



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

**Pramod Noatia<sup>1</sup>, Abhinav Sao<sup>1\*</sup>, Ajay Tiwari<sup>1</sup>, S. K. Nair<sup>1</sup> and Deepak Gauraha<sup>1</sup>**

<sup>1</sup>Department 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.*

### **Article Information**

DOI: 10.9734/IJPSS/2021/v33i2030638

#### Editor(s):

- (1) Dr. Hon H. Ho, State University of New York, USA.  
(2) Dr. Sangita Sahni, Dr. Rajendra Prasad Central Agricultural University, India.

#### Reviewers:

- (1) Kannan CS Warriar, Institute of Forest Genetics and Tree Breeding, India.  
(2) Kumari Anjani, Dr. Rajendra Prasad Central Agricultural University, India.  
Complete Peer review History: <https://www.sdiarticle4.com/review-history/71653>

**Original Research Article**

**Received 02 June 2021**  
**Accepted 12 August 2021**  
**Published 27 September 2021**

### **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,

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, hulling %, 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 ( $h^2$ ) 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)

$$h^2 = \sigma_g^2 / \sigma_p^2$$

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;

$$GA = K \cdot \sigma_p \cdot h^2$$

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  $x_1$ ,  $x_2$  and  $x_3$ , a path diagram must be formulated. As a result, we get the following set of simultaneous equations:

- I.  $r(x_1, y) = a + r(x_1, x_2) b + r(x_1, x_3) c$
- 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.  $x_1$ ,  $x_2$  and  $x_3$ , the simultaneous equation given above can be matrix notation as;

$$\begin{bmatrix} r_{x_1 y} \\ r_{x_2 y} \\ r_{x_3 y} \end{bmatrix} = \begin{bmatrix} r_{x_1 x_1} & r_{x_1 x_2} & r_{x_1 x_3} \\ r_{x_2 x_1} & r_{x_2 x_2} & r_{x_2 x_3} \\ r_{x_3 x_1} & r_{x_3 x_2} & r_{x_3 x_3} \end{bmatrix} \begin{bmatrix} a \\ b \\ c \end{bmatrix}$$

A                                  B                                  C

Where,

$r_{x_1 y}$ : Correlation coefficient between character  $x_1$  and y.  
 $r_{x_2 y}$ : Correlation coefficient between character  $x_2$  and y.  
 $r_{x_3 y}$ : Correlation coefficient between character  $x_3$  and y.  
A: Direct effect of character  $x_1$  and y.  
B: Direct effect of character  $x_2$  and y.  
C: Direct effect of character  $x_3$  and y.

The solution for vector C may be obtained as follows;

$$A = B \cdot C \quad \text{or,} \quad C = B^{-1}A$$

Where,

$B^{-1}$  = inverse of matrix B.

The residual effect can be estimated using the following formula after determining the values of the path coefficient, i.e. the 'C' vector.

$$R = 1 - \sum(r_{ij})$$

Where,

R= Residual effect

$r_{ij}$ = Correlation coefficient between  $i^{\text{th}}$  character and  $j^{\text{th}}$  dependent variable.

### 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 harvest index (32.33 and 26.07), filled spikelet per panicle (29.43 and 25.59), 1000 seed weight (26.73 and 26.49) and number of spikelet per panicle (26.17 and 23.62 %, respectively). This suggested that the genotypes used in the research have a broad genetic base, indicating the likelihood of genetic change by selection of above mentioned traits. Similar result were also reported earlier by Mohanty et al. [7], Tuwar et al. [8], Singh et al. [9], Acharya et al. [10], Priyanka et al. [11] and Sudeepthi et al. [12].

Moderate PCV and GCV values were recorded for head rice recovery percentage (19.11 and 18.82), 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). The results are in agreement with those of Akter et al. [13], Mohanty et al. [7], Dhanwani et al. [14], Sharma and Koutu. [15], Singh et al. [9], 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**

<b>S. No.</b>	<b>Entry number</b>	<b>S. No.</b>	<b>Entry number</b>	<b>S. No.</b>	<b>Entry number</b>
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 2409-494-264-1	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 <i>d.f. (1)</i>	Treatments <i>d.f.(52)</i>	Errors <i>d.f.(52)</i>
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%

**Table 3. Parameters of genetic variability of yield and yield contribution traits**

Characters	Mean	Range		CV (%)		Heritability (h <sup>2</sup> ) %	GA	GAM %
		Min.	Max.	PCV	GCV			
Days to 50 % flowering	105.02	90.50	125.50	8.80	8.78	99.49	18.96	18.05
Days to maturity	132.98	115.50	155.50	8.21	8.20	99.65	22.43	16.86
Plant height	133.61	89.30	187.90	16.84	16.69	98.16	45.52	34.07
Total tillers per plant	7.91	5.60	10.10	14.71	7.07	23.10	0.55	7.00
Effective tillers per plant	7.14	4.80	9.00	15.99	8.46	27.96	0.66	9.22
Panicle length	25.74	21.70	29.50	6.56	5.80	78.22	2.72	10.58
Number of spikelet per panicle	219.44	134.50	416.00	26.17	23.62	81.47	96.40	43.93
Filled spikelet per panicle	174.10	91.00	350.50	29.43	25.59	75.60	79.80	45.84
Spikelet fertility %	79.54	44.00	94.65	12.88	8.15	40.04	8.45	10.62
1000 seed weight	18.16	10.15	31.50	26.73	26.49	98.21	9.82	54.09
Harvest index	30.74	11.55	48.75	32.33	26.07	65.05	13.32	43.32
Kernel length	5.54	4.05	6.95	10.91	10.81	98.24	1.22	21.98
Kernel breadth	2.10	1.75	2.60	9.96	9.28	86.78	0.37	17.73
Kernel length : breadth ratio	2.66	1.80	3.31	12.14	11.55	90.47	0.60	22.53
Grain length	8.56	5.75	10.55	11.28	11.21	98.92	1.96	22.88
Grain breadth	2.64	2.10	3.27	10.29	9.98	94.11	0.53	19.92
Grain length to breadth ratio	3.27	2.08	4.57	13.64	13.29	94.95	0.87	26.58
Head rice recovery %	51.59	34.22	68.45	19.11	18.82	96.99	19.61	38.02
Amylose content (%)	22.09	16.75	28.60	12.75	11.96	87.95	5.09	23.03
Hulling percentage	71.93	54.96	78.84	7.74	7.55	95.10	10.86	15.10
Milling percentage	65.39	50.91	73.71	7.96	7.58	90.76	9.69	14.82
Grain yield per plant	13.80	5.40	22.10	36.71	27.98	58.12	6.07	43.96

(96.40), filled spikelet per panicle (79.80), plant height (45.52), days to maturity (22.43), head rice recovery percentage (19.61), days to 50% flowering (18.96) and harvest index (13.32), hulling percentage (10.86). Similar findings were reported earlier by Ekka et al. [25], Islam et al. [24], Konate et al. [26] and Sudeepthi et al. [12]. High (>20 %) genetic advance as percent mean were obtained 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 ( $r_p=0.207^*$ ;  $r_g=0.255^{**}$ ), days to maturity ( $r_p=0.218^*$ ;  $r_g=0.275^{**}$ ), effective tillers per plant ( $r_p=0.387^{**}$ ;  $r_g=0.454^{**}$ ), harvest index ( $r_p=0.810^{**}$ ;  $r_g=0.918^{**}$ ), spikelet fertility percentage ( $r_p=0.191^*$ ;  $r_g=0.309^{**}$ ), 1000 seed weight ( $r_p=0.276^{**}$ ;  $r_g=0.363^{**}$ ). Total tillers per plant ( $r_g=0.271^{**}$ ) 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 ( $r_g=-0.239^*$ ) at genotypic level. Panicle length ( $r_g=-0.009$ ) at genotypic level, number of spikelet per panicle ( $r_p=-0.146$ ) and plant height ( $r_p=-0.095$ ;  $r_g=-0.153$ ), filled spikelet per panicle ( $r_p=-0.159$ ;  $r_g=-0.156$ ) 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 ( $r_g=0.138$ ) at genotypic level and panicle length ( $r_p=0.064$ ) 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], Thippiani 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	<b>1.000</b>											
Days to maturity	0.997**	<b>1.000</b>										
Plant height	0.435**	0.428**	<b>1.000</b>									
Total tillers/plant	0.158	0.176	0.022	<b>1.000</b>								
Effective tillers/plant	0.225*	0.247*	-0.070	0.777**	<b>1.000</b>							
Panicle length	0.061	0.060	0.531**	-0.116	-0.241*	<b>1.000</b>						
Number of spikelet/panicle	0.011	0.004	0.084	-0.257**	-0.246*	0.145	<b>1.000</b>					
Filled spikelet/panicle	-0.006	-0.016	0.094	-0.420**	-0.326**	0.079	0.870**	<b>1.000</b>				
Spikelet fertility %	-0.140	-0.152	-0.081	-0.097	-0.017	0.016	-0.091	0.130	<b>1.000</b>			
1000 seed weight	-0.051	-0.057	-0.107	-0.118	-0.024	0.027	-0.534**	-0.362**	0.248*	<b>1.000</b>		
Harvest index	0.096	0.101	-0.352**	0.057	0.226*	-0.067	-0.050	-0.063	0.115	0.234*	<b>1.000</b>	
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**	<b>1.000</b>

\*\*= 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	<b>1.000</b>											
Days to maturity	0.997**	<b>1.000</b>										
Plant height	0.439**	0.432**	<b>1.000</b>									
Total tillers/plant	0.314**	0.361**	0.049	<b>1.000</b>								
Effective tillers/plant	0.414**	0.463**	-0.130	0.542**	<b>1.000</b>							
Panicle length	0.068	0.066	0.604**	-0.108	-0.415**	<b>1.000</b>						
Number of spikelet/panicle	0.007	-0.001	0.096	-0.539**	-0.507**	0.131	<b>1.000</b>					
Filled spikelet/panicle	-0.002	-0.015	0.115	-0.666**	-0.419**	0.059	0.954**	<b>1.000</b>				
Spikelet fertility %	-0.221*	-0.240*	-0.136	-0.280**	-0.178	-0.106	-0.131	0.172	<b>1.000</b>			
1000 seed weight	-0.053	-0.059	-0.108	-0.249*	-0.059	0.013	-0.595**	-0.417**	0.419**	<b>1.000</b>		
Harvest index	0.104	0.115	-0.431**	0.100	0.525**	-0.150	-0.061	-0.078	0.195*	0.278**	<b>1.000</b>	
Grain yield/plant	0.255**	0.275**	-0.153	0.138	0.454**	-0.009	-0.239*	-0.156	0.309**	0.363**	0.918**	<b>1.000</b>

**Table 6. Direct and indirect effects of different characters on grain yield per plant at genotypic level**

	<b>DF</b>	<b>DM</b>	<b>PH</b>	<b>TTP</b>	<b>ETP</b>	<b>PL</b>	<b>NSP</b>	<b>FSP</b>	<b>SF %</b>	<b>TW</b>	<b>HI</b>	<b>GYP</b>
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	0.309**
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, FS: 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.

#### ACKNOWLEDGEMENT

The authors are highly thankful to the financial assistance from the Indira Gandhi Krishi Vishwavidyalaya, Raipur, India for providing all the financial and physical support for Post graduate research work.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

#### REFERENCES

1. Anonymous. Report of expert consultation on the technological evolution and impact for sustainable rice production in Asia and Pacific; FAO-RAP Publ. No. 1996/14, 20 pp. FAO-RAP Bangkok, Thailand;1996.
2. Sao, Abhinav, Panigrahi, Praveen, Kumar, Prafull, Sahu, Hemant. Molecular Distinguishness among rice (*Oryza sativa* L.) landrace of Central India using microsatellite markers. Intl. J. Chemi. Stud. 2020;8(4):1046-1050.
3. Fisher RA. The correlation between relatives on the supposition of Mendelian inheritance. Trans. R. Edinb. 1918;53:399-433.
4. Burton GN. Quantitative inheritance in grasses. Proceedings of Sixth International Grassland Congress. 1952;277-283.
5. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlations in soybean and their implications in selections. J. of Agro. 1955;477-483.
6. Dewey DR, Lu KH. Correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomy Journal. 1959;51:515-518.
7. Mohanty, Nibedita, Sekhar, M. Reddi, Reddy, D. Mohan and Sudhakar P. Genetic variability and character association of agro-morphological and

- quality characters in rice. *Oryza*. 2012;49(2):88-92.
8. Tuwar, Ashok Kumar, Singh SK, Sharma, Amita, Bhati PK. Appraisal of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). *Biolife, An International Quarterly Journal of Biology & Life Sciences*. 2013;1(3):84-89.
  9. Singh AK, Nandan R, Singh PK. Genetic variability and association analysis in rice germplasm under rainfed conditions. *Crop Res.* 2014;47 (1, 2 & 3):7-11.
  10. Acharya, Shiva, Shrestha, Abhisek, Acharya, Narayan, Poudel, Ankur and Acharya, Suvarna. Genetic variability, heritability and correlation analysis in quantitative traits of irrigated rice (*Oryza Sativa* L.). *Biosciences Biotechnology Research Asia*. 2018;15(3):729-735.
  11. Priyanka, Sao, Abhinav, Gauraha, Deepak. Genetic variability studies for yield and quality parameters in aromatic breeding lines of rice (*Oryza sativa* L.). *Journal of Pharmacology and Phytochemistry*. 2020;9(6):1637-1640.
  12. Sudeepthi K, Srinivas T, Kumar BNVS, Ravi, Jyothula DPB, Umar, Nafeez. Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). *Ele. J. of Pl. Breed*. 2020;11(1):144-148.
  13. Akter T, Ivy NA, Rasul MG, Mian MAK. Variability and character association of reproductive traits in exotic rice germplasm. *Bangladesh J. Pl. Breed. Genet*. 2010;23(1):39-43.
  14. Dhanwani, Rakesh Kumar, Sarawgi AK, Solanki, Akash, Tiwari, Jitendra Kumar. Genetic variability analysis for various yield attributing and quality traits in rice (*O. sativa* L.). *The Bioscan*. 2013;8(4):1403-1407.
  15. Sharma, Amita and Koutu, GK. Study of heritability, genetic advance and variability for yield attributing characters in exotic germplasm of rice. *Oryza*. 2013;50(4):404-408.
  16. Nirmaladevi G, Padmavathi G, Kota, Suneetha, Babu VR. Genetic variability, heritability and correlation coefficients of grain quality characters in rice (*Oryza sativa* L.). *SABRAO J. Breed. Genet.*, 2015;47 (4):424-433.
  17. Singh PK, Birah, Ajanta, Singh, Awnindra K, Gautam SK, Ahmed, Zamir, Roy SK. Dam. Genetic variability and characters association among quality traits of medium duration rice under island conditions. *Oryza*. 2016;53(2):196-200.
  18. Aditya JP, Bhartiya, Anuradha. Genetic variability, correlation and path analysis for quantitative characters in rainfed upland rice of Uttarakhand hills. *Journal of Rice Research*. 2013;6(2):24-34.
  19. Rashid MM, Nuruzzaman M, Hassan L, Begum SN. Genetic variability analysis for various yield attributing traits in rice genotypes. *J. Bangladesh Agril. Univ*. 2017;15(1):15–19.
  20. Akinwale MG, Gregorio G, Nwilene F, BO, Akinyele, Ogunbayo SA, Odiyi AC. Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *African Journal of Plant Science*. 2011;5 (3):207-212.
  21. Babu V. Ravindra, Shreya K, Dangi, Kuldeep Singh, Usharani G, Nagesh P. Genetic variability studies for qualitative and quantitative traits in popular rice (*Oryza sativa* L.) hybrids of India. *Intl. J. of Sci. and Res. Pub*. 2012;2(6):1-5.
  22. Karuppaiyan R, Kapoor, Chandan, Gopi R. Variability, heritability and genetic divergence in lowland rice genotypes under the mid-hills of Sikkim. *Oryza*. 2013;50(1):81-84.
  23. Chouhan SK, Singh AK, Singh, Aparajita, Singh NK, Yadav, Sujit Kumar, Singh PK. Genetic variability and association analysis in wild rice (*Oryza nivara* and *Oryza rufipogon*). *Ann. of Pl. and Soil Res*. 2014;16(3):219-223.
  24. Islam MA, Raffi SA, Hossain MA, Hasan AK. Analysis of genetic variability, heritability and genetic advance for yield and yield associated traits in some promising advanced lines of rice. *Progressive Agriculture*. 2015;26:26-31.
  25. Ekka, Ruth Elizabeth, Sarawgi AK, Kanwar Raja R. Genetic variability and inter-relationship analysis for various yield attributing and quality traits in traditional germplasm of rice (*Oryza sativa* L.). *Plant Archives*. 2015;15(2):637-645.
  26. Konate, Abdourasmane K, Zongo, Adama, Kam, Honore, Sanni, Ambaliou and Audebert, Alain. Genetic variability and correlation analysis of rice (*Oryza sativa* L.) inbred lines based on agromorphological traits. *African Journal of Agricultural Research*. 2016;11(35):3340-3346.

27. Sarangi DN, Pradhan B, Sial P, Mishra, CHHP. Genetic variability, correlation and path-coefficient analysis in early rice genotypes. *Env. & Eco.* 2009;27 (1A): 307-312.
28. Khare R, Singh AK, Eram S, Singh PK. Genetic variability, association and diversity analysis in upland rice (*Oryza sativa* L). *SAARC J. Agri.*, 2014;12(2):40-51.
29. Devi K. Rukmini, Parimala K, Venkanna V, Lingaiah N, Hari Y, Chandra B. Satish. Estimation of variability for grain yield and quality traits in rice (*Oryza sativa* L.). *Int. J. Pure App. Biosci.*, 2016;4(2): 250-255.
30. Edukondalu B, Reddy V, Ram, Rani, T. Shobha, Kumari, Ch. Aruna, Soundharya B. Studies on variability, heritability, correlation and path analysis for yield, yield attributes in rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci.*, 2017;6(10):2369-2376.
31. Naik Deepak, Sao Abhinav, Sarawgi AK. Association analysis for quality and yield components in some indigenous scented rice accessions. *Indian J. of Pl. Gen. Reso.* 2005;18(2):266-268.
32. Rashid, Kashif, Khaliq, Ihsan, Farooq, Muhammad Omer and Ahsan, Muhammad Zahir. Correlation and cluster analysis of some yield and yield related traits in rice (*Oryza sativa* L.). *Intl. JI of Agril. Sci. and Res.*, 2013;3(4):25-30.
33. Kumar, Prafull, Sao, Abhinav, Mukherjee SC, Netam RS. Secondary genetic productivity factors (SGPFs) in expression of grain yield in rainfed upland rice of Bastar plateau. *Asian J. of Bio. Sci.* 2015;10(2):174-177.
34. Thippani , Srikanth, Kumar, S. Sudheer, Senguttavel, P., Madhav, M. Sheshu. Correlation analysis for yield and yield components in rice (*Oryza sativa* L.). *Int. J. Pure App. Biosci.*, 2017;5(4):1412-1415.
35. Kalyan B, Krishna KV, Radha, Rao LV. Subba. Correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.) genotypes. *Int. J. Curr. Microbiol. App. Sci.* 2017;6(7):2425-2430.
36. Nanda, Kalpataru, Bastia DN, Nanda, Ashutosh. Character association and path coefficient analysis for yield and its component traits in slender grain rice (*Oryza sativa* L.). *Ele. J. of Pl. Breed.*, 2019;10 (3):963-969.
37. Surek, Halil, Beser, Necmi. Correlation and path coefficient analysis for some yield-related traits in rice (*Oryza Sativa* L.) under thrace conditions. *Turk. J. Agric. For.* 2003;27:77-83.
38. Kumar, Sujeet, Singh PK, Verma OP, Verma GP, Singh Karan, Chaudhary RK, Kumar Manoj. Interrelationships for yield and component traits in rainfed upland rice. *Oryza.* 2012;49(1):57-59.
39. Nayak R, Singh, Vivek K, Singh AK, Singh PK. Genetic variability, character association and path analysis of rice genotypes. *Ann. of Pl. and Soil Res.* 2016;18(2):161-164.
40. Jaiswal HK, Srivastava AK, Dey A. Variability and association studies in indigenous aromatic rice (*Oryza sativa* L.). *Oryza.* 2007;44(4):351-353.
41. Debnath, Keya, Das, Bimal, Sikder, Subhamoy, Sarkar KK. Assessment of genetic variability character association and path coefficient for yield and its component characters in rice. *The Ecoscan.* 2015;9(1&2):455-459.
42. Gupta, Sneha, Upadhyay, Sameer, Koli, Ganesh Kumar, Rathi, Sanket Rajendra, Bisen, Prashant, Loitongbam, Bapsila, Singh, Pawan Kumar and Sinha, Brajesh. Trait association and path analysis studies of yield attributing traits in rice (*Oryza sativa* L.) Germplasm. *Intl. J. of Bio-reso. and Stre. Man.* 2020;11(6):508-517.

© 2021 Noatia et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

*Peer-review history:*

The peer review history for this paper can be accessed here:  
<https://www.sdiarticle4.com/review-history/71653>