Unveiling the Rice hybrid parental lines - A study of genetic variability for yield attributing traits (*Oryza sativa*. L)

Abstract:

Sixty-five rice hybrid lines along with five checks were evaluated in augmented block design (ABD) at ICAR-IIRR Hyderabad, to determine the genetic variability, heritability and genetic advance for ten traits during Kharif 2023. Analysis of variance showed that significant variation was present in the hybrid parental lines studied. The phenotypic coefficient of variation was found to be higher than the genotypic coefficient of variation for all the traits. High GCV (Genotypic Coefficient of Variation) and PCV (Phenotypic Coefficient of Variation) levels were recorded for number of productive tillers (20.12% and 22.28%) and grain yield per plant (21.82% and 23.88%) respectively. Heritability was high for all the traits studied. High heritability coupled with high genetic advance as percent of mean was recorded for majority of the traits suggesting importance should be given to these characters during selection.

Keywords: Rice, genetic variability, heritability, genetic advance as percent of mean

Introduction:

Rice is the most significant grain and staple food for over 100 countries, earning it the title "Global Grain". Despite being the second largest rice producer worldwide, India faces challenges with low productivity. Rice contains 80-90 grams of carbohydrates and 7-8 grams of protein per 100 grams of uncooked grains (Juliano [11], Kennedy, Burlingame, & Nguyen [10]). Rice has 0.3-0.5 grams of fiber (Slavin [16]). The increasing demand for rice, coupled with limited cultivable land and low domestic output, may result in future shortages. By 2025, an estimated 785 million tons of paddy will be required, a 70% increase from current levels, to meet this demand. The FAO (2020) reports that productivity of rice in India is 3.21 t/ha, significantly lower than China (6.35 t/ha) and the global average (4.15 t/ha). This low productivity is mainly due to the lack of high-yielding rice varieties, making it crucial for India to focus on enhancing rice productivity to sustain its population.

The existence of genetic variation is paramount for the efficacy of any agricultural enhancement initiative. A comprehensive understanding of genetic parameters such as variability, heritability, and genetic advance is imperative for the augmentation of crop breeding endeavours. Genetic diversity among traits is indispensable for the identification of favourable genotypes and the establishment of a robust genetic framework for selective breeding practices. Investigations into heritability, genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and genetic advance yield critical insights into the traits being examined. This accumulated knowledge facilitates an understanding of gene action and the identification of the most appropriate breeding methodologies to adopt. In light of these considerations, the current study was undertaken to assess genetic variability within rice hybrid parental lines.

Rice is cultivated on 154 million hectares worldwide, producing 470 million tonnes of milled rice, with over 90% of both production and consumption occurring in Asia (Sarwar [21]). According to (James [20]) global demand for rice is projected to increase from 490 million tonnes in 2020 to 555 million tonnes by 2035. To face the upcoming challenge, hybrids are need to be developed. However, hybrid lines play a vital role in modern agriculture by harnessing hybrid vigor (heterosis) to achieve higher yields, i.e., 15-20% increase in yield when compared with pure lines (Soujanya [22]).

Materials and methods:

The present study was conducted at ICAR- Indian Institute of Rice Research, Rajendranagar, Hyderabad during *Kharif*, 2023. Experiment was comprised of 65 hybrid parental lines and five checks (ISM, Tetep, CO 101A 51, BPT 5204 and TN-1) evaluated in Augmented block design. The experimental field was divided into five blocks. Recommended agronomic practices were followed during crop growth period. The parental lines were evaluated for the following traits: Days to 50 % flowering, plant height, panicle length, number of productive tillers, filled grains, 1000 seed weight, kernel length, kernel breadth, kernel length/ breadth and grain yield per plant.

The analysis of variance for the design of the experiment was carried out according to the procedure outlined by Panse and Sukhatme [13], Ferderer [5]. “The phenotypic and genotypic coefficients of variation were estimated” according to the method suggested by Burton and de Vane [3]. “Broad sense heritability (h^2) expressed as the percentage of the ratio of the genotypic variance ($\sigma^2 g$) to the phenotypic variance ($\sigma^2 p$) and was estimated on genotype mean basis” as described by Allard [2] and “Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes was estimated in accordance with the methods” illustrated by Johnson *et al*. [9]

Results and Discussions:

Analysis of variance:

In the current study, the examination of variance concerning yield and its associated attributes indicated that significant discrepancies existed among the parental lines. The outcomes of the variance analysis for the augmented block design pertaining to all ten attributes are displayed in Table 1. The variability observed in the blocks was statistically significant for the traits assessed *viz*., days to 50% flowering, plant height, filled grains, 1000 seed weight, grain yield per plant. The difference among the checks was found to be highly significant for all the traits under study.

Mean performance:

A wider range of mean variability was observed for the traits *viz*., filled grains (78-242), plant height (69.05 cm -145.0 cm), days to 50% flowering (82-114), number of productive tillers (4-17) and 1000 seed weight (10.13 gm -24.15 gm). The results showed that these traits should be used as selection prospects to improve performance through a breeding procedure like selection and hybridization.

Genetic variability:

The degree of variability for any specific trait holds significant relevance for the enhancement of a population through selective breeding (Reddy [23]). The estimations of genotypic variation, phenotypic variation, heritability, genetic gain, genotypic coefficient of variation (GCV), and phenotypic coefficient of variation (PCV) across various traits are delineated in Table 2. The extent of environmental influence on any trait signifies the magnitude of the disparity between the genotypic and phenotypic coefficients of variation. A substantial difference denotes a greater environmental impact, while a minimal difference indicates a predominance of genetic influence. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) in all the studied characters which indicates the presence of environmental influence on the phenotypic expression of the character to some degree.

The difference between PCV and GCV was less for the characters, days to 50% flowering, panicle length, plant height, thousand seed weight. Phenotypic coefficient of variation ranged from 5.87% (days to 50% flowering) to 21.82% (Grain yield / plant), while GCV ranges from 6.28% (days to 50% flowering) to 23.88% (Grain yield /plant). (Fig.1)

Table 1. Analysis of variance for yield components in sixty-five hybrid parental lines of rice

S.No	Traits	Block (df = 4)	Treatments (df = 64)	Treatment: Check (df = 4)	Treatment: Test vs. Check (df = 1)	Residuals (df = 16)
1	**DFF**	159.57 **	81.84 **	940.66 **	48.74 **	4.83
2	**PH**	312.51 **	347.91 **	4097.44 **	8.14 ns	18.14
3	**PL**	3.48 ns	12.33 **	39.45 **	123.65 **	2.09
4	**NPTS**	10.91 ns	6.81 ns	51.14 **	5.97 ns	5.14
5	**FG**	2018.28 **	1432.94 **	8236.26 **	25756.52 **	139.06
6	**TSW**	14.16 **	7.18 **	22.31 **	2.07 ns	1.23
7	**KL**	0.03 ns	0.20 **	2.68 **	2.48 **	0.05
8	**KB**	0.02 ns	0.06 ns	0.41 **	1.75 **	0.03
9	**L*B**	0.05 ns	0.05 **	0.48 **	0.83 **	0.02
10	**GYP**	22.15 **	31.53 **	99.34 **	246.40 **	4.14

^{ns} P > 0.05; * P <= 0.05; ** P <= 0.01

DFF- days to 50% flowering, PH- Plant height, PL- panicle length, NPTS- number of productive tillers, FG- filled grains, TSW- 1000 seed weight, KL- kernel length, KB- kernel breadth, L*B-kernel length/breadth, GYP-grain yield per plant

Table 2. Genetic parameters for yield components in sixty-five hybrid parental lines of rice

Trait	Mean	GCV (%)	PCV (%)	h^2 (%)	GAM (%) at 5%
DFF	98.79	5.87	6.28	87.43	11.32
PH	96.75	11.25	12.08	86.72	21.61
PL	23.41	11.22	12.8	76.72	20.27
NPTS	9.51	20.12	22.28	74.67	44.32
FG	163.75	14.85	16.5	80.96	27.57
TSW	16.01	15.19	16.69	82.74	28.49
KL	5.46	8.22	10.32	79.20	19.27
KB	2.29	9.16	11.56	86.32	22.51
L*B	2.4	14.28	16.62	89.68	28.30
GYP	20.93	21.82	23.88	83.43	41.11

(DFF- Days to 50% flowering; PH- Plant Height; PL- Plant Length; NPT- Number of productive tillers; FG- Filled grains; TSW- Thousand Seed Weight; KL- Kernal length; KB- Kernal breadth; L*B- Kernal length /breadth ratio; GYP- Grain yield per plant.)

High GCV and PCV values were recorded for grain yield per plant (21.82% and 23.88 %) and number of productive tillers (20.12% and 22.28%). Similar results were reported by Hemalatha et al. [8], Gayathridevi et al. [6], Pradhan et al. [14], Gupta et al. [7], Yashwanth et al. [19] for grain yield per plant.

Moderate GCV and PCV values were recorded for plant height (11.25 and 12.08), panicle length (11.22% and 12.80%), filled grains (14.85% and 16.50%), 1000 seed weight (15.19% and 16.69%), kernel length / breadth (14.28% and 16.62%). This suggests moderate variability for these traits, which can be exploited for improvement through selection in advanced generations.

Low PCV and GCV values recorded for days to 50% flowering (5.87% and 6.28%). Vanaja and Babu et al. [18], Uma Devi et al. [17], Mythili et al. [12], Rashid et al. [15] observed low values for days to 50% flowering. Low GCV values were noticed for kernel length (8.22%) and kernel breadth (9.16) while PCV values are moderate (10.32% and 11.56%). Lower GCV and PCV suggest a narrow genetic base for these traits. Enhancing these traits may require hybridization or induced mutagenesis to broaden the genetic base, followed by pedigree selection in later generation

Heritability:

Broad-sense heritability is valuable for selecting elite genotypes from homozygous lines, while narrow-sense heritability is more useful for segregating populations. Broad-sense heritability estimates for different traits ranged from 74.67% (number of productive tillers) to 89.68% (kernel length / breadth).

Heritability estimates were high for traits such as days to 50% flowering (87.43), plant height (86.72%), panicle length (76.72%), number of productive tillers (74.67%), filled grains (80.96%), 1000 seed weight (82.74%), kernel length (79.20%), kernel breadth (86.32%), kernel length/breadth (89.68%), grain yield per plant (83.43%). (Fig. 2)

Genetic advance:

Genetic advance as percent of mean was high for plant height (21.61%), panicle length (20.27%), number of productive tillers (44.32%), filled grains (27.57%), 1000 seed weight (28.49%), kernel breadth (22.51%), kernel length / breadth (28.30%), grain yield per plant (41.11%) and moderate for days to 50 % flowering (11.32%) and kernel length (19.27%).

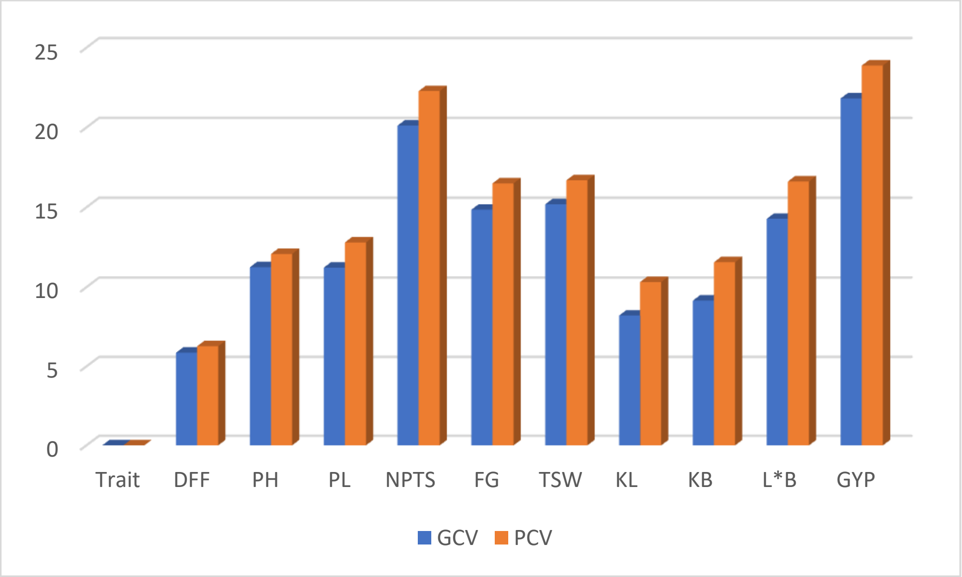

Fig 1. Genotypic and phenotypic coefficients of variation for yield components in rice hybrid parental lines

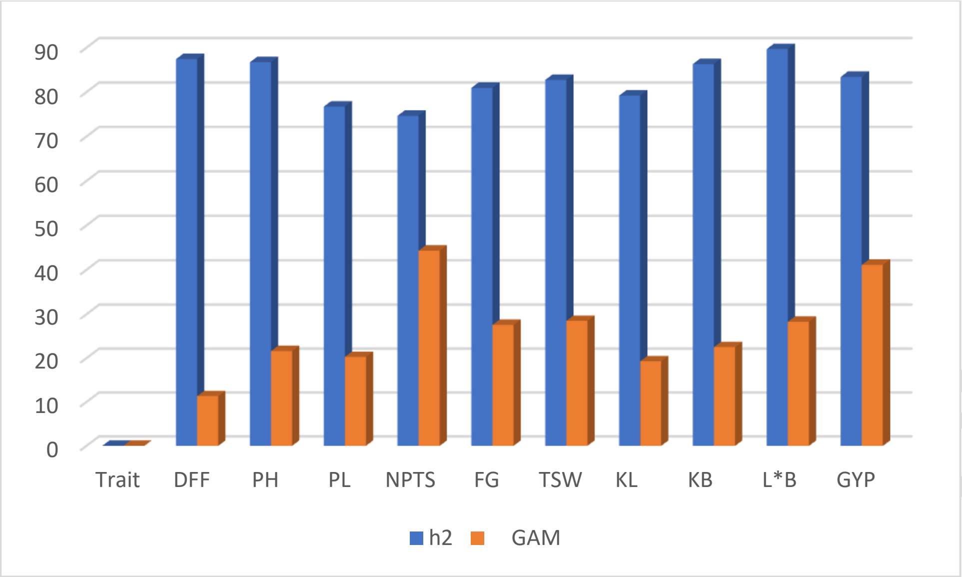

Fig 2. Heritability and genetic advance as per cent of mean for yield components in rice hybrid parental lines

High genetic advance coupled with high heritability was recorded for plant height, panicle length, number of productive tillers, filled grains, 1000 seed weight, kernel breadth, kernel length/ breadth and grain yield per plant. Similar results for plant height were reported by Akinwale et al. [1], Gayathridevi et al. [6], Pradhan et al. [14] for grain yield per plant. Demeke et al. [4] reported similar results for plant height, number of productive tillers, filled grains, 1000 seed weight and grain yield per plant. Generally, traits with high heritability and high genetic advance are controlled by additive gene action and can be improved through simple or progeny selection methods.

High heritability coupled with moderate genetic advance was recorded for days to 50% flowering and kernel length. High heritability with moderate or low genetic advance can be improved by intermating superior genotypes of segregating populations developed from combination breeding.

Conclusion:

Selecting superior genotypes is more likely when there is greater genetic variety. We can gauge the level of diversity in these traits within a genetic population by looking at high estimates of the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) on the number of productive tillers and grain yield per plant. Compared to heritability estimates alone, additive gene action predicted genetic gain under selection, as evidenced by high heritability and high genetic advancement as a percentage of mean for all parameters except days to 50% flowering and kernel length. Therefore, in order to create rice hybrid lines with increased grain production, plant breeding activities should concentrate on modifying the current genetic diversity in the desired direction through suitable crop improvement initiatives.

Disclaimer (Artificial intelligence)

Option 1:

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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