Genetic Dissection of Yield Determinants in Advance Breeding Lines (ABLs) of Rice (*Oryza sativa* L.) under Irrigated Condition of Chhattisgarh, India

Pramod Noatia¹, Abhinav Sao†, Ajay Tiwari¹, S. K. Nair¹ and Deepak Gauraha¹

¹Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, India.

**Authors’ contributions**

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

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**ABSTRACT**

The present study was undertaken to study the extent of genetic variability, character association and path analysis in 53 irrigated late duration breeding lines for 12 quantitative and 10 quality parameters. Analysis of variance revealed the presence of significant variation among the breeding lines for all the characters except for total tillers per plant, effective tillers per plant, spikelet fertility percentage and grain yield per plant. The highest magnitude of PCV and GCV were displayed by grain yield per plant followed by harvest index, filled spikelet per panicle and 1000 seed weight. The greater extent of heritability in broad sense were recorded for days to maturity, days to 50% flowering, 1000 seed weight, plant height, total spikelet per panicle, kernel length, kernel L:B ratio, grain length, head rice recovery percentage, amylose content, hulling and milling percentage. However, high heritability coupled with high genetic advance as percent of mean were displayed by plant height, number of spikelet per panicle, filled spikelet per panicle, 1000 seed weight, kernel length, kernel L:B ratio, grain length, head rice recovery percentage and amylose content. Grain yield per plant exhibited positive significant correlation with harvest index, effective tillers per plant.

*Corresponding author: E-mail: saoabhi27@yahoo.co.in;*
1000 seed weight, spikelet fertility %, days to maturity and days to 50% flowering. Path analysis revealed direct effect on grain yield were exerted by days to 50% flowering followed by harvest index, 1000 seed weight, total tillers per plant, number of spikelet per plant, effective tillers per plant and plant height indicating their importance in rice breeding programs.

Keywords: Genetic variability; heritability; correlation coefficient; path analysis.

1. INTRODUCTION

Rice serves as staple food crop for more than 55 % of the world’s population. Rice production is mainly concentrated in Asian developing countries and consumes 90 % of world’s rice production [1]. Rice grain contains decent amounts of carbohydrates, proteins, amino acid, fiber and vitamin that play a vital role against malnutrition. To ensure food security of the population outbreaks is expected to meet through production of high yielding varieties and improvement in production technology. Yield improvement is the main thrust in any crop improvement program. Presence of genetic variability among genotypes and their magnitude is prerequisite for any breeding to be successful. As an established fact, yield is a quantitative trait which is governed by interaction between a numbers of polygenic traits and selecting for yield alone will not be very rewarding. One of the important approaches to rice breeding is hybridization and subsequent selection. Parents’ choice is the first step in plant breeding program through hybridization [2]. Hence, it is prerequisite to understand the associations between yield and its component characteristics as well as direct and indirect effects of various yield component traits on grain yield. In view of the above concerns, the current experiment were carried out and planned with the goals, to estimate genetic variability parameters for yield and its contributing traits and to estimate correlation of yield and yield contributing traits along with their direct and indirect contribution yield through path coefficient analysis.

2. MATERIALS AND METHODS

2.1 Experimental Site

The experiment was carried out at the Research Cum Instructional Farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, India during Kharif, (wet season) 2020, in a randomized complete block design (RCBD) with two replications. Geographically the experimental site is situated between 17.14 and 24.45° North latitude and 79.16 and 84.15° East latitude and 289.60 m above mean sea level.

2.2 Experimental Material

A set of fifty-three late-duration advanced breeding lines of rice representing diverse genetic base (Table 1) were taken as experimental materials including four checks viz., Swarna, Mashuri, Pooja and Jaldubi. Twenty one days old seedlings were transplanted in a plot sized of 3.60 m × 1.80 m for each line and adopting a spacing of 20 cm ×15 cm. The crop was supplied with fertilizer (N, P and K) dose of 120:60:40 kg/ha respectively. The recommended standard agronomic package of practices was followed with plant protection measures.

2.3 Data Collections

The observations were recorded for both quantitative traits as well as qualitative traits during the peak crop growth stage. Five randomly selected plants from each plot for each breeding lines were considered for recording data. The characters undertaken for studies are days to 50 % flowering, days to maturity, plant height (cm), total tillers per plant, effective tillers per plant, Panicle length (cm), number of spikelet per panicle, filled spikelet per panicle, spikelet fertility %, 1000 seed weight (g), harvest index (%), grain yield per plant (g). Grain quality traits like Grain length (mm), grain breadth (mm), grain length: breadth ratio, kernel length (mm), kernel breadth (mm), kernel length: breadth ratio, hulking %, milling %, head rice recovery % and amylose content (%) were estimated in Crop Quality Lab, Department of Genetics and Plant Breeding, IGKV, Raipur.

2.4 Statistical Analysis

The treatment means for all the characters were subjected to analysis of variance techniques on the basis of model proposed by Fisher [3]. The genotypic and phenotype variance was also calculated as per the formulae proposed by Fisher [3]. Heritability in broad sense (h²) was determined by the formula given by Burton [4].
From the heritability estimates, the genetic advance (GA) was calculated by the following formula given by Johnson et al. [5]. Correlation and path analysis was estimated by using the methods suggested by Dewy and Lu [6].

**Coefficient of variation**

**Phenotypic coefficient of variation (PCV)**

\[ PCV \% = \frac{\sigma_p^2}{\bar{X}} \times 100 \]

Where,
- \( \sigma_p^2 \) = Phenotypic variance.
- Grand mean = \( \bar{X} \)

**Genotypic coefficient of variation (GCV)**

\[ GCV \% = \frac{\sigma_g^2}{\bar{X}} \times 100 \]

Where,
- \( \sigma_g^2 \) = Genotypic variance
- Grand mean = \( \bar{X} \)

**Heritability (broad sense)**

\[ h^2 = \frac{\sigma_g^2}{\sigma_p^2} \]

Where,
- \( \sigma_g^2 \) = Genotypic variance
- \( \sigma_p^2 \) = Phenotypic variance

**Genetic advance (GA)**

Genetic advance was calculated from the heritability estimates by using the formula;

\[ GA = K \times \sigma_p \times h^2 \]

Where,
- GA: Genetic advance
- \( K \): Selection differential at 5% selection intensity
- \( \sigma_p \): Phenotypic standard deviation
- \( h^2 \): Heritability

**Genetic advance as % of mean**

\[ GAM = \frac{\text{Genetic Advance}}{\text{General mean}} \times 100 \]

**Phenotypic correlation coefficients (r_p)**

\[ r_p (XY) = \frac{\text{Cov}(XY)}{\sqrt{\text{Var}(X) \times \text{Var}(Y)}} \]

Where,
- \( r_p (XY) \) = Phenotypic correlation coefficient.
- Cov. (XY) = Covariance between characters X and Y.
- Var. (X) = Variance for X character.
- Var. (Y) = Variance for Y character.

**Genotypic correlation coefficients (r_g)**

\[ r_g (XY) = \frac{\text{Cov}(XY)}{\sqrt{\text{Var}(X) \times \text{Var}(Y)}} \]

Where,
- \( r_g (XY) \) = Genotypic correlation coefficient
- Cov. (XY) = Covariance between characters X and Y.
- Var. (X) = Variance for X character.
- Var. (Y) = Variance for Y character.

**Path coefficient analysis**

If a character y is determined by correlated characters x1, x2 and x3, a path diagram must be formulated. As a result, we get the following set of simultaneous equations:

I. \( r (x_1, y) = a + r (x_1, x_3) c \)
II. \( r (x_2, y) = b + r (x_2, x_1) a + r (x_2, x_3) c \)
III. \( r (x_3, y) = c + r (x_3, x_1) a + r (x_3, x_2) b \)

Considering the three factors i.e. x1, x2 and x3, the simultaneous equation given above can be matrix notation as;

\[
\begin{bmatrix}
\Gamma x_1y \\
\Gamma x_2y \\
\Gamma x_3y
\end{bmatrix} = \begin{bmatrix}
\Gamma x_1x_1 & \Gamma x_1x_3 & \Gamma x_1x_3 \\
\Gamma x_2x_1 & \Gamma x_2x_2 & \Gamma x_2x_3 \\
\Gamma x_3x_1 & \Gamma x_3x_2 & \Gamma x_3x_3
\end{bmatrix} \begin{bmatrix}
a \\
b \\
c
\end{bmatrix}
\]

Where,
- \( r_{x_1y} \): Correlation coefficient between character x1 and y.
- \( r_{x_2y} \): Correlation coefficient between character x2 and y.
- \( r_{x_3y} \): Correlation coefficient between character x3 and y.
- A: Direct effect of character x1 and y.
- B: Direct effect of character x2 and y.
- C: Direct effect of character x3 and y.

The solution for vector C may be obtained as follows;

\[ A = B.C \text{ or, } C = B^{-1}A \]
3. RESULTS AND DISCUSSION

Genetic variability is prerequisite for selection of superior genotypes over the existing cultivars. The analysis of variance indicated the existence of significant differences among all genotypes for all the characters except total tiller per plant, productive tillers per plant, spikelet fertility percentage, kernel length: breadth ratio and grain yield per plant (Table-2). This suggested that there were inherent genetic differences among the genotypes. The results on mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean for the yield and yield component traits are depicted in Table No.3. The maximum range of mean variation was observed for number of spikelet per panicle (134 to 416) followed by filled spikelet per panicle (91 to 350), plant height (89.30 to 187.90 cm) and least for kernel length (1.75 to 2.60 cm).

The value of phenotypic coefficient of variation (PCV %) was higher than genotypic correlation coefficient (GCV %), which indicated a strong environmental impact on the expression of the characters. The phenotypic and genotypic coefficients of variation ranged from 6.56 and 5.80 in panicle length to 36.71 and 27.98, respectively in grain yield per plant. In the present investigation grain yield (36.71 and 27.98) had the highest PCV and GCV, followed by plant height (16.84 and 16.691), effective tillers per plant (15.98 and 8.46), total tillers per plant (14.71 and 7.07), grain L:B ratio (13.64 and 13.29), spikelet fertility percentage (12.88 and 8.15), amylose content (12.75 and 11.96), kernel L:B ratio (12.14 and 11.55), grain length (11.28 and 11.21), kernel length (10.91 and 10.81) and grain breadth (10.29 and 9.98 % respectively). Similar result were also by selection of those traits interacted with environmental factors to some extent in their expression. Similar results were also reported by Aditya et al. [18], Dhanwani et al. [14], Nirmaladevi et al. [16], Singh et al. [17] and Sudeepthi et al. [12].

The lowest PCV and GCV value were observed for panicle length (6.56 and 5.80) followed by hulling percentage (7.74 and 7.55), milling percentage (7.96 and 7.58), days to maturity (8.21 and 8.20) and days to 50 % flowering (8.80 and 8.78) and kernel breadth (9.96 and 9.28 % respectively) indicating that these traits interacted with environmental factors to some extent in their expression. Similar results were also reported by Aditya et al. [18], Dhanwani et al. [14], Nirmaladevi et al. [16], Singh et al. [17], Rashid et al. [19] and Sudeepthi et al. [12].

The range of heritability varied from 99.65 % for days to maturity to 23.10 % for total tillers per plant. Days to maturity (99.65%) showed maximum heritability, followed by days to 50 % flowering (99.49 %), 1000 seed weight (98.21 %), plant height (98.16 %), grain length (98.92 %), kernel length (98.24 %), head rice recovery percentage (96.99 %), hulling percentage (95.11 %), grain L:B ratio (94.95 %), grain breadth (94.11 %), milling percentage (90.76 %), kernel L:B ratio (90.47 %), amylose content (87.95 %), kernel breadth (86.78 %), number of spikelet per panicle (81.47 %), panicle length (78.22 %) and filled spikelet per panicle (75.60 %). This suggested that these traits are good indices for selection. Whereas moderate heritability was exerted by harvest index (65.05 %) and grain yield per plant (58.12 %). The lowest magnitude of heritability was observed for tillers per plant (23.10 %), effective tillers per plant (27.96 %) and spikelet fertility percentage (40.04 %). These results are in conformity with the findings of Akter et al. [13], Akinwale et al. [20], Babu et al. [21], Karupaiyan et al. [22], Tuwar et al. [8], Chouhan et al. [23], Singh et al. [9], Islam et al. [24] and Priyanka et al. [11].

The highest amount of genetic advance was observed for number of spikelet per panicle...
Table 1. List of 53 rice genotypes used as experimental material

| S. No. | Entry number | S. No. | Entry number | S. No. | Entry number |
|--------|--------------|--------|--------------|--------|--------------|
| 1.     | R 2307-76-1-39-1 | 19.    | R 2405-376-1-188-1 | 37.    | R 2419-1272-1-630-1 |
| 2.     | R 2303-38-1-19-1 | 20.    | R 2405-283-1-192-1 | 38.    | R 2408-739-2-438-1 |
| 3.     | R 2307-53-1-28-1 | 21.    | R 2405-391-200-1 | 39.    | R 2408-739-3-439-1 |
| 4.     | R 2307-59-1-31-1 | 22.    | R 2406-418-2-219-1 | 40.    | R 2408-739-4-440-1 |
| 5.     | R 2321-97-1-54-1 | 23.    | R 2406-422-1-222-1 | 41.    | R 2408-740-4-444-1 |
| 6.     | R 2325-104-1-59-1 | 24.    | R 2408-424-1-223-1 | 42.    | R 2408-740-5-445-1 |
| 7.     | R 2326-108-1-61-1 | 25.    | R 2409-467-1-252-1 | 43.    | Swarna (Check) |
| 8.     | R 2328-129-1-69-1 | 26.    | R 2409-469-1-254-1 | 44.    | Mahsuri (Check) |
| 9.     | R 2340-143-1-73-1 | 27.    | R 2409-487-1-258-1 | 45.    | Pooja (Check) |
| 10.    | R 2370-263-1-114-1 | 28.    | R 2409-4809-1-260-1 | 46.    | Jaldubi (Check) |
| 11.    | R 2370-265-1-116-1 | 29.    | R 2409-490-1-261-1 | 47.    | DH-19-1-1 |
| 12.    | R 2370-268-1-117-1 | 30.    | R 2409-490-1-262-1 | 48.    | DH-19-1-2 |
| 13.    | R 2370-268-2-118-1 | 31.    | R 2409-493-1-263-1 | 49.    | DH-19-1-3 |
| 14.    | R 2370-272-1-122-1 | 32.    | R 2409-494-1-264-1 | 50.    | DH-19-1-4 |
| 15.    | R 2373-277-1-123-1 | 33.    | R 2409-494-1-267-1 | 51.    | DH-19-1-5 |
| 16.    | R 2372-292-1-131-1 | 34.    | R 1771-529-1-274-1 | 52.    | DH-19-1-6 |
| 17.    | R 2374-299-1-135-1 | 35.    | R 2419-1248-1-610-1 | 53.    | DH-19-1-7 |
| 18.    | R 2404-346-1-164-1 | 36.    | R 2419-1250-611-1 |         |              |
### Table 2. Analysis of variance (ANOVA) for different traits in 53 rice genotypes

| Sl. no | Characters                        | Source of Variation | Replication d.f. (1) | Treatments d.f.(52) | Errors d.f.(52) |
|--------|----------------------------------|---------------------|----------------------|---------------------|-----------------|
| 1      | Days to 50% flowering            |                     | 5.434                | 170.653 **          | 0.434           |
| 2      | Days to maturity                 |                     | 6.377                | 238.269 **          | 0.416           |
| 3      | Plant height                     |                     | 103.614              | 1,004.020 **        | 9.325           |
| 4      | Total tillers per plant          |                     | 0.666                | 1.666               | 1.041           |
| 5      | Effective tillers per plant      |                     | 0.085                | 1.670               | 0.940           |
| 6      | Panicle length                   |                     | 0.097                | 5.094 **            | 0.622           |
| 7      | Number of spikelet per panicle   |                     | 2.123                | 5,987.38 **         | 611.39          |
| 8      | Number of filled spikelet per panicle |                 | 744.92               | 4,610.43 **         | 640.55          |
| 9      | Spikelet fertility %             |                     | 135.17               | 146.98              | 62.94           |
| 10     | 1000 seed weight                 |                     | 0.60                 | 46.70 **            | 0.42            |
| 11     | Harvest index                    |                     | 72.06                | 163.06 *            | 34.53           |
| 12     | Kernel length                    |                     | 0.006                | 0.724 **            | 0.006           |
| 13     | Kernel breadth                   |                     | 0.000                | 0.082 **            | 0.006           |
| 14     | Kernel L:B                       |                     | 0.002                | 0.199 **            | 0.010           |
| 15     | Grain length                     |                     | 0.059                | 1.854 **            | 0.010           |
| 16     | Grain breadth                    |                     | 0.046                | 0.143 **            | 0.004           |
| 17     | Grain L:B                        |                     | 0.031                | 0.389               | 0.010           |
| 18     | Head rice recovery %             |                     | 5.056                | 191.57 **           | 2.923           |
| 19     | Amylose content                  |                     | 2.325                | 14.93 **            | 0.957           |
| 20     | Hulling percentage               |                     | 0.452                | 60.51 **            | 1.519           |
| 21     | Milling percentage               |                     | 2.223                | 51.73 **            | 2.504           |
| 22     | Grain yield per plant            |                     | 21.917               | 40.60               | 10.754          |

** = Significance level at 0.01%, * = Significance level at 0.05%
| Characters                        | Mean   | Range  | CV (%) | Heritability (h²) % | GA     | GAM % |
|----------------------------------|--------|--------|--------|---------------------|--------|-------|
|                                  |        | Min.   | Max.   | PCV                 |        |       |
| Days to 50 % flowering           | 105.02 | 90.50  | 125.50 | 8.80                | 99.49  | 18.96 |
| Days to maturity                 | 132.98 | 115.50 | 155.50 | 8.21                | 99.65  | 22.43 |
| Plant height                     | 133.61 | 89.30  | 187.90 | 16.84               | 98.16  | 45.52 |
| Total tillers per plant          | 7.91   | 5.60   | 10.10  | 14.71               | 23.10  | 0.55  |
| Effective tillers per plant      | 7.14   | 4.80   | 9.00   | 15.99               | 27.96  | 0.66  |
| Panicle length                   | 25.74  | 21.70  | 29.50  | 6.56                | 78.22  | 2.72  |
| Number of spikelet per panicle   | 219.44 | 134.50 | 416.00 | 26.17               | 81.47  | 96.40 |
| Filled spikelet per panicle      | 174.10 | 91.00  | 350.50 | 29.43               | 75.60  | 79.80 |
| Spikelet fertility %             | 79.54  | 44.00  | 94.65  | 12.88               | 8.15   | 40.04 |
| 1000 seed weight                 | 18.16  | 10.15  | 31.50  | 26.73               | 98.21  | 9.82  |
| Harvest index                    | 30.74  | 11.55  | 48.75  | 32.33               | 26.07  | 65.05 |
| Kernel length                    | 5.54   | 4.05   | 6.95   | 10.91               | 10.81  | 98.24 |
| Kernel breadth                   | 2.10   | 1.75   | 2.60   | 9.96                | 9.28   | 86.78 |
| Kernel length : breadth ratio    | 2.66   | 1.80   | 3.31   | 12.14               | 11.55  | 90.47 |
| Grain length                     | 8.56   | 5.75   | 10.55  | 11.28               | 11.21  | 98.92 |
| Grain breadth                    | 2.64   | 2.10   | 3.27   | 10.29               | 9.98   | 94.11 |
| Grain length to breadth ratio    | 3.27   | 2.08   | 4.57   | 13.64               | 13.29  | 94.95 |
| Head rice recovery %             | 51.59  | 34.22  | 68.45  | 19.11               | 18.82  | 96.99 |
| Amylose content (%)              | 22.09  | 16.75  | 28.60  | 12.75               | 11.96  | 87.95 |
| Hulling percentage               | 71.93  | 54.96  | 78.84  | 7.74                | 7.55   | 95.10 |
| Milling percentage               | 65.39  | 50.91  | 73.71  | 7.96                | 7.58   | 90.76 |
| Grain yield per plant            | 13.80  | 5.40   | 22.10  | 36.71               | 27.98  | 58.12 |

Table 3. Parameters of genetic variability of yield and yield contribution traits.
High heritability does not always imply high genetic gain; however, when selecting superior varieties, heritability combined with high genetic progress can be used to predict the eventual outcome. The high heritability coupled with high genetic advance as percent of mean were observed for 1000 seed weight (54.09 %), filled spikelet per panicle (45.84 %), grain yield (43.96 %), number of spikelet per panicle (43.93 %), harvest index (43.32 %), head rice recovery percentage (38.02 %), plant height (34.07 %), grain L:B ratio (26.58 %), amylose content (23.03 %), grain length (22.88 %), kernel L:B ratio (22.53 %) and kernel length (21.98 %). These results are in agreement with the previous report by Sarangi et al. [27], Akinwale et al. [20], Sharma and Koutu et al. [15] and Islam et al. [24].

High heritability does not always imply high genetic gain; however, when selecting superior varieties, heritability combined with high genetic progress can be used to predict the eventual outcome. The high heritability coupled with high genetic advance as percent of mean were observed for 1000 seed weight, filled spikelet per panicle, number of spikelet per panicle, plant height, head rice recovery %, kernel length, kernel length to breadth ratio, grain length, grain length to breadth ratio and amylose content. These traits show the supremacy of additive gene effects in their expression, as well as the lack of environmental factors that would strengthen genetic inherent associations through selection. High heritability in association with moderate GA as % of mean were obtained for the character days to 50 percent flowering, days to maturity, panicle length, grain breadth, kernel breadth, hulling and milling %. These result revealed existence of substantial genetic variability among the genotypes and potential for selection, since variability is a pre requisite for success in selection programmes. Whereas, total tillers per plant, effective tillers per plant exhibited low heritability in association with low genetic advance as percent of mean. These findings are in accordance with those of Akinwale et al. [20], Babu et al. [21], Aditya et al. [18], Karuppaiyan et al. [22], Khare et al. [28], Ekka et al. [25], Devi et al. [29], Edukondalu et al. [30], Priyanka et al. [11] and Sudeepthi et al. [12].

3.1 Correlation Analysis

Since, crop grain yield is a quantitative character conditioned by interaction between many component characters knowledge of nature and association among the characters is pre requisite. When the characters are correlated, selection of one character would bring changes in another character. In present research attempt was made to study correlation coefficient for quantitative characters at both phenotypic and genotypic level. The phenotypic correlation coefficient was recorded higher than the genotypic correlation coefficient. It indicated existence of environmental influence on the expression of characters. The result of phenotypic correlation coefficient and genotypic correlation coefficient are depicted in Table-4 and Table-5 respectively.

3.1.1 Correlation between grain yield and yield contributing characters

At both phenotypic and genotypic level grain yield per plant showed positive significant correlation with days to 50 % flowering (rp=0.207*; rg=0.255**), days to maturity (rp=0.218*; rg=0.275**), effective tillers per plant (rp=0.387**; rg=0.454**), harvest index (rp=0.810**; rg=0.918**), spikelet fertility percentage (rp=0.191*; rg=0.309**), 1000 seed weight (rp=0.276**; rg=0.363**). Total tillers per plant (rg=0.271**) at genotypic level also showed positive significant correlation with grain yield. According to the findings of the study, rice grain yield can be increased by selecting these characters. When one character is selected, all positively correlated characters advance and negatively correlated features regress. A negative significant correlation was observed for number of spikelet per panicle (rg=-0.239*) at genotypic level. Panicle length (rg=-0.009) at genotypic level, number of spikelet per panicle (rp=-0.146) and plant height (rp=-0.095; rg= -0.153), filled spikelet per panicle (rp=-0.159; rg=-0.156) at both level showed negative non-significant correlation with grain yield. These results are in agreement with Babu et al. (2012). Whereas, total tillers per plant (rg=0.138) at genotypic level and panicle length (rp=0.064) at phenotypic level had positive non-significant correlation with grain yield per plant. Similar findings in rice were also reported by Naik et al. [31], Rashid et al. [32], Kumar et al. [33], Thippani et al. [34], Kalyan et al. [35] and Nanda et al. [36].

3.2 Path Coefficient Analysis

Since, simple correlation does not represent the true contribution of the characters to the yield,
### Table 4. Phenotypic correlation for yield and quantitative traits

|                        | Days to flowering | Days to maturity | Plant height | Total tillers/plant | Effective tillers/plant | Panicle length | Number of spikelet/panicle | Filled spikelet/panicle | Spikelet fertility % | 1000 seed weight | Harvest index | Grain yield/plant |
|------------------------|-------------------|------------------|--------------|---------------------|-------------------------|---------------|---------------------------|------------------------|---------------------|------------------|---------------|-----------------|
| Days to flowering      | 1.000             |                  |              |                     |                         |               |                           |                        |                    |                  |               |                 |
| Days to maturity       |                   | 1.000            |              |                     |                         |               |                           |                        |                    |                  |               |                 |
| Plant height           | 0.997*            | 0.435*           | 0.428*       | 1.000               |                         |               |                           |                        |                    |                  |               |                 |
| Total tillers/plant    | 0.158             | 0.176            | 0.022        | 1.000               |                         |               |                           |                        |                    |                  |               |                 |
| Effective tillers/plant| 0.225*            | 0.247*           | -0.070       | 0.777*              | 1.000                   |               |                           |                        |                    |                  |               |                 |
| Panicle length         | 0.061             | 0.060            | 0.531**      | -0.116              | -0.241*                 | 1.000         |                           |                        |                    |                  |               |                 |
| Number of spikelet/panicle | 0.011             | 0.004            | 0.084        | -0.257*             | -0.246*                 | 0.145         | 1.000                     |                        |                    |                  |               |                 |
| Filled spikelet/panicle| -0.006            | -0.016           | 0.094        | -0.420**            | -0.326**                | 0.079         | 0.870**                   | 1.000                  |                    |                  |               |                 |
| Spikelet fertility %   | -0.140            | -0.152           | -0.081       | -0.097              | -0.017                  | 0.016         | -0.091                   | 0.130                  | 1.000               |                  |               |                 |
| 1000 seed weight       | -0.051            | -0.057           | -0.107       | -0.118              | -0.024                  | 0.027         | -0.534**                 | -0.362*                | 0.248               | 1.000            |               |                 |
| Harvest index          | 0.096             | 0.101            | -0.352*      | 0.057               | 0.226*                  | -0.067        | -0.050                   | -0.063                 | 0.115               | 0.234*           | 1.000         |                 |
| Grain yield/plant      | 0.207*            | 0.218*           | -0.095       | 0.271**             | 0.387**                 | 0.064         | -0.146                   | -0.159                 | 0.191               | 0.276**          | 0.810**       | 1.000          |

**= Significance level at 0.01 %, *= Significance level at 0.05 %

### Table 5. Genotypic correlation for yield and quantitative traits

|                        | Days to flowering | Days to maturity | Plant height | Total tillers/plant | Effective tillers/plant | Panicle length | Number of spikelet/panicle | Filled spikelet/panicle | Spikelet fertility % | 1000 seed weight | Harvest index | Grain yield/plant |
|------------------------|-------------------|------------------|--------------|---------------------|-------------------------|---------------|---------------------------|------------------------|---------------------|------------------|---------------|-----------------|
| Days to flowering      | 1.000             |                  |              |                     |                         |               |                           |                        |                    |                  |               |                 |
| Days to maturity       | 0.997*            | 0.439*           | 0.432*       | 1.000               |                         |               |                           |                        |                    |                  |               |                 |
| Plant height           | 0.314*            | 0.361            | 0.049        | 1.000               |                         |               |                           |                        |                    |                  |               |                 |
| Total tillers/plant    | 0.414*            | 0.463*           | -0.130       | 0.542*              | 1.000                   |               |                           |                        |                    |                  |               |                 |
| Effective tillers/plant| 0.068             | 0.066            | 0.504*       | -0.108              | -0.415**                | 1.000         |                           |                        |                    |                  |               |                 |
| Panicle length         | 0.007             | -0.001           | 0.096        | -0.539*             | -0.507**                | 0.131         | 1.000                     |                        |                    |                  |               |                 |
| Number of spikelet/panicle | -0.002            | -0.015           | 0.115        | -0.666**            | -0.419**                | 0.059         | 0.954**                   | 1.000                  |                    |                  |               |                 |
| Filled spikelet/panicle| -0.221*           | -0.240*          | -0.136       | -0.280*             | -0.178                  | -0.106        | -0.131                   | 0.172                  | 1.000               |                  |               |                 |
| Spikelet fertility %   | -0.053            | -0.059           | -0.108       | -0.249*             | -0.059                  | 0.013         | -0.585*                  | -0.417**                | 0.419*              | 1.000            |               |                 |
| 1000 seed weight       | 0.104             | 0.115            | -0.431*      | 0.100               | 0.525*                  | -0.150        | -0.061                   | -0.078                 | 0.195               | 0.278**          | 1.000         |                 |
| Harvest index          | 0.255*            | 0.275*           | -0.153       | 0.138               | 0.454**                 | -0.009        | -0.239*                  | -0.156                 | 0.309               | 0.363**          | 0.918**       | 1.000          |
| Grain yield/plant      |                   |                  |              |                     |                         |               |                           |                        |                    |                  |               |                 |

**= Significance level at 0.01 %, *= Significance level at 0.05 %
Table 6. Direct and indirect effects of different characters on grain yield per plant at genotypic level

|       | DF     | DM     | PH    | TTP   | ETP   | PL    | NSP   | FSP   | SF %  | TW    | HI    | GYP   |
|-------|--------|--------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| DF    | 1.151  | -1.197 | 0.062 | 0.099 | 0.115 | 0.009 | 0.002 | -0.003| -0.042| -0.020| 0.075 | 0.255*|
| DM    | 1.147  | -1.201 | 0.061 | 0.114 | 0.129 | 0.009 | -0.002| -0.001| -0.046| -0.022| 0.083 | 0.275*|
| PH    | 0.505  | -0.519 | 0.143 | 0.015 | -0.036| 0.082 | 0.029 | 0.001 | -0.025| -0.040| -0.310| -0.153|
| TTP   | 0.361  | -0.433 | 0.007 | 0.315 | 0.151 | -0.015| -0.167| -0.008| -0.053| -0.092| 0.072 | 0.138 |
| ETP   | 0.476  | -0.556 | -0.019| 0.171 | 0.279 | -0.056| -0.158| -0.004| -0.034| -0.022| 0.378 | 0.454*|
| PL    | 0.079  | -0.079 | 0.086 | -0.034| -0.116| 0.137 | 0.040 | 0.006 | -0.020| 0.004 | -0.108| -0.009|
| NSP   | 0.008  | 0.001  | 0.014 | -0.170| -0.141| 0.018 | 0.311 | 0.010 | -0.025| -0.221| -0.043| -0.239*|
| FSP   | -0.003 | 0.018  | 0.016 | -0.210| -0.117| 0.008 | 0.297 | 0.011 | 0.032 | -0.155| -0.056| -0.156|
| SF %  | -0.255 | 0.288  | -0.020| -0.088| -0.050| -0.015| -0.041| 0.002 | 0.190 | 0.156 | 0.140 | 0.305*|
| TW    | -0.061 | 0.071  | -0.015| -0.079| -0.016| 0.002 | -0.185| -0.005| 0.079 | 0.372 | 0.200 | 0.363*|
| HI    | 0.120  | -0.138 | -0.062| 0.031 | 0.147 | -0.020| -0.019| -0.008| 0.037 | 0.103 | 0.719 | 0.918*|

DF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, TTP: Total tillers per plant, ETP: Effective tillers per plant, PL: Panicle length, NSP: Number of spikelet per panicle, FSP: Filled spikelet per panicle, SF %: Spikelet fertility percentage, TW: 1000 Seed weight, HI: Harvest index, GYP: Grain yield per plant.
path co-efficient analysis was determined using genotypic correlation data to estimate the indirect and direct contribution of different traits (Table-6). Path coefficient analysis provides a critical examination of the specific effects acting to produce a given correlation, as well as measures the relative importance of the characters. In present investigation genotypic correlation coefficient were used to estimate the direct and indirect effect of different yield contributing traits on grain yield.

The maximum positive direct effect on grain yield were exerted by days to 50 % flowering (1.151), followed by harvest index (0.719), 1000 seed weight (0.372), total tillers per plant (0.315) and number of spikelet per panicle (0.311). The characters also showed positive significant correlation with grain yield except total tillers per plant; hence, it indicated these characters to be prioritized in the selection process in order to isolate superior lines with high yield potential. The non-significant association with grain yield of total tillers per plant indicated the need for adoption of restricted selection on simultaneous basis to eliminate the undesirable indirect effects and make use of the high direct effects. Similar result were also reported by earlier workers Surek et al. [37], Kumar et al. [38], Khare et al. [28], Nayak et al [39]; Nanda et al. [36] and Sudeepthi et al. [12].

A moderate to low positive direct effect were recorded for effective tillers per plant (0.279) following that spikelet fertility percentage (0.190), plant height (0.143), panicle length (0.137) and negligible for filled spikelet per panicle (0.011).

Negative direct effect on grain yield of days to crop maturity (-1.201) were observed through its indirect effect via plant height, total tillers per plant, effective tillers per plant, panicle length and harvest index. These results are in agreement with the earlier reports by Jaiswal et al. [40], Debnath et al. [41] and Gupta et al. [42].

4. CONCLUSION

The results of the present study showed that there is a potential of adequate genetic variability present in the material studied. Study on correlation showed, the characters days to 50 % flowering, days to maturity, total tillers per plant, effective tillers per plant, harvest index, spikelet fertility percentage and 1000 seed weight had positive significant association with grain yield per plant. Path analysis also revealed days to 50 % flowering, total tillers per plant, number of spikelet per panicle, harvest index and 1000 seed weight contributed directly on grain yield. The indirect selection through total tillers per plant, number of spikelet per panicle, harvest index and 1000 seed weight will be useful in improving the high yield potential of the rice genotype. Therefore, selections of these desirable traits would be effective in accumulation of favourable genes into a common genetic background of cultivated rice.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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