Advances
in
Bioresearch

ORIGINAL ARTICLE

Correlation and path analysis for identifying key morphological and yield-contributing traits for breeding and genetic improvements in rice (*Oryza sativa* L.)

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ABSTRACT

The present investigation was aimed at estimating correlation and path coefficients using observations on thirteen yield and its components in forty-six rice genotypes, comprising 10 parental lines, 3 testers, and their resulting 30 F_1 crosses with 3 check varieties. The genotypes were evaluated in RBD at SIF (Student's Instructional Farm), Department of Genetics and Plant Breeding, ANDUA&T Kumarganj, Ayodhya (U.P.) during kharif, 2023. and ANOVA results revealed the highly significant mean sum of squares among the genotypes for all the characters. Correlation analysis revealed that grain yield showed highly significant and positive correlation with biological yield/plant followed by productive tillers per plant, 1000-grain weight, harvest index, panicle length, flag leaf area, spikelet fertility, number of fertile spikelets per panicle, number of spikelets per panicle. This suggested that selection would be quite efficient in improving yield and yield components. Path coefficient analysis revealed that the highest positive direct effect on grain yield per plant was exerted by biological yield per plant followed by harvest index and number of fertile spikelets per panicle while the highest negative direct effect on grain yield per plant was exerted by number of spikelets per panicle followed by spikelet fertility. These relationships may be helpful in crop improvement, if selection favours high grain yield, then the remaining characters which are positively associated will be automatically improved. The path-coefficient analysis helps to understand the causal factor better, because it divides total effects of paired traits into direct and indirect effects via other characters. These characters could be utilized as indices of selection for future breeding programme.
Keywords: Correlation, rice, yield, path coefficient, genotypic & phenotypic.

INTRODUCTION

Rice (*Oryza sativa* L.) is a self-pollinated cereal crop belonging to the family Poaceae with the chromosome number 2n = 24 [9]. The cultivated rice plant is an annual grass, leaves are long and flat and with hollow stems grows to about 1.2 metres in height. It is stands as the predominant staple food for a

significant portion of the global populace [17]. Over half of the world's inhabitants rely on rice for essential sustenance, with its cultivation spanning across Asia, parts of Africa, and Latin America, encompassing three main types: *japonica, indica,* and *javanica.* Total production of rice in world is estimated at record 502.98 million metric tonnes. In India, estimated the area, production and productivity of rice was 46.38 million hectares (mha), 130.29 million tonnes (mt) and 2809 kg/ha, respectively, during 2021-22 (Anonymous, 2021-22, Dett. of Agriculture and Farmers Welfare, MoA & FW). The rice grain comprises significant proportions of starch, protein, fiber, lipids, minerals (such as potassium, phosphorus, magnesium, calcium, sodium, and iodine), and essential nutrients (including thiamine, riboflavin, niacin, pyridoxine, and folic acid), along with vitamins [13]. The future of rice cultivation is poised for significant advancements due to technological innovations and sustainable practices. With the advent of genetic engineering, high-yield, and pest-resistant rice varieties are being developed, which promise to increase productivity and reduce losses. Climate-smart agriculture practices are also being adopted to mitigate the effects of climate change on rice production. As global demand for rice continues to rise, ensuring sustainable and resilient rice production systems will be essential for food security and economic stability.

Usually, the traits of interest to plant breeders are complex and result from the interplay of multiple components. Direct selection for crop yield in breeding programs is often challenging because yield is a complex trait influenced by numerous underlying factors. Yield is a quantitative trait controlled by many genes with small effects, known as polygenes. Therefore, yield is the cumulative result of its component traits, which can impact yield either directly or indirectly. Enhancing yield components can maximize yield, provided there are no negative associations. The correlation coefficient provides insights into the relationships among yield components, indicating the strength of association between any two traits. Understanding these associations is crucial for the simultaneous improvement of yield and its components. Correlation coefficient analysis quantifies the mutual relationship between various plant traits and identifies the component traits on which selection can be based for genetic improvement of yield. A positive correlation indicates that changes in two variables occur in the same direction, meaning high values of one trait are associated with high values of another, and vice versa. Correlation coefficient analysis is a statistical method used to measure the strength and direction of the relationship between two or more variables. In rice breeding, it is a valuable tool to identify traits that are positively or negatively correlated with grain yield and other agronomic characteristics. Understanding these correlations helps breeders select for desirable traits, enhancing breeding efficiency and achieving higher yields. For instance, positive correlations between yield and biomass indicate that selecting for high biomass can indirectly improve yield [26]. Path coefficient analysis is a statistical technique that helps in understanding the direct and indirect effects of various traits on grain yield in rice. This method decomposes the correlation coefficients into direct and indirect effects, providing a clearer picture of how different traits influence yield. Path coefficient analysis thus aids breeders in identifying key traits that can be targeted for improving yield. For example, a high direct effect of number of grains per panicle suggests that increasing this trait could directly enhance yield [10]. Similarly, understanding indirect effects helps in making more informed selection decisions in breeding programs [27].

MATERIAL AND METHODS

The present investigation was carried out during *kharif*, 2023-2024 in SIF (Student's Instructional Farm), Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya (U.P.) India. A total of 46 genotypes were utilized in the study, comprising 10 parental lines, 3 testers, and their resulting 30 F1 crosses with 3 check varieties. The parental lines (Germplasm lines) included Akhtahwa BBK, IET-6663, Bhadani-I, Bhadani-II, Tinpakhiya, IET-16605, Sorahi, Binni Deoria, Dhaniya, and Akhtahwa, while the testers consisted of NDR-6093, NDR-702, and HUR-1304, alongside the check varieties Sarju-52, NDR-97, and NDR-2065. Crosses were generated through a line × tester mating scheme, resulting in a total of 30 crosses among the three testers and ten lines. The experimental setup involved 46 genotypes evaluated with three replications in a Randomized Block Design during the 2023 kharif, at SIF (Student's Instructional Farm). Seedlings aged 25 days were transplanted at a spacing of 20 cm between rows and 15 cm within rows, with meticulous attention to maintaining uniform plant populations across treatments per replication. Various agronomic traits such as days to 50% flowering, days to maturity, plant height, flag leaf area (cm^2), number of spikelets per panicle, number of fertile spikelets per panicle, spikelet fertility (%), 1000 grain weight (g), biological yield per plant (g), harvest index (%), and grain yield per plant (g) were recorded and subjected to statistical analysis. The correlation coefficients at genotypic and phenotypic levels and direct

and indirect effects of yield contributing traits on grain yield, following the methods suggested by Searle [18].

RESULTS AND DISCUSSION
Correlation Analysis for Identifying Key Traits in Rice

Complete knowledge on interrelationship of grain yield with other characters is of paramount importance to the breeder for making improvement in complex quantitative character like grain yield for which direct selection is not much effective. Correlation coefficient as another fundamental tool showing relationships among independent characteristics. Hence, association analysis was undertaken to determine the direction of selection and number of characters to be considered in improving grain yield. Genotypic correlation coefficients in general were higher than phenotypic correlation coefficients indicating strong inherent association between the traits. Phenotypic and genotypic correlations between yield and yield components were estimated in the Table 3.1.

Table 3.1 (a): Genotypic Correlation coefficients among yield and different yield components of thirteen characters in rice

Characters	DM	PH	PTP	PL	FLA	NSPS	NFSP	SF	TGW	BY	HI	GY
DF	0.967**	-0.248	-0.032	0.347*	0.146	0.037	0.022	0.0011	-0.025	-0.097	0.130	-0.388**
DM		0.270	-0.107	0.296*	0.138	-0.010	-0.029	-0.038	-0.118	-0.214*	0.019	-0.377**
PH			-0.208	0.355**	-0.160	0.327**	0.339**	0.486**	0.328**	-0.257	-0.442**	-0.311**
PTP				0.909**	0.873**	0.739**	0.819**	0.729**	0.916**	0.992**	0.918**	0.990**
PL					0.918**	0.893**	0.931**	0.728**	0.902**	0.884**	0.906**	0.946**
FLA						0.715**	0.774**	0.647**	0.755**	0.762**	0.842**	0.808**
NSPS							0.948**	0.513**	0.477**	0.570**	0.463**	0.559**
NFSP								0.758**	0.634**	0.676**	0.623**	0.679**
SF									0.803**	0.690**	0.808**	0.734**
TGW										0.931**	0.904**	0.978**
BY											0.933**	0.999**
HI												0.954**

Table 3.2 (b): Phenotypic Correlation coefficients among yield and different yield components of thirteen characters in rice

Characters	DM	PH	PTP	PL	FLA	NSPS	NSSP	SF	TGW	BY	HI	GY
DF	0.928**	0.219**	-0.013	0.151	0.127	0.030	0.018	-0.004	-0.012	-0.068	0.070	-0.219**
DM		0.250**	-0.078	0.174*	0.108	-0.005	-0.025	-0.042	-0.087	-0.1807*	0.032	-0.120**
PH			-0.237**	0.261**	-0.127	-0.177*	-0.273**	0.338**	-0.297**	-0.205*	-0.283**	-0.267**
PTP				0.501**	0.634**	0.584**	0.631**	0.442**	0.678**	0.735**	0.516**	0.769**
PL					0.489**	0.477**	0.480**	0.264**	0.444**	0.441**	0.376**	0.493**
FLA						0.573**	0.618**	0.430**	0.578**	0.582**	0.406**	0.603**
NSPS							0.920**	0.359**	0.379**	0.482**	0.251**	0.468**
NSSP								0.692**	0.473**	0.550**	0.345**	0.550**
SF									0.447**	0.425**	0.383**	0.477**
TGW										0.792**	0.689**	0.876**
BY											0.415**	0.900**
HI												0.767**

Table 3.2 (a): Genotypic path coefficients among yield and different yield components of thirteen characters in rice

Characters	DF	DM	PH	PTP	PL	FLA	NSPS	NFSP	SF	TGW	BY	HI
GY	-0.388**	-0.377**	-0.311**	0.990 **	0.946 **	0.808 **	0.559**	0.679 **	0.734 **	0.978 **	0.999 **	0.954 **
HI	-0.1491	-0.1374	-0.1665	0.3453	0.3786	0.3169	0.1745	0.2343	0.3039	0.3939	0.3512	**0.3761**
BY	-0.0710	-0.0569	-0.0882	0.7264	0.6472	0.5584	0.4176	0.4952	0.5051	0.6820	**0.7320**	0.6835
TGW	0.0022	0.0103	0.0301	-0.0792	-0.0780	-0.0654	-0.0413	-0.0549	-0.0695	**-0.0865**	-0.0806	-0.0906
SF	-0.0001	0.0040	0.0507	-0.0759	-0.0759	-0.0674	-0.0534	-0.0790	**-0.1041**	-0.0837	-0.0719	-0.0842
NFSP	0.0061	-0.0077	-0.0906	0.2188	0.2486	0.2067	0.2531	**0.2670**	0.2025	0.1694	0.1806	0.1664
NSPS	-0.0068	0.0019	0.0416	-0.1354	-0.1636	-0.1310	**-0.1831**	-0.1735	-0.0939	-0.0875	-0.1044	-0.0849
FLA	-0.0002	-0.0002	0.0002	-0.0010	-0.0013	**-0.0011**	-0.0008	-0.0008	-0.0007	-0.0008	-0.0008	-0.0009
PL	-0.0029	-0.0025	0.0026	-0.0093	**-0.0084**	-0.0100	-0.0075	-0.0079	-0.0062	-0.0076	-0.0075	-0.0085
PTP	-0.0002	-0.0006	-0.0016	**0.0051**	0.0056	0.0044	0.0038	0.0042	0.0037	0.0047	0.0050	0.0047
PH	0.0029	0.0031	**0.0116**	-0.0036	-0.0035	-0.0019	-0.0026	-0.0039	-0.0056	-0.0040	-0.0030	-0.0051
DM	0.1125	**0.0129**	0.0035	-0.0014	0.0038	0.0018	-0.0001	-0.0004	-0.0005	-0.0015	-0.0028	0.0003
DF	**-0.0204**	-0.0197	-0.0051	0.0007	-0.0071	-0.0030	-0.0008	-0.0005	0.0000	0.0005	0.0020	-0.0027

Table 3.2 (b): Phenotypic path coefficients among yield and different yield components of thirteen characters in rice

Characters	DF	DM	PH	PTP	PL	FLA	NSPS	NFSP	SF	TGW	BY	HI
GY	-0.219**	-0.120**	-0.267**	0.769**	0.493**	0.603**	0.468**	0.55**	0.477**	0.876**	0.900**	0.767**
HI	-0.1345	-0.1156	-0.1389	0.2527	0.1844	0.1987	0.1233	0.1690	0.1876	0.3373	0.2035	**0.4896**
BY	-0.0478	-0.1268	-0.1439	0.5160	0.3099	0.4088	0.3389	0.3866	0.2984	0.5563	**0.7017**	0.2916
TGW	0.0004	0.0027	0.0093	-0.0211	-0.0138	-0.0180	-0.0118	-0.0147	-0.0139	**-0.0312**	-0.0247	-0.0215
SF	0.0000	-0.0001	-0.0005	0.0007	0.0004	0.0007	0.0006	0.0011	**0.0016**	0.0007	0.0007	0.0006
NFSP	-0.0002	0.0002	0.0024	-0.0055	-0.0042	-0.0054	-0.0081	**-0.0088**	-0.0061	-0.0042	-0.0048	-0.0030
NSPS	0.0005	-0.0001	-0.0027	0.0088	0.0072	0.0086	**0.0150**	0.0138	0.0054	0.0057	0.0072	0.0038
FLA	-0.0001	-0.0001	0.0001	-0.0005	-0.0004	**-0.0009**	-0.0005	-0.0005	-0.0004	-0.0005	-0.0005	-0.0003
PL	0.0012	0.0014	-0.0013	0.0041	**0.0081**	0.0040	0.0039	0.0039	0.0022	0.0036	0.0036	0.0031
PTP	-0.0002	-0.0012	-0.0037	**0.0154**	0.0077	0.0097	0.0090	0.0097	0.0068	0.0104	0.0113	0.0079
PH	0.0036	0.0041	**0.0164**	-0.0039	-0.0026	-0.0021	-0.0029	-0.0045	-0.0056	-0.0049	-0.0034	-0.0047
DM	-0.0376	**-0.0405**	-0.0102	0.0032	-0.0071	-0.0044	0.0002	0.0010	0.0017	0.0035	0.0073	-0.0013
DF	**0.0265**	0.0246	0.0058	-0.0003	0.0040	0.0034	0.0008	0.0005	-0.0001	-0.0003	-0.0018	0.0019

At genotypic level, days to 50% flowering exhibited highly positive and significant correlation with days to maturity (0.967) and positive significant association with panicle length (0.347). and days to maturity showed significant and positive association with number of panicle length (0.296). It did not show significant negative correlation with any other traits. Plant height exhibited positive and highly significant correlation with spikelet fertility (0.486) followed by panicle length (0.355), number of fertile spikelets

per panicle (0.339), 1000-grain weight (0.328), number of spikelets per panicle (0.327) and while highly significant negative correlation was observed with harvest index (-0.442). The results are in conformity with the findings of Ahamed *et al.* [1], Naseem *et al.* [12], Ratna *et al.* [15], Kumar *et al.* [10] and Manivelan *et al.* [11].

Highly significant and positive correlation of productive tillers per plant had been observed with biological yield/plant (0.992) followed by harvest index (0.918), 1000-grain weight (0.916), panicle length (0.909), flag leaf area (0.873), number of fertile spikelets per panicle (0.819), number of spikelets per panicle (0.739) and spikelet fertility (0.729). Panicle length showed highly significant and positive association with number of fertile spikelets per panicle (0.931) followed by flag leaf area (0.918), harvest index (0.906), 1000-grain weight (0.902), number of spikelets per panicle (0.893) biological yield per plant (0.884) and spikelet fertility (0.728) while it was not negatively associated with any characters. These results are in agreement with the findings of Aparna *et al.* [2], Bhargava *et al.* [3], Jangala *et al.* [7] and Reshma *et al.* [16].

Flag leaf area possessed highly significant and positive correlation with harvest index (0.842) followed by number of fertile spikelets per panicle (0.774), biological yield/plant (0.762), 1000-grain weight (0.755), number of spikelets per panicle (0.715) and spikelet fertility (0.647). Number of spikelets per panicle exhibited highly significant positive correlation with number of fertile spikelets per panicle (0.948), biological yield/plant (0.570), spikelet fertility (0.513), 1000-grain weight (0.477) and harvest index (0.463). Highly significant and positive association were recorded between number of fertile spikelets per panicle and spikelet fertility (0.758) followed by biological yield /plant (0.676), 1000-grain weight (0.634) and harvest index (0.623) and no any character showed negative correlation. The trait spikelet fertility had highly significant and positive association with harvest index (0.808), 1000-grain weight (0.803) and biological yield/plant (0.690). These results are in agreement with the findings, Dhavaleshvar *et al.* [5] and Singh *et al.* [22].

Grain yield per plant exhibited highly significant and positive correlation with biological yield/plant (0.999) followed by productive tillers per plant (0.990), 1000-grain weight (0.978), harvest index (0.954), panicle length (0.946), flag leaf area (0.808), spikelet fertility (0.734), number of fertile spikelets per panicle (0.679), number of spikelets per panicle (0.559). It showed negative and highly significant correlation with days to 50% flowering (-0.388), days to maturity (-0.377) and plant height (-0.311). These results are in agreement with the findings Gour *et al.* [6], Bhujel *et al.* [4], Shrestha *et al.* [19], Singh *et al.* [21], Parimala *et al.* [14], Jangala *et al.* [7] and Singh *et al.* [22].

At phenotypic level, grain yield per plant exhibited highly significant and positive correlation with biological yield/plant (0.900) followed by 1000 grain weight (0.876), productive tillers per plant (0.769), harvest index (0.767), flag leaf area (0.603), number of fertile spikelets per panicle (0.550), panicle length (0.493), spikelet fertility (0.477), number of spikelets per panicle (0.468). It showed negative and highly significant correlation with plant height (-0.268), days to 50% flowering (-0.219) and days to maturity (-0.120). The correlation at phenotypic level is very close to genotypic level. These results are in agreement with the findings Parimala *et al.* [14].

Path coefficient analysis for Identifying Key Traits in Rice
Correlation gives only the relation between two variables whereas path coefficient analysis allows the separation of direct effect and their indirect effects through other attributes by partitioning the correlations (Wright, 1921) for better interpretation of cause-and-effect relationship. Based on the data presented the genotypic and phenotypic correlations were estimated to determine direct and indirect effects of yield and yield contributing characters. If the correlation coefficient between a casual factor and the effect is almost equal to its direct effect, it explains the true relationship and a direct selection through this trait may be useful. If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects appear to be the cause of that positive correlation. In such situation the other factors are to be considered simultaneously for selection. However, if the correlation coefficient is negative but direct effect is positive and high, a restriction has to be imposed to nullify the undesirable indirect effects in order to make use of direct effect. The estimates of path coefficient analysis are provided for yield and yield component characters in (Table 3.2). Among all the characters studied.

The highest positive direct effect on grain yield per plant was exerted by biological yield per plant (0.7320) followed by harvest index (0.3761) and number of fertile spikelets per panicle (0.2670) while the highest negative direct effect on grain yield per plant was exerted by number of spikelets per panicle (-0.1831) followed by spikelet fertility (-0.1041). These characters have also been identified as major direct contributors towards grain yield by Sritama *et al.* [24]; Gour *et al.* [6], Kumar *et al.* [10]; Shrestha *et al.* [19], Aparna *et al.* [2]; Bhargava *et al.* [3]; The direct effects of remaining five characters were too low to be considered important.

In genotypic path analysis, days to 50% flowering exerted considerable amount of positive indirect effect on grain yield *via* days to maturity (0.1125). Productive tillers per plant exerted high order of positive significant indirect effect on grain yield *via* biological yield per plant (0.7264) followed by harvest index (0.3453) number of fertile spikelets per panicle (0.2188); panicle length *via* biological yield per plant (0.6472) followed by harvest index (0.3786), number of fertile spikelets per panicle (0.2486); flag leaf area *via* biological yield per plant (0.5584) followed by harvest index (0.3169), number of fertile spikelets per panicle (0.2067); number of spikelets per panicle *via* biological yield per plant (0.4176) followed by number of fertile spikelets per panicle (0.2531), harvest index (0.1745); number of fertile spikelets per panicle *via* biological yield per plant (0.4952) followed by harvest index (0.2343); spikelet fertility *via* biological yield per plant (0.5051) followed by harvest index (0.3039), number of fertile spikelets per panicle (0.2025); 1000-grain weight *via* biological yield per plant (0.6820) followed by harvest index (0.3939), number of fertile spikelets per panicle (0.1694); biological yield per plant *via* harvest index (0.3512) followed by number of fertile spikelets per panicle (0.1806); harvest index *via* biological yield per plant (0.6835) followed by number of fertile spikelets per panicle (0.1806) high order of positive indirect effects on grain yield per plant. While, days to 50% flowering, days to maturity and plant height exerted high considerable extent of negative indirect effects on grain yield *via* harvest index, i.e., -0.1491, -0.1374 and -0.1665 respectively. Remaining other component traits of grain yield had either negative or too low amount of indirect effect to be of any consequences. These results are in agreement with the findings Ahamed *et al.* [1], Naseem *et al.* [12], Ratna *et al.* [15], Bhujel *et al.* [4], Singh *et al.* [21] , Dhavaleshvar *et al.* [5], Aparna *et al.* [2] . The indirect effects of remaining characters were too low to be considered important.

In phenotypic path analysis, the highest positive direct effect on grain yield per plant was exerted by biological yield per plant (0.7017) followed by harvest index (0.4896). while the highest negative direct effect on grain yield per plant was exerted by flag leaf area (-0.0009) followed by number of fertile spikelets per panicle (-0.0088). These results are in agreement with the findings Reshma *et al.* [16].

In addition to emerging as most important direct yield contributors owing to their very high positive direct effects on grain yield per plant; biological yield per plant and harvest index having considerable positive indirect effects via different characters, also appeared as most important indirect yield components. Gour *et al.* [6], Kumar *et al.* [8] and Shrestha *et al.* [19], have also identified biological yield and harvest index as important direct and indirect yield contributing characters. The indirect effects of remaining characters were too low to be considered important. Results revealed that, path analysis identified biological yield per plant followed by harvest index and number of fertile spikelets per panicle as most important direct as well as indirect yield contributing traits which merit due consideration at time of devising selection strategy aimed at developing high yielding varieties in rice.

The salient findings of present study are summarized as:

1. Grain yield per plant exhibited highly significant and positive correlation with biological yield/plant, productive tillers per plant, 1000-grain weight, harvest index, panicle length, spikelet fertility, number of fertile spikelets per panicle and number of spikelets per panicle to emerge as most important associates of grain yield in rice. This suggested that selection would be quite efficient in improving yield and yield components.

2. Path analysis revealed that the highest positive direct effect on grain yield per plant was exerted by biological yield per plant followed by harvest-index and number of fertile spikelets per panicle, while number of spikelets per panicle followed by spikelet fertility exerted highest negative direct effect on grain yield per plant. It refers that more emphasis should be given to select these traits to increase the production and productivity of rice under sodic soil.

3. Productive tillers per plant exerted high order of positive significant indirect effect on grain yield *via* biological yield per plant (0.7264) followed by harvest index (0.3453) number of fertile spikelets per panicle (0.2188), While, days to 50% flowering, days to maturity and plant height exerted high considerable extent of negative indirect effects on grain yield *via* harvest index respectively which can be taken into consideration to devise suitable strategy.

Conclusion

The characters biological yield/plant, productive tillers per plant, 1000-grain weight, harvest index, panicle length, spikelet fertility, number of fertile spikelets per panicle and number of spikelets per panicle showed significant positive genotypic correlation and would result in improvement of yield. Path analysis revealed that biological yield per plant, harvest-index and number of fertile spikelets per panicle and productive tillers per plant are the most important characters which could be used as selection criteria for effective improvement of grain yield.

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