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# Genetic variability, correlation and path analyses for selection in elite breeding materials of rice (*Oryza sativa* L.) genotypes in Madhya Pradesh

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### Abstract
The present investigation was conducted to estimate genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) along with correlations and path coefficients from data collected on 83 rice genotypes. Analysis of variance indicated significant differences among the genotypes for different morphological characters. High GCV and PCV were observed for grain yield per plant, Panicle weight/plant, Biological yield/plant, Filled spikletes/plant, 1000 seed weight, Harvest index, Number of tillers/plant, where as moderate GCV and PCV was observed for Plant height. High heritability coupled with high genetic advance as percent of mean were observed for grain yield per plant, panicle weight/plant, biological yield/plant, filled spikletes/plant, harvest index, 1000 seed weight, number of tillers/plant, panicle length/plant, where as high heritability coupled with moderate genetic advance as percent of mean for days to 50% flowering and days to maturity. The filled spikletes/plant, harvest index, biological yield per plant showed high genetic advance that helped in effective and reliable selection through these characters for crop improvement. Grain yield per plant showed positive association with panicle weight/plant, biological yield/plant, number of tillers/plant and Harvest index, while, negative association with plant height. The biological yield per plant had maximum direct effect on grain yield/plant followed by panicle length/plant, harvest index, filled spikletes/plant, panicle length/plant and days to maturity. Hence, biological yield per plant, harvest index and number of seeds per plant are identified as key traits for developing high yielding genotypes of rice for future breeding programme.

**Keywords:** Correlation coefficient, Seed yield, Rice, Path analysis

## 1. Introduction
Rice (*Oryza sativa* L.) is the world's most important cereal crop and serves as the primary source of staple food for more than half of the global population (Emani *et al*., 2008) [5]. The large scale spread of modern, high yielding varieties has replaced the traditional varieties especially in the irrigated rice ecosystem leading to reduced genetic base and thus increased genetic vulnerability. In past few decades, increase in share of high yielding varieties and shrinkage in the area of local varieties have been reported in India (Hore 2005; Rana *et al*., 2009) [7, 17] as well as in several other countries (Chaudhary *et al*., 2006; Itani, 1993) [3, 8]. There is an urgent need to broaden the genetic base of the important crop by introgressing genes from diverse sources. Thus, there is a need to collect, exploit and evaluate the untapped germplasm.
Direct selection based on crop yields is often a paradox in breeding programmes because yield is a complex polygenically inherited character, influenced by its component traits. Breeding programmes should therefore take into consideration character association of various component traits with yield and among themselves (Veni *et al*. 2013) [24]. The breeder has to isolate desired genotypes from the knowledge of components of variations. The essential feature is the partitioning of total variation into phenotypic, genotypic & environmental components and determines the magnitude of these components for various traits which is a measure of the type of gene action thus helps in deciding a breeding procedure for the genetic improvement of a trait.
The information about heritability along with genetic advance may provide a clear picture for selection of a particular trait. The relative contribution of individual traits may be accomplished by correlation studies. Therefore, the technique of path coefficient analysis is utilised to have an idea of direct and indirect contribution of a trait towards the yield which enables the breeder to rank genetic attributes according to their contribution (Dewey and Lu, 1959) [4].

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In this context, an attempt was made to characterize a set of rice germplasm accessions for different morphological and agronomic trials and to identify the variability available in the collection.

## Method and Material
The material for the present investigations consisted of 83 rice germplasm lines & released varieties received from Department of Plant Breeding and Genetics of JNKVV, Jabalpur. These lines were planted in randomized complete block design with three replications. Each entry was sown in a plot comprising three rows having three meter length at spacing of 20 cm between rows and 15 cm between plants. The recommended agronomical practices were followed to raise good crop in the season. Observations were recorded on five randomly chosen plants of each accession for eleven morphological and agronomical traits. The traits studied were days to 50 % flowering, days to maturity, thousand grain weight, Filled spikletes/plant, Number of tillers/plant, panicle length (cm), panicle weight per plant (g), biological yield per plant, plant height (cm), harvest Index (%) and grain yield per plant (g). The mean values were subjected to analysis of variance for the experimental design as per Panse and Sukhatme (1985) [16]. Phenotypic and genotypic coefficients of variation were calculated as per the formula suggested by Burton (1952) [1]. Heritability and genetic advance were worked out as per the procedure given by Johnson *et al*., (1955) [10]. Correlation coefficient was worked out for all possible combination of characters as per the procedure outlined by Miller *et al*. (1958) [14]. Path analysis was carried out following the method suggested by Dewey and Lu (1959) [4].

## Results and Discussion
The analysis of variance carried out for the seed yield and its component character is presented in Table 1. The variations among the genotypes were highly significant for all the characters under study indicating the existence of considerable genetic variation in the experimental material. The genetic components using appropriate statistical formulae for all eleven characters in rice are presented in Table 2.

**Estimation of variability:** The range of variation on the basis of mean values was more for the trait Filled spikletes/plant, days to maturity, Harvest index and Days to 50% flowering. The present studies, the genotypic coefficients of variation for all the characters were lower than the phenotypic coefficient of variation. This relationship indicated that there was small effect of environment on these traits and phenotypic selection for such traits may be effective. In this study, high genotypic and phenotypic coefficient of variation were observed for seed yield per plant, days to 50% flowering, biological yield per plant, filled spikletes/plant, 1000 seed weight, harvest index, number of tillers/plant and Plant height. For the remaining traits value of GCV and PCV were lower. The low genotypic and phenotypic coefficients of variations were observed for days to maturity and days to 50% flowering. This was in agreement with the findings reported by Saxena *et al*. (2005) [18], Padmaja *et al*. (2008) [15], Shrivastava *et al*. (2014) [22] and Kumar *et al*. (2015) [13]. The range of broad sense heritability was from 14.10 per cent for number of seeds/pod to oil percent 98.60 per cent. Higher broad sense heritability values were also associated with the all traits (Table 2). The result was in agreement with that reported by Kole *et al*. (2008) [12], Jha *et al*. (2014) [9] and Selvaraj *et al*. (2011) [19].

**Correlation coefficients analysis:** The genotypic and phenotypic correlation coefficients among yield and yield contributing traits (Table 3) showed that all the traits have higher genotypic correlation coefficients than corresponding phenotypic correlation coefficients indicating a low influence of environmental factors and relative stability of the genotypes. In the present study, among the eleven component characters studied, six exhibited significant positive association with seed yield per plant. Based on the strength of correlations, these six characters were ordered as Panicle weight/plant followed by biological yield/plant, Number of tillers/plant, Filled spikletes/plant, Harvest index and 1000 seed weight indicating the importance of these traits as selection criteria in succeeding generations for yield improvement. The result was in agreement with that reported by Shashidhar *et al*. (2005) [21], Girish *et al*. (2006) [6], Ketan & Sarkar (2014) [11] and Shrivastava *et al*. (2014) [22]. 1000 grain yield/plant had positive significant association with grain yield/plant, harvest index, Panicle length/plant, Panicle weight/plant, biological yield per plant and plant height. Biological yield/plant had showed significant phenotypic and genotypic correlation with grain yield/plant and harvest index. Harvest index showed positive significant association with Plant height, Panicle weight/plant, Panicle length/plant, Days to 50% flowering, Days to maturity, 1000 seed weight and Filled spikletes/plant. From the present investigation, it is inferred that traits biological yield/plant followed by harvest index, and 1000 seed weight are highly correlated with seed yield per plant and need to be considered for selection. The results revealed that there is scope for simultaneous improvement of these traits through selection.

**Path coefficient**: With the help of path coefficient analysis, the correlation coefficient is partitioned into direct and indirect effects (Table 4). Biological yield per plant showed highest positive direct effect on grain yield per plant followed by harvest index, panicle weight per plant, filled spikletes/plant, panicle length/plant and days to maturity. However, number of tillers per plant, 1000 seed weight and days to 50% flowering showed direct negative effect but its negligible. Panicle weight per plant having direct effect on grain yield per plant and indirect positive effect via character but It's also have indirect negative effect on grain yield through character days to 50% flowering, days to maturity, panicle length per plant and harvest index. These results are in agreement with the findings of Shanthala (2004) [20], Surek and Beser (2003) [23] and Chakraborty *et al*. (2010) [2]. A positive and high direct effect of a trait on grain yield reveals the effectiveness of a trait for direct selection. High direct effect along with positive and high indirect through other traits provides a better chance for a character to be selected through breeding programmes. Therefore biological yield per plant, harvest index, panicle weight/plant, filled spikletes/plant, panicle length/plant and days to maturity are the traits which can be directed in selection programmes to obtain higher grain yield.

## Conclusion
The genetic architecture of grain yield is based on the balance or overall net effect produced by various yield components interacting with one another. It is inferred that traits biological yield/plant followed by harvest index, and 1000 seed weight are highly correlated with seed yield per plant and need to be considered for selection. So it is concluded that there is scope

for simultaneous improvement of these traits through selection. A positive and high direct effect of a trait on grain yield reveals the effectiveness of a trait for direct selection. Therefore biological yield per plant, harvest index, panicle weight/plant, filled spikletes/plant, panicle length/plant and days to maturity are the traits which can be directed in selection programmes to obtain higher grain yield. High direct effect along with positive and high indirect through other traits provides a better chance for a character to be selected through breeding programmes. Hence, utmost importance should be given to these characters during selection for single plant yield improvement.

**Table 1:** Analysis of variance for yield & yield attributing traits of in rice genotypes.

| Source of variation | D.F | Mean sums of square | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | DF | DM | PH | FSPP | NTPP | PLL | PLW | BYPP | TGW | HI% | GYPP |
| Replication | 2 | 317.89 | 209.86 | 428.31 | 169.37 | 5.84 | 97.71 | 31.94 | 82.61 | 105.79 | 3.86 | 12.30 |
| Treatment | 82 | 264.93** | 266.09** | 1854.49** | 3344.78** | 9.75** | 22.38** | 173.98** | 1062.25** | 57.68** | 113.99** | 132.91** |
| Error | 164 | 0.70 | 0.52 | 0.54 | 0.63 | 0.03 | 0.20 | 0.34 | 1.29 | 0.19 | 0.58 | 0.05 |

**Table 2:** Genetic parameters of variability for yield & yield attributing traits in rice genotypes.

| Characters | Mean | Range | | GCV (%) | PCV (%) | Heritability % (Bs) | Genetic Advance | GA as % of Mean |
|---|---|---|---|---|---|---|---|---|
| | | Min. | Max. | | | | | |
| Days to 50% flowering | 98.22 | 76.00 | 121.00 | 09.56 | 09.59 | 99.20 | 19.26 | 19.61 |
| Days to maturity | 128.19 | 106.00 | 151.00 | 07.34 | 07.36 | 99.40 | 19.33 | 15.08 |
| Plant height | 24.59 | 10.23 | 34.07 | 17.80 | 17.89 | 99.00 | 08.97 | 36.49 |
| Filled spikletes/plant | 138.66 | 63.20 | 209.33 | 24.08 | 24.09 | 99.90 | 68.76 | 49.59 |
| Number of tillers/plant | 08.47 | 04.80 | 13.20 | 21.26 | 21.35 | 99.10 | 03.69 | 43.59 |
| Panicle length/plant | 24.94 | 19.58 | 33.34 | 10.91 | 11.05 | 97.40 | 05.53 | 22.17 |
| Panicle weight/plant | 27.16 | 14.81 | 50.06 | 28.01 | 28.09 | 99.40 | 15.63 | 57.53 |
| Biological yield/plant | 70.06 | 37.80 | 113.60 | 26.84 | 26.89 | 99.60 | 38.67 | 55.20 |
| 1000 seed weight | 28.09 | 14.54 | 46.47 | 21.89 | 22.06 | 98.50 | 12.57 | 44.75 |
| Harvest index | 114.23 | 70.83 | 165.58 | 21.76 | 21.77 | 99.90 | 51.19 | 44.81 |
| Grain yield/plant | 19.56 | 07.43 | 36.20 | 34.02 | 34.04 | 99.90 | 13.70 | 70.04 |

**Table 3:** Genotypic and phenotypic correlation coefficients for different characters and their correlation with seed yield of rice.

| Characters | DF | DM | TGW | FSPP | NTPP | PLL | PLW | BYPP | PH | HI% | GYPP |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to 50% flowering | 1.0000 | 0.9950 ** | -0.2745** | 0.2610** | -0.0600 | -0.1466* | -0.1325* | 0.0548 | -0.2393 ** | 0.1898** | -0.1415** |
| Days to maturity | | 1.0000 | -0.2691 ** | 0.2590 ** | -0.0600 | -0.1472* | -0.1313* | 0.0581 | -0.2424 ** | 0.1874** | -0.1413** |
| 1000 seed weight | | | 1.0000 | -0.3870 ** | -0.1256* | 0.3452 ** | 0.1485* | 0.2200 ** | 0.0246 | 0.0882** | 0.1465** |
| Filled spikletes/plant | | | | 1.0000 | 0.1783** | -0.1194 | 0.4167** | 0.2502 ** | 0.2522 ** | 0.0804** | 0.4098** |
| Number of tillers/plant | | | | | 1.0000 | -0.1422* | 0.5797 ** | 0.4771 ** | 0.3237 ** | -0.4319** | 0.6106** |
| Panicle length/plant | | | | | | 1.0000 | -0.0914 | -0.0823 | -0.0354 | 0.2946** | -0.1118** |
| Panicle weight/plant | | | | | | | 1.0000 | 0.7177** | 0.5268 ** | 0.3243** | 0.9682** |
| Biological yield/plant | | | | | | | | 1.0000 | -0.0999 | 0.0778 | 0.7979** |
| Plant height | | | | | | | | | 1.0000 | 0.4181** | 0.5510** |
| Harvest index | | | | | | | | | | 1.0000 | -0.3607 ** |
| Grain yield/plant | | | | | | | | | | | 1.0000 |

**Table 4:** Direct and indirect effects for different characters on seed yield per plant at gen otypic level in rice.

| Characters | DF | DM | TGW | FSPP | NTPP | PLL | PLW | BYPP | PH | HI% | GYPP |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to 50% flowering | -0.0164 | -0.0164 | 0.0045 | -0.0043 | 0.0010 | 0.0024 | 0.0022 | -0.0009 | 0.004 | -0.0031 | -0.1423 |
| Days to maturity | 0.0538 | 0.0538 | -0.0145 | 0.0140 | -0.0032 | -0.0080 | -0.0071 | 0.0031 | -0.0132 | 0.0101 | -0.1410 |
| 1000 seed weight | 0.0058 | 0.0057 | -0.0211 | 0.0082 | 0.0027 | -0.0075 | -0.0031 | -0.0047 | -0.0005 | -0.0019 | 0.1474 |
| Filled spikletes/plant | 0.0654 | 0.0649 | -0.0971 | 0.2494 | 0.0447 | -0.0301 | 0.1043 | 0.0625 | 0.0633 | -0.0201 | 0.4100 |
| Number of tillers/plant | 0.0015 | 0.0015 | 0.0033 | -0.0046 | -0.0254 | 0.0037 | -0.0148 | -0.0122 | -0.0083 | 0.011 | 0.6132 |
| Panicle length/plant | -0.0079 | -0.0080 | 0.0191 | -0.0065 | -0.0078 | 0.0539 | -0.0051 | -0.0045 | -0.0018 | 0.0159 | -0.1125 |
| Panicle weight/plant | -0.1576 | -0.1568 | 0.1777 | 0.4981 | 0.6943 | -0.1122 | 1.1912 | 0.8582 | 0.6345 | -0.3877 | 0.9711 |
| Biological yield/plant | -0.0476 | -0.0508 | -0.1927 | -0.2180 | -0.4177 | 0.0725 | -0.6264 | 0.8695 | 0.0825 | 0.0678 | 0.7494 |
| Plant height | 0.0018 | 0.0018 | -0.0002 | -0.0019 | -0.0024 | 0.0003 | -0.0040 | 0.0007 | -0.0074 | 0.0031 | 0.4679 |
| Harvest index | 0.0562 | 0.0555 | 0.0262 | -0.0238 | -0.1278 | 0.0871 | -0.0959 | -0.023 | -0.1241 | 0.2946 | 0.554 |

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