# Association Studies in Red Rice Mutant Lines of IRGA-318-11-6-9-2B

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***Authors' contributions***

*This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.*

*Original Research Article*

## ABSTRACT

Rice is the important cereal food crop. It provides 20% of the world's dietary energy and predominant dietary energy source. It is estimated that the demand for rice will be 137.30 million tonnes by 2050. In order to achieve this, the production per unit area needs to be increased by mutation in turn creating variation. Induced mutants were grown in the field during Kharif 2022 at the Zonal Agricultural and Horticultural Research Station, Brahmavar, Udupi District, Karnataka the results showed grain yield had positive correlations with several traits including number of productive tillers, number of grains per panicle, panicle weight, spikelet fertility, flag leaf length and width but negative correlations with days to fifty per cent flowering, days to maturity, and plant height. Days to maturity, flag leaf length, plant height, panicle weight, number of productive tillers

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per plant per plant, number of grains per panicle, spikelet fertility and grain length showed a direct positive effect on grain yield. This indicated the effectiveness of direct selection for these traits in improvement of grain yield per plant. Days to fifty per cent flowering, flag leaf width, panicle length, test weight, number of filled grains per panicle, panicle length, and grain breadth had negative direct effects on grain yield per plant.

## 1. INTRODUCTION

Rice (*Oryza sativa* L.) is an annual $C_3$ cereal crop with a diploid chromosome number of 2n = 2x = 24, classified under the genus *Oryza* and the family *Poaceae*. It is most popular and important staple food for nearly half of the world's population and in general is consumed widely as polished white rice after milling. Rice with a red bran layer is called as red rice. Though, the colour is confined to the bran layer, a tinge of red remains even after milling and unmilled red rice has a higher nutrient content than polished white rice [1]. Traditional red rice varieties are grown in India and many other rice growing countries since ancient times. However, have disappeared from commercial cultivation in early nineties and remained confined to few areas.

Crop improvement through mutagenesis helps to obtain superior mutants for different traits. The purpose of mutation induction is to enhance the mutation rate in a short duration for developing new variants. Spontaneous mutation sometimes is not able to provide genetic variability rapidly and accurately, therefore inducing mutations artificially is an important tool to improve and increase the productivity of crop plants [2].

To determine the degree of association of characters with yield and also among the yield components, the correlation coefficients were calculated. Phenotypic correlation coefficient helps in determining selection index which may be useful for overall improvement of yield. It is the magnitude of relationship between various plant characters that determines the component characters on which selection can be made for further improvement in yield and quality parameters. It may be either due to pleiotropic action of genes or linkage. If the correlation between yield and a character is due to the direct effect of the character, it reflects a true relationship between them and selection can be practiced for such characters in order to ameliorate yield. But, if the correlation is mainly

due to indirect effect of the character through another component trait, the breeder has to select for the trait through which the indirect effect is expected. A great yield response is obtained when the character for which indirect selection is practiced which intern, has a high heritability and positive correlation with yield. Phenotypic coefficient of correlation between two characters are determined by using the variance and covariance components as suggested by Al-Jibouri et al. [3].

## 2. MATERIALS AND METHODS

Induced mutants were grown in the field during *Kharif* 2022 at the Zonal Agricultural and Horticultural Research Station, Brahmavar, Udupi District, Karnataka. The experiment was carried out in acidic soil with pH of 5.27, EC of 0.053 dS m$^{-1}$, Fe of 14.16 mg, kg$^{-1}$, and Zn of 1.93 mg kg$^{-1}$ which is located at the latitude 13° 25' North and 75°45' East longitude.

IRGA-318-11-6-9-2B line, International Network for Genetic Evaluation of Rice, (INGER), International Rainfed Lowland Rice Observational Nursery, Module 2 from IRRI, Philippines is a mid-duration (130-135 days) variety with long slender red seeds, erect flag leaf, 95 cm tall, non-lodging and is resistant to gall midge. Initially, 200 seeds of this variety were exposed to 15kR, 25kR, 35kR and 45kR gamma ray treatment from Cobalt 60 at BARC Mumbai.

Plant to progeny method was followed to forward the individual plants from $M_1$ to $M_2$. Plants with semi-dwarf, earliness, and medium bold red grain type that were primarily selected and forwarded to $M_3$ from each treatment (15, 25, 3,5 and 45kR) and mutants showing severe diseases incidence like false smut, blast, brown leaf spot, lodging type were rejected. Healthy plants attributing good agronomic traits compared with parent were selected and forwarded to the $M_4$ generation. The material for the present study consists of 25, 11, 21 and 2 lines from the 15kR, 25kR,

35kR and 45kR gamma treatments respectively, total of 59 $M_5$ mutant lines with one untreated parent check (IRGA-318-11-6-9-2B) were grown in the *Kharif* 2022.

The experiment was laid out in a Randomized Complete Block Design (RCBD) with two replications. A total of 59 mutant lines (25, 11, 21 and 2) from each treatment and one untreated parent check were randomized and sown in each replication. The spacing was maintained with the plant-to-plant spacing of 15 cm within a row and row-to-row spacing of 20cm in 5 square meter area.

Correlation coefficient and Path analysis was carried out using RStudio software, *Version 4.3.1* by using packages, '*metan*' and '*variability*'.

## 3. RESULTS AND DISCUSSION

The analysis of variance of all mutant lines and one untreated parent check in the $M_6$ generation with respect to fifteen quantitative traits revealed that the mutant lines exhibited highly significant mean sum of squares for all the traits studied indicating the presence of genetic variability. The analysis of variance for yield and yield related traits are presented in Table 1.

Correlation is an amount of degree and direction of association of one variable with other variables and governs how these aspects vary together or whether there is any relationship between any two such characters. In order to find the nature of association present within the characters, phenotypic correlation was evaluated among the fifteen characters. The results of correlation coefficient are presented in Table 2.

Grain yield per plant (g) exhibited positive and significant association with the traits like flag leaf length (r = 0.2754), flag leaf width (r = 0.2531), number of productive tillers per plant (r = 0.6473), number of grains per panicle (r = 0.3184), number of filled grains per panicle (r = 0.4762), spikelet fertility (r = 0.4112), panicle length (r = 0.3655) and panicle weight (r = 0.5007). These results are in accordance with Ekka et al. [4] for panicle length, Reddy et al. [5] for flag leaf length and flag leaf width, Lakshmi et al. [6] for number of productive tillers per plant and number of grains per panicle, Fentie et al. [7] for number of filled grains per panicle, Kulsum et
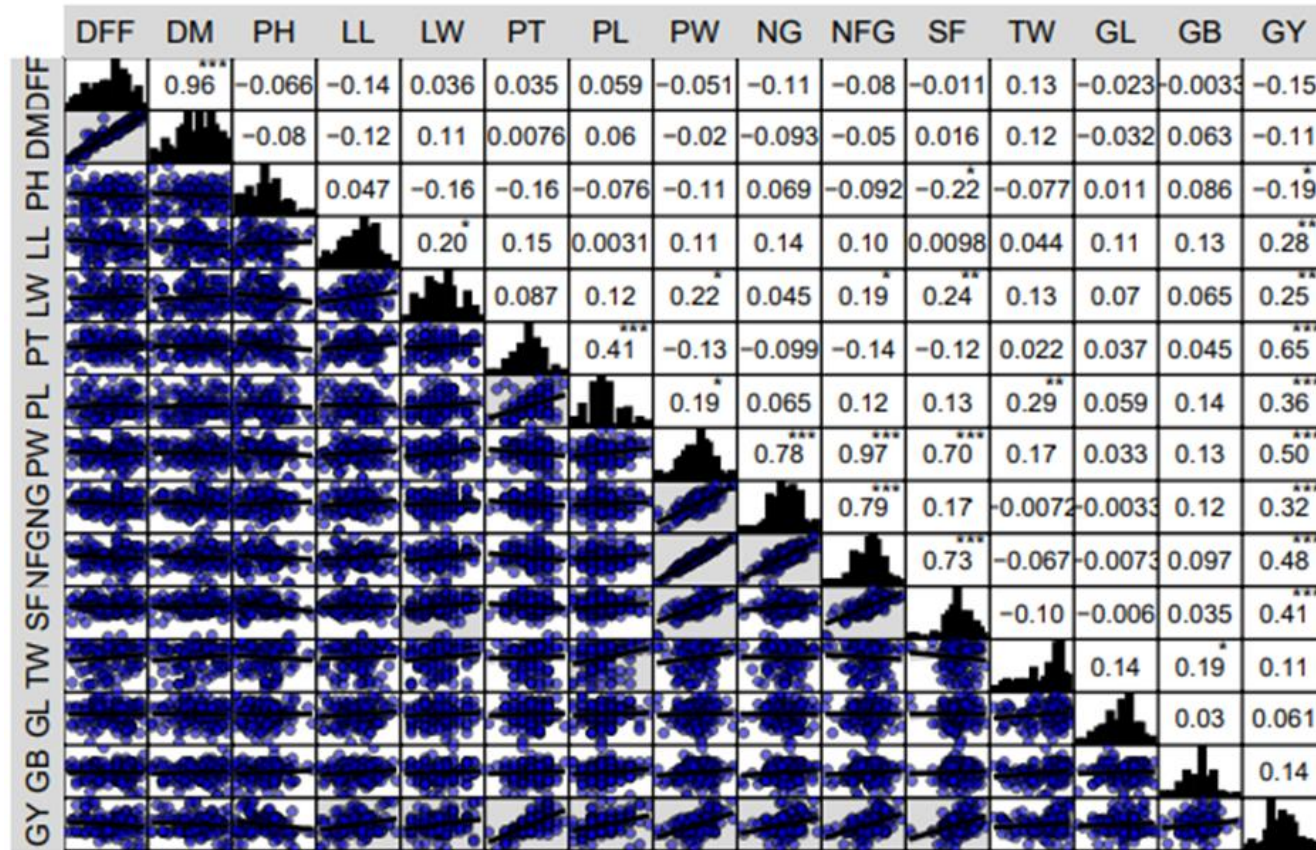
al. [8] for panicle weight and Kiran et al. [9] for spikelet fertility.

For grain yield per plant the traits like, test weight (r = 0.1138), grain length (r = 0.0596), grain breadth (r = 0.1374) exhibited positive and non-significant association, days to fifty *per cent* flowering (r = -0.1453) and days to maturity (r = -0.1107) exhibited non-significant and negative association. Plant height (r = -0.1932) exhibited significant and negative association. These findings were analogous to the works of, Gangashetty et al. [10] for days to fifty *per cent* flowering, days to maturity, plant height, Allam et al. [11] for grain length, Sameera et al. [12] for test weight and Priyanka [13] for grain breadth.

The Path coefficient analysis was computed to estimate the contribution of individual traits to grain yield. It is performed to understand the causes and effects of chain relationships of different yield contributing traits with yield. The path coefficient analysis was conducted using grain yield as dependent variable and all other traits studied as independent variables. In this study, the phenotypic direct and indirect effects of different traits on grain yield are presented in Table 3.

Out of fourteen characters, phenotypic path, nine characters had a positive and direct effect on grain yield through days to maturity (0.47175), flag leaf length (0.11801), plant height (0.03055), panicle weight (5.32089), number of productive tillers per plant (0.78001), number of grains per panicle (0.04676), spikelet fertility (0.21734) and grain length (0.12409) This indicated the effectiveness of direct selection for these traits in improvement of grain yield per plant. The traits such as, days to fifty *per cent* flowering (-0.57250), flag leaf width (-0.03980), panicle length (-0.06850), number of filled grains per panicle (-4.83880), test weight (-1.03440) and grain breadth (-0.00020) had negative direct effects on grain yield. These results were similar to the results depicted by Edukondalu et al. [14] for number of filled grains per panicle, test weight, grain breadth, Archana et al. [15] for plant height, Bagudam et al. [16] for number of productive tillers per plant, Dhavaleshvar et al. [17] for days to maturity, Sari et al. [18] for flag leaf length and spikelet fertility, Deepthi et al. [19] for days to fifty *per cent* flowering, test weight, panicle length and Kulsum et al. [8] for panicle weight and number of grains per panicle.

**Table 1. Estimates of phenotypic correlation for fifteen yield and yield attributing traits in the mutant lines of M$_6$ generation of red rice IRRI line IRGA-318-11-6-9-2B**



|     | DFF | DM | PH | LL | LW | PT | PL | PW | NG | NFG | SF | TW | GL | GB | GY |
|-----|-----|----|----|----|----|----|----|----|----|-----|----|----|----|----|----|
| DFF |     | 0.96*** | -0.066 | -0.14 | 0.036 | 0.035 | 0.059 | -0.051 | -0.11 | -0.08 | -0.011 | 0.13 | -0.023 | -0.0033 | -0.15 |
| DM  |     |    | -0.08 | -0.12 | 0.11 | 0.0076 | 0.06 | -0.02 | -0.093 | -0.05 | 0.016 | 0.12 | -0.032 | 0.063 | -0.11 |
| PH  |     |    |    | 0.047 | -0.16 | -0.16 | -0.076 | -0.11 | 0.069 | -0.092 | -0.22* | -0.077 | 0.011 | 0.086 | -0.19* |
| LL  |     |    |    |    | 0.20* | 0.15 | 0.0031 | 0.11 | 0.14 | 0.10 | 0.0098 | 0.044 | 0.11 | 0.13 | 0.28** |
| LW  |     |    |    |    |    | 0.087 | 0.12 | 0.22* | 0.045 | 0.19 | 0.24** | 0.13 | 0.07 | 0.065 | 0.25** |
| PT  |     |    |    |    |    |    | 0.41*** | -0.13 | -0.099 | -0.14 | -0.12 | 0.022 | 0.037 | 0.045 | 0.65*** |
| PL  |     |    |    |    |    |    |    | 0.19* | 0.065 | 0.12 | 0.13 | 0.29** | 0.059 | 0.14 | 0.36*** |
| PW  |     |    |    |    |    |    |    |    | 0.78*** | 0.97*** | 0.70*** | 0.17 | 0.033 | 0.13 | 0.50*** |
| NG  |     |    |    |    |    |    |    |    |    | 0.79*** | 0.17 | -0.0072 | -0.0033 | 0.12 | 0.32*** |
| NFG |     |    |    |    |    |    |    |    |    |    | 0.73*** | -0.067 | -0.0073 | 0.097 | 0.48*** |
| SF  |     |    |    |    |    |    |    |    |    |    |    | -0.10 | -0.006 | 0.035 | 0.41*** |
| TW  |     |    |    |    |    |    |    |    |    |    |    |    | 0.14 | 0.19* | 0.11 |
| GL  |     |    |    |    |    |    |    |    |    |    |    |    |    | 0.03 | 0.061 |
| GB  |     |    |    |    |    |    |    |    |    |    |    |    |    |    | 0.14 |
| GY  |     |    |    |    |    |    |    |    |    |    |    |    |    |    |    |

*Where,*

DFF- Days to fifty per cent flowering  PH- Plant height (cm)  NG- Number of grains per panicle  DM- Days to maturity  GB- Grain breadth (cm)
GL- Grain length (cm)  SF- Spikelet fertility (%)  LL- Flag leaf length (cm)  PT- Number of productive tillers per plant
TW- Test weight (g)  LW- Flag leaf width  PL- Panicle length (cm)  GY- Grain yield per plant (g)

**Table 2. Analysis of variance for yield and yield components in the mutant lines of $M_6$ generation of red rice IRRI line IRGA-318-11-6-9-2B**

| Source of Variation | Degrees of freedom | Days to 50 % flowering | Days to maturity | Plant height(cm) | Leaf length (cm) | Leaf width (cm) | Panicle length (cm) | Number of productive tillers per plant | Panicle weight (g) |
|---|---|---|---|---|---|---|---|---|---|
| Replication | 1 | 0.075 | 0.075 | 17.633 | 1.408 | 0.0009 | 0.300 | 1.408 | 0.128 |
| Mutant lines | 59 | 31.85** | 23.24** | 103.49** | 25.14** | 0.11** | 6.00** | 287.09** | 0.41** |
| Error | 59 | 3.74 | 2.80 | 10.51 | 5.65 | 0.0033 | 1.32 | 34.09 | 0.08 |
| **CD (5%)** | | 3.87 | 3.35 | 6.49 | 4.75 | 0.12 | 2.30 | 1.52 | 0.57 |
| **CD (1%)** | | 5.14 | 4.46 | 8.63 | 6.32 | 0.15 | 3.05 | 2.02 | 0.76 |
| **CV (%)** | | 1.90 | 1.28 | 3.96 | 9.47 | 5.23 | 6.03 | 6.95 | 10.76 |

| Source of variation | Degrees of freedom | Number of grains per panicle | Number of filled grains per panicle | Spikelet fertility (%) | Test weight (g) | Grain length (cm) | Grain breadth (cm) | Grain yield per plant (g) |
|---|---|---|---|---|---|---|---|---|
| Replication | 1 | 53.33 | 200.21 | 6.88 | 0.0096 | 0.00012 | 0.00000083 | 5.80 |
| Mutant lines | 59 | 578.02** | 711.39** | 92.00** | 0.86** | 0.0013** | 0.00045** | 59.17** |
| Error | 59 | 111.59 | 140.67 | 22.94 | 0.13 | 0.00041 | 0.00011 | 17.09 |
| **CD (5%)** | | 21.14 | 23.73 | 9.58 | 0.73 | 0.04 | 0.02 | 8.27 |
| **CD (1%)** | | 28.12 | 31.57 | 12.75 | 0.97 | 0.05 | 0.03 | 11.00 |
| **CV (%)** | | 8.11 | 11.14 | 5.90 | 1.53 | 2.86 | 3.42 | 15.53 |

**Table 3. Estimates of phenotypic path coefficient analysis for fifteen yield and yield attributing traits in the mutant lines of M$_6$ generation of red rice IRRI line IRGA-318-11-6-9-2B**

| | DFF | DM | PH | LL | LW | PT | PL | PW | NG | NFG | SF | TW | GL | GB | r Values |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DFF | **-0.57250** | 0.45085 | -0.00201 | -0.01630 | -0.00140 | 0.02691 | -0.00403 | -0.27315 | -0.00514 | 0.38662 | -0.00239 | -0.13017 | -0.00265 | 0.00009 | -0.14530 |
| DM | -0.54722 | **0.47175** | -0.00245 | -0.01460 | -0.00435 | 0.00632 | -0.00410 | -0.10798 | -0.00437 | 0.24146 | 0.00348 | -0.12251 | -0.00309 | -0.02302 | -0.11068 |
| PH | 0.03773 | -0.03778 | **0.03055** | 0.00561 | 0.00631 | -0.12605 | 0.00521 | -0.56181 | 0.00320 | 0.44517 | -0.04736 | 0.07974 | 0.00104 | -0.03476 | -0.19320* |
| LL | 0.07907 | -0.05835 | 0.00145 | **0.11801** | -0.00808 | 0.11521 | -0.00028 | 0.59869 | 0.00646 | -0.49694 | 0.00191 | -0.04567 | 0.01245 | -0.04853 | 0.27540** |
| LW | -0.02004 | 0.05123 | -0.00481 | 0.02379 | **-0.03980** | 0.06607 | -0.00851 | 1.19632 | 0.00211 | -0.92953 | 0.05312 | -0.13711 | 0.00012 | 0.00016 | 0.25310** |
| PT | -0.01975 | 0.00380 | -0.00494 | 0.01740 | -0.00339 | **0.78001** | -0.02816 | -0.68850 | -0.00454 | 0.66146 | -0.02630 | -0.02413 | 0.00451 | -0.02013 | 0.64734** |
| PL | -0.03366 | 0.02825 | -0.00232 | 0.00048 | -0.00498 | 0.32066 | **-0.06850** | 1.03863 | 0.00300 | -0.59082 | 0.02821 | -0.30291 | 0.00638 | -0.05693 | 0.36549** |
| PW | 0.02926 | -0.00953 | -0.00321 | 0.01322 | -0.00897 | -0.10047 | -0.01331 | **5.32089** | 0.03443 | -4.68684 | 0.15251 | -0.17885 | 0.00201 | -0.05043 | 0.50071** |
| NG | 0.06298 | -0.04410 | 0.00209 | 0.01631 | -0.00181 | -0.07574 | -0.00440 | 4.16467 | **0.04676** | -3.84732 | 0.03827 | 0.00777 | -0.00032 | -0.04675 | 0.31841** |
| NFG | 0.04575 | -0.02354 | -0.00281 | 0.01212 | -0.00770 | -0.10663 | -0.00836 | 5.17763 | 0.03718 | **-4.83880** | 0.15974 | 0.06908 | -0.00083 | -0.03665 | 0.47620** |
| SF | 0.00630 | 0.00755 | -0.00666 | 0.00104 | -0.00979 | -0.09438 | -0.00889 | 3.75092 | 0.00823 | -3.55651 | **0.21734** | 0.10718 | -0.00059 | -0.01055 | 0.41119** |
| TW | -0.07197 | 0.05575 | -0.00235 | 0.00520 | -0.00530 | 0.01817 | -0.02004 | 0.92316 | -0.00035 | 0.32333 | -0.02249 | **-1.03440** | 0.01588 | -0.07085 | 0.11379 |
| GL | 0.01357 | -0.01307 | 0.00028 | 0.01326 | 0.00001 | 0.03151 | -0.00391 | 0.00050 | -0.00014 | 0.03581 | -0.00115 | -0.14726 | **0.12409** | 0.00610 | 0.05960 |
| GB | -0.00120 | 0.02925 | 0.00286 | 0.01542 | -0.00230 | 0.04228 | -0.01050 | 0.72592 | 0.00589 | -0.47759 | 0.00617 | -0.19759 | -0.00099 | **-0.00020** | 0.13741 |

*Residual effect (P) = 0.1611*

*Where,*

*DFF- Days to fifty per cent flowering      PH- Plant height (cm)      NG- Number of grains per panicle   DM- Days to maturity   NFG- Number of filled grains per panicle*
*GL- Grain length (cm)                SF- Spikelet fertility (%)      GB- Grain breadth (cm)            PT- Number of productive tillers per plant*
*TW- Test weight (g)                  LL- Flag leaf length (cm)      LW- Flag leaf width              PL- Panicle length (cm)*

## 4. CONCLUSION

The trait grain yield per plant had significant positive correlation with traits like flag leaf length, flag leaf width, panicle length, panicle weight, number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle and spikelet fertility, indicating that these trait improvements can enhance the grain yield per plant. Very low residual effect of 0.1611 depicted that the traits included in the study explained high percentage of variation in grain yield. Days to maturity, flag leaf length, plant height, panicle weight, number of productive tillers per plant, number of grains per panicle, spikelet fertility and grain length had positive and direct effect on grain yield at phenotypic path analysis. Hence, selection for these traits would be more rewarding for yield improvement strategy.

## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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