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**M Madhuri**
(1) Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India
(2) ICAR- Indian Institute of Rice Research, Rajendranagar, Hyderabad, Telangana, India

**Nandan Mehta**
Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

**R Abdul Fiyaz**
ICAR- Indian Institute of Rice Research, Rajendranagar, Hyderabad, Telangana, India

**LV Subba Rao**
ICAR- Indian Institute of Rice Research, Rajendranagar, Hyderabad, Telangana, India

**N Himaja**
ICAR- Indian Institute of Rice Research, Rajendranagar, Hyderabad, Telangana, India

**K Chaitanya**
ICAR- Indian Institute of Rice Research, Rajendranagar, Hyderabad, Telangana, India

**M Bharath**
ICAR- Indian Institute of Rice Research, Rajendranagar, Hyderabad, Telangana, India

**GD Dileep Kumar**
ICAR- Indian Institute of Rice Research, Rajendranagar, Hyderabad, Telangana, India

**Akshat Joshi**
ICAR- Indian Institute of Rice Research, Rajendranagar, Hyderabad, Telangana, India

**Corresponding Author:**
**R Abdul Fiyaz**
ICAR- Indian Institute of Rice Research, Rajendranagar, Hyderabad, Telangana, India

# Studies on PCV, GCV, heritability, and genetic advance for yield related traits in rice germplasm lines (*Oryza sativa* L.)

**M Madhuri, Nandan Mehta, R Abdul Fiyaz, LV Subba Rao, N Himaja, K Chaitanya, M Bharath, GD Dileep kumar and Akshat Joshi**

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## Abstract

The goal of the current study was to assess the genetic diversity of twenty-one rice germplasm lines throughout the course of two seasons, Rabi 2023 and Kharif 2021, using a Randomized Block Design with three replications. Eleven quantitative traits were noted in order to investigate genetic advance, PCV, heritability, and GCV. All eleven variables have extremely significant differences according to the analysis of variance (ANOVA), suggesting that there is genetic heterogeneity among the germplasm lines under evaluation. For every trait under investigation, the estimations of PCV were somewhat more than GCV, indicating a reduced impact of the environment on the trait expression. Therefore, by direct selection, the evaluated characters might gain from genetic enhancement. Both seasons showed high values for the phenotypic and genotypic coefficient of variation for the number of productive tillers, filled and unfilled grains, and panicle weight; however, for the number of tillers, the PCV was high and the GCV was moderate. Conversely, there were only small coefficients of variation for plant height, panicle length, spikelet fertility, and yield from a single plant. Days to fifty percent showed low coefficients of variance in combination with moderate phenotypic and genotypic coefficients of variation in spikelet fertility in Kharif 2021, compared to higher variation in Rabi 2023. With the exception of days to 50% blooming with moderate genetic advancement, all traits showed high heritability as well as high genetic advancement in both seasons.

**Keywords:** Genetic advance, coefficient of variation, germplasm, heritability

## Introduction

The staple diet of more than half of the world's population is rice (*Oryza sativa* L.). It is imperative to enhance rice cultivars in order to feed the growing global population. Continuous efforts are made to increase rice production and yield-related factors in order to satisfy the rising demand for grains and ensure food security. Genetic study determines rice genotypes' intrinsic potential, the heritability of traits, and the potential for genetic development (Demeke *et al.*, 2023) [2]. It is crucial to comprehend the genetic diversity that a crop possesses before initiating any kind of crop development effort (Demeke *et al.*, 2023) [2]. An understanding of the existing genetic variability in a crop is very essential for beginning a crop improvement programme. A plant breeder can identify traits for effective selection by using information on heritability, genetic advancement, and associations of traits. Determining the degree of heritability aids in distinguishing between genetic and environmental variables contributing to individual differences. The extent to which a trait benefits from phenotypic selection is determined by genetic progress or the organism's reaction to selection. The degree of gain derived from phenotypic selection for a character is explained by genetic advancement or responsiveness to selection. Genetic advance and heritability estimates combined are more accurate and useful than evaluating them individually. With a focus on the effects of these factors on "yield and yield-related traits, the present investigation reviews the literature on heritability, genetic advance, PCV (Phenotypic Coefficient Of Variation), GCV (Genotypic Coefficient Of Variation), and genetic advance in rice germplasm lines.

## Materials and Methods

At the ICAR-Indian Institute of Rice Research (ICAR-IIRR) Farm in Rajendranagar, Hyderabad, twenty-one rice germplasm lines had been assessed for yield-related attributes in the Kharif 2021 and Rabi 2023 seasons employing a Randomized Block Design" with 3 replications. Twenty-centimeter row spacing and fifteen-centimeter plant spacing were used while transplanting seedlings that were 25 days old. All suggested and accepted methods for the primary crop and crop nursery were followed throughout the study. For every genotype in each replication, three representative plants were chosen at random, and measurements were made of the following: "plant height (cm), panicle length (cm), number of tillers (cm), productive tillers (n), panicle weight (g), number of filled grains (n), number of unfilled grains" (n), spikelet fertility (%), single plant yield (g), and test weight (g). Plot-based evaluation of the days to 50% flowering was done, and statistical analysis was applied to the data.

## Statistical Analysis

The ANOVA procedure recommended by Panse and Sukhatme (1967) [16] was used to assess the variability. The Burton formulas were used to calculate the genotypic and phenotypic variances. Heritability levels were classified by (Robinson *et al.*, 1949) as low (between 0 and 30%), moderate (between 30 and 60%), and high (above 60%). R 4.4.1 software was used to do a statistical analysis on the mean of three plants for each trait. ANOVA revealed very significant differences between the twenty-one germplasm lines for each of the 11 characteristics that were looked at in both the kharif and rabi seasons. This indicates that there is enough genetic variability among the genotypes that are being considered.

## Results and Discussion

The existence of genetic variability is crucial in any germplasm line to be utilized in the breeding programme. ANOVA demonstrated that there is greater genetic variability across the assessed genotypes, with substantial variations found between the twenty-one germplasm lines for each of the eleven variables examined in both the kharif and rabi seasons. Table 1. For each of the 11 variables, Table 2 shows an examination of the estimated coefficients of variation (both genotypic as well as phenotypic), broad sense heritability (h2), as well as genetic progress at 5% of the mean. Figures 1 and 2 provide the variability parameters in a graphical format. The PCV was marginally higher than the GCV for every trait, suggesting that environmental factors had less of an effect on these characteristics. Because the characters are not significantly impacted by their environment, these features can therefore be used for direct selection. In both the rabi and kharif seasons, GCV & PCV were low for characteristics such as plant height, spikelet fertility, and single plant yield. But in the kharif season, they were high for features like test weight, panicle weight, filled and unfilled grains, and the number of productive tillers. In kharif 2021, the number of tillers and panicle length demonstrated a high PCV whereas the GCV was low and moderate, respectively. With the exception of modest coefficients of variation for test weight and panicle length and larger amounts of variation for spikelet fertility during Rabi 2023, the results were identical. The only characteristic that showed low GCV and PCV in both seasons was days to 50% flowering and the findings were similar to those (Sumanth *et al.*, 2017) [17]. Graphical representations of GCV and PCV values in Kharif 2021 and Rabi 2023 were mentioned in Figure 1 and Figure 2. Similar observations were made for the above seven characters "by Chaudhary *et al.*, 2004 [5]; Babar *et al.*, 2009 [4]; Anjaneyulu *et al.*, 2010 [1]; Jayasudha and Sharma, 2010 [6]; Karthikeyan *et al.*, 2010 [7]; Akhtar *et al.*, 2011 [8]; Garg *et al.*, 2011 [9]; Pandey, 2012 [10]; Basavaraja *et al.*, 2013 [3]; Sathya and Jebaraj 2013 [12]; Warkad *et al.*, 2013) [13]. The number of productive tillers, panicle length, test weight, plant height, panicle" length, spikelet fertility, and test weight were observed to be similar to the reports of Chacko *et al.* (2023) [14]. Every attribute had a considerable genetic advance at 5% "mean, along with high heritability, except for the character days to fifty percent of the bloom which showed a moderate genetic advance.

**Table 1:** Analysis of variance for yield-related traits in rice germplasm lines

| S. No. | Traits | Mean squares (Kharif 2021) | | | Mean squares (Rabi 2023) | | |
|---|---|---|---|---|---|---|---|
| | | Replication (df= 2) | Treatment (df=20) | Error (df=40) | Replication (df= 2) | Treatment (df=20) | Error (df=40) |
| 1 | DFF | 5.78 | 184.34*** | 1.328 | 1.19 | 81.45*** | 1.257 |
| 2 | PH | 7.53 | 1014.56*** | 7.00 | 6.81 | 753.28*** | 6.37 |
| 3 | PL | 1.0076 | 16.9081*** | 0.278 | 0.014 | 18.29*** | 0.1950 |
| 4 | NT | 2.6825 | 10.6540*** | 1.1325 | 0.21 | 6.10*** | 0.7563 |
| 5 | NPT | 2.4 | 7.6200*** | 0.8135 | 0.587 | 7.80*** | 0.6540 |
| 6 | NFG | 0.8 | 6198.1*** | 2.5 | 4.8 | 6289.1*** | 4.0 |
| 7 | NUFG | 1.19 | 1266.17*** | 1.54 | 0.30 | 1465.21*** | 1.57 |
| 8 | SF | 3.70 | 436.010*** | 0.85 | 2.57 | 2013.84*** | 2.63 |
| 9 | PW | 0.038 | 2.5710*** | 0.00369 | 0.042 | 2.590*** | 0.0181 |
| 10 | SPY | 0.789 | 28.9537*** | 0.3910 | 0.034 | 30.97*** | 0.3901 |
| 11 | TW | 0.046 | 59.62*** | 0.017 | 0.043 | 57.49*** | 0.136 |

* Significance at 1% level DFF- Days to 50 percent" "Flowering; Panicle Length; NT-Number of Tillers; NUFG- Number of Unfilled Grains; NPT- Number of Productive Tillers; PW- Panicle Weight; SF- Spikelet Fertility; PH- Plant Height; SPY- Single Plant Yield; NFG-Number of Filled" Grains; TW- Test weight

**Table 2:** Estimation “of components of variance and genetic parameters for 11 characters in rice germplasm lines

| S.No | Traits | Kharif 2021 | | | | Rabi 2023 | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | **GCV** | **PCV** | **h2 (bs) (%)** | **GA as % of mean** | **GCV** | **PCV** | **h2 (bs) (%)** | **GA as % of mean** |
| 1 | DFF | 7.69 | 7.77 | 97.87 | 15.67 | 5.42 | 5.54 | 95.51 | 10.9 |
| 2 | PH | 17.4 | 17.58 | 97.96 | 35.47 | 15.11 | 15.3 | 97.5 | 30.74 |
| 3 | PL | 9.95 | 10.2 | 95.23 | 20.00 | 10.77 | 10.94 | 96.87 | 21.83 |
| 4 | NT | 18.77 | 21.86 | 73.70 | 33.19 | 18.75 | 22.34 | 70.18 | 30.16 |
| 5 | NPT | 20.06 | 23.38 | 73.61 | 35.46 | 24.06 | 27.17 | 78.45 | 43.9 |
| 6 | NFG | 38.65 | 38.68 | 99.88 | 79.58 | 41.38 | 41.42 | 99.81 | 85.17 |
| 7 | NUFG | 64.35 | 64.47 | 99.64 | 132.32 | 53.3 | 53.38 | 99.68 | 109.61 |
| 8 | SF | 15.24 | 15.28 | 99.42 | 31.30 | 36.87 | 36.94 | 99.61 | 75.81 |
| 9 | PW | 34.24 | 34.32 | 99.57 | 70.38 | 36.48 | 36.87 | 97.92 | 74.37 |
| 10 | SPY | 16.33 | 16.66 | 96.06 | 32.97 | 16.77 | 17.1 | 96.31 | 33.91 |
| 11 | TW | 20.29 | 20.3 | 99.91 | 41.78 | 19.92 | 19.99 | 99.29 | 40.89 |

DFF- Days to 50 percent” Flowering; NT- “Number of Tillers; NPT- Number of Productive Tillers; PW- Panicle Weight; Panicle Length; NFG- Number of Filled Grains; PH- Plant” Height; SF- Spikelet Fertility; NUFG- Number of Unfilled Grains; SPY- Single Plant Yield; TW- Test weight

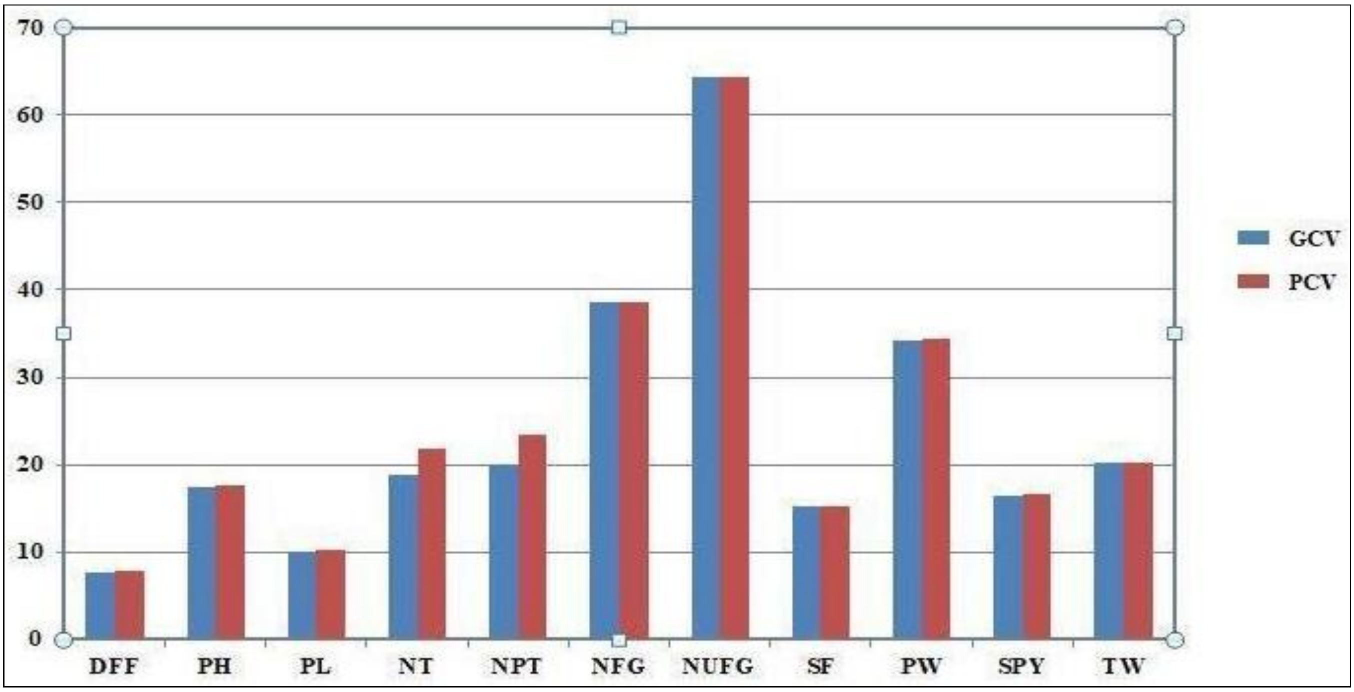

**Fig 1:** Graphical representation of PCV and GCV in Kharif 2021 season

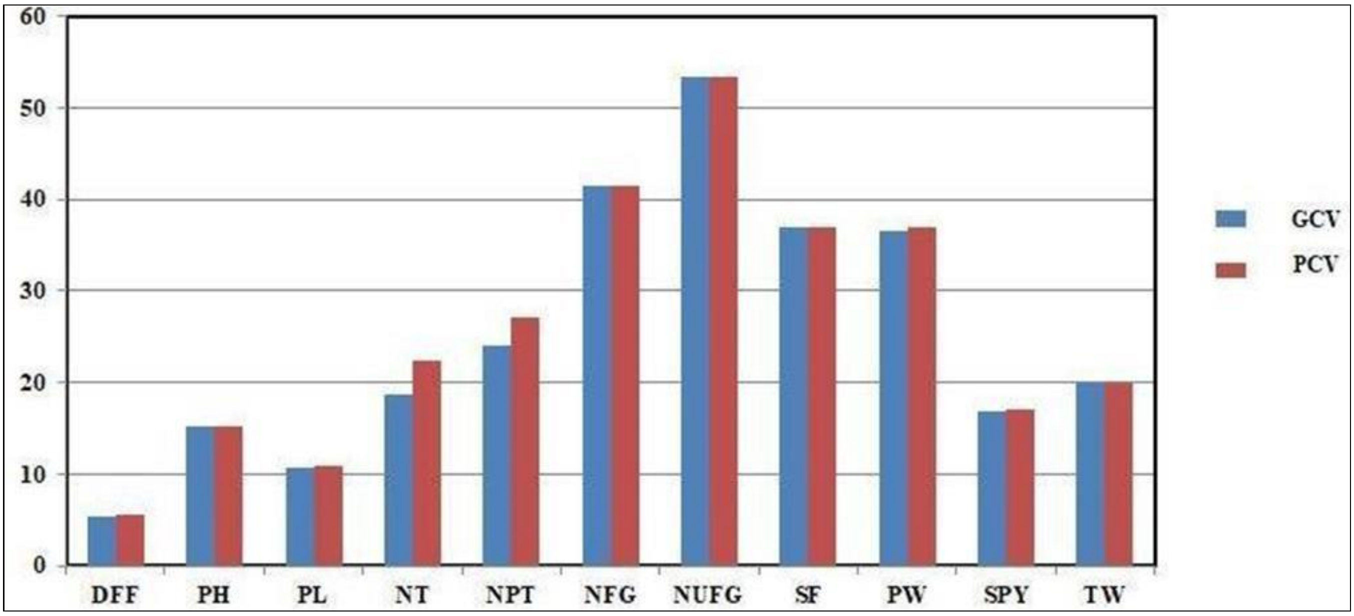

**Fig 2:** Graphical representation of PCV and GCV in the Rabi 2023 season

## Conclusion

The goal of the present investigation, which used 21 rice genotypes, was to analyze the kind and degree of variability, heritability (in the broadest sense), and genetic advancement for 11 quantitative variables. A significant difference was found for ever y characteristic examined in the analysis of variance across the 23 genotypes. It was revealed that additive gene action dominated the yield-related variables and that simple selection might be able to improve them. As a fraction of the mean, all attributes exhibited strong heritability and high to moderate genetic advancement. The majority of the traits had moderate to high GCV & PCV, indicating that direct selection could readily enhance the trait and that additive gene action was the "cause of the diversity in the rice germplasm lines.

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