

Reprint

ISSN 1991-3036 (Web Version)

**International Journal of Sustainable Crop Production (IJSCP)**

*(Int. J. Sustain. Crop Prod.)*

---

**Volume: 12**

**Issue: 2**

**May 2017**

---

*Int. J. Sustain. Crop Prod. 12(2): 1-6 (May 2017)*

**CORRELATION AND PATH COEFFICIENT ANALYSIS OF YIELD AND YIELD  
CONTRIBUTING TRAITS IN RICE**

M.M. RASHID, L. HASSAN, B. DAS AND S.N. BEGUM



An International Scientific Research Publisher

**Green Global Foundation<sup>®</sup>**

Web address: <http://ggfjournals.com/e-journals archive>

E-mails: [editor@ggfjournals.com](mailto:editor@ggfjournals.com) and [editor.int.correspondence@ggfjournals.com](mailto:editor.int.correspondence@ggfjournals.com)



## CORRELATION AND PATH COEFFICIENT ANALYSIS OF YIELD AND YIELD CONTRIBUTING TRAITS IN RICE

M.M. RASHID<sup>1</sup>, L. HASSAN<sup>1\*</sup>, B. DAS<sup>1</sup> AND S.N. BEGUM<sup>2</sup>

<sup>1</sup>Department of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU), Mymensingh-2202, Bangladesh; <sup>2</sup>Senior Scientific Officer, Plant Breeding Division, Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh-2202, Bangladesh.

\*Corresponding author & address: Dr. Lutful Hassan, E-mail: lutfulhassan@yahoo.co.uk

Accepted for publication on 25 April 2017

### ABSTRACT

Rashid MM, Hassan L, Das B, Begum SN (2017) Correlation and path coefficient analysis of yield and yield contributing traits in rice. *Int. J. Sustain. Crop Prod.* 12(2), 1-6.

Studies on character association and path-coefficient analysis were conducted on ten rice genotypes including seven landraces and three released variety for their yield and yield contributing traits. Character association of the yield attributing traits revealed significantly positive association of yield panicle<sup>-1</sup> with days to 50% flowering, days to maturity, plant height and number of filled grains panicle<sup>-1</sup>. Hence, selection for these traits can improve yield. Path coefficient analysis revealed that Days to maturity, number of filled grains panicle<sup>-1</sup>, number of unfilled grains panicle<sup>-1</sup>, and 1000 grains weight exhibited direct positive effect on yield panicle<sup>-1</sup> at genotypic level and days to 50% flowering, plant height, panicle length, number of effective tillers plant<sup>-1</sup>, percent fertility exhibited direct positive effect on yield panicle<sup>-1</sup> at phenotypic level. Hence, selection for this character could bring improvement in yield and yield components. This study revealed that genetic improvement of yield in rice is admissible by selecting characters having high positive correlation and positive direct effect on grain yield.

**Key words:** correlation, path coefficient, yield, yield contributing traits, rice

### INTRODUCTION

Rice (*Oryza sativa* L.) is one of the momentous staple cereal crops feeding more than half of the world population. 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 2014. But salinity is one of the major hindrances in increasing production in rice growing areas worldwide, which is an ever present threat to crop yield. Therefore, development of salt tolerant varieties has been considered as one of the strategies to increase rice production in saline prone coastal areas. Yield and yield contributing parameters are the most widely targeted traits for rice improvement programmes worldwide. Yield is a complex polygenic character, resulting from multiple interactions between many yield contributing traits. Associations between these traits can be evaluated by correlation analysis, which helps in the simultaneous selection for more than one character (Akhtar *et al.* 2011; Sathya and Jebaraj, 2013; Semahegn and Tesfaye, 2016). The degree of connection between important plant traits is an index that can be used to predict yield responses in relation to changes associated with a particular character (Malek *et al.* 2014). So, for rice genotypes, identification of key characters associated with yield and other contributing components is important for maximizing yields (Aditya *et al.* 2011; Meitei *et al.* 2014; Jain *et al.* 2015). Correlation coefficients alone are insufficient to understand cause and effect relationships among traits associated with yield, whereas path coefficient analysis allows a better understanding of associations between different characters, by breaking down correlation coefficients associated with the main character into direct and indirect effects (Rahman *et al.* 2011; Hossain *et al.* 2015). The correlation value denotes only the nature and extent of association existing between pairs of characters. The yield is dependent on several contributing characters that are mutually associated which will in turn impair the true association existing between a yield contributing characters and economic characters and change in any one component is likely to disturb the whole network of cause and effect. Each contributing characters has two parts of action *viz.*, the direct effect and the indirect effects through yield contributing characters on economic characters which are not revealed from the correlation studies. Path coefficient analysis provides an applicable means to partition correlation coefficients into unidirectional and alternative pathways, thus permitting a critical examination of the specific factors that produce a given correlation; this can then be employed to formulate an effective selection programme (Salahuddin *et al.* 2010; Lal *et al.* 2011; Parmar *et al.* 2013; Jain *et al.* 2015). Considering the above facts, the present research study was undertaken to evaluate the associations among yield and yield contributing traits for rice genotypes, using correlation and path analysis. This investigation provides information that could lead to the development of desirable genotypes in future breeding programmes.

### MATERIALS AND METHODS

The present experiment was carried out in the experimental site of the Plant Breeding Division at Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh during the period from June to December 2015. Ten rice genotypes including seven landraces and three released varieties *viz.*, Hogla, Dakh Shail, Kute Patnai, Ghunshi, Mondeshor, Tal Mugur, Nona Bokhra, Binadhan-8, Binadhan-10 and BRRI dhan47 were used as plant material. The seedlings were grown in earthen pot filled with field soil and five seedlings were finally kept in each pot. Randomized Complete Block Design (RCBD) with five replications and three different salt treatments *viz.*, EC-6 dSm<sup>-1</sup>, EC-8 dSm<sup>-1</sup>, EC-12 dSm<sup>-1</sup> with one control condition were used for this study. Management practices

such as irrigation and fertilization were performed by following the standard procedures (IRRI 2002). Other intercultural operations were done whenever necessary. Morphological data were collected at appropriate growth stage of rice plant following the standard evaluation system indicated by IRRI (IRRI 2013). The characters that were studied included days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), number of effective tillers plant<sup>-1</sup>, number of filled grains panicle<sup>-1</sup>, number of unfilled grains panicle<sup>-1</sup>, fertility (%), 1000 grains weight (g) and yield panicle<sup>-1</sup> (g). The recorded data for different parameters were assembled and organized properly for statistical analysis using BASICA. Estimation of phenotypic and genotypic correlation coefficients were estimated by the formula suggested by (Miller *et al.* 1958). The path coefficients were calculated as per the formula given by Dewey and Lu (1959).

## RESULTS AND DISCUSSION

### Estimation of the correlation coefficient

The degree of correlation between the traits is important in plant breeding. It can be used as tool for indirect selection. Correlation studies help the plant breeder during selection and provide the understanding of yield components. The estimates of genotypic and phenotypic correlation coefficients are presented in Table 1. The results revealed that the estimates of genotypic coefficients were higher than phenotypic correlation coefficients for most of the characters under study, which indicated strong inherent association between the characters, which might be due to masking or modifying effects of environment. Significant positive correlations at both genotypic and phenotypic level were recorded for yield panicle<sup>-1</sup> with days to 50% flowering, days to maturity, plant height and number of filled grains panicle<sup>-1</sup> and negatively correlated with 1000 grains weight (g). The number of effective tillers plant<sup>-1</sup> negatively correlative with yield panicle<sup>-1</sup> only at genotypic level. The observed positive correlation of days to 50% flowering was supported by earlier researchers such as (Zhou *et al.* 2010; Khan *et al.* 2014) for number of panicle. (Ekka *et al.* 2011) also reported positive correlation of grain yield with plant height and that with plant height and effective tillers per plant (Patel *et al.* 2014). (Bhadru *et al.* 2011) reported that plant height had a significant positive association with yield. The results also supported by (Rokonuzzman *et al.* 2008; Khan *et al.* 2009) for filled grains per panicle and by (Rasheed *et al.* 2002 and Girish *et al.* 2006) for plant height. The yield panicle<sup>-1</sup> negatively correlated with 1000 grains weight at both phenotypic and genotypic level. (Ullah *et al.* 2011) also found that grain yield had negative and significant correlation with thousand grains weight.

Overall, the results of the present study indicate that selection of high yielding rice genotypes would be possible by carefully balancing days to 50% flowering, days to maturity, plant height with moderate number of filled grains panicle<sup>-1</sup>. These results should be considered when determining the selection criteria for future varietal improvement of rice. Any traits, which do not show any significant association or very negligible association, can be discarded to reduce the number of traits considered.

### Estimation of path coefficients

The path coefficient analysis was performed using correlation coefficients to determine the direct and indirect effects of 10 yield contributing characters. The values are shown in Table (2&3). In this analysis days to maturity, number of filled grains panicle<sup>-1</sup>, number of unfilled grains panicle<sup>-1</sup>, and 1000 grains weight had direct positive effect on yield panicle<sup>-1</sup> at genotypic level (Table 2) and days to 50% flowering, plant height, panicle length, number of effective tillers plant<sup>-1</sup>, fertility percentage, had direct positive effect on yield panicle<sup>-1</sup> at phenotypic level (Table 3). Similar results had also been reported by (Osman *et al.* 2012; Akhtar *et al.* 2011). (Zahid *et al.* 2006) reported that number of filled grains panicle<sup>-1</sup> has highest positive direct effect on yield. (Akhter *et al.* 2010) conducted an experiment and reported that days to maturity has highest positive direct effect on yield followed by plant height and days to 50% flowering. The above information revealed that highly significant positive correlation with highest positive direct effect was observed in number of filled grains panicle<sup>-1</sup>. So the number of number of filled grains panicle<sup>-1</sup> could be considered as critical criteria for yield improvement in these genotypes of rice. Similar results had also been reported by (Samonte *et al.* 1998; Mahto *et al.* 2003). The residual effect determines how best the causal factors account for the variability of the dependent factor, the yield per plant in this case. In case of the present study the residual effect was 0.3965 and 0.1409 at genotypic and phenotypic level respectively. The residual effect 0.1409 at phenotypic level indicates that the nine traits explain 86% of variability in yield per panicle. The reason seems to be very low and non-significant correlation of some traits with yield.

Table 1. Phenotypic ( $r_p$ ) and genotypic ( $r_g$ ) correlation coefficients among 10 traits in ten rice genotypes

Characters		DM	PH (cm)	PL (cm)	NETPP	NFGPP	NUGPP	PF	TGW (g)	YP (g)
DFF	$r_p$	0.847**	0.898**	0.771**	-0.523	0.511	-0.316	0.242	0.019	0.762*
	$r_g$	0.858**	0.919**	0.792**	-0.599	0.534	-0.350	0.269	0.024	0.851**
DM	$r_p$		0.822**	0.929**	-0.407	0.604	-0.401	0.575	0.019	0.640*
	$r_g$		0.831**	0.983**	-0.459	0.620	-0.432	0.602	0.018	0.709*
PH (cm)	$r_p$			0.952**	-0.452	0.660*	-0.385	0.520	0.154	0.869**
	$r_g$			0.896**	-0.521	0.683*	-0.377	0.527	0.166	0.958**
PL (cm)	$r_p$				-0.934**	0.326	-0.742*	-0.751*	-0.867**	0.434
	$r_g$				-0.963**	0.029	-0.824**	-0.730*	-0.992**	0.118
NETPP	$r_p$					-0.190	0.116	-0.684*	-0.965**	-0.487
	$r_g$					-0.287	-0.015	-0.971**	-0.766**	-0.734*
NFGPP	$r_p$						-0.460	0.686*	-0.817**	0.625*
	$r_g$						-0.522	0.596	-0.982**	0.636*
NUGPP	$r_p$							-0.516	-0.641*	-0.435
	$r_g$							-0.517	-0.911**	-0.519
FP	$r_p$								-0.877**	0.221
	$r_g$								-0.838**	0.053
TGW (g)	$r_p$									-0.715*
	$r_g$									-0.818**

\*\* Indicates significant at 0.01 probability level and \* indicates significant at 0.05 probability level

Note:

DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, PL: Panicle length, NETPP: Number of effective tiller per plant, NFGPP: Number of filled grains per panicle, NUGPP: Number of unfilled grains per panicle, PF: percent fertility, TGW: 1000 grains weight, YP: Yield per panicle

Table 2. Partitioning of genotypic correlation into direct and indirect effects of morphological characters of 10 rice genotypes by path coefficient analysis (bold values indicate the direct effect)

Characters	DFF	DM	PH (cm)	PL (cm)	NETPP	NFGPP	NUGPP	PF	TGW (g)	YP (g)
DFF	<b>-2.22</b>	1.82	-0.71	-0.15	0.96	2.30	-0.54	-0.65	0.04	0.85**
DM	-1.91	<b>2.13</b>	-0.65	-0.18	0.74	2.67	-0.66	-1.46	0.03	0.71*
PH (cm)	-2.04	1.77	<b>-0.78</b>	-0.17	0.83	2.94	-0.58	-1.27	0.25	0.96**
PL (cm)	-1.76	2.09	-0.70	<b>-0.18</b>	1.54	0.13	-1.26	1.76	-1.50	0.12
NETPP	1.33	-0.98	0.41	0.18	<b>-1.60</b>	-1.24	-0.02	2.35	-1.16	-0.73*
NFGPP	-1.18	1.32	-0.53	-0.01	0.46	<b>4.31</b>	-0.80	-1.44	-1.49	0.64*
NUGPP	0.79	-0.92	0.29	0.15	0.02	-2.25	<b>1.53</b>	1.25	-1.38	-0.52
FP	-0.59	1.28	-0.41	0.13	1.55	2.56	-0.79	<b>-2.41</b>	-1.27	0.053
TGW (g)	-0.05	0.04	-0.13	0.18	1.23	-4.23	-1.39	2.03	<b>1.51</b>	-0.82**

Residual effect = 0.3965

\*\* Indicates significant at 0.01 probability level and \* indicates significant at 0.05 probability level

Note:

DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, PL: Panicle length, NETPP: Number of effective tiller per plant, NFGPP: Number of filled grains per panicle, NUGPP: Number of unfilled grains per panicle, PF: percent fertility, TGW: 1000 grains weight, YP: Yield per panicle

Table 3. Partitioning of phenotypic correlation into direct and indirect effects of morphological characters of 10 rice genotypes by path coefficient analysis (bold values indicate the direct effect)

Characters	DFF	DM	PH (cm)	PL (cm)	NETPP	NFGPP	NUGPP	PF	TGW (g)	YP (g)
DFF	<b>1.10</b>	-0.97	0.53	0.30	-0.10	-0.34	0.09	0.16	-0.01	0.76*
DM	0.94	<b>-1.15</b>	0.48	0.33	-0.08	-0.40	0.12	0.38	-0.01	0.64*
PH (cm)	0.99	-0.95	<b>0.59</b>	0.37	-0.09	-0.44	0.11	0.34	-0.07	0.87**
PL (cm)	0.85	-1.07	0.56	<b>0.39</b>	-0.18	-0.22	0.22	-0.49	0.37	0.43
NETPP	-0.58	0.47	-0.27	-0.37	<b>0.19</b>	0.13	-0.03	-0.45	0.42	-0.49
NFGPP	0.56	-0.69	0.39	0.13	-0.04	<b>-0.67</b>	0.14	0.45	0.35	0.63
NUGPP	-0.35	0.46	-0.23	-0.29	0.02	0.31	<b>-0.29</b>	-0.34	0.27	-0.44
FP	0.27	-0.66	0.31	-0.29	-0.13	-0.46	0.15	<b>0.66</b>	0.38	0.22
TGW (g)	0.02	-0.02	0.09	-0.34	-0.19	0.54	0.19	-0.57	<b>-0.43</b>	-0.72*

Residual effect = 0.1409

\*\* Indicates significant at 0.01 probability level and \* indicates significant at 0.05 probability level

Note:

DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, PL: Panicle length, NETPP: Number of effective tiller per plant, NFGPP: Number of filled grains per panicle, NUGPP: Number of unfilled grains per panicle, PF: percent fertility, TGW: 1000 grains weight, YP: Yield per panicle

## CONCLUSION

From this present study when the result of correlation and path coefficient analysis are examined, it can be concluded that the character *viz.*, days to 50% flowering, days to maturity, plant height and number of filled grains per panicle could be used as an important selection indices for the improvement of yield in rice. In addition, these traits had significant and positive correlations with yield per panicle and its may be utilized for pure line selection in late generations for the betterment of breeding program.

## REFERENCES

- Aditya JP, Pushpendra BP, Anuradha B (2011) Genetic variability, heritability and character association for yield and component characters in soybean (*G. max* (L.) Merrill), *Journal of Central European Agriculture* 12(1), 27-34.
- Akhtar N, Nazir MF, Rabnawaz A, Mahmood T, Safdar ME, Asif M, Rehman A (2011) Estimation of heritability, correlation and path coefficient analysis in fine grain rice (*Oryza Sativa* L.). *Journal of Animal and Plant Science* 21(4), 660-664.
- Akhter T, Ivy NA, Rasul MG, Mian MAK (2010) Variability and character association of reproductive traits in exotic rice germplasm, *Bangladesh Journal of Plant Breeding and Genetics*, 23(1), 39-43.
- Bhadru D, Reddy DL, Ramesha MS (2011) Correlation and path coefficient analysis of yield and yield contributing traits in rice hybrids and their parental lines. *Electronic Journal of Plant Breeding* 2(1), 112-116.
- Dewey DR, Lu KH (1959) A correlation and path-coefficient analysis of components of crested wheat grass seed production, *Agronomy Journal*, 51, 515-518.
- Ekka RE, Sarawgi AK, Kanwar RR (2011) Correlation and Path Analysis in Traditional Rice Accessions of Chhattisgarh. *J. of Rice Research* 4(2), 11-18.
- Girish TN, Giresha TM, Vaishali MG, Hanamareddy BG, Hittalmani S (2006) Response of a new IR 50/Moroberekan recombinant inbred population of rice (*Oryza sativa* L.) from an indica × japonica cross for growth and yield traits under aerobic condititions. *J. Euphytica*, 152(2), 149-161.
- Hossain S, Maksudu HMD, Jamilur RJ (2015) Genetic Variability, Correlation and Path Coefficient Analysis of Morphological Traits in some Extinct Local Aman Rice (*Oryza sativa* L). *J. Rice Res.* 3, 158.
- IRRI (2013) Standard evaluation system for rice. 5th Edition, IRRI, Philippines.
- IRRI (2002) International Rice Research Institute. Annual Report for 2002. Los Banos, Laguna, Philippines. pp. 308.
- Jain S, Srivastava SC, Singh KS, Indapurkar YM, Singh BK (2015) Studies on genetic variability, character association and path analysis for yield and its contributing traits in soybean [*Glycine max* (L.) Merrill], Agricultural Research Communication Center, Legume Research, 38(2), 182-184.
- Khan AS, Imran M, Ashfaq M (2009) Estimation of genetic and environmental variability in soybeans. *Agron. J.*, 47, 314-318.
- Khan MSK, Iqbal J, Saeed M (2014) Comparative study of agronomic traits of different rice varieties grown under saline and normal conditions. *J. Anim. Plant Sci.* 24(2), 634-642.
- Lal H, Rai M, Verma A, Vishwanath (2011) Analysis of genetic divergence of Dolichos Bean (*Lablab purpureus* L.) genotypes, *Vegetable Science*, 32(2), 129-132.
- Mahto RN, Yadava MS, Mohan KS (2003) Genetic variation, character association and path analysis in rainfed upland rice. *Indian Journal of Dryland Agriculture Research and Development, Central Research Institute for Dryland Agriculture, Hyderabad, India.* 18(2), 196-198.
- Malek MA, Raffi MY, Afroj MSS, Nath UK, Mondol MMA (2014) Morphological characterization and assessment of genetic variability, character association, and divergence in soybean mutants. *The Scientific World Journal* 1-12.
- Meitei KM, Bora GC, Singh JS, Sinha KA (2014) Morphology based genetic variability analysis and identification of important characters for tomato (*Solanum lycopersicum* L.) crop improvement. *American-Eurasian Journal of Agricultural & Environmental Sciences* 14(10), 1105-1111.
- Miller P, Williams J, Robinson H, Comstock R (1958) Estimates of genotypic and environmental variances and co-variances in upland cotton and their implications in selection, *Agronomy Journal* 50, 126-131.

- Osman KA, Mustafa AM, Ali F, Yonglain Z, Fazhan Q (2012) Genetic variability for yield and related attributes of upland rice genotypes in semi-arid zone (Sudan). *African Journal of Agricultural Research*. 7(33), 4613-4619.
- Parmar AM, Singh AP, Dhillon NPS, Jamwal M (2013) Genetic variability studies for morphological and yield traits in Dolichos bean (*Lablab purpureus* L.), *World Journal of Agricultural Sciences*, 9(1), 24-28.
- Patel DB, Patel DA, Bhatt MM, Jadeja GC, Pathak AR (2014) Variability for salinity tolerance in rice genotypes at germination stage. *Res. Crops* 5, 168- 175.
- Rahman MM, Rasul MG, Bashir MK, Syed MA, Islam MR (2011) Parent selection for transplanted aman rice breeding by morphological, physiological and molecular diversity analysis. *Libyan Agriculture Research Center Journal International* 2(1), 29-35.
- Rasheed MS, Sadaqat HA, Babar HA (2002) Correlation and path coefficient analysis for yield and its components in rice. *Asian J. Pl. Sci.*, 1(3), 241-244.
- Rokonuzzaman M, Zahangir MS, Hussain MDI (2008) Genotype variability of components and their effects on the rice yield: Correlation and path analysis study. *Ital. J. Agron.*, 2, 131-134.
- Salahuddin S, Abro M, Kandhro M, Salahuddin L, Laghari S (2010) Correlation and path coefficient analysis of yield components of upland cotton [*Gossypium hirsutum* (L.)] sympodial, *World Applied Sciences Journal*, 8, 71-75.
- Samonte SOPB, Wilson LT, McClung AM (1998) Path analyses of yield and yield related traits of fifteen diverse rice genotypes. *Crop Science*. 38(5), 1130-1136.
- Sathya R, Jebaraj S (2013) Inter-Relationship and cause effect analysis among drought and physiological traits in three line aerobic rice hybrids. *Plant Gene and Trait* 4, 70-73.
- Semahegn Y, Tesfaye M (2016) Characters associations and path analysis in safflower (*Carthamus tinctorious*) accessions. *Molecular Plant Breeding* 7(31), 1-5.
- Ullah MZ, Bashir MK, Bhuiyan MSR, Khalequzzamana M, Hasan MJ (2011) Interrelationship and cause-effect analysis among morpho-physiological traits in birain rice of Bangladesh. *Int. J. Plant Breed. Genet.*, 5, 246-254.
- Zahid MA, Akhtar M, Sabir M, Manzoor Z, Awan TH (2006) Correlation and path analysis studies of yield and economic traits in Basmati rice (*Oryza Sativa* L.). *Asian Journal of Plant Science*. 5, 643-645.
- Zhou HK, Hayat Y, Fang LJ, Guo RF, He JM, Xu HM (2010) Analysis of genetic and genotype X environment interaction effects for agronomic traits of rice (*Oryza sativa* L.) in salt tolerance. *Pak. J. Bot.* 42, 3239- 3246.