

## Genetic Variability and Traits Association Analysis on Segregating Population of Basmati and Red Rice

Aman Verma<sup>1</sup>, Daisy Basandrai<sup>2\*</sup>, Om Prakash Raigar<sup>3</sup>, Kritesh Thakur<sup>1</sup>, Sakshi Verma<sup>1</sup>, Amritpal Mehta<sup>4</sup> and Ashwani K Basandrai<sup>5</sup>

<sup>1</sup>Department of Genetics and Plant Breeding, Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishwavidyalaya, Palampur, Kangra (H.P)-176062, India

<sup>2</sup>ICAR-National Institute of Biotic Stress Management, Baronda, Raipur (Chhattisgarh)-493225, India

<sup>3</sup>Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana-141004, India

<sup>4</sup>Guru Kashi University, Talwandi Sabo, Mansa (Punjab)-151302, India

<sup>5</sup>Department of Plant Pathology, Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishwavidyalaya, Palampur, Kangra (H.P)-176062, India

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**\*Corresponding author:** E-mail: [daisybasandrai@gmail.com](mailto:daisybasandrai@gmail.com)

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Rice is cultivated over an area of about 47.8 million hectares with a total production of approximately 137.8 million tonnes and an average productivity of 4.32 t/ha in India (USDA-FAO, 2024) and in Himachal Pradesh, rice is cultivated in approximately 68 thousand hectares with production exceeding 138 thousand tonnes (Anonymous, 2024). Rice landraces offer significant potential for enhancing grain yield through incorporation of adaptability related genes. The indigenous rice germplasm of the North Western Himalayas, including Himachal Pradesh, represents a rich reservoir of genetic diversity. Red rice has higher nutritional and medicinal value in terms of high iron, zinc, calcium and anthocyanin as compared to common rice and it is classified as functional food (Rathna Priya *et al.*, 2019). Red rice variety HPR-2795 (improved Sukara land race) is tall, high yielding, early maturing, disease resistant variety and possess superior nutritional attribute. It has been released for Himachal Pradesh, Manipur and Uttarakhand. However, this variety is prone to lodging due to its tallness and heavy panicles. *Basmati* group surpasses all other scented rices in cooking, aroma and organoleptic taste and eating qualities and has found wider acceptance all over the world. However, requirement of

specific agro-climatic conditions restricts the extent of its area of cultivation. Major area of *Basmati* cultivation lies between Punjab of Pakistan and erstwhile Punjab (Punjab, Haryana, and Himachal), J & K, Uttarakhand and western U.P (Ahuja *et al.*, 2019). Rice variety PB-3 is an aromatic *Basmati* rice cultivar with desirable grain quality, aroma and dwarf stature. Hybridization between these contrasting parents offers opportunities for combining premium long grain quality, short stature and aroma with enhanced nutritional value and resistance to lodging. Biofortified and specialty rice breeding has gained considerable attention, however information on genetic variability and trait associations in populations derived from *basmati* × red rice crosses remain limited. Verma *et al.* (2026) studied marker assisted selection for semi-dwarf trait in F<sub>2</sub> Population of *Basmati* and Red Rice and confirmed the introgression of the gene *sd1* from PB 3 in the segregating progenies having red pericarp. The usefulness of genetic variability parameters and heritability estimates for identifying efficient selection criteria in segregating populations has been well documented by several researchers (Sandhu *et al.*, 2021; Yadav and Gabrial 2021, Kumar *et al.*, 2023). Determining association of yield



with its component traits is critical based on nature and magnitude of genetic variability, heritability, genetic advance, genetic divergence and character association, particularly in segregating populations. Keeping this in view, 11 characters were studied in the  $F_2$  segregating populations of the cross PB-3  $\times$  HPR-2795 to estimate the genetic variability and traits association analysis along with frequency distribution parameters, skewness and kurtosis for agro-morphological traits.

Present study was carried out in the experimental fields of department of Genetics and Plant Breeding, CSKHPKV, Palampur (~ 1290 m amsl; latitude and longitude of 36°6'N and 76°3'E, respectively). The  $F_1$  seed was produced by crossing PB-3 (female) with HPR-2795 (male) during Kharif 2019 and advanced to generate  $F_2$  population. The  $F_2$  population comprising 165 individual plants was evaluated during Kharif 2020 using augmented design with three checks, PB-3, HPR-2795 and HPR-2880 repeated frequently. Standard agronomic practices recommended for irrigated rice cultivation were uniformly followed (Anonymous, 2020).

The observations were recorded on each plant for agro-morphological traits viz., days to 50% flowering (DFF), days to 75% maturity (DTM), plant height (PH), flag leaf length (FLL), panicle length (PL) in cm, number of tillers per plant (NOT), grain length (GL) and grain breadth (GB) in mm, length and breadth ratio L/B ratio (L/B), thousands grain weight (TGW) and grain yield per plant (GY) in grams. Broad-sense heritability ( $h^2_{bs}$ ) was estimated as the ratio of genotypic variance to phenotypic variance (Burton and DeVane 1953). Expected genetic advance under selection was calculated according to Johnson *et al.* (1955). The association analysis was performed using “corrplot” package of R software version 4.5.2 (<https://cran.rstudio.com/>). The correlation coefficients were determined by estimating the direct and indirect contribution of traits towards grain yield following Dewey and Lu (1959). Frequency distributional characteristics were assessed using skewness and kurtosis statistics as suggested by Snedecor and Cochran (1989).

The  $F_2$  population from cross PB-3  $\times$  HPR-2795 exhibited substantial variation for all the traits studied, indicating sufficient genetic variability for effective selection. The broad phenotypic range observed for PH, grain dimensions and TGW reflected the contrasting parental

backgrounds of aromatic *Basmati* rice (PB-3) and red rice (HPR-2795). Such variability provides opportunities for identifying superior transgressive segregants combining desirable grain quality traits with nutritional attributes.

The estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability and genetic advance as percent of mean (GA) are given in Table 1. High PCV values (>20%) were observed for TGW (25.83%) and FLL (21.66%), indicating a high degree of phenotypic variability for these traits whereas, DFF (1.17%), DTM (0.81%) and GYP (7.80%) exhibited low PCV values. Similarly, GCV estimates were high for TGW (25.36%), moderate for FLL (18.87%), L/B (17.14%), GL (12.67%), GB (12.54%), PH (12.59%) and NOT (10.56%), and low for PL (6.74%), GY (2.97%), DFF (0.72%) and DTM (0.05%). The close correspondence between PCV and GCV values for traits such as TGW, PH, GL and GB suggested relatively low environmental influence on their expression. In contrast, comparatively wider differences between PCV and GCV for FLL, PL and NOT indicated greater environmental influence. Similar observations have been reported by Bhat *et al.* (2018), Kalaiselvan *et al.* (2019) and Kumar *et al.* 2025 in segregating rice populations.

High heritability (>70%) was recorded for PH (96.87%), TGW (96.40%), GL (86.69%), GB (81.75%), FLL (75.86%) and L/B ratio (75.03%), indicating that a major proportion of variation in these traits was genetically controlled. Moderate to low heritability was observed for DTF, DTM, PL, NOT and GYP, suggesting a greater influence of environmental factors on their expression. Similar findings were also reported by Ogunbayo *et al.* (2014) and Bhargava *et al.* (2021). High GA as percent of mean (>20%) was observed for TGW (51.38%), FLL (33.90%), L/B ratio (30.63%), PH (25.56%), GL (24.34%) and GB (23.39%). The combination of high heritability and high GA for these traits indicated the predominance of additive gene effects and suggested that selection for these characters would be effective in early segregating generations. Moderate GA was observed for NOT (12.43%), while GY (2.34%), DTF (0.91%) and DTM (0.01%) exhibited low GA, indicating the probable involvement of non-additive gene action and/or environmental effects as reported by Nandeshwar *et al.* (2010) and Kalaiselvan *et al.* (2019) for grain shape and flag leaf traits in rice.



Table 1: Estimates of genetic parameters of variability for various traits

| Traits | Mean ± SD      | Range         | GCV (%) | PCV (%) | Heritability (%) | Genetic Advance (%) Over mean | Skewness*1 | Kurtosis* |
|--------|----------------|---------------|---------|---------|------------------|-------------------------------|------------|-----------|
| DTF    | 88.72 ± 1.28   | 79.33-90.67   | 0.72    | 1.17    | 37.74            | 0.91                          | -3.616**   | 29.57**   |
| DTM    | 108.9 ± 0.97   | 106.56-110.56 | 0.05    | 0.81    | 0.38             | 0.01                          | -0.051     | -1.272**  |
| PH     | 112.05 ± 14.34 | 73.18-146.04  | 12.59   | 12.79   | 96.87            | 25.56                         | -0.09      | 0.42      |
| NOT    | 7.44 ± 2       | 2.89-11.56    | 10.56   | 18.5    | 32.55            | 12.43                         | 0.364*     | -0.239    |
| PL     | 26.04 ± 2.95   | 17.97-33.97   | 6.74    | 11.27   | 35.82            | 8.33                          | -0.043     | -0.238    |
| FLL    | 33.4 ± 7.34    | 14.29-52.36   | 18.87   | 21.66   | 75.86            | 33.9                          | 0.112      | -0.435    |
| GL     | 7.56 ± 1.19    | 4.62-9.92     | 12.67   | 13.61   | 86.69            | 24.34                         | -0.184     | 0.009     |
| GB     | 2.45 ± 0.39    | 1.84-3.08     | 12.54   | 13.87   | 81.75            | 23.39                         | 0.011      | -1.633**  |
| L/B    | 3.14 ± 0.73    | 1.59-4.71     | 17.14   | 19.79   | 75.03            | 30.63                         | 0.109      | -0.71     |
| TGW    | 24.76 ± 6.32   | 20.31-38.94   | 25.36   | 25.83   | 96.4             | 51.38                         | 2.088**    | 8.615**   |
| GYP    | 18.37 ± 1.5    | 15.07-22.27   | 2.97    | 7.8     | 14.56            | 2.34                          | 0.422**    | -0.402**  |

\*Values of skewness and kurtosis are presented to assess distributional characteristics of traits in the F<sub>2</sub> population. DTF= Days to 50% flowering, DTM=Days to 75% maturity, PH=Plant height (PH), FLL= Flag leaf length, PL= Panicle length (in cm), NOT= Number of tillers per plant, GL= Grain length, GB= Grain breadth (in mm), L/B ratio=length/ breadth ratio, TGW= Thousand grain weight and GYP=Grain yield per plant (GY) in grams

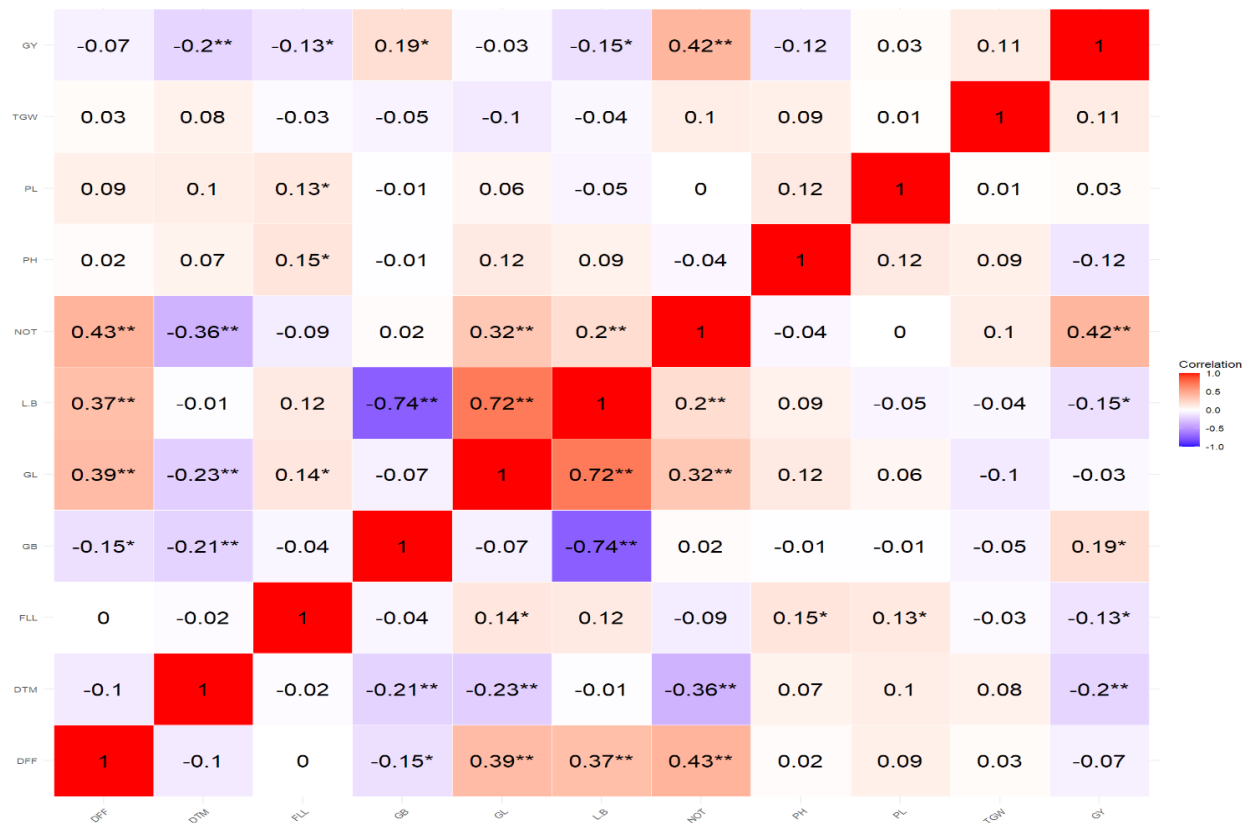


Fig. 1: Estimation of correlation coefficient among yield and yield contributing traits in rice.

\*Significant at  $p < 0.05$ \*\*Significant at  $p < 0.01$ 

Correlation analysis revealed significant associations among yield and its component traits (Figure 1). GYP exhibited a significant positive correlation with NOT, indicating that improvement in these traits is likely to contribute positively towards yield enhancement. The positive association of GYP with productive tillering is biologically meaningful because increased tiller number contributes to greater sink capacity and grain production. GYP showed a negative association with DTM, suggesting the possibility of identifying relatively early maturing and high-yielding segregants within the population. Negative associations were also observed with L/B ratio and FLL. These findings indicated that selection solely for grain slenderness or larger flag leaves may not necessarily result in yield improvement in the present genetic background.

Similar positive associations between GYP and NOT have been reported by Kiani and Nematzadeh 2012, Kahani and Hittalmani 2015, Ratna *et al.* 2015 and Bhargava *et al.* (2021).

The frequency distribution analysis revealed considerable variation among the  $F_2$  segregants for the test traits, indicating ample genetic variability available. Differences in skewness and kurtosis among traits suggested variation in the nature of gene action and genetic architecture governing trait expression. Positive skewness observed for TGW indicated the predominance of complementary gene interaction, suggesting that favourable alleles were concentrated in relatively fewer segregant (Table 1, Figure 2).

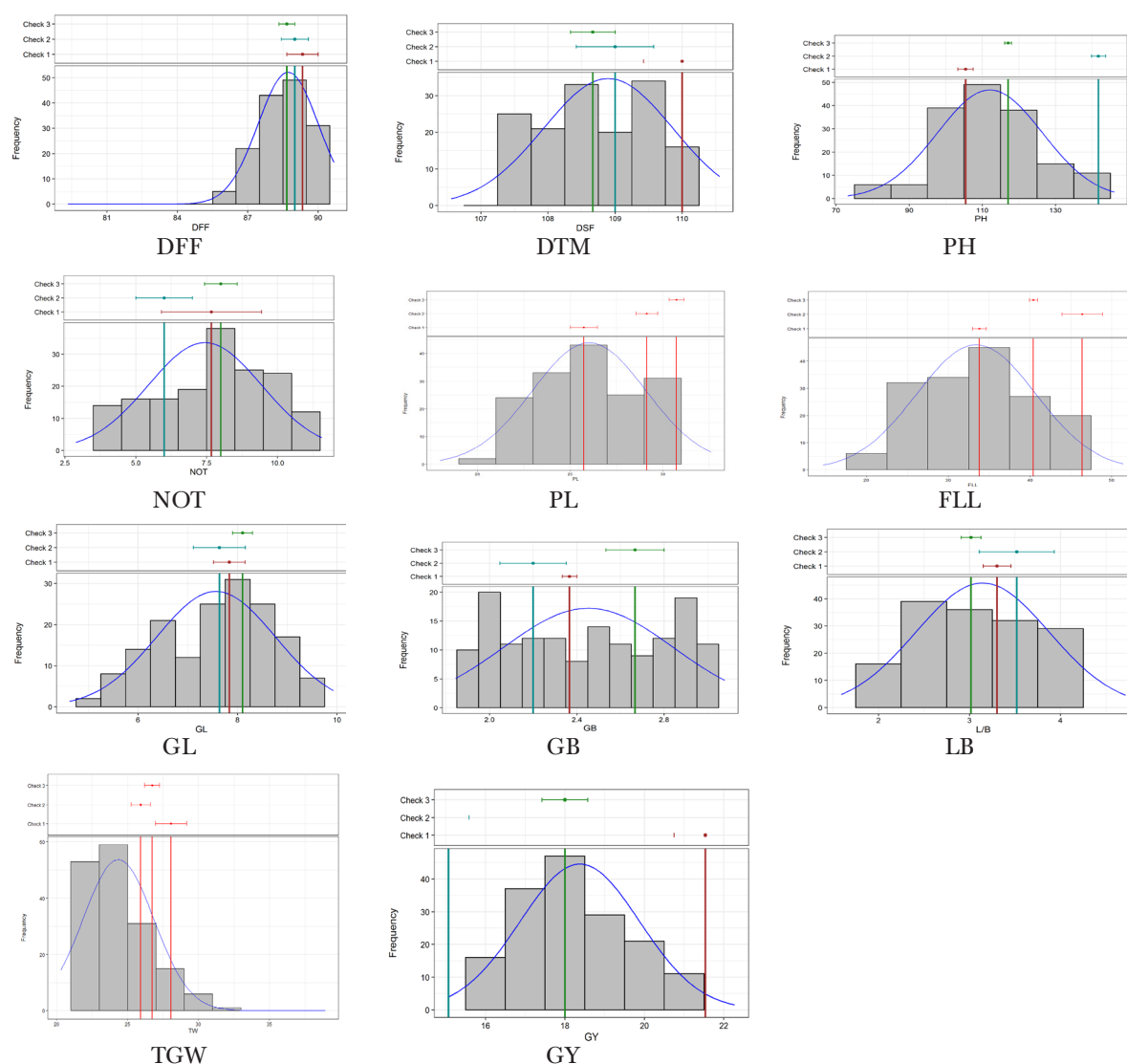


Fig. 2. Descriptive statistics, frequency distribution parameters, skewness and kurtosis estimates for agro-morphological traits in the  $F_2$  population derived from PB-3  $\times$  HPR-2795 rice cross. PB-3 (check 1); HPR-2795 (check 2) and HPR-2880 (check 3)



Conversely, negative skewness recorded for DTF indicated duplicate gene interaction, where desirable alleles were distributed among a larger proportion of the population. Similar observations have been reported in rice segregating populations by Bharath *et al.* (2018) and Seneega *et al.* (2019).

Kurtosis analysis provided insight into the number of genes involved in trait inheritance. TGW exhibited a leptokurtic distribution, indicating the involvement of relatively fewer major genes with higher concentration of observations around the mean. In contrast, PH and GL displayed near-normal (mesokurtic) distributions, suggesting polygenic inheritance controlled by several genes with small individual effects. Such traits generally exhibit continuous variation and provide greater scope for selection in segregating generations. The combined interpretation of skewness and kurtosis indicated that both additive and non-additive gene effects contributed to the inheritance of yield and related traits in the PB-3 × HPR-2795 population. The presence of diverse distribution patterns among traits reflected the complex genetic architecture of this *Basmati* × red rice cross and highlights the potential for selecting superior recombinants possessing desirable agronomic and grain-quality attributes. However, validation in advanced generations and across environments is required before making definitive breeding recommendations.

## Conclusion

The F<sub>2</sub> population derived from PB-3 × HPR-2795 exhibited substantial genetic variability for several agronomic and grain-related traits. High heritability coupled with high genetic advance for PH, FLL, GL, GB, L/B ratio and TGW suggested predominance of additive gene effects and the potential effectiveness of selection. Correlation coefficient analyses identified number of tillers as an important contributors to GY. The results provide useful preliminary information for selecting superior recombinants. However, validation in advanced generations and multi-environment trials is required before making definitive breeding recommendations. The combined interpretation of skewness and kurtosis indicated that both additive and non-additive gene effects contributed to the inheritance of yield and related traits in the PB-3 × HPR-2795 population.

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## Authors' contributions

AV, DB, AKB, KT conceptualization and execution of research, compilation and editing of the manuscript; SV, AM helped in the statistical analysis of the findings and in editing of the manuscript.

## Conflict of interest

The authors declare that they have no conflict of interest.

## Ethical Approval

The article doesn't contain any study involving ethical approval.

## Use of Generative AI or AI assisted technologies

Authors declare that no Generative AI or AI assisted technologies have been used in preparation of this manuscript.

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