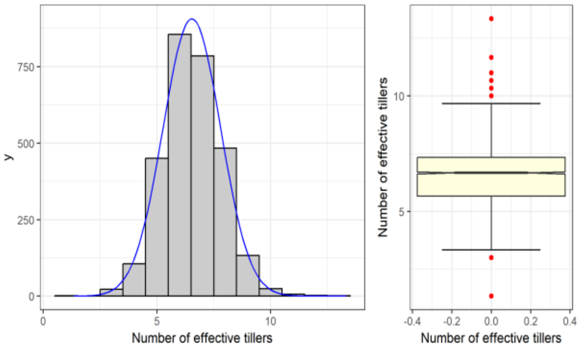
Plant height

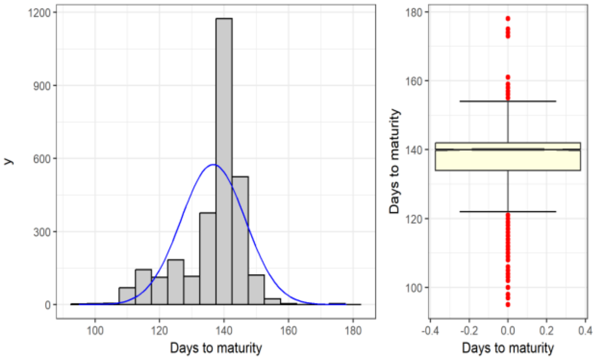




Days to 50% flowering

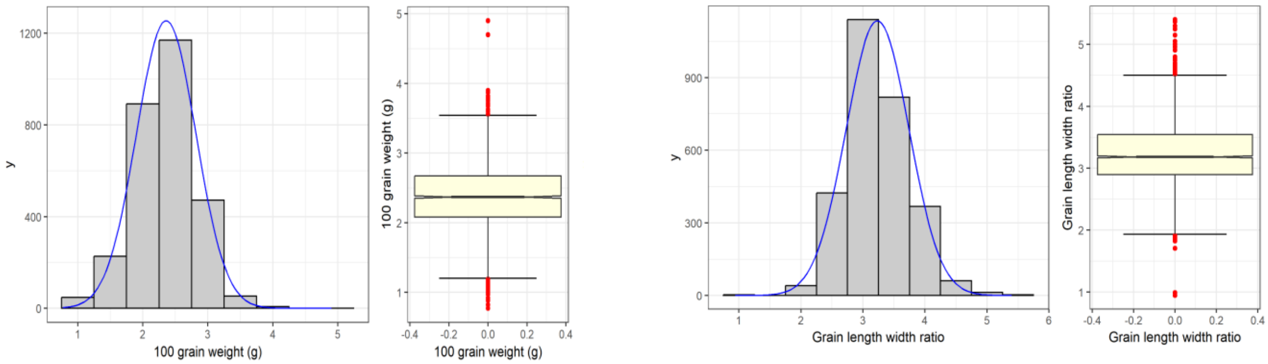
Panicle length





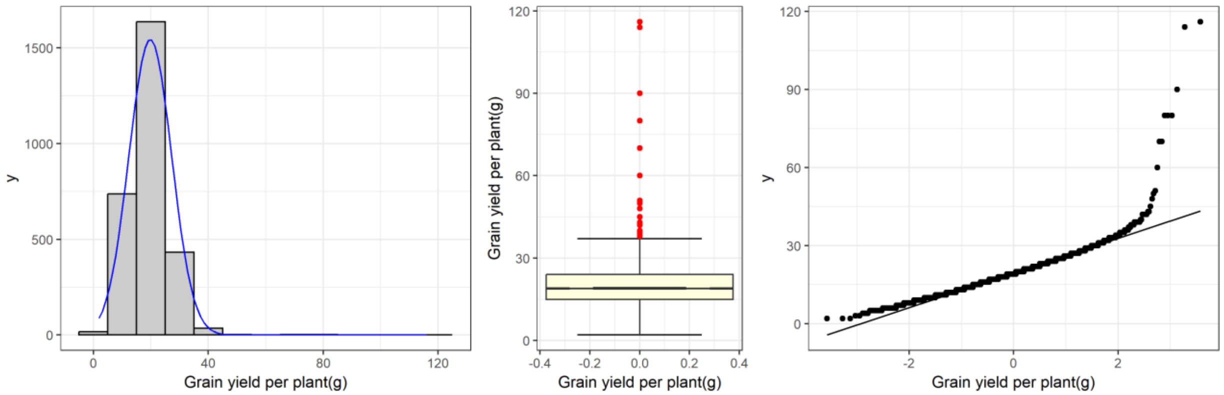
No. of effective tillers

Days to maturity



100 grain weight

Grain L/B ratio



Grain yield per plant

Fig.1. Graphical representation of variability parameters for different quantitative characters.

CONCLUSION

The present study aimed at the assessment of the extent of variability present in the germplasm accessions. The PCV was slightly higher than the GCV for most of the characters, indicating a little bit of influence of environment on the expression of traits. High variability was observed for grain yield per plant and moderate for other traits means ample diversity is present in the germplasm accessions. High heritability coupled with high genetic advance was also observed for flowering, maturity duration and yield traits indicating the selection for these traits will also be passed on to the next generation, hence genotypes are useful for future breeding programmes.

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