***Original Research Article***

**Genetic Parameters of Variability and Selection Potential for Yield and Quality Traits in Rice** **under North Western Himalayan Conditions**

ABSTRACT

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| The existence of wide morpho-genetic variability acts as a prerequisite for any crop improvement programme. It provides the basis for effective selection and breeding of superior genotypes for targeted genetic improvement and sustainable crop development. The present study aimed to estimate genetic variability, heritability and genetic advance for 16 agro-morphological and grain quality traits in 17 rice genotypes. Genotypes were evaluated in a Randomized Block Design (RBD) with three replications during *kharif,* 2024 at the Rice and Wheat Research Centre, Malan, Himachal Pradesh. The analysis of variance revealed that the mean sum of squares due to genotypes were significant for all the studied traits, thus sufficient genetic variability prevailed. Genetic variability studies revealed that high Genotypic Coefficient of Variation (GCV) and high Phenotypic Coefficient of Variation (PCV) were exhibited by five traits *viz*., spikelets per panicle, grains per panicle, grain breadth, L:B ratio and gel consistency. These traits also exhibited high heritability coupled with high genetic advance which suggests that there is predominance of additive gene action and selection would be effective. High heritability coupled with high genetic advance provided more realistic results. Therefore, by evaluating genetic parameters *viz*., PCV, GCV, heritability and genetic advance, breeders can efficiently determine the extent of variability present in a population, predict the effectiveness of selection and maximize genetic gain for various target traits which ultimately helps in developing stable and superior varieties, suitable for diverse agro-ecological regions. Thus, present study helped to unravel the hidden genetic potential among the genotypes, enabling its strategic exploitation for crop improvement. |

*Keywords: Genetic variability; Heritability; Genetic advance; Randomized Block Design*

1. INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important staple food globally. China and India are the leading producers of rice in the world. Global area under rice cultivation is 166.09 million hectares with an annual production of 522.08 million tonnes (USDA, 2024). India ranks second with production of 137.83 million tonnes in 47.83 million hectares area (USDA, 2024).

Genetic variability studies are very crucial for effective selection in any breeding programme. The expansion of rice cultivation depends not only on agronomic management practices but also on the inherent genetic variability and advancements in breeding (Chitanda et al. 2022). The development of high-yielding rice cultivars with enhanced grain quality and tolerance to biotic and abiotic stresses (Demeke et al. 2023), necessitates a comprehensive understanding of genetic variability of the genotypes. The success of trait improvement in any breeding program is closely linked to the magnitude of genetic divergence among parental lines (Khatri et al. 2019). Hence, greater genetic variability contributes significantly to broader adaptability, resilience to biotic and abiotic challenges, and overall enhancement in yield and grain quality. Therefore, the presence of substantial morpho-genetic variation is critical for achieving genetic gains and advancing trait-specific improvement goals (Anis et al. 2016).

Rice has abundant genetic resources with high genetic variability which could be exploited for the development of superior high yielding genotypes through selection and hybridization programmes. Phenotypic and genotypic coefficients of variation (PCV and GCV) help breeders distinguish between the phenotypic expression and the actual genetic potential of traits, which is important for effective selection. A higher GCV value coupled with a minimal difference between PCV and GCV suggests that the trait is less affected by the environment and largely controlled by genetic factors which in turn implies that direct selection based on phenotype would be rewarding. However, greater difference between PCV and GCV indicates that there is a strong environmental effect and selection based solely on phenotype might not be effective.

Heritability and genetic advance also play an important role in assessing the gene action and potential response to selection. High heritability for a trait indicates that the selection based on phenotype would be rewarding but heritability alone does not help to predict the response to selection. Therefore, genetic advance is considered along with heritability to get more realistic and accurate results. Thus, assessing the extent of genetic variability through parameters like PCV, GCV, heritability and genetic advance help breeders to understand the underlying genetic control and the potential for selection as well as to design efficient breeding strategies which ultimately facilitate the development of stable, high-yielding superior varieties suitable for diverse agro-ecological conditions.

Thus, the aim of the present research was to investigate the genetic basis of various agro-morphological traits in rice cultivars under Northwestern Himalayan conditions. The findings of this study would aid in identifying highly suitable genetic material and assist in designing subsequent breeding programs to facilitate crop improvement.

**2.** **MATERIALS AND METHODS**

**2.1 Experimental location:** The present study was conducted at the Rice and Wheat Research Centre, Malan, H.P., India during *kharif*, 2024 to study the genetic variability, heritability and genetic advance for 16 agro-morphological and grain traits.

The Research Centre lies 950 m above mean sea level, at latitude of 32°12' N and longitude of 76°20' E in the lap of majestic Dhauladhar range of North Western Himalayas. The temperature varies from 15.6 ºC to 28.6 ºC with sub-humid mid-hill conditions. The soil type is silty clay loam.

**2.2 Experimental materials:** The experimental materials consisted of three Cytoplasmic Male Sterile (CMS) lines *viz*., IR 58025A, IR 79156A and IR 68897A and 14 released varieties for Himachal Pradesh *viz*., HPR 1068, HPR 1156, HPR 2143, HPR 2612, HPR 2656, HPR 2720, HPR 2795, HPR 2880, HPU 2216, RP 2421, Koshikari, Kasturi, Naggar Dhan and Varun Dhan (Table 1). These were evaluatedin a Randomized Block Design (RBD) with three replications. The seeds were initially grown in the nursery bed and later transplanted after 25 days to the main field with an inter-row spacing of 20cm and plant-to-plant spacing of 15cm. All the standard agronomic package of practices were properly followed and observations were recorded for 16 agro-morphological and grain traits *viz*., days to 50% flowering, days to 75% maturity, plant height at maturity (cm), effective tillers per plant, panicle length (cm), spikelets per panicle, grains per panicle, grain yield per plant (g), spikelet fertility (%), 1000-grain weight (g), grain length (mm), grain breadth (mm), L:B ratio, protein content (%), amylose content (%) and gel consistency (mm).

**Table 1: List of rice genotypes used in the study along with their parentage/source**

|  |  |
| --- | --- |
| **Genotypes** | **Parentage/Source** |
| 1. IR 58025A | Wild Abortive (WA) – IRRI Philippines / IIRR, Hyderabad |
| 2. IR 79156A | Wild Abortive (WA) – IRRI Philippines / IIRR, Hyderabad |
| 3. IR 68897A | Wild Abortive (WA) – IRRI Philippines / IIRR, Hyderabad |
| 4. HPR 1068 | IR 42015-83-3-22/IR 9758-K2 |
| 5. HPR 1156 | IR 32429-122-3-1-2/IR 31868-64-2-3-3-3 |
| 6. HPR 2143 | Phul Patas/HUP 741 |
| 7. HPR 2612 | Hassan Serai/T23//IR 66295-36-2 |
| 8. HPR 2656 | RP2421/VL Dhan 221 |
| 9. HPR 2720 | Pure line selection from Begmi (IC455333) |
| 10. HPR 2795 | Selection from IC 3131180 germplasm |
| 11. HPR 2880 | HPU2216/Tetep |
| 12. HPU 2216 | IR8/IR2053-521-1-1//IR36 |
| 13. RP 2421 | IR36/Kathwar |
| 14. Kasturi | Basmati 370/CR 88-17-1-5 |
| 15. Koshikari | *Japonica* rice germplasm |
| 16.Naggar Dhan | Ching Shi-15 (Acc.36852) |
| 17. Varun Dhan | Kunjen 4 (HPR K 2001) |

**2.3 Estimation of parameters of variability**

**2.3.1 Range**

It is the difference between the largest and the smallest values in the data.

Range = Largest value – Smallest value

**2.3.2 Mean (X̅)**

Mean refers to the average of any given data.

$$\overbar{X}= \frac{Sum of individual observations}{Number of observations}$$

**2.3.3 Coefficients of variation**

The genotypic, phenotypic and environmental coefficients of variation were estimated following Burton and De Vane (1953):

$$Genotypic coefficient of variation \left(GCV\%\right)= \sqrt{\frac{σ^{2 }g}{\overbar{X}}} ×100 $$

$$Phenotypic coefficient of variation \left(PCV\%\right)= \sqrt{\frac{σ^{2 }p}{\overbar{X}}} ×100 $$

$$Environmental coefficient of variation \left(ECV\%\right)= \sqrt{\frac{σ^{2 }e}{\overbar{X}}} ×100 $$

where,

$\sqrt{σ^{2 }g}$ = Genotypic standard deviation

$\sqrt{σ^{2 }p}$ = Phenotypic standard deviation

$\sqrt{σ^{2 }e}$ = Environmental standard deviation

$$\overbar{X}=Population mean$$

For PCV and GCV, ranges used were:

> 20% - High

10% - 20% - Moderate

< 10% - Low

**2.3.4 Heritability in broad sense (**$h\_{bs}^{2}$**)**

Heritability in broad sense ($h\_{bs}^{2}$) was calculated by Burton and De Vane (1953) and Johnson et al. (1955) formula:

$Heritability \left(broad sense\right)=\frac{σ^{2}g}{σ^{2}p} ×100$

$$σ^{2}g= genotypic variance $$

$$σ^{2}p= phenotypic variance $$

Ranges for heritability ($h\_{bs}^{2}$)

> 80% - High

50% - 80% - Moderate

< 50% - Low

**2.3.5 Genetic advance as per cent of mean (GAM)**

The expected genetic advance (GA) was calculated as per Burton and De Vane (1953) and Johnson et al. (1955).

GA = K x σp x h2bs

where,

K = 2.06 (selection differential at 5% selection intensity)

h2bs = heritability (broad sense)

 σp = phenotypic standard deviation

$Genetic advance as percentage of mean = \frac{Expected genetic advance}{Grand mean (\overbar{X})} ×100$

Ranges for genetic advance (GA) :

> 40% - High

20% - 40% - Moderate

< 20% - Low

3. results and discussions

**3.1 Analysis of variance**

The results of analysis of variance depicted that the mean sum of squares due to genotypes were found to be significant for all the traits *viz*., days to 50% flowering, days to 75% maturity, plant height at maturity (cm), effective tillers per plant, panicle length (cm), spikelets per panicle, grains per panicle, grain yield per plant (g), spikelet fertility (%), 1000-grain weight (g), grain length (mm), grain breadth (mm), L:B ratio, protein content (%), amylose content (%) and gel consistency (mm) which indicated the presence of high genetic variability in the present set of rice genotypes (Table 2). The presence of sufficient genetic variation for agro-morphological and grain quality traits in rice genotypes indicated the scope for selecting high yielding rice genotypes with superior quality traits.

Significant high amount of genetic variability for various yield and quality traits in rice were also documented by Dhanwani et al. (2013), Sameera et al. (2015), Ali et al. (2018), Kalpana et al. (2018), Nanda et al. (2021), Pathak et al. (2024) and Sharmila et al. (2025).

Puren (2017) also reported high heritability for plant height, effective tillers per plant, yield per plant, grains per panicle and 1000-grain weight in rice genotypes.

**3.2 Assessment of genetic variability**

Various genetic parameters such as range, mean, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance as per cent of mean for yield attributing and quality traits are presented (Table 3). PCV was higher than the corresponding GCV for all the studied traits which indicated role of environment in governing the variation and thus, selection should be practiced carefully. However, a close correspondence between PCV and GCV estimates for all the traits studied indicates minimal environmental influence. Patel et al. (2019) also reported close alignment between PCV and GCV values for various traits in rice, suggesting less influence by environmental variation.

**3.2.1 Coefficients of variation**

High magnitudes of PCV and GCV (>20%) were observed for five traits *viz*., spikelets per panicle (28.12%, 26.93%) followed by L:B ratio (26.32%, 26.12%), grains per panicle (24.56%, 22.91%), gel consistency (21.87%, 21.82%) and grain breadth (20.45%, 20.24%). Moderate PCV and GCV (10% - 20%) estimates were exhibited by eight traits *viz*., grain yield per plant (19.34%, 17.56%), effective tillers per plant (19.28%, 17.99%), 1000-grain weight (13.50%, 13.08%), panicle length (12.49%, 12.20%), protein content (12.02%, 11.73%), plant height at maturity (11.74%, 11.56%), grain length (11.52%, 11.30%) and amylose content (11.00%, 10.86%). Low PCV and GCV (<10%) estimates were exhibited by three traits *viz*., spikelet fertility (9.49%, 9.14%), days to 50% flowering (5.21%, 5.05%) and days to 75% maturity (3.68%, 3.56%). Low PCV values indicated limited phenotypic variation. Similar to present findings, low PCV for days to 50% flowering has been reported earlier by Sameera et al. (2015) and Soundharya et al. (2024). High PCV and high GCV has also been reported earlier by Ali et al. (2018) and Nanda et al. (2021) for grains per panicle. Results of higher PCV than corresponding GCV were similar to that of Islam et al. (2015) and Ali et al. (2018).

**Table 2: Analysis of variance for yield and quality traits in rice**

|  |
| --- |
| **Mean sum of squares** |
|  |  **Sources** | **Replications** | **Genotypes** | **Error** |
| **Traits** |  **df** | **2** | **16** | **32** |
| Days to 50% flowering | 3.549 | 57.130\* | 1.237 |
| Days to 75% maturity | 3.314 | 49.157\* | 1.105 |
| Plant height at maturity | 11.620 | 508.312\* | 5.362 |
| Effective tillers per plant | 0.055 | 5.940\* | 0.279 |
| Panicle length | 1.264 | 31.264\* | 0.506 |
| Spikelets per panicle | 109.973 | 5168.499\* | 150.232 |
| Grains per panicle | 109.162 | 2909.791\* | 137.730 |
| Grain yield per plant | 1.099 | 36.462\* | 2.421 |
| Spikelet fertility | 2.869 | 201.590\* | 5.112 |
| 1000- grain weight | 4.833 | 34.087\* | 0.713 |
| Grain length  | 0.083 | 1.670\* | 0.021 |
| Grain breadth  | 0.010 | 0.627\* | 0.004 |
| L:B ratio | 0.073 | 1.926\* | 0.010 |
| Protein content  | 0.004 | 3.066\* | 0.050 |
| Amylose content | 1.176 | 14.720\* | 0.128 |
| Gel consistency | 2.965 | 520.157\* | 0.693 |

\* Significant at P ≤ 0.05

**Table 3: Estimates of genetic parameters of variability for yield and quality traits in rice**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  Range |  |  |  |  |  |  |  |  |
|  | max | min | mean | PV | GV | EV | PCV | GCV  | h2bs (%) | GA (% of mean) |
| Days to 50% flowering | 95 | 80 | 85.51 | 19.87 | 18.63 | 1.24 | 5.21 | 5.05 | 93.78 | 10.07 |
| Days to 75% maturity | 120 | 107 | 112.43 | 17.12 | 16.02 | 1.11 | 3.68 | 3.56 | 93.54 | 7.09 |
| Plant height at maturity | 136.00 | 78.67 | 112.02 | 173.01 | 167.65 | 5.36 | 11.74 | 11.56 | 96.90 | 23.44 |
| Effective tillers per plant | 10.44 | 5.44 | 7.63 | 2.17 | 1.89 | 0.28 | 19.28 | 17.99 | 87.12 | 34.60 |
| Panicle length | 33.33 | 20.00 | 26.26 | 10.76 | 10.25 | 0.51 | 12.49 | 12.20 | 95.30 | 24.53 |
| Spikelets per panicle | 234.78 | 82.33 | 151.86 | 1822.99 | 1672.76 | 150.23 | 28.12 | 26.93 | 91.76 | 53.15 |
| Grains per panicle | 198.56 | 76.89 | 132.66 | 1061.75 | 924.02 | 137.73 | 24.56 | 22.91 | 87.03 | 44.03 |
| Grain yield per plant | 24.11 | 12.59 | 19.18 | 13.77 | 11.35 | 2.42 | 19.34 | 17.56 | 82.42 | 32.84 |
| Spikelet fertility | 96.70 | 64.57 | 88.54 | 70.60 | 65.49 | 5.11 | 9.49 | 9.14 | 92.76 | 18.13 |
| 1000-grain weight | 31.90 | 17.67 | 25.49 | 11.84 | 11.12 | 0.71 | 13.50 | 13.08 | 93.98 | 26.13 |
| Grain length | 7.64 | 5.31 | 6.56 | 0.57 | 0.55 | 0.02 | 11.52 | 11.30 | 96.27 | 22.85 |
| Grain breadth | 3.11 | 1.81 | 2.25 | 0.21 | 0.21 | 0.00 | 20.45 | 20.24 | 97.93 | 41.26 |
| L:B ratio | 4.60 | 1.76 | 3.06 | 0.65 | 0.64 | 0.01 | 26.32 | 26.12 | 98.48 | 53.39 |
| Protein content | 10.20 | 6.77 | 8.55 | 1.06 | 1.01 | 0.05 | 12.02 | 11.73 | 95.29 | 23.59 |
| Amylose content | 22.21 | 15.03 | 20.31 | 4.99 | 4.86 | 0.13 | 11.00 | 10.86 | 97.44 | 22.08 |
| Gel consistency | 96.20 | 43.00 | 60.29 | 173.85 | 173.15 | 0.69 | 21.87 | 21.82 | 99.60 | 44.87 |

*PV- Phenotypic variance, GV- Genotypic variance, EV- Environmental variance, PCV- Phenotypic coefficient of variance, GCV- Genotypic coefficient of variance, h2bs (%)- Broad sense heritability, GA (% of mean)- Genetic advance*

**3.2.2 Heritability (h2bs)**

Higher magnitude of broad sense heritability (>80%) was observed for all the traits under study *viz.,* gel consistency (99.60%) followed by L:B ratio (98.48%), grain breadth (97.93%), amylose content (97.44%), plant height at maturity (96.90%), grain length (96.27%), panicle length (95.30%), protein content (95.29%), 1000-grain weight (93.98%), days to 50% flowering (93.78%), days to 75% maturity (93.54%), spikelet fertility (92.76%), spikelets per panicle (91.76%), effective tillers per plant (87.12%), grains per panicle (87.03%) and grain yield per plant (82.42%). Out of all the traits studies, highest heritability was depicted by gel consistency (99.60%) while least was exhibited by grain yield per plant (82.42%). Puren (2017) reported high heritability for plant height, effective tillers per plant, yield per plant, grains per panicle and 1000-grain weight in rice genotypes. Nanda et al. (2021) also reported high heritability for days to 50% flowering, plant height, panicle length, filled grains per panicle, fertility and grain yield per plant.

**3.2.3 Genetic advance**

High genetic advance (>40%) as per cent of means (GAM) was exhibited by L:B ratio (53.39%) followed by spikelets per panicle (53.15%), gel consistency (44.87%), grains per panicle (44.03%) and grain breadth (41.26%). Moderate GAM (20-40%) was observed for eight traits *viz*., effective tillers per plant (34.60%) followed by grain yield per plant (32.84%), 1000-grain weight (26.13%), panicle length (24.53%), protein content (23.59%), plant height at maturity (23.44%), grain length (22.85%) and amylose content (22.08%). While, low GAM (<20) was observed for three traits *viz*., spikelet fertility (18.13%) followed by days to 50% flowering (10.07%) and days to 75% maturity (7.09%). High genetic advance indicated predominance of additive gene action and thus selection would be effective for improvement of such traits while low genetic advance indicated non-additive gene action.

In order to determine the real progress that can be made through selection, it is important to implement both genetic advance and heritability of characters simultaneously. High heritability (>80%) coupled with high genetic advance (>40%) were observed for traits *viz.,* L:B ratio (53.39%) followed by spikelets per panicle (53.15%), gel consistency (44.87%), grains per panicle (44.03%) and grain breadth (41.26%). This indicated that these traits may be under the control of additive gene action and selection would be rewarding. However, high heritability (>80%) coupled with low genetic advance (<20%) was observed for spikelet fertility, days to 50% flowering and days to 75% maturity which indicated that selection would not be effective. High heritability coupled with high genetic advance was reported earlier by Sameera et al. (2015) for spikelets per panicle and grains per panicle, Nanda et al. (2021) and Hariharan et al. (2025) for grains per panicle while Sao et al. (2024) for L:B ratio, which justified the present results.

4. Conclusion

The results of analysis of variance depicted that the mean sum of squares due to genotypes were found to be significant for all the 16 agro-morphological and grain quality traits studied which highlight substantial genetic variability in genotypes for these traits, indicating a promising scope for genetic improvement through selection. Differences between PCV and GCV were minimal for all the traits, which indicated less influence of environmental factors. High PCV coupled with high GCV was exhibited by five traits *viz*., spikelets per panicle, grains per panicle, grain breadth, L:B ratio and gel consistency. These traits also exhibited high heritability coupled with high genetic advance, confirming presence of additive gene action and therefore, selection would be effective for these traits. Overall, the findings of the present study proved to be valuable in assessing the extent of genetic variability and idea of gene action involved which further enables its efficient strategic exploitation in rice improvement programmes.

**DISCLAIMER (ARTIFICIAL INTELLIGENCE)**

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

**COMPETING INTERESTS**

Author(s) have declared that no competing interests exist.

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