



ISSN (E): 2277-7695

ISSN (P): 2349-8242

NAAS Rating: 5.23

TPI 2023; 12(6): 2726-2728

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Received: 05-03-2023

Accepted: 15-04-2023

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## Exploring the role of genetic variability in Rice yield stability and production efficiency

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### Abstract

The research on genetic variability studies for yield and its component traits in Rice (*Oryza sativa* L.) is carried out using 45 accessions at field experimentation centre, department of Genetics and Plant Breeding, Lovely Professional University, during *Kharif* 2022. The analysis of variance found significant differences in all variables for all genotypes available. The study finds PCV is higher than GCV. High PCV and GCV recorded for number of unfilled grains and harvest index. High Heritability observed for all the characters. High genetic advance as mean recorded for number of spikelets per panicle and number of filled grains per panicle.

**Keywords:** *Oryza sativa* L., Heritability, PCV and GCV

### Introduction

Rice (*Oryza sativa* L.), belonging to the family of Gramineae (Poaceae) is a self-pollinating and diploid species (AA) composed of 12 chromosomes ( $2n=24$ ). Rice is the most important staple food for 1/3rd of the world's population, and almost 90% of the world's rice supply is produced in Asia. Rice cultivation in Asia constitutes approximately 90% of the overall output (Faysal *et al.*, 2022) [7]. China (28%), India (23.7%) and Indonesia (7.2%) are the 3rd largest rice producing countries worldwide, as reported by the data from 2019 (Fentie *et al.*, 2021) [8]. Nearly 3.4 crore tons of rice are harvested from about 11 million hectares of land (Rabbany *et al.*, 2022; Faysal *et al.*, 2022) [15, 7]. Rice includes a wide array of nutrient-dense compounds, including carbohydrates, fats, and protein, in addition to a sufficient amount of calcium and riboflavin in a moderate proportion (Juliano and Villareal 1993; Maurya *et al.*, 2022) [11, 14]. The ample amount of genetic variability should be present in genotypes or entries for successful breeding. So, variation should be present in genotypes for yield and yield attributing traits is the primary aspect that should be taken into consideration throughout the selection process (Fentie *et al.*, 2021) [8]. Heritability quantifies the proportion of phenotypic variation in a trait that is due to genetic differences, while genetic advance represents the increase in average trait values achieved through selective breeding. Heritability in combination with genetic advance will be more precise in estimating genetic gain under selection (Demeke *et al.*, 2023) [6].

### Materials and Methods

The experimental study was conducted at the Field Experimentation Centre of the Department of Genetics and Plant Breeding, Lovely Professional University, located in Phagwara, Punjab.

### Plant Material and experimental design

The experiment involved a total of 45 rice genotypes. Among these, 5 genotypes were check varieties. In this experiment most of the genotypes are Landraces. The experiment was augmented (incomplete block design). On June 21, nursery bed was prepared, and seedlings were transplanted by July 16 to main field.

### Observations recorded

Days to 50% flowering, days to maturity, plant height, panicle length, number of effective tillers per plant, number of spikelets per panicle, number of filled grains per panicle, number of unfilled grains per panicle, test weight, biological yield, harvest index and grain yield per plant.

## Statistical Analysis

Mean values were computed and data were analysed for analysis of variance as suggested Fisher (1938) <sup>[9]</sup> given in table 1. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were given by

Burton (1952) <sup>[4]</sup>. Heritability in broad sense was given by Lush (1949) <sup>[13]</sup> and Burton and Devane (1953) <sup>[3]</sup>. Genetic advance was given by Lush (1949) <sup>[13]</sup> and Johnson *et al.*, (1955) <sup>[10]</sup>.

**Table 1:** Assessment of various genetic parameters for yield and yield contributing traits in rice germplasm

Characters	General mean	Range		Coefficient of variation		Heritability (%)	Genetic advance (5%)
		Mini.	Max.	Genotypic	Phenotypic		
DFE	101.51	73.00	121.98	10.90	10.91	99.90	22.77
DM	137.60	106.00	155.84	7.53	7.54	99.70	21.32
PH	123.13	75.92	158.73	18.49	18.50	99.90	46.87
PL	25.92	19.54	34.55	11.66	11.69	99.40	6.21
NETP	10.52	7.06	13.38	15.55	15.61	89.40	3.36
NSP	191.22	145.09	256.87	14.92	14.94	99.70	58.69
NFGP	161.93	118.36	214.20	15.17	15.19	99.70	50.52
NUGP	29.67	15.88	58.00	32.55	32.56	86.90	19.89
TSW	18.93	11.41	27.50	21.10	21.12	99.80	8.22
BY	111.67	75.04	131.69	12.51	12.53	99.80	28.76
HI	22.71	12.94	38.90	26.82	27.04	98.30	12.44
GYP	24.66	16.26	34.79	17.79	17.97	98.00	8.95

DFE Days to 50% flowering, DM days to maturity, PH plant height, PL panicle length, NETP number of effective tillers per plant, NSP number of spikelets per panicle, NFGP number of filled grains per panicle, NUGP number of unfilled grains per panicle, TSW test weight, BY biological yield, HI harvest index and GYP grain yield per plant.

## Results and Discussion

The analysis of variance (ANOVA) conducted in study revealed that mean sum of squares attributed to genotypes was significant for all the characters under investigation. Similar results were observed by Abebe *et al.*, (2017) <sup>[1]</sup>.

### Mean performance

The mean performance for 12 characters are days to 50% flowering (101.51), days to maturity (137.60), plant height (123.13 cm), panicle length (25.92), number of effective tillers per plant (10.52), number of spikelets per panicle (191.22), number of filled grains per panicle (161.93), number of unfilled grains per panicle (29.67), test weight (18.93 gm), biological yield (111.67 gm), harvest index (22.71) and grain yield per plant (24.66 gm). Similar results were recorded for days to 50% flowering and test weight by Akshay *et al.*, (2022) <sup>[2]</sup>.

### PCV and GCV

The phenotypic coefficient of variation (PCV) was higher in magnitude compared to the genotypic coefficient of variation (GCV) for all the traits studied suggests that the observed variation is not solely attributable to genetic factors. It indicates that external environmental factors also have a significant influence on the expression of these traits. Maurya *et al.*, (2022) <sup>[14]</sup> and Akshay *et al.*, (2022) <sup>[2]</sup>.

This study found high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values for the number of unfilled grains (32.55, 32.56), harvest index (26.82, 27.04) and test weight (21.10, 21.12). Similar results recorded for test weight by Akshay *et al.*, (2022) <sup>[2]</sup>. Moderate GCV and PCV were recorded traits such as plant height (18.49, 18.50), grain yield per plant (17.79, 17.97), number of filled grains (15.17, 15.19), number of effective tillers per plant (15.55, 15.61), number of spikelets per panicle (14.92,

14.94), biological yield (12.51, 12.53), panicle length (11.66, 11.69) and days to flowering (10.90, 10.91). Similar findings recorded for plant height, number of effective tillers, panicle length, and grain yield per plant by Akshay *et al.*, (2022) <sup>[2]</sup>. Low GCV and PCV recorded for days to maturity (7.53, 7.54).

**Heritability:** Heritability evaluates additive gene-induced phenotypic variation. Heritability recorded range from 86.90 to 99.90. High heritability was recorded for days to flowering (99.90), plant height (99.90), test weight (99.80), biological yield (99.80), number of spikelets per panicle (99.70), grain yield per plant (98.00), panicle length (99.40), harvest index (98.30), number of filled grains (99.70), days to maturity (99.70), number of effective tillers per plant (89.40), and number of unfilled grains (86.90), similar results were recorded for plant height, number of spikelets per panicle, test weight, and days to maturity by Keerthiraj & Biju (2020) <sup>[12]</sup>. None of the results revealed moderate and low heritability, similar findings by Akash *et al.*, (2022), which says that these traits were least affected by environment specifies the phenotypic expression depends on the genotypic ability of the cultivars to carry on genes to the next generation.

### Genetic Advance

The genetic advance as a percentage of the mean ranges from 3.36 – 58.69. Highest genetic advance recorded for number of spikelets per panicle (58.69), number of filled grains per panicle (50.52), plant height (46.87), biological yield (28.76), days to 50% flowering (22.77), and days to maturity (21.32), similar outcomes recorded for plant height, number of spikelets per panicle by Singh and Verma (2018) <sup>[17]</sup>, days to 50% flowering by Deepthi *et al.*, (2022). Moderate genetic advance recorded for number of unfilled grains per panicle (19.89), and harvest Index (12.44), similar results recorded for harvest index by (Sravani *et al.*, 2022) <sup>[16]</sup>, (Thakur *et al.*, 2023) <sup>[18]</sup>, and (Thuy *et al.*, 2023). Low genetic advance percentage recorded for grain yield per plant (8.95), test weight (8.22), panicle length (6.21), and number of effective tillers per plant (3.36), similar findings recorded for number of effective tillers per plant by Maurya *et al.*, (2022) <sup>[14]</sup>, panicle length by Venkanna *et al.*, (2022) <sup>[20]</sup>.

## Conclusion

In a nutshell, the studied landraces of rice have the ability to include some important and valuable traits. Estimations of genetic parameters high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values for the number of unfilled grains, heritability days to flowering, genetic advance high number of spikelet's per panicle.

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