ORIGINAL ARTICLE

Correlation and path coefficient analysis for different quantitative traits in rice (*Oryza sativa* **L.)**

Kapil Gautam1, S.C. Vimal1, Shrigovind1, Mayank Chaudhary2*, Madhusri Pramanik³ Ashok Kumar**, Govind Mishra1, Rishabh Gupta¹**

¹Research scholar, Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

1**Professor, Dept. of Seed Science and Technology, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh (224229), India.

**Assistant Professor, Dept. of Seed Science and Technology, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh (224229), India.

²*Research scholar, Department of Genetics and Plant Breeding, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut, Uttar Pradesh, India

³Assistant Professor, Department of Agriculture, Brainware University, Barasat, Kolkata, West Bengal

(700125)

***Corresponding author: E-mail**: Mayankchahal2709@gmail.com

ABSTRACT

The present investigation is carried out to study the correlation and path analysis in forty-six genotypes of rice (Oryza sativa L.), comprising 10 parental lines, 3 testers, and their resulting 30 F1 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. Character association of the yield attributing traits revealed significantly positive association of biological yield per plant, followed by harvest index, spikelet fertility, 1000-grain weight, plant height and panicle length. Hence, selection for these traits can improve grain yield in rice. Path coefficient analysis revealed that the highest positive direct effect on grain yield per plant was exerted by identified biological yield per plant followed by harvest-index as most important direct yield contributing traits, 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. The selection strategy aimed at developing high yielding varieties in rice. Among these characters, highly significant and positive association of productive tillers per possessed and biological yield per plant highly significant and positive direct effects on biological yield per plant. Hence, selection for this character could bring improvement in yield and yield components.

Keywords: Correlation, path coefficient analysis, rice, (Oryza sativa L.) and yield

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INTRODUCTION

Rice *(Oryza sativa* L) one of the world's most important staple cereal crop growing at least 114 countries under diverse conditions. Rice is also called "Grain of Life", because itis not only the staple food for more than 70 per cent of the Indians and half of the world population but also a feeding source of livelihood for millions of rural households. Rice belongs to the genus *Oryza* of (Gramineae) family *Poaeceae* (*Oryza sativa*, L. 2n = 24) [27]. In view of the growing population, the basic objective of the plant breeders would always be towards yield improvement in staple food crops. It has been estimated that the world will have to produce 60% more rice by 2030 than what it produced in 1995. Rice constitutes a significant portion of the daily diet particularly in developing countries of Asia, supplying 50-80% of the daily caloric intake, proteins, minerals and vitamins etc. This year's 513.02 estimated millions of tons could represent an increase of 4.18 million tons or 0.82% in rice production around the globe [11,3]**.**

Rice is an effective supply of carbohydrate, proteins, fiber, lipid and fat, minerals (potassium, phosphorous, magnesium, calcium, sodium and iodine) and nutrients (thiamine, riboflavin, niacin, pyridoxine and folic acid). The population growth in most of the Asian countries, except China, continues to be around 2% per year [12]. Hence it is very pertinent to critically consider whether the rice production can be further increased to keep pace with population growth. To meet the demand of rapidly increasing population of our country, at the current rate of population growth of 1.58% in India, the requirement of rice by 2025 is estimated to be around 140.7 million tonnes [3], which can be achieved by increasing rice production by over 2.0 million tonnes per year in the coming decades. There is need for a paradigm shift in rice research to meet the challenges of the future decades for ensuring food security [20, 14].

Information on association of characters, direct and indirect effects contributed by each character towards yield will be an added advantage in aiding the selection process. Correlation and path analysis establish the extent of association between yield and its components and also bring out relative importance of their direct and indirect effects, thus giving an obvious understanding of their association with grain yield. Ultimately, this kind of analysis could help the breeder to design his selection strategies to improve grain yield. In the light of the above scenario, the present investigation is carried out with the objective of studying the character associations in rice hybrids for yield improvement.

MATERIAL AND METHODS

The present experimental materials are consisting ten germplasm lines having the *viz*., Sabarmati, IET 18517, Heera, Ferni, Moti Farm, Paudhan, Binni, IET 18933, Bhadani III and Dudhia used as lines and three promising rice varieties *viz*., NDR 359, WGL-32100 and NDR 2064 were used as testers, three checks (Sarju 52, NDR 9930111 and BPT 5204) were the experimental materials of this study. The crosses will be made into "line x tester" mating design [14] to produce 30 crosses. All the forty-six seeds of rice genotype were sown in nursery bed. After 22 days, single seedling per hill was transplanted standard spacing of 20 cm row to row and 15 cm plant to plant spacing in Randomized Block Design (RBD) with three replications at Student Instructional farm of ANDUA&T, Kumarganj, Ayodhya during *Kharif 2023-24*. Recommended packages of practices were followed during the crop growth period. Observations were recorded for thirteen characters *viz.*, Days to 50% flowering, days to maturity, plant height (cm), productive tillers per plant, panicle length (cm), flag leaf area (cm2), The number of spikelets per panicle, Number of fertile spikelets per panicles, spikelet fertility (%), biological yield per plant (g), harvest index (%), 1000-grain weight (g), grain yield per plant (g). Correlation and direct & indirect effects were estimated for all thirteen characters. Observations were recorded and the data was subjected to statistical analysis [24, 9]. The simple correlations (r) between different characters at phenotypic (p) and genotypic (g) levels were worked out.

RESULTS AND DISCUSSION

Correlation Analysis

Selection based on the detailed knowledge of magnitude and direction of association between grain yield and its attributes is very important in identifying the key characters, which can be exploited for crop improvement through suitable breeding programme. 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 Table-1 (a) and Table-1 (b).

At genotypic level, days to 50% flowering exhibited highly positive and significant correlation with days to maturity (0.983) and negative significant association with harvest index (-0.375) and 1000-grain yield (-0.325). Days to maturity showed significant and negative association with flag leaf area (-0.469) followed by harvest index (-0.393) and 1000-grain yield (-0.376). Plant height exhibited positive and highly significant correlation with panicle length (0.337) followed by biological yield per plant (0.318) and while highly significant negative correlation was observed with harvest index (-0.371). The results are in conformity with the findings of Aditya *et al.* [1], Sarwar *et al.* [23], Dhavaleshvar *et al.* [10], Parimala *et al.* [19], Manivelan *et al.* [15] and Reshma *et al.* [22].

Highly significant and positive correlation of productive tillers per plant had been observed with 1000 grain weight (0.962), followed by harvest index (0.952), biological yield/plant (0.882), spikelet fertility (0.740), flag leaf area (0.726), number of fertile spikelets per panicle (0.663), number of spikelets per panicle (0.548) and panicle length (0.394).Panicle length showed highly significant and positive association with harvest index (0.940) followed by 1000-grain weight (0.921), biological yield per plant (0.851), flag leaf area (0.742), spikelet fertility (0.717), number of fertile spikelets per panicle (0.631) and number of spikelets per panicle (0.893) while it was not negatively associated with any characters. These results are in agreement with the findings of Sarwar *et al.* [23], Singh *et al.* [25], Bhargava *et al* (2021), Reshma *et al.* [22] and Singh *et al.* [24].

Flag leaf area possessed highly significant and positive correlation with 1000-grain weight (0.779) followed by biological yield/plant (0.644), harvest index (0.600), spikelet fertility (0.541), number of fertile spikelets per panicle (0.441) and number of spikelets per panicle (0.342). Number of spikelets per panicle exhibited highly significant positive correlation with number of fertile spikelets per panicle (0.965), spikelet fertility (0.569), biological yield/plant (0.449) and positive significant with association 1000-grain weight (0.369) and harvest index (0.341). Highly significant and positive association were recorded between number of fertile spikelets per panicle and spikelet fertility (0.762) followed by biological yield /plant (0.535), 1000-grain weight (0.485) and harvest index (0.418) and no any character showed negative correlation. The trait spikelet fertility had highly significant and positive association with 1000-grain weight (0.778), biological yield/plant (0.648) and harvest index (0.523). 1000-grain weight showed highly significant positive association with harvest index (0.970) and biological yield per plant (0.905). Biological yield per plant showed highly significant positive association with harvest index (0.925). These results are in agreement with the findings**,** Dhavaleshvar *et al.* [10] and Singh *et al.* [25].

Grain yield per plant exhibited highly significant and positive correlation with productive tillers per plant (0.998) followed by 1000-grain weight (0.997), harvest index (0.991), panicle length (0.980), biological yield/plant (0.952), flag leaf area (0.684), spikelet fertility (0.682), number of fertile spikelets per panicle (0.531), number of spikelets per panicle (0.443). It showed negative and highly significant correlation with days to 50% flowering (-0.394), days to maturity (-0.385) and plant height (-0.316). Cyprien *et al.* [8], Ekka *et al.* [11], Ratna *et al.* [21], Muthuramu, S., & Sakthivel, [16], Singh *et al.* [24], Jangala *et al.* [13], Reshma *et al.* [22].

At phenotypic level, grain yield per plant exhibited highly significant and positive correlation with 1000 grain weight (0.901) followed by harvest index (0.813), biological yield/plant (0.780), productive tillers per plant (0.710), panicle length (0.601), flag leaf area (0.475), number of fertile spikelets per panicle (0.404), spikelet fertility (0.365), number of spikelets per panicle (0.317). It showed negative and highly significant correlation with days to maturity (-0.288), days to 50% flowering (-0.267) and plant height (- 0.240). The correlation at phenotypic level is very close to genotypic level. These results are in agreement with the findings Singh *et al.* [26].

Path coefficient analysis

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. The direct and indirect effects of thirteen characters on grain yield per plant estimated by path coefficient analysis using phenotypic as well as genotypic correlation coefficients are given in Table-2 (a) and table-2 (b).

At genotypic level, the highest positive direct effect on grain yield per plant was exerted by biological yield per plant (0.6304) followed by harvest index (0.4553) and number of fertile spikelets per panicle (0.1825).

In genotypic path analysis, days to 50% flowering exerted considerable amount of positive indirect effect on grain yield *via* days to maturity (0.1327). Productive tillers per plant exerted high order of positive significant indirect effect on grain yield *via* biological yield per plant (0.5559) followed by harvest index (0.4335), number of fertile spikelets per panicle (0.1210); panicle length *via* biological yield per plant (0.5369) followed by harvest index (0.4281), number of fertile spikelets per panicle (0.1152); flag leaf area *via* biological yield per plant (0.4064) followed by harvest index (0.2732); number of spikelets per panicle *via* biological yield per plant (0.2836) followed by number of fertile spikelets per panicle (0.1762), harvest index (0.1556); number of fertile spikelets per panicle *via* biological yield per plant (0.3378) followed by harvest index (0.1904); spikelet fertility *via* biological yield per plant (0.3693) followed by harvest index (0.2094), number of fertile spikelets per panicle (0.1391); 1000-grain weight *via* biological yield per plant (0.5174) followed by harvest index (0.3979); biological yield per plant *via* harvest index (0.2852); harvest index *via* biological yield per plant (0.3949) 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., -0.1709, - 0.1793 and -0.1690 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 Chandra *et al.* [7], Sarwar *et al.* [23], Bhujel *et al.* [6], Singh *et al.* [25]*,* Dhavaleshvar *et al.* [10], Jangala *et al.*[13],The indirect effects of remaining characters were too low to be considered important.

Characters	Daysto 50% flowering	Days to Maturity	Plant height (cm)	Productive tillers per plant	Panicle length (cm)	Flagleaf area (cm ²)	Number of spikelets per panicle	spikelets per panicle Number of fertile	Spikelet fertility Ę	1000 grain waiahtfal	Biological yield per plant (g)	Harvest index (%)	Grain yield per plant (g)
flowering Daysto %0S	1.0001	$0.983**$	-0.040	-0.145	-0.212	-0.413	0.073	0.073	0.055	$-0.325*$	-0.214	$-0.375*$	$-0.394**$
Maturity Days to		1.0001	-0.022	-0.201	-0.287	$-0.469**$	820.0	0.042	-0.007	$-0.376**$	-0.249	$-0.393**$	$-0.385**$
height Plant (mn)			1.0001	0.355	$0.337**$	811.0-	-0.213	-0.200	41114	-0.262	$0.318**$	-0.371 ∗	-0.316 $*$
Productive tillers per plant				1.0001	$0.394**$	$0.726**$	$0.548**$	$0.663**$	$0.740**$	$0.962**$	$0.882**$	0.952 **	** 866'0
Panicle length (mn)					1.0001	$0.742**$	$0.520**$	$0.631**$	0.717**	$0.921**$	$0.851**$	$0.940**$	$0.980**$
Flag leaf cm^2 area						1.0001	$0.342*$	$0.441**$	$0.541**$	0.779 **	0.644**	$0.600**$	$0.684**$
per panicle Number of spikelets							1.0001	$0.965***$	0.569**	$0.369*$	$0.449**$	$0.341*$	$0.443**$
ner nanicle Number of spikelets fertile								1.0001	$0.762**$	$0.485***$	$0.535***$	$0.418**$	$0.531**$
Spikelet fertility (9)									1.0001	$0.778**$	$0.648**$	$0.523**$	$0.682**$
weight $1000 -$ ureng lal										1.0001	$0.905***$	$0.970**$	** 7997
Biologica per plant I yield رەر											1.0001	$0.925***$	$0.952**$
index $(%$ Harvest												1.0001	** 1660

Table 1(a): Estimates of genotypic correlation coefficients between 13 characters of rice (*Oryza sativa* **L.).**

*, ** Significant at 5 % and 1 % probability levels, respectively**.**

In phenotypic path analysis, the highest positive direct effect on grain yield per plant was exerted by harvest index (0.6570) followed by biological yield per plant (0.6060), while the highest negative direct effect on grain yield per plant was exerted by flag leaf area (-0.0033) followed by spikelet fertility (- 0.0027). Reshma *et al.* [22]. Path analysis revealed that the amount of phenotypic path coefficient was very close to their genotypic path coefficient in most cases, suggesting the existence of inherent direct and indirect effects on grain yield per plant *via* biological yield per plant and harvest index as presented in table 2(a).

The rest of the estimates of direct and indirect effects obtained in genotypic and phenotypic path analysis were too low to be of any consequences. The estimate of residual factors for genotypic and phenotypic path were 0.00013 and 0.003 respectively obtained in this path analysis was low. The remaining estimates of indirect effects in this analysis were too low to be considered of any consequence. The estimates of residual factors were negligible. These results are similar to Nayak *et al*. [18], Babu et al [4], Naseem *et al*. [17], Sarwar, *et al.* [24], Shrestha, *et al.* [24], Dhavaleshvar *et al.* [10] and Singh *et al.* [24].

*, ** Significant at 5 % and 1 % probability levels, respectively**.**

Table 2(a): Direct (Bold diagonal figures) and indirect effects of different characters on grain yield per plant at genotypic level in rice (*Oryza sativa* **L.).**

R SQUARE = 0.0013 RESIDUAL EFFECT =SQRT (0.0013)' *, ** significant at 5% and 1% level, respectively.

Table 2(b): Direct (Bold diagonal figures) and indirect effects of different characters on grain yield per plant at phenotypic level in rice (*Oryza sativa* **L.).**

R SQUARE = 0.0030 ;*, ** significant at 5% and 1% level, respectively.

CONCLUSION

The characters biological yield/plant, plant height, 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 are the most important characters which could be used as selection criteria for effective improvement of grain yield.

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