# Genetic Variability, Correlation and Path Analysis Studies in Early Transplanted Rice

## Prathamesh Kalpande [a++], Milind Meshram [b#*] and Vaishali Borkar [b†]

*[a] College of Agriculture, Nagpur, Maharashtra, India.*
*[b] ARS, Sakoli, Dist. Bhandara, Maharashtra, India.*

***Authors' contributions***

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

*Original Research Article*

## ABSTRACT

**Aims:** The aim of this study was to evaluate the genetic variation, heritability, and direct and indirect effects of various traits on grain yield in 64 rice genotypes under early transplanted conditions.
**Study Design:** The study utilized a randomized block design with two replications.
**Place and Duration of Study:** The research was conducted at the Agriculture Research Station, Sakoli, District. Bhandara under Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra, India during the Kharif season of 2022.
**Methodology:** The experimental material comprised 64 rice genotypes along with the regional check Sakoli-6. Observations were recorded on the following traits: days to 50% flowering, days to

_____

[++] *Post Graduate Student;*
[#] *Junior Rice Breeder;*
[†] *Technical Assistant;*
*Corresponding author: E-mail: mpmeshram358@gmail.com;*

maturity, plant height (cm), number of panicles per square meter (panicles/m²), and grain yield (kg/ha). Data were analyzed for genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance, correlation, and path analysis to determine the direct and indirect effects of these traits on grain yield in early transplanted condition.

**Results:** High GCV and PCV were observed for grain yield, with moderate values for the number of panicles/m², indicating significant variability conducive to improvement. Grain yield, number of panicles/m², and plant height exhibited high heritability and genetic advance. Whereas, correlation analysis showed significant positive correlations between the number of panicles/m² and grain yield, and significant negative correlations between days to 50% flowering and days to maturity with grain yield. Path analysis indicated that days to 50% flowering, followed by the number of panicles/m² and plant height, had the highest positive direct effects on grain yield.

**Conclusion:** The study identified the number of panicles/m² as a critical trait for selecting superior genotypes. Based on these findings, the rice genotypes RP 6496-JB 202-4-6-1-1-1-1, OR 2800-4, and KNM 13557 were recommended for further breeding programs under early transplanted conditions.

## 1. INTRODUCTION

"Rice is a staple food of world as well as in India, whereas India ranks first in area and second in production after China. Rice is a self-pollinated crops belonging to genus *Orzya* of the family Poaceae having chromosome number 2n = 24 comprising two species, *Orzya sativa* L. and *Orzya glaberrima* Steud. *Oryza sativa* L. is cultivated in all countries worldwide whereas *Oryza glaberrima* Steud. specifically cultivated in West African countries" [1]. The demand for food will be doubled by the year 2025 and tripled by 2050 [2]. In 2022-23, rice occupied an area of around 47,000 ha, resulting in a production of 2 lakh tons, indicating a productivity of 4.3 tons ha$^{-1}$ [3]. "With rising food security, various climate changes and increasing population pressure, improving rice yield becomes a critical challenge for breeders. In addition to solving the problem by understanding genetic variability, correlation and path analysis of agronomically important characters holds prime importance" [3].

Early transplanting is the cultural practice aimed at exploiting favorable environmental conditions, which have the potential for resource utilization and significant improvement in yield [4]. However, the effectiveness of early transplanted rice highly depends on the genetic composition of the varieties, as different varieties respond differently in various environments [5-7].

"The advancement in breeding for yield and yield contributing characters in any crop is governed by polygenic inheritance and also affected by environmental influence which is determined by the extent and nature of their genetic variability"
[8,9]. "Heritability is the extent to which a trait can be transmitted in further generations, whereas for crop improvement in any crop the knowledge of heritability of the character holds prime importance that too in association with genetic advance which states genetic gain under selection along with heritability of the trait" [10]. "Character association revels the relative influence of the attributing characters on grain yield. Path analysis revels the influence of each contributing trait to yield directly as well as indirectly and also enable the breeders to rank the genetic attributes according to their contribution" [2].

Considering all above points, the present investigation was undertaken to understand genetic variability, correlation and path analysis of yield and yield contributing characters in rice genotypes in early transplanted condition.

## 2. MATERIALS AND METHODS

The present investigation was carried out at research farm of Agriculture Research Station, Sakoli, District. Bhandara under Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra, India during *kharif* 2022 using 64 rice genotypes with the help of randomized block design in two replications in early transplanted condition. The nursery was sown in raised beds and healthy nursery was raised following uniform package of practices. Twenty-one days old seedlings were transplanted at spacing of 20 cm x 15 cm and observations were recorded on five randomly selected plants *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of panicles per meter square

(panicles/m$^2$) and grain yield (kg/ha). The experimental materials for experiment were comprised of 63 genotypes (Table. 1) along with one regional check Sakoli-6. Fertilizer dose of 100 kg N, 50 kg P$_2$O$_5$ and 50 kg K$_2$O was applied. The standard agronomic practices were adopted for normal crop growth.

The data underwent statistical analysis as recommended by Panse and Sukhatme [11] for analysis of variance using a randomized block design. Meanwhile, parameters of genetic variability, including mean, range, genotypic, and phenotypic coefficient of variation, were computed following the method outlined by Burton and Devane [12]. Broad-sense heritability for grain yield and its components was determined using the formula proposed by Burton and Devane [12]. Genetic advancement was calculated using the method suggested by Johnson *et al.* [13]. Genotypic and phenotypic correlation coefficients for all possible comparisons were computed according to the formula provided by Johnson *et al.* [13]. The partitioning of genotypic and phenotypic correlation coefficients into direct and indirect effects was carried out using the procedure outlined by Dewey and Lu [14].

## Table 1. List of genotypes under study

| Code No. | Designation | Code No. | Designation |
|---|---|---|---|
| 3601 | RP 6112- MS-M-4-11-5-3-7- 9-4-1 | 3633 | RP 6496-JB 202-4-6-1-1-1-1 |
| 3602 | Pusa 2091-26 | 3634 | KNP-241 |
| 3603 | JGL 28639 | 3635 | CR 3506-1-2-3-1-2-1 |
| 3604 | CR 4075-1341-3-3-2-2-1-4-3 | 3636 | R 1902-97-1-77-1 |
| 3605 | CR 4401-1-7-IR 117834-10-1 RGA-1 RGA-1 RGA-1 | 3637 | WGL 1719 |
| 3606 | CSR AP10 | 3638 | OR 2800-4 |
| 3607 | CSR M1-4 | 3639 | KPS-10321 |
| 3608 | RNR 35105 | 3640 | CR 4388-RGA-245 |
| 3609 | KNM 12509 | 3641 | HKR 18-32 |
| 3610 | CR 3745-3-2-1-2-1-1 | 3642 | RCPR 95-IR 97046-39-2-1-2 |
| 3611 | CB 18611 | 3643 | Sahbhagidhan |
| 3612 | RP 6468-JB 396-9-7-2-1-1-1 | 3644 | CRR-DH8 |
| 3613 | NVSR 3211 | 3645 | RP 5599-240-B-7-3 (PSV-56) |
| 3614 | NWGR-16032 | 3646 | CR 4386-RGA-134 |
| 3615 | AD 19215 | 3647 | TRC H2N 422-B-B-7-4 |
| 3616 | CR 4396-1-13-11 | 3648 | HURS 19-9-IR 128773-4-3-1-4-B |
| 3617 | TRC B3N 693-B-B-9-4 | 3649 | UPR 4304-12-1-1-1 |
| 3618 | CO-51 (NC) | 3650 | RP-6529-1780-28-7-16 |
| 3619 | RCPR 94-IR97030-7-2-2-2 | 3651 | CB 17529 |
| 3620 | RP 6166-47-1-23 | 3652 | MTU 1390 (IR17M1172) |
| 3621 | CSR M1-5 | 3653 | CR 3842-62-5-1-1-1 |
| 3622 | CR 3516-11-2-2-1-15 | 3654 | NWGR-16034 |
| 3623 | KJTR 4 | 3655 | IIABR-10 / IIAB-309/IR 13T144 |
| 3624 | IIABR-9/IIAB-54/IR 16A3098 | 3656 | CRR - DH6 |
| 3625 | WGL 1720 | 3657 | RP 6680- RMS-1703-55-89-66 |
| 3626 | AD (Bio) 13060 | 3658 | NVSR 750 |
| 3627 | ORJ 1345 (TP 30531) | 3659 | RNR 35109 |
| 3628 | KNM 13557 | 3660 | RP 6420-C10-269-12 |
| 3629 | CR 3843-22-2 | 3661 | NDR 8806-TFR-3 |
| 3630 | BRR 0156 | 3662 | RDR-2747 |
| 3631 | UPR 4546-4-1-1-1 | 3663 | CRR 778-B-B-2-2 |
| 3632 | AD 18028 | 3664 (LC) | SKL-6 |

# 3. RESULTS AND DISCUSSION

## 3.1 Analysis of variance

Analysis of variance revealed significant differences for all traits studied (Table 2). Variance due to genotype was highly significant for all the traits indicating the presence of significant variability in all 64 genotypes under study. The estimates of genetic variability parameter showed that phenotypic variability is higher than genotypic variability indicating the influence of environment on expression of the traits.

## 3.2 Genetic Variability

Among the yield attributes, maximum PCV and GCV was depicted by grain yield (23.97, 20.40) having high GCV and PCV *i. e.* above 20% followed by number of panicles /m$^2$ (17.96, 17.62) which reported into moderate level ranged between 10 – 20% and in low variability (<10%) for the trait's days to 50% flowering (6.68, 6.64), plant height (6.48, 6.44) and days to maturity (5.03, 4.99) (Table 3). A close resemblance of phenotypic and genotypic variation for all the characters indicates stable expression of attributes and absence of high environmental influence. In the present study, grain yield and number of panicles /m$^2$ reported high variation in these traits and predicting greater scope for improvement of these traits. Similarly, Williams *et*

*al.* [1] reported higher estimates for number of panicles per hill and grain yield.

The highest heritability (%) was recorded for plant height (98.97%) followed by days to 50% flowering, days to maturity (98.60%) and number of panicles /m$^2$ (96.20%). Similar results were exhibited by Akinwale *et al.* [15] for rice genotypes with high heritability for days to heading, days to maturity, plant height, grain yield and number of panicles /m$^2$. The higher genetic advance as per cent of mean observed for grain yield (35.75) followed by number of panicles per m$^2$ (35.60) which is followed by days to 50% flowering (13.58) and plant height (13.20) indicating high genetic advance as per cent of mean. Whereas, days to maturity (10.22%) reported moderate level of genetic gain as per cent of mean. Since high heritability do not always indicate high genetic gain, heritability with genetic advance considered together should be used in predicting the ultimate effect for selecting superior varieties [15]. In the present investigation, all the traits showed high heritability with high genetic gain except for days to maturity reporting moderate gain as per cent of mean. For selection, it can be concluded that on the basis of variation, heritability and genetic advance as per cent of mean, the characters grain yield, number of panicles /m$^2$ and plant height holds prime importance. Similar results were also reported by Akinwale *et al.* [15], Sheena and Lavanya [2] and Kavyashree *et al.* [16].

**Table 2. Analysis of variance for grain yield and yield contributing characters of rice**

| Source of variation | Degrees of freedom | Days to 50% flowering | Days to maturity | Plant height (cm) | Number of panicles per m$^2$ | Grain yield (g) |
|---|---|---|---|---|---|---|
| Replication | 1 | 1.76 | 1.76 | 0.13 | 132.03 | 65868.72 |
| Treatment | 63 | 73.93** | 73.93** | 94.65** | 4010.82** | 1732667.30** |
| Error | 63 | 0.52 | 0.52 | 0.49 | 77.68 | 277523.68 |

*\*, \*\* Significant at 5% and 1% level of significance*

**Table 3. Estimates of heritability, genotypic and phenotypic coefficient of variation, and genetic advance and genetic advance as per cent of mean in rice genotypes**

| Characters | Heritability | GCV | PCV | GA | GAM |
|---|---|---|---|---|---|
| Days to 50% flowering | 98.60 | 6.64 | 6.68 | 12.39 | 13.58 |
| Days to maturity | 98.60 | 4.99 | 5.03 | 12.39 | 10.22 |
| Plant height | 98.97 | 6.44 | 6.48 | 14.06 | 13.20 |
| Number of panicles per m$^2$ | 96.20 | 17.62 | 17.96 | 89.60 | 35.60 |
| Grain yield | 72.39 | 20.40 | 23.97 | 1495.12 | 35.75 |

### 3.3 Correlation Analysis

In the study, genotypic correlation coefficient was higher in magnitude for almost all traits than phenotypic coefficient indicating the depression of phenotypic expression by environmental influence (Table 4). Number of panicles per $m^2$ showed highly positive significant correlation with grain yield followed by positive correlation with plant height in early transplanted situation. However, days to 50% flowering and days to maturity showed negative significant correlation with grain yield. Whereas, days to 50% flowering and days to maturity showed highest positive correlation between them and number of panicles per $m^2$ reported negative significant correlation with days to 50% flowering and days to maturity. Similar results were reported by Ogunbayo et al. [17], where grain yield showed highly positive correlation with number of panicles per $m^2$. Kavyashree et al. [16] also reported negative correlation between grain yield and days to 50% flowering along with flag leaf length. Kiran et al. [18] reported days to maturity as negatively correlated to grain yield.

### 3.4 Path analysis

Path analysis offers plant breeders to study direct and indirect effects simultaneously with multiple independent and dependent variables. In the present investigation, direct and indirect effect was represented in Table 5. The residual effect was found to be 0.1683 which reveals that sufficient characters were included in the path coefficient and hence the information drawn can be used. Direct effect of any character on yield gives an idea about effective selection of traits that can be made to bring improvement in breeding program. The indirect effect indicates the inter-relationship of component characters towards contribution of yield [19]. Days to 50% flowering (0.8619) exhibited highest direct effect on seed yield followed by number of panicles per $m^2$ (0.7933) and plant height (0.0986) whereas negative effect was reported by the trait days to maturity (-1.1362). In indirect effect on grain yield reported highest by number of panicles per $m^2$ (0.8671) followed by plant height (0.0460) and negative effect was reported in relation with days to 50% flowering (-0.5126) and days to maturity (-0.5114). Sheena and Lavanya [2] reported positive direct effect of number of panicles per hill, panicle length, test weight, number of spikelet per panicle, biological yield with grain yield per plant and negative direct effects with days to 50% flowering, days to maturity, number of tillers per hill, flag leaf width and harvest index. Results were also supported by Madishetty et al. [20] in findings showed negative effect between days to maturity and days to 50% flowering with grain yield.

**Table 4. Estimates of genotypic correlation (above diagonal) and phenotypic correlation (below diagonal) for all the traits**

| Characters | Days to 50% flowering | Days to maturity | Plant height | Number of panicles per $m^2$ | Grain yield |
|---|---|---|---|---|---|
| Days to 50% flowering | 1.00 | 1.00** | -0.02 | -0.30* | -0.51** |
| Days to maturity | 1.00** | 1.00 | -0.02 | -0.30* | -0.51** |
| Plant height | -0.02 | -0.02 | 1.00 | -0.07 | 0.05 |
| Number of panicles per $m^2$ | -0.29* | -0.29* | -0.07 | 1.00 | 0.87** |
| Grain yield | -0.44** | -0.44** | 0.05 | 0.73** | 1.00 |

*(*, ** Significant at 5% and 1% level of significance)*

**Table 5. Direct and indirect effect of different characters in grain yield at genotypic level in rice (R = 0.1683)**

| Characters | Days to 50% flowering | Days to maturity | Plant height | Number of panicles per $m^2$ | Grain yield |
|---|---|---|---|---|---|
| Days to 50% flowering | 0.8619 | -1.1367 | -0.0020 | -0.2358 | -0.5126 |
| Days to maturity | 0.8623 | -1.1362 | -0.0020 | -0.2355 | -0.5114 |
| Plant height | -0.0178 | 0.0234 | 0.0986 | -0.0583 | 0.0460 |
| Number of panicles per $m^2$ | -0.2562 | 0.3372 | -0.0072 | 0.7933 | 0.8671 |

*Values in the bold are the direct effect*

## 4. CONCLUSION

In the present investigation, based on high GCV, PCV, high heritability along with genetic advance, positive significant genotypic correlation with yield and path coefficient analysis studied in this experiment, suggested only one character *i.e.,* number of panicle /m² was useful under selection in early transplanted condition. Considering this character, RP 6496-JB 202-4-6-1-1-1-1, OR 2800-4 and KNM 13557 are isolated as superior genotypes over all the genotypes for further rice breeding program in early transplanted condition.

## COMPETING INTERESTS

Authors have declared that no competing interests exist.

## REFERENCES

1. Williams K, Mishra A, Akansha Verma, Suresh BG and Lavnya GR. Genetic variability and correlation studies for yield and yield related traits in Rice (*Oryza sativa* L.) genotypes. Int. J. Curr. Microbiol. App. Sci. 2021;10 (1): 752-764.
2. Sheena Shaik and Roopa Lavanya G. Genetic variability, heritability, correlation and path analysis of yield component characters in Rice (*Oryza sativa* L.) genotypes. Int. J. Environ. Clim. Change. 2023;13 (8): 2118-2127.
3. USDA report - India Rice Area, Yield and Production; 2024.
Available:https://ipad.fas.usda.gov/country summary/Default.aspx?id=IN&crop=Rice
4. Pasuquin E, Lafarge T and Tubana B. Transplanting young seedlings in irrigated rice fields: Early and high tiller production enhanced grain yield. Field Crops Res. 2008;105 (1-2):141-155.
5. Khaire AR, Singh SK, Vijay HS, Mounika K, Singh DK, Jayasudha ., Singh A, Majhi PK, Madankar KS. Analysis of Rice (Oryza sativa L.) Accessions Genetic Variability Related to Yield and Its Components. Curr. J. Appl. Sci. Technol. [Internet]. 2022 Sep. 20 [cited 2024 May 22];41(33):41-9.
Available:https://journalcjast.com/index.php/CJAST/article/view/3950
6. Manjunatha B, Kumara BN. Genetic Variability Analysis for Quantitative Traits in Rice (Oryza sativa L.). J. Exp. Agric. Int. [Internet]. 2019 Feb. 9 [cited 2024 May 22];30(4):1-4.
Available:https://journaljeai.com/index.php/JEAI/article/view/1239
7. Guleria S, Aggarwal R, Thind TS, Sharma TR. Morphological and pathological variability in rice isolates of Rhizoctonia solani and molecular analysis of their genetic variability. Journal of Phytopathology. 2007 Dec;155(11-12):654-61.
8. Wright S. The analysis of variance and correlations between relative with respect to deviations from an optimum. J. Genetics. 1935;30.
9. Fisher RA. The correlation among relative on the supposition of Mendelian Inheritance. Trans. Royal Soc. Edinberg. 1981;52: 314-318.
10. Ajmera S, Kumar SS and Ravindra babu V. Evaluation of genetic variability, heritability and genetic advance for yield and yield components in rice genotypes. Int. J. Curr. Microbiol. App. Sci. 2017; 6 (10):1657-1664.
11. Panse VG and Sukhatme PV. Statistical methods for agricultural workers. 2nd Edn ICAR, New Delhi pp. 1961; 361.
12. Burton GW and Devane EH. Estimating heritability in tall fescue (*Festuca arundinacea* Schreb.) from replicated clonal material. Agron J. 1953; 45: 478-481.
13. Johanson HW, Robinson HF and Comstock RE. Estimates of genetic and environmental variability in soybean. Agron. J. 1955; 47 (7): 314- 315.
14. Dewey DR and Lu KH. Correlation and path coefficients analysis of components of crested wheat grass seed production. Agron. J., 1959; 51: 575-581.
15. Akinwale MG, Gregorio G, Nwilene F, Akinyele BO, Ogunbayo SA, and Odiyi AC. Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). Afr. J.Plant Sci. 2011; 5(3):207-212.
16. Kavyashree NM, Diwan JR, Mahantashivayogayya K, Lokesha R and Naik NM. Genetic variability and correlation studies on yield and yield-related traits in Rice (*Oryza sativa* L.) and their implications in selection. BFAIJ. 2022; 14 (1):595-600.
17. Ogunbayo SA, Sie M, Ojo DK, Sanni KA, Akinwale MG, Toulou B, *et al.* Genetic variation and heritability of yield and related traits in promising rice genotypes

(*Oryza sativa* L.) J. Plant Breed. Crop Sci. 2014; 6(11):153-159.

18. Kiran AK, Sharma DJ, Subbarao LV, Gireesh C and Agrawal AP. Correlation coefficient and path coefficient analysis for yield, yield attributing traits and nutritional traits in rice genotypes. J. Pharm. 2023;12 (2):1978-1983.

19. Singh S, Kumar V, Singh SK and Daneva V. Genetic variability, interrelation and path analysis for yield and yield characters in Indian mustard (*Brassica juncea* L.). Journal of oilseed Brassica. 2022; 13 (2):112-118.

20. Madishetty AR, Gaibriyal ML and Adarsh K. Genetic variability and correlation studies for yield and yield related traits in Rice (*Oryza sativa* L.) Int. J. Plant Sci. 2023; 35 (20):1165-1176.

---

---