***Original Research Article***

**Genetic Variability, Heritability and Genetic advance for** **Yield, Yield-attributing and Quality traits in Rice under Northwestern Himalayan conditions**

ABSTRACT

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| The present study intends to estimate the genetic variability, heritability and genetic advance for 16 yield, yield attributing and quality traits in 17 rice genotypes which were evaluated in Randomized Block Design (RBD) with three replications during *kharif,* 2024 at the Rice and Wheat Research Centre, Malan, Himachal Pradesh. The observations were recorded for 16 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). Analysis of variance depicted significant differences among genotypes for all traits studied. 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. Therefore, by evaluating genetic parameters *viz*., PCV, GCV, heritability and genetic advance, breeders can efficiently determine the extent of variability present in a population and predict the effectiveness of selection for various target traits since exploitation of genetic variability is critical for 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; Genotypic Coefficient of Variation; Phenotypic Coefficient of Variation*

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. 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.

Therefore, present investigation was done to estimate the genetic variability, heritability and genetic advance for yield, yield-attributing and quality traits in rice.

**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 estimate the genetic variability, heritability and genetic advance for 16 agronomically important traits.

The Research Centre lies at an elevation of 950 m above mean sea level, 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 17 rice genotypes including three 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 sown in the nursery 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 agronomically important traits *viz*., days to 50% flowering, days to 75% maturity, plant height at maturity, effective tillers per plant, panicle length, spikelets per panicle, grains per panicle, grain yield per plant, spikelet fertility, 1000-grain weight, grain length, grain breadth, L:B ratio, protein content, amylose content and gel consistency.

**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.

Where, 𝑋= Mean

**2.3.3 Coefficients of variation**

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

where,

= Genotypic standard deviation

= Phenotypic standard deviation

= Environmental standard deviation

For PCV and GCV, ranges used were:

> 20% - High

10% - 20% - Moderate

< 10% - Low

**2.3.4 Heritability in broad sense ()**

Heritability in broad sense () was calculated according to the formula given by Burton and De Vane (1953) and Johnson et al. (1955):

Ranges for heritability ()

> 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

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 revealed that the mean sum of squares due to genotypes were 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 grain yield, yield attributing and 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 % of mean for various yield attributing and quality traits were presented in 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 Phenotypic Coefficient of variation and Genotypic coefficient 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 estimates of PCV and GCV (10% - 20%) were observed for 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 estimates of PCV and GCV (<10%) were observed for 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 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 the findings of Islam et al. (2015) and Ali et al. (2018).

**Table 2: Analysis of variance for yield, yield attributing 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, yield attributing 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)**

High 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 shown 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 percentage of means (GAM) was recorded for 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 selection would be rewarding for these traits. 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 by Sameera et al. (2015) for spikelets per panicle and grains per panicle, Nanda et al. (2021) for grains per panicle and Sao et al. (2024) for L:B ratio, which justified the present results.

4. Conclusion

The analysis of variance revealed that the mean sum of squares due to genotypes were significant for all the 16 yield, yield-attributing and quality traits which indicated presence of sufficient genetic variability among the genotypes for all the traits studied, indicating a promising scope for genetic improvement through selection. Differences between PCV and GCV were low for all the traits, indicating less environmental influence. High PCV and 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 which indicated presence of additive gene action and selection would be effective for these traits. Overall, these findings 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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