



Assessment of Genetic Variability Parameters Among the F₂ Population of a Cross Between Jaya × Isogenic Line of MTU1010 for Yield and its Component Traits in Rice

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Abstract

An experiment was carried out during *Rabi* 2021-22 at the experimental plot of ICAR-Indian Institute of Rice Research, Hyderabad. Two diverse elite indica lines of rice (Jaya and isogenic line of MTU1010) were used to generate the F₂ population to study genetic variability parameters, heritability, and expected genetic advance under selection. Higher GCV, PCV, and heritability coupled with high genetic advance were estimated for the number of productive tillers, panicle weight, number of filled grains, and single plant yield, which indicated that heritability of these traits was under the control of additive gene action. Stringent selection for such traits will be rewarding.

Keywords: Variability, Jaya, MTU1010 (IL), GCV, PCV, Expected genetic advance, Rice

Introduction

Rice (*Oryza sativa* L.) is the most preferable staple cereal crop around the world. More than 90% of the world's rice is produced and consumed in Southeast Asia and tropical Latin America. It accounts for almost 35-60% of the calories consumed by more than 3 billion Asians. India is the largest rice-growing country, while China is the largest producer of rice (Fiyaz *et al.*, 2022). To meet the growing demand of nearly 5.0 billion consumers with an annual average population growth of ~1.5% and estimated per capita consumption of about 250g of rice per day, the demand for rice is expected to increase to 40% by 2030 (Khush, 2005). Yield is one of the important complex traits influenced by environmental, agronomical, and genetic factors. Yield-related traits are mostly governed by several additive loci which always show continuous variation. Basically, for any crop improvement strategy, the availability of genetic

variability is a must criterion. With the available genetic variation, knowing the inheritance pattern and adopting appropriate selection techniques together gives good results in crop improvement (Rani *et al.*, 2016). The higher heritability values generally are the reflection of the closed value of respective phenotypic and genotypic variances and indicate that selection of this character is useful in improving plant type. Heritability by itself does not indicate the amount of genetic progress that would result from selecting the best individuals, rather it depends on the amount of genetic variance. Therefore, genetic advance and genetic advance over mean gain importance in providing an idea of the amount of progress that can be achieved by selection. Among the segregating populations, the F₂ generation is more vital for improving plant types because of its highly variable population structure. Heritability coupled with genetic advance would provide a clear-cut approach to the selection of desirable traits (Shet *et al.*, 2012). Hence,

the present study aims to estimate genetic variability parameters among the diverse cross of Indica rice varieties. Genetic parameters' effectiveness is determined by genetic parameters that include gene action, the number of genes controlling the trait, the magnitude of genetic variability, heritability, and genetic advance (Fisher *et al.*, 1932).

Materials and Methods

The experimental study was carried out in the experimental plots of ICAR-Indian Institute of Rice Research, Rajendranagar, Hyderabad during Rabi 2021-22. Single seedlings per hill were maintained at a spacing of 20 × 15 cm and all cultural practices were followed as per the recommended package of practices. In F₂, a total of 257 plants were selected randomly and observations were recorded on plant height, number of productive tillers per plant, panicle length, panicle weight, number of filled grains per panicle, number of unfilled grains per panicle, 1000 grain weight and single plant yield. The phenotypic and genotypic coefficient of variation was computed by the method reported by Burton and De Vane (1953). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were classified as suggested by Sivasubramanian and Menon (1973) that are, low (<10 %), moderate (10 - 20%) and high (>20 %). The heritability percentage was classified as low (0-30%), moderate (30–60%), and high (>60%) by Robinson *et al.* (1949). The genetic advance was computed by using the formula given by Robinson *et al.* (1949) and the genetic advance over the mean was calculated by the given formulas below.

Phenotypic variance

The individual observation made for each trait on the F₂ population is used for calculating the phenotypic, genotypic, and environmental variance.

$$\text{Phenotypic variance } (\sigma^2p) = \text{Var } F_2$$

Where, Var F₂ = variance of F₂ population

Genotypic variance

$$\text{Genotypic variance } (\sigma^2g) = \sigma^2p - \sigma^2e$$

σ^2p = Phenotypic variance

σ^2e = Environmental variance

Environmental variance

The average variance of parents and their corresponding F₁ is used as the environmental variance for single crosses.

Where,

$$\sigma^2p1 = \text{Variance of parent P1}$$

$$\sigma^2p2 = \text{Variance of parent P2}$$

$$\sigma^2F1 = \text{Variance of cross F1}$$

$$\text{Environmental variance } (\sigma^2e) = \frac{(\sigma^2p1) + (\sigma^2p2) + (\sigma^2F1)}{3}$$

The genetic advance as per cent mean was categorized as low up to 10 per cent, 10 to 20 per cent consider as moderate and more than 20 per cent noticed as high (Johnson *et al.*, 1955).

$$\text{Genetic advance over mean} = \frac{\text{Genetic Advance}}{\text{Mean}} \times 100$$

Broad-sense heritability (h_{2b}) was calculated as

$$h_{2b} = V_G / V_P$$

Where V_G is genetic variance and V_P is phenotypic variance

Results and Discussion

Genetic variability is a prerequisite for any crop improvement program. The pedigree method of selection from F₂ onwards from the cross-between genetically diverse parents has been known to be one of the effective means of generating and maintaining genetic variability. The present study attempted to evaluate genetic variability, heritability, and GAM in the F₂ population derived from the cross of two popular indica rice varieties, Jaya, and an isogenic line of MTU1010. Statistical analysis revealed the presence of a considerable level of genetic variability for all the characters in this study (**Table 1**). Statistically, the range is a difference between the highest and lowest, breeders generally used to know the existing range of variability for interested traits in the working population. Single plant yield recorded the range from 21.06-84.6g, number of filled grains (116-320), number of unfilled grains (1-63), panicle weight (3.56-11.3g), 1000 grain weight (18-27.71g), panicle length (21-32cm), plant height (93.5-107cm) and number of productive tillers (5-30).

**Table 1. Genetic variability parameters in F₂ population of across Jaya × MTU1010 (IL)**

Sl. No.	Traits	Mean	GCV (σ^2g)	PCV(σ^2p)	ECV (σ^2e)	Heritability (h^2)	GA	GAM
1	PH	108.52	5.42	6.04	0.62	80.41	10.87	10.02
2	NPT	15.42	32.76	33.14	0.38	97.7	10.3	66.8
3	PL	25.84	6.68	7.13	0.45	87.84	3.34	12.92
4	PW	5.71	20.2	20.67	0.47	95.51	2.33	40.72
5	TW	22.44	9.92	10.17	0.25	95.22	4.48	19.97
6	NFG	191.97	21.05	21.32	0.27	97.47	82.31	42.87
7	NUFG	16.96	52.28	56.87	4.59	84.52	16.82	99.16
8	SPY	43.09	29.45	29.76	0.31	97.93	25.91	60.11

PH- Plant Height; NPT- Number of Productive Tillers; PL- Panicle Length; PW- Panicle Weight; TW- Thousand Grain Weight; NFG- Number of Filled Grains; NUFG- Number of Unfilled Grains; SPY- Single Plant Yield; GCV- Genotypic coefficient of variation; ECV- Environment coefficient variance; PCV- phenotypic coefficient of variation; GAM- Genetic advance over mean; GA- Genetic advance

Of the 257 F₂ plants, 57 plants recorded higher yield than F₁ (44.4 g/plant), plant number F-103 recorded the highest 84.6 g (90.54% superior over F₁), followed by F-252 recorded 83.98 g (89.14 % more than F₁), F-67 recorded 81.1 g (82.65% more than F₁) and F-114 shown 70.7 g (59.23% greater than F₁). These results confirmed that genetic variation can be created through hybridization between diverse parents. There were many reports available on this aspect, the most related study by Savita and Usha (2015) reported the presence of a wide range for single plant yield (21.46-61.15g) in 200 F₂ population of a cross IR72 × Veeradangan.

The coefficients of variation expressed in percentage at phenotypic and genotypic levels (PCV and GCV) have been used to compare the variability observed among the different characters. The number of productive tillers (33.14), panicle weight (20.67), number of filled grains (21.32), number of unfilled grains (56.87), and single plant yield (29.76) recorded higher PCV (>20%), whereas 1000 grain weight (10.17) recorded moderate PCV (10-20%), but plant height (6.04) and panicle length (7.13) recorded low PCV (<10%). Similarly, for GCV, the number of productive tillers (32.76), panicle weight (20.2), number of filled grains (21.05), number of unfilled grains (52.28), and single plant yield (29.45) recorded higher GCV, whereas plant height (5.42), panicle length (6.68) and 1000 grain weight (9.92) shown

less GCV. In the present investigation, the Phenotypic Coefficient of Variation (PCV) was greater than the Genotypic Coefficient of Variation (GCV) for all traits studied in the F₂ population, representing the magnitude of environmental influence (**Table 1**). The narrow difference between the genotypic coefficient of variation and phenotypic coefficient of variation indicates that characters were less affected by the environment, and the comparison between GCV and PCV is depicted in **Figure 1**.

The number of productive tillers, panicle weight, number of filled grains, number of unfilled grains, and single plant yield recorded higher PCV and GCV which were in accordance with the results of Rani *et al.*, (2016). Plant height and panicle length recorded low PCV and GCV, similar results were earlier reported by Sala *et al.*, (2015) and Rani *et al.*, (2016). Only one character *i.e.*, 1000 grain weight had recorded moderate PCV along with low GCV, and the observed result found similar to that reported by Dhanwani *et al.*, (2013).

Heritability (h^2) is a ratio of genotypic to the phenotypic variance that indicates the effectiveness with which the selection of genotypes can be based on phenotypic performance. Heritability of different traits was classified as high (>60%), moderate (30-60%), and low (<30%) (Robinson *et al.*, 1949). High heritability was reported for all the traits in the present

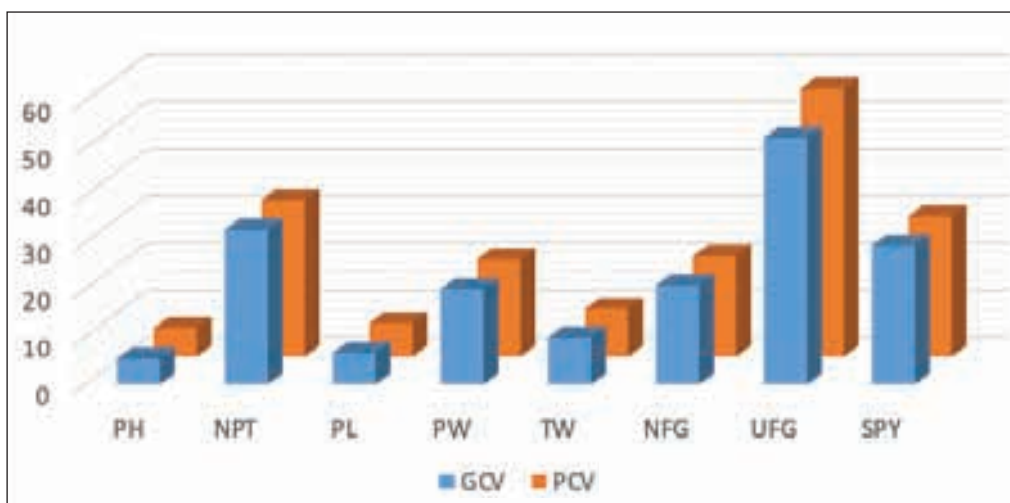


Figure 1: Comparison between PCV and GCV for yield and its component traits

study (Table 1). Similar results were reported by many researchers. The study by Seneega *et al.*, (2019) reported higher heritability for plant height, panicle length, panicle weight, number of productive tillers per plant, number of filled and unfilled grains per panicle, and single plant yield.

Heritability estimates along with genetic advance over mean will be more useful in predicting the outcome of selecting the best individuals. The high GAM (>20 %) was observed for different traits *viz.*, Number of productive tillers (66.8), panicle weight (40.72), number of filled grains (42.87), and single

plant yield (60.11). Similar results were reported for the number of productive tillers per plant, number of filled grains per panicle, single plant yield by Seneega *et al.*, (2019) in F₂ population of the cross CO 52 × CR Dhan 310. Moderate GAM (10-20%) was observed for plant height (10.02), panicle length (12.92), and 1000 grain weight (19.97). Similar results were reported by many researchers, a more relevant study by Shet *et al.*, (2012) reported moderate GAM for plant height and 1000-grain weight. Comparison among heritability, genetic advance, and genetic advance over mean is depicted in Figure 2.

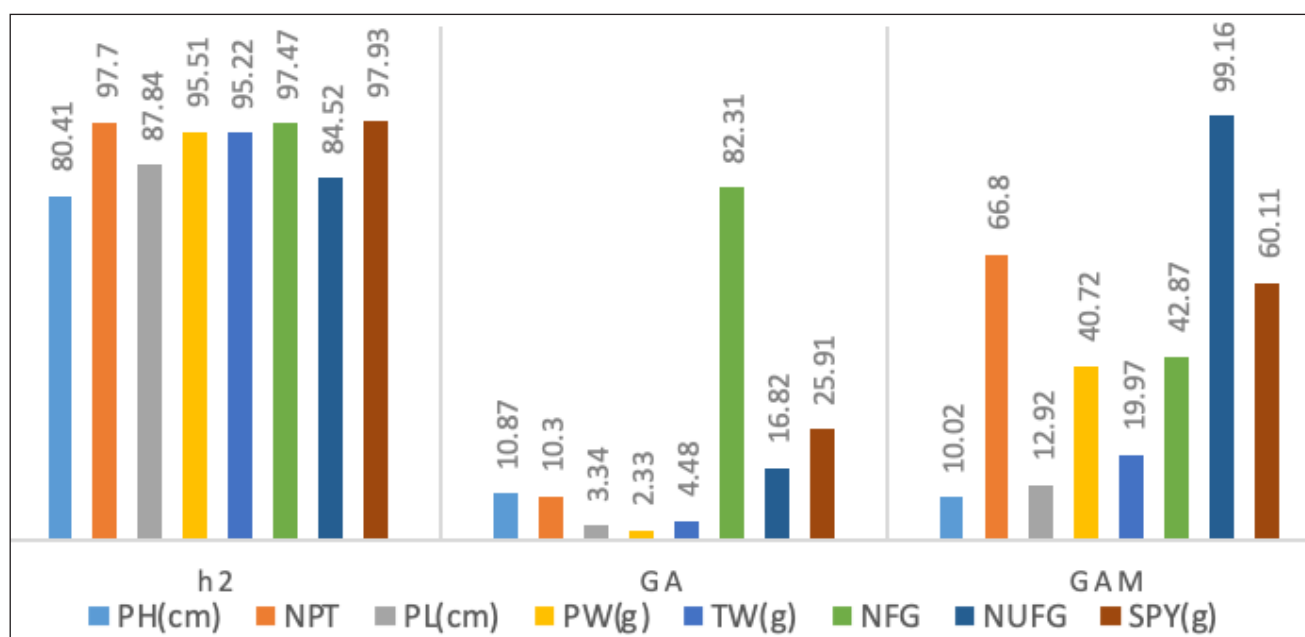


Figure 2: Comparison among heritability (h₂), genetic advance (GA), and GAM for yield and its component traits



Conclusions

High heritability coupled with high genetic advance indicates the presence of additive gene effect and it is inferred that simple selection may be effective for the improvement of these traits. In our study, higher heritability along with a high genetic advance over the mean observed for a number of productive tillers per plant, panicle weight, number of filled grains, and single plant yield. These results indicate high chances of recovery of transgressive segregants for yield and its related characters in the forwarded generations, hence selection for these traits leads to better results for selecting high-yielding lines among the forwarded generation from the cross Jaya × isogenic line of MTU1010.

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Authors' contribution

The study was timely planned and analyzed by DGD, RAF; supervised by KPV, LVS, VPC, KSR, VLA and DGD, KCR, BK, SD, RPVS, and SB helped in the collection and interpretation of data; the manuscript was critically edited by RAF and KPV.

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