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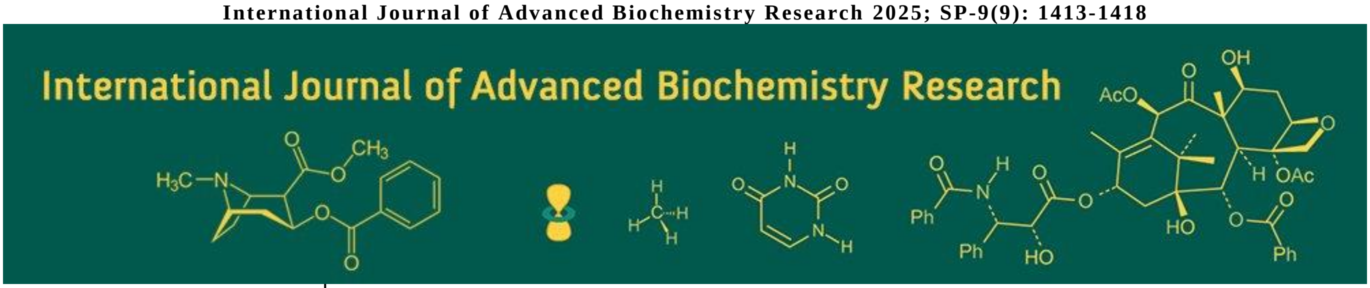

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# Evaluation of advanced breeding lines of rice (*Oryza sativa* L.) for enhancing yield potential

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## Abstract

The present investigation entitled “Evaluation of advanced breeding lines of rice (*Oryza sativa* L.) for enhancing yield potential” was carried out during *Kharif* 2024 at the Instructional cum Research Farm, S.G. College of Agriculture and Research Station, Jagdalpur, Bastar (C.G.). Fourteen advanced breeding lines including checks were evaluated in a Randomized Block Design with three replications to assess genetic variability and to study association among yield and its attributing traits. Analysis of variance revealed highly significant differences among genotypes for all traits, indicating substantial genetic variability. High heritability with high genetic advance was observed for number of filled grains per panicle and grain yield, suggesting the predominance of additive gene action. Correlation analysis revealed grain yield had a strong positive association with biological yield and panicle length. Path analysis further confirmed biological yield exerted the highest direct effect on grain yield, followed by kernel and grain L:B ratios. These results suggest that selection for these traits could effectively enhance yield potential in rice breeding programs.

**Keywords:** Genetic variability, heritability, correlation, path analysis, yield-attributing traits, rice (*Oryza sativa* L.), breeding lines, biological yield

## Introduction

Rice (*Oryza sativa* L.) is one of the most important staple food crops, feeding more than half of the global population. It contributes nearly 75% of daily calorie intake and about 55% of protein intake in Asia, where nearly 90% of the world’s rice is produced and consumed (Devi *et al*., 2020) [7]. Globally, rice is cultivated on 168.36 million hectares with a production of 532.7 million metric tonnes and productivity of 5830 kg ha$^{-1}$ (Anonymous, 2025a) [1]. India ranks as the largest producer and consumer of rice, accounting for 27% of world production with 147 million tonnes during 2024 and productivity of 3570 kg ha$^{-1}$ (Anonymous, 2025b) [2]. Chhattisgarh, often called the “Rice Bowl of India,” has 3.82 million hectares under rice cultivation, producing 9.73 million tonnes with an average productivity of 2708 kg ha$^{-1}$ (Anonymous, 2025c) [3]. Despite its importance, rice productivity in Chhattisgarh remains below the national average due to limited irrigation, suboptimal agronomic practices, and lack of high-yielding varieties suitable to diverse ecosystems. Narrowing genetic base and increased vulnerability of modern cultivars further threaten yield stability (Choudhary *et al*., 2013) [6]. Hence, there is an urgent need to broaden the genetic base through evaluation and utilization of advanced breeding lines with desirable agronomic traits. Yield in rice is a complex quantitative trait governed by polygenic interactions and strongly influenced by the environment. Thus, direct selection for yield alone may be misleading. Understanding genetic variability, heritability, and genetic advance provides insight into the extent of transmissible variation available for selection (Paul *et al*., 2006) [17]. Similarly, correlation analysis helps to determine the degree of association among yield-attributing traits, while path coefficient analysis partitions these correlations into direct and indirect effects, thereby identifying key traits contributing effectively to yield (Dewey and Lu, 1959) [8]. Considering these aspects, the present investigation was undertaken with the following objectives: To assess the genetic variability for yield and attributing traits. To study character association using correlation and path analysis.

## 2. Materials and Methods

The experiment was conducted at the Instructional cum Research Farm, S.G. College of Agriculture and Research Station, Jagdalpur, Bastar (Chhattisgarh) during *Kharif* 2024. The farm is situated at 19°04′N latitude, 81°95′E longitude, and 553 m above mean sea level. The soil is sandy loam with medium fertility. The area receives ~1200-1400 mm rainfall annually. Fourteen genotypes including checks were evaluated in Randomized Block Design (RBD) with three replications. The experimental field was properly prepared before sowing. Each genotype was transplanted in a gross plot size of 3m × 5 m and net plot size of 2.6 m× 4.6 m, maintaining a spacing of 20 cm × 15 cm (row × plant). Recommended package of practices was followed, with fertilizer application of 80:60:40 N:$P_2O_5$: $K_2O$ kg $ha^{-1}$ in split doses. The experimental material comprised 14 advanced breeding lines and including checks. Observations were taken on growth, yield, and yield contributing traits traits like days to 50% flowering and days to maturity were evaluated on a plot basis, while other traits were recorded from five randomly selected plants per plots. such as plant height (cm), number of tillers $plant^{-1}$, panicle length (cm), flag leaf length and breadth, number of filled grains $panicle^{-1}$, spikelet fertility (%), test weight (g), biological yield, harvest index (%), and grain yield (q $ha^{-1}$). Grain and kernel size measurements (length, breadth and L/B ratio) were recorded using standard methods, including digital vernier calipers. Climatic conditions during the crop period included temperatures from 10.8 °C to 34.3 °C and total rainfall of 1356.9 mm, with July receiving the highest rainfall (398.3 mm). Data were subjected to ANOVA (Panse and Sukhatme, 1967) [15] for RBD. Genetic parameters such as GCV, PCV, heritability ($H^2$), and genetic advance (GA as% of mean) were estimated. Correlation analysis was performed at phenotypic levels. Path coefficient analysis (Dewey and Lu, 1959) [8] was carried out to partition direct and indirect effects.

## 3. Results and Discussion

Analysis of variance revealed significant differences among the genotypes for all traits studied, confirming the presence of wide genetic variability. Morphological characterisation revealed a wide range of variability among the genotypes. Days to 50% flowering ranged from 88 days in Gontra Bidhan-3 to 104 days in CR 4077-1357-5-4-2-1-1, classifying two genotypes as early and twelve as medium duration. Days to maturity varied from 119 days in MTU 1010 to 134 days in CR 4077-1357-5-4-2-1-1. Plant height ranged between 101.6 cm (MTU 1010) and 128.0 cm (RRX-3341), with three genotypes falling under short stature and eleven under medium stature. The number of effective tillers per plant varied from 6 in Gontra Bidhan-3 to 11 in CR 4077-1357-5-4-2-1-1. Panicle length was found to be shortest in MTU 1010 (22.2 cm) and longest in RRX-3341 (28.2 cm). Flag leaf length ranged from 25.4 cm (MTU 1010) to 37.40 cm (LG-90303), whereas flag leaf breadth varied from 1.7 cm (CR 4077-1357-5-4-2-1-1) to 2.2 cm (CR 4415-3-1-3-1-3-1). The number of filled grains per panicle ranged from 101 (HRI-217) to 306 (NPH-X69), while spikelet fertility percentage ranged between 93.6% (HRI-217) and 96.6% (NPH-X69). Test weight varied from 23.2 g in US 312 to 26.0 g in IGKV R 1. The harvest index recorded a minimum of 37.0% (US 312) and a maximum of 47.6% in both CR 4077-1357-5-4-2-1-1 and YNPK-7258. Grain length ranged from 7.93 mm (CR 4415-3-1-3-1-3-1) to 10.03 mm (RNC-0992), while grain breadth varied from 2.36 mm (US 312) to 2.86 mm (NPH-X69). The grain L:B ratio ranged from 2.92 (NPH-X69) to 3.76 (RNC-0992). Kernel length was shortest in CR 4415-3-1-3-1-3-1 (6.03 mm) and longest in MTU 1010 (8.16 mm), whereas kernel breadth varied from 2.16 mm (US 312) to 2.70 mm (IGKV R 1). The kernel L:B ratio ranged from 2.55 (NPH-X69) to 3.55 (MTU 1010). Biological yield ranged from 90.3 q/ha (MTU 1010) to 170.1 q/ha (LG-90303), while grain yield varied between 41.70 q/ha (MTU 1010) and 77.27 q/ha (LG-90303). Similar findings were reported Islam *et al.* (2025) [12] found high heritability and genetic advance for thousand-grain weight, grain length and yield. High heritability was recorded for traits such as harvest index (98.9%), number of filled grains per panicle (95.9%), days to 50% flowering (95.4%), and grain yield (61.5%), while high heritability coupled with high genetic advance was observed for number of filled grains per panicle (47.97%) and grain yield (29.1%), indicating the predominance of additive gene action. High heritability values indicate a strong genetic component underlying trait variation and suggest effective phenotypic selection potential (Asante *et al.*, 2019; Ashfaq *et al.*, 2012) [4, 5]. In the present study, traits such as harvest index (98.9%), number of filled grains per panicle (95.9%), days to 50% flowering (95.4%), days to maturity (84.4%), grain length (67.9%), kernel L:B ratio (67.5%), plant height (66.3%), kernel breadth (61.6%), grain yield (61.5%), and kernel length (61.3%) showed high heritability, whereas number of effective tillers (58.0%), biological yield (57.5%), panicle length (55.6%), grain L:B ratio (43.4%), flag leaf breadth (36.2%), test weight (30.6%), spikelet fertility (23.0%), grain breadth (22.0%), and flag leaf length (18.7%) exhibited moderate heritability. Similar findings were reported Singh *et al.* (2024) [19] reported heritability ranging from 32% to 97%, notably, days to 50% flowering achieved the highest value at 97%. Genetic advance as percent of mean was high for number of filled grains per panicle (47.97%), grain yield (29.1%), biological yield (25.48%), number of effective tillers (20.35%). Moderate genetic advance as percent of mean was recorded for harvest index (14.77%), kernel L: B ratio (15.85%), kernel length (12.39%), grain length (10.64%), plant height (10.44%), days to 50% flowering (10.07%). Low genetic advance as percent of mean was recorded for panicle length (9.83%), kernel breadth (9.81%), grain L: B ratio (9.39%), flag leaf breadth (6.35%), flag leaf length (6.09%), Days to maturity (6.10%), grain breadth (3.22%), test weight (2.13%), spikelet fertility percentage (0.59). High heritability coupled with high genetic advance was reported for characters like number of filled grains per panicle and grain yield. Similar findings were reported Rani *et al.* (2020) [18] for plant height and days to 50% flowering; Meena *et al.* (2023) [14] for panicle length and kernel breadth. High heritability coupled with moderate genetic advance was reported for characters like harvest index, Days to 50% flowering, Grain length, kernel L: B ratio, plant height and kernel length. High heritability coupled with moderate genetic advance was reported for characters like days to maturity and kernel breadth. Moderate genetic advance coupled with High heritability was reported for characters like number of effective tillers and biological yield. Moderate heritability coupled with low genetic advance was reported for Panicle length, Flag leaf breadth, Test weight and grain L: B ratio. Low heritability coupled with low genetic advance flag leaf length, spikelet fertility percentage, Grain breadth. PCV values were found to be slightly higher than GCV values showing the influence of environment on character expression. High GCV and PCV values were observed for the character Number of filled grains per panicle. Moderate GCV and high PCV values were observed for the character biological yield, Grain yield. Moderate GCV and PCV values were observed for the character number of effective tillers per plant. Low GCV and moderate PCV values were observed for characters like flag leaf length, grain L: B ratio and kernel L; B ratio. Low PCV and GCV values were observed for 50% flowering, days to maturity, plant height, panicle length, flag leaf breadth, spikelet fertility percentage, test weight, grain length, grain breadth, kernel length, and kernel breadth, harvest index. Similar findings were reported by Hasan *et al*. (2022) [11] (number of filled grains per panicle, grain yield, biological yield), Lakshmi *et al*. (2021) [13] (number of effective tillers per plant, plant height, days to maturity), Gupta *et al*. (2021) [10] (flag leaf length, flag leaf breadth). Correlation analysis indicated that grain yield had a highly significant positive association with biological yield (0.915**) and a significant positive association with panicle length (0.360*). Similar findings were reported by Perween *et al*. (2020) [16] (biological yield and harvest index). Path coefficient analysis showed that biological yield (0.903), kernel L:B ratio (0.511), and grain L:B ratio (0.467) exerted the highest positive direct effects on grain yield.

**Table 1:** Analysis of variance for yield and yield attributing traits

| | | **Mean sum of square** | | |
|---|---|---|---|---|
| **S. No.** | **Source of variation** | **Replication (df = 2)** | **Treatment (df = 13)** | **Error (df = 26)** |
| 1 | Days to 50% flowering | 0.02 | 70.07** | 1.10 |
| 2 | Days to maturity | 0.45 | 53.35** | 3.09 |
| 3 | Plant height (cm) | 39.53 | 186.54** | 27.03 |
| 4 | Number of effective tillers | 2.28 | 4.63** | 0.90 |
| 5 | Panicle length (cm) | 3.78 | 9.60** | 2.01 |
| 6 | Flag leaf length (cm) | 24.63 | 35.55 | 21.05 |
| 7 | Flag leaf breadth (cm) | 0.001 | 0.04* | 0.01 |
| 8 | Number of filled grains per panicle | 355 | 7832** | 110.96 |
| 9 | Spikelet fertility percentage | 6.12 | 2.28 | 1.20 |
| 10 | Test weight(g) | 0.21 | 1.15* | 0.49 |
| 11 | Grain length(mm) | 0.41 | 1.04** | 0.14 |
| 12 | Grain breadth (mm) | 0.45 | 0.05 | 0.02 |
| 13 | Grain L:B ratio | 0.59 | 0.22** | 0.06 |
| 14 | Kernel length (mm) | 0.22 | 1.05** | 0.18 |
| 15 | Kernel breadth (mm) | 0.02 | 0.07** | 0.01 |
| 16 | Kernel L:B ratio | 0.11 | 0.25** | 0.03 |
| 17 | Biological yield(q/ha) | 213.93 | 1837.23** | 363.39 |
| 18 | Harvest index (%) | 0.11 | 29.78** | 0.11 |
| 19 | Grain yield (q/ha) | 40.85 | 401.33** | 69.31 |

(*, **, Significant at 5% and 1% level, respectively)

**Table 2:** Minimum, maximum, mean, standard error, coefficient of variation of 14 characters under study

| **Characters** | **Minimum $X_{min}$** | **Maximum $X_{max}$** | **Mean ($\bar{X}$)** | **Std. Error (SE)** | **Coefficient of variation (CV%)** |
|---|---|---|---|---|---|
| Days to 50% flowering | 88 | 104 | 95 | 0.60 | 1.09 |
| Days to maturity | 119 | 134 | 126 | 1.01 | 1.38 |
| Plant height (cm) | 101 | 128 | 117 | 3.00 | 4.44 |
| Number of effective tillers | 6 | 11 | 8 | 0.54 | 11.03 |
| Panicle length (cm) | 22.2 | 28.2 | 24.8 | 0.81 | 5.71 |
| Flag leaf length (cm) | 25.4 | 37.4 | 32.1 | 2.64 | 14.29 |
| Flag leaf breadth (cm) | 1.7 | 2.2 | 1.8 | 0.07 | 6.82 |
| Number of filled grains per panicle | 101 | 306 | 213 | 6.08 | 4.93 |
| Spikelet fertility percentage | 93.6 | 96.6 | 94.8 | 0.63 | 1.15 |
| Test weight(g) | 23.2 | 26.0 | 25.0 | 0.40 | 2.82 |
| Grain length(mm) | 7.9 | 10.0 | 8.7 | 0.21 | 4.31 |
| Grain breadth (mm) | 2.3 | 2.8 | 2.6 | 0.09 | 6.26 |
| GL/GB ratio | 2.9 | 3.7 | 3.3 | 0.15 | 7.90 |
| Kernel length (mm) | 6.0 | 8.1 | 7.0 | 0.24 | 6.10 |
| Kernel breadth (mm) | 2.1 | 2.7 | 2.4 | 0.06 | 4.78 |
| KL/KB ratio | 2.5 | 3.5 | 2.8 | 0.10 | 6.49 |
| Biological yield(q/ha) | 90.3 | 170.1 | 135.8 | 11.00 | 14.03 |
| Harvest index (%) | 37.0 | 47.6 | 43.6 | 0.19 | 0.76 |
| Grain yield (q/ha) | 41.7 | 77.2 | 58.3 | 4.80 | 14.26 |

**Table 3:** Genetic parameters of variation for yield and yield attributing characters

| Characters | Heritability (%) | GA | GA% Mean | GCV | PCV |
|---|---|---|---|---|---|
| Days to 50% flowering | 95.4 | 9.64 | 10.07 | 5.00 | 5.12 |
| Days to maturity | 84.4 | 7.74 | 6.10 | 3.22 | 3.50 |
| Plant height (cm) | 66.3 | 12.23 | 10.44 | 6.22 | 7.65 |
| Number of effective tillers | 58.0 | 1.75 | 20.35 | 12.96 | 17.02 |
| Panicle length (cm) | 55.6 | 2.44 | 9.83 | 6.40 | 8.58 |
| Flag leaf length (cm) | 18.7 | 1.95 | 6.09 | 6.84 | 15.84 |
| Flag leaf breadth (cm) | 36.2 | 0.11 | 6.35 | 5.13 | 8.53 |
| Number of filled grains per panicle | 95.9 | 102.32 | 47.97 | 23.78 | 24.29 |
| Spikelet fertility percentage | 23.0 | 0.59 | 0.62 | 0.63 | 1.31 |
| Test weight(g) | 30.6 | 0.53 | 2.13 | 1.87 | 3.39 |
| Grain length(mm) | 67.9 | 0.93 | 10.64 | 6.27 | 7.61 |
| Grain breadth (mm) | 22.0 | 0.08 | 3.22 | 3.33 | 7.09 |
| Grain length/Grain breadth ratio | 43.4 | 0.31 | 9.39 | 6.92 | 10.50 |
| Kernel length (mm) | 61.3 | 0.86 | 12.39 | 7.68 | 9.81 |
| Kernel breadth (mm) | 61.6 | 0.23 | 9.81 | 6.07 | 7.73 |
| Kernel length/Kernel breadth ratio | 67.5 | 0.45 | 15.85 | 9.36 | 11.39 |
| Biological yield(q/ha) | 57.5 | 34.61 | 25.48 | 16.31 | 21.52 |
| Harvest index (%) | 98.9 | 6.44 | 14.77 | 7.21 | 7.25 |
| Grain yield (q/ha) | 61.5 | 16.99 | 29.1 | 18.02 | 22.98 |

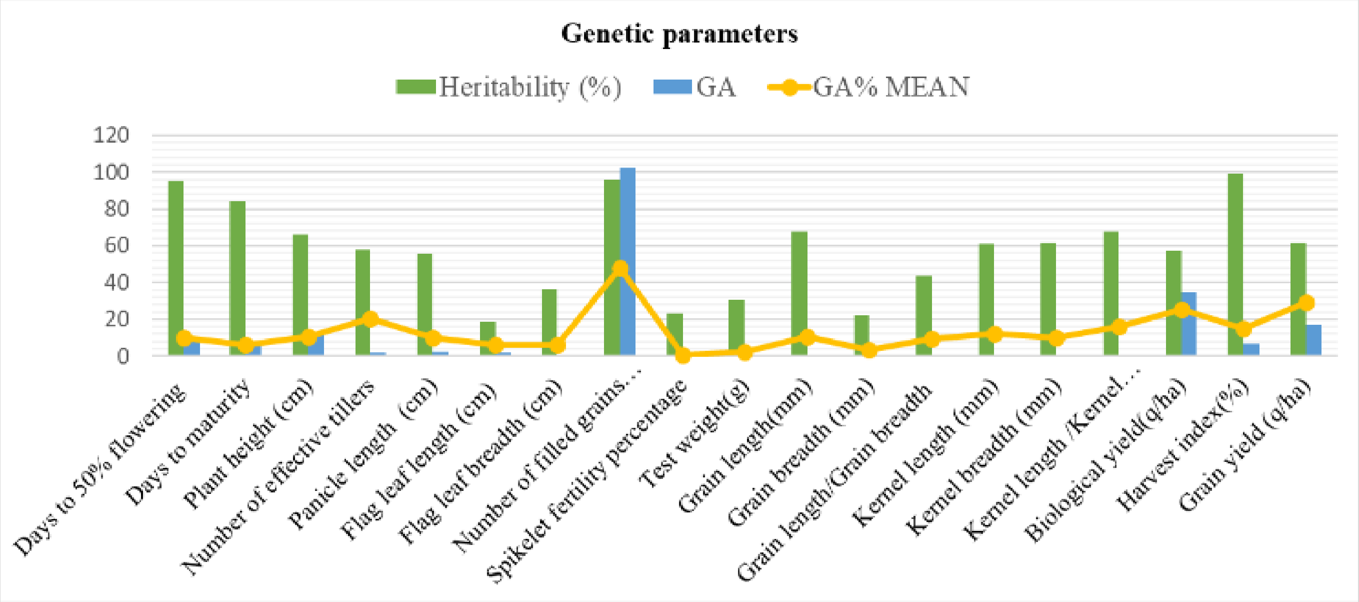

**Fig 1:** Bar graph representing heritability coupled with genetic advance as percent of mean for yield and yield attributing traits

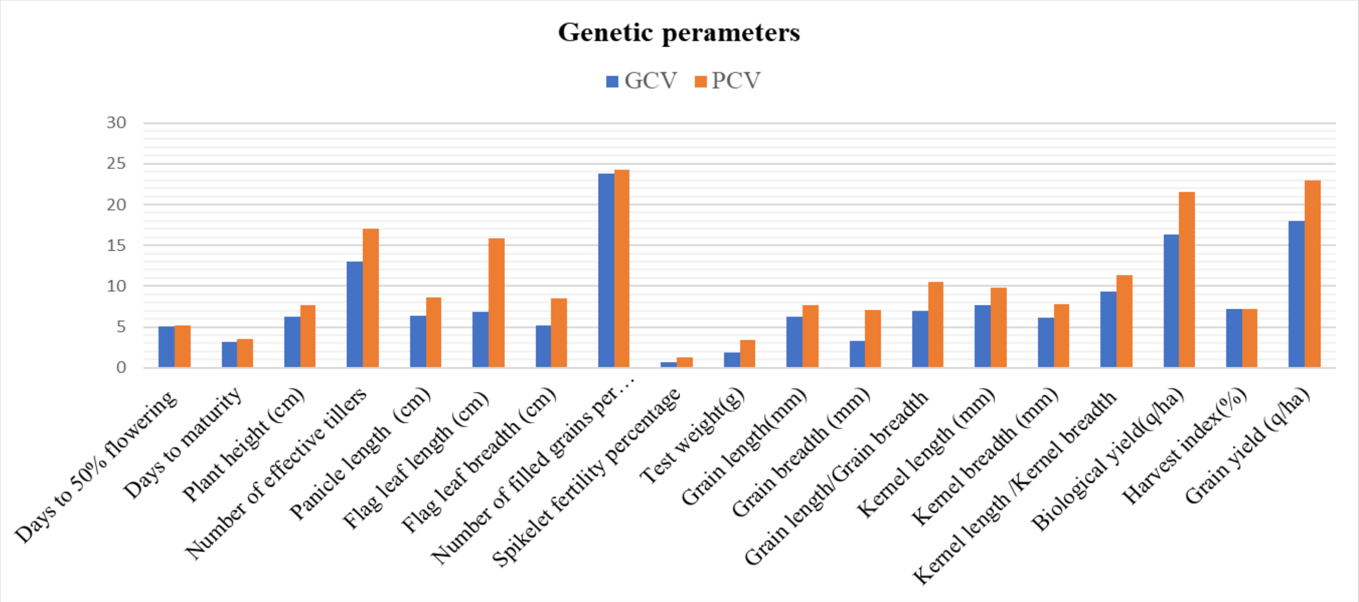

**Fig 2:** Bar graph representing phenotypic and genotypic coefficient of variability for yield and yield attributing characters

**Table 4:** Phenotypic correlation coefficients of yield and yield attributing characters

| Traits | DF | DM | PH | NET | PL | FLL | FLB | NFGP | SFP | TW | GL | GW | GL/GB | KL | KW | KL/KB | BY | HI | GY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DF | 1.000 | 0.884** | -0.009 | 0.544** | 0.027 | 0.028 | -0.057 | -0.061 | 0.042 | 0.219 | -0.217 | -0.060 | -0.142 | -0.276 | -0.031 | -0.227 | -0.083 | 0.302 | 0.112 |
| DM | | 1.000 | 0.079 | 0.517** | 0.164 | 0.041 | 0.018 | 0.008 | 0.032 | 0.067 | -0.234 | -0.054 | -0.153 | -0.315* | -0.079 | -0.222 | -0.009 | 0.203 | 0.165 |
| PH | | | 1.000 | -0.158 | 0.667** | 0.304* | -0.234 | 0.094 | 0.082 | -0.154 | 0.292 | -0.072 | 0.267 | 0.025 | 0.021 | -0.004 | 0.214 | -0.295 | 0.172 |
| NET | | | | 1.000 | 0.030 | 0.137 | -0.189 | -0.158 | 0.176 | 0.135 | -0.263 | -0.172 | -0.084 | -0.247 | -0.057 | -0.164 | 0.047 | 0.295 | 0.237 |
| PL | | | | | 1.000 | 0.296 | -0.245 | 0.006 | 0.082 | -0.246 | 0.206 | -0.080 | 0.184 | -0.026 | 0.013 | -0.034 | 0.337* | -0.158 | 0.360* |
| FLL | | | | | | 1.000 | -0.119 | 0.145 | 0.182 | -0.164 | -0.235 | -0.056 | -0.137 | -0.317* | 0.097 | -0.349* | 0.300 | 0.095 | 0.264 |
| FLB | | | | | | | 1.000 | 0.102 | -0.275 | 0.051 | -0.035 | 0.033 | -0.042 | -0.121 | -0.116 | -0.036 | 0.125 | -0.087 | 0.062 |
| NFGP | | | | | | | | 1.000 | 0.418** | -0.289 | -0.392* | -0.063 | -0.236 | -0.158 | 0.028 | -0.153 | -0.034 | 0.149 | -0.017 |
| SFP | | | | | | | | | 1.000 | -0.109 | -0.346* | 0.136 | -0.333* | -0.162 | 0.099 | -0.195 | 0.063 | 0.333* | 0.170 |
| TW | | | | | | | | | | 1.000 | 0.022 | 0.406** | -0.301 | 0.174 | 0.426** | -0.161 | -0.078 | 0.135 | -0.012 |
| GL | | | | | | | | | | | 1.000 | 0.033 | 0.701** | 0.712** | 0.031 | 0.583** | -0.131 | -0.176 | -0.117 |
| GW | | | | | | | | | | | | 1.000 | -0.680** | 0.081 | 0.771** | -0.440** | -0.023 | 0.149 | 0.030 |
| GL/KB | | | | | | | | | | | | | 1.000 | 0.452** | -0.535** | 0.738** | -0.055 | -0.247 | -0.089 |
| KL | | | | | | | | | | | | | | 1.000 | 0.162 | 0.747** | -0.370* | 0.103 | -0.270 |
| KW | | | | | | | | | | | | | | | 1.000 | -0.532** | -0.047 | 0.130 | 0.017 |
| KL/KB | | | | | | | | | | | | | | | | 1.000 | -0.296 | -0.004 | -0.253 |
| BY | | | | | | | | | | | | | | | | | 1.000 | -0.037 | 0.915** |
| HI | | | | | | | | | | | | | | | | | | 1.000 | 0.300 |

*, ** significant at 5% and 1% level, respectively

Key words: DF = Days to 50% flowering; DM = Days to maturity; PH = Plant height; NET = Number of effective tillers; PL = Panicle length; FLL = Flag leaf length; FLB = Flag leaf breadth; NFGP = Number of filled grains per panicle; SEP = Spikelet fertility percentage TW = Test weight; GL = Grain length; GB = Grain breadth; GL/GB = Grain L/B ratio; KL = Kernel length; KB = Kernel breadth; KL/KB = Kernel L/B ratio; BY = Biological yield; HI = Harvest index; GY = Grain yield

**Table 5:** Estimation Path coefficient analysis of yield and yield attributing traits

| Traits | DF | DM | PH | NET | PL | FLL | FLB | NFGP | SFP | TW | GL | GW | GL/GB | KL | KW | KL/KB | BY | HI | GY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DF | 0.031 | 0.037 | 0.000 | 0.048 | 0.003 | -0.002 | -0.003 | -0.007 | -0.005 | 0.003 | 0.068 | -0.017 | -0.066 | 0.110 | -0.012 | -0.116 | -0.075 | 0.104 | 0.112 |
| DM | 0.028 | 0.041 | 0.004 | 0.045 | 0.017 | -0.003 | 0.001 | 0.001 | -0.004 | 0.001 | 0.074 | -0.015 | -0.072 | 0.126 | -0.032 | -0.113 | -0.008 | 0.070 | 0.165 |
| PH | 0.000 | 0.003 | 0.046 | -0.014 | 0.070 | -0.020 | -0.011 | 0.010 | -0.009 | -0.002 | -0.092 | -0.020 | 0.124 | -0.010 | 0.008 | -0.002 | 0.194 | -0.102 | 0.172 |
| NET | 0.017 | 0.021 | -0.007 | 0.088 | 0.003 | -0.009 | -0.009 | -0.017 | -0.020 | 0.002 | 0.083 | -0.049 | -0.039 | 0.099 | -0.023 | -0.084 | 0.043 | 0.102 | 0.237 |
| PL | 0.001 | 0.007 | 0.031 | 0.003 | 0.105 | -0.019 | -0.012 | 0.001 | -0.009 | -0.004 | -0.065 | -0.023 | 0.086 | 0.010 | 0.005 | -0.018 | 0.304 | -0.054 | 0.360* |
| FLL | 0.001 | 0.002 | 0.014 | 0.012 | 0.031 | -0.064 | -0.006 | 0.016 | -0.021 | -0.003 | 0.074 | -0.016 | -0.064 | 0.127 | 0.039 | -0.178 | 0.271 | 0.033 | 0.264 |
| FLB | -0.002 | 0.001 | -0.011 | -0.017 | -0.026 | 0.008 | 0.048 | 0.011 | 0.031 | 0.001 | 0.011 | 0.009 | -0.020 | 0.049 | -0.047 | -0.018 | 0.113 | -0.030 | 0.062 |
| NFGP | -0.002 | 0.000 | 0.004 | -0.014 | 0.001 | -0.009 | 0.005 | 0.107 | -0.048 | -0.004 | 0.123 | -0.018 | -0.110 | 0.063 | 0.011 | -0.078 | -0.031 | 0.051 | -0.017 |
| SFP | 0.001 | 0.001 | 0.004 | 0.015 | 0.009 | -0.012 | -0.013 | 0.045 | -0.114 | -0.002 | 0.109 | 0.039 | -0.156 | 0.065 | 0.040 | -0.099 | 0.057 | 0.115 | 0.170 |
| TW | 0.007 | 0.003 | -0.007 | 0.012 | -0.026 | 0.011 | 0.003 | -0.031 | 0.013 | 0.015 | -0.007 | 0.115 | -0.140 | -0.070 | 0.170 | -0.082 | -0.071 | 0.046 | -0.012 |
| GL | -0.007 | -0.010 | 0.013 | -0.023 | 0.022 | 0.015 | -0.002 | -0.042 | 0.040 | 0.000 | -0.315 | 0.009 | 0.327 | -0.285 | 0.012 | 0.298 | -0.118 | -0.061 | -0.117 |
| GW | -0.002 | -0.002 | -0.003 | -0.015 | -0.008 | 0.004 | 0.002 | -0.007 | -0.016 | 0.006 | -0.011 | 0.283 | -0.317 | -0.033 | 0.308 | -0.225 | -0.021 | 0.051 | 0.030 |
| GL/GB | -0.004 | -0.006 | 0.012 | -0.007 | 0.019 | 0.009 | -0.002 | -0.025 | 0.038 | -0.005 | -0.221 | -0.192 | 0.467 | -0.181 | -0.214 | 0.377 | -0.050 | -0.085 | -0.089 |
| KL | -0.009 | -0.013 | 0.001 | -0.022 | -0.003 | 0.020 | -0.006 | -0.017 | 0.019 | 0.003 | -0.224 | 0.023 | 0.211 | -0.400 | 0.065 | 0.381 | -0.334 | 0.035 | -0.270 |
| KW | -0.001 | -0.003 | 0.001 | -0.005 | 0.001 | -0.006 | -0.006 | 0.003 | -0.011 | 0.007 | -0.010 | 0.218 | -0.250 | -0.065 | 0.400 | -0.272 | -0.043 | 0.045 | 0.017 |
| KL/KB | -0.007 | -0.009 | 0.000 | -0.014 | -0.004 | 0.022 | -0.002 | -0.016 | 0.022 | -0.002 | -0.184 | -0.124 | 0.344 | -0.299 | -0.213 | 0.511 | -0.268 | -0.001 | -0.253 |
| BY | -0.003 | 0.000 | 0.010 | 0.004 | 0.035 | -0.019 | 0.006 | -0.004 | -0.007 | -0.001 | 0.041 | -0.007 | -0.026 | 0.148 | -0.019 | -0.151 | 0.903 | -0.013 | 0.915** |
| HI | 0.009 | 0.008 | -0.014 | 0.026 | -0.017 | -0.006 | -0.004 | 0.016 | -0.038 | 0.002 | 0.056 | 0.042 | -0.115 | -0.041 | 0.052 | -0.002 | -0.034 | 0.344 | 0.300 |

*, ** significant at 5% and 1% level, respectively

Key words: DF = Days to 50% flowering; DM = Days to maturity; PH = Plant height; NET = Number of effective tillers; PL = Panicle length; FLL = Flag leaf length; FLB = Flag leaf breadth; NFGP = Number of filled grains per panicle; SEP = Spikelet fertility percentage TW = Test weight; GL = Grain length; GB = Grain breadth; GL/GB = Grain L/B ratio; KL = Kernel length; KB = Kernel breadth; KL/KB = Kernel L/B ratio; BY = Biological yield; HI = Harvest index; GY = Grain yield

## 4. Conclusion

The present study revealed substantial genetic variability among advanced breeding lines of rice for yield and its attributing traits, providing ample scope for effective selection. High heritability coupled with high genetic advance for traits such as filled grains per panicle, biological yield, and grain yield indicated the predominance of additive gene action, suggesting that direct selection would be effective for genetic improvement. Correlation analysis demonstrated that grain yield had a strong positive and significant association with biological yield and harvest index, highlighting the importance of these traits in determining productivity. Path coefficient analysis further confirmed that biological yield exerted the highest positive direct effect on grain yield, followed by kernel and grain L:B ratios. This study substantiates that the integration of variability assessment with correlation and path analysis provides a robust framework for the formulation of precise selection criteria. Emphasis on biological yield, harvest index, and grain quality parameters offers an effective strategy for developing high-yielding and regionally adapted rice cultivars. The findings not only validate the utility of advanced breeding lines as valuable genetic reservoirs but also furnish a scientific basis for accelerating genetic gains in rice improvement programmes under the Bastar Plateau and analogous agro-ecological environments.

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