Fundamental and Applied Agriculture
Vol. 4(4), pp. 1019–1024: 2019
doi: 10.5455/faa.60679

Genetics and Plant Breeding
ORIGINAL ARTICLE

Traits association, path analyses and multiple linear regression estimates in rice (*Oryza sativa* L.)

Joynulalam Talukder[1*], Md. Abdullah Al Bari[2,3], Mirza Mofazzal Islam[4], Majharul Islam[5], Rashedullah Jewel[6], Israt Jahan[7]

[1]Horticulture Centre, Department of Agricultural Extension, Shulakia, Kishoreganj, Bangladesh
[2]Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh 2202, Bangladesh
[3]Applied Wheat Genomics Lab, Department of Plant Pathology, Kansas State University, 4701 Throcmorton PSC, Manhattan, KS 66506, USA
[4]Plant Breeding Division, Bangladesh Institute of Nuclear Agriculture, Mymensingh 2202, Bangladesh
[5]Soil Science Division, Bangladesh Institute of Nuclear Agriculture, Mymensingh 2202, Bangladesh
[6]Bayer Crop Science, Vadra, Rajshahi 6000, Bangladesh
[7]Department of Agricultural Extension, Netrakona Sadar, Netrakona, Bangladesh

ARTICLE INFORMATION

Article History
Submitted: 08 Aug 2019
Revised: 11 Sep 2019
Accepted: 22 Sep 2019
First online: 11 Nov 2019

Academic Editor
Md Amir Hossain
amirgpb@bau.edu.bd

*Corresponding Author
Joynulalam Talukder
joynulalam.hstu@gmail.com

ABSTRACT

Screening of segregating breeding lines based on only yield may mislead selection in the breeding programs. So the research objectives were to measure the association existed among yield and yield related traits, measuring the direct and indirect effects of yield associated traits on grain yield and estimate the influence of secondary traits in determining yield of rice. Forty seven rice genotypes including BINA dhan10, BINA dhan17, NERICA mutant and rest developed genetic materials were planted following randomized complete block design using three replications at BINA complex from July 2015 to December 2016. The statistical program MSTAT-C, BASICA and multiple linear regression analyses model implemented in R were used to analyze the data. Traits association analyses suggested that yield plant^{-1} had highly significant and positive association existed with plant height (r_p = 0.577, r_g = 0.591) followed by active tillers number plant^{-1} (r_p = 0.372, r_g = 0.364) and tillers number plant^{-1} (r_p = 0.337, r_g = 0.342) and negative significant association with days to first flowering (r_p = −0.095, r_g = −0.094). Plant height had the highest positive direct effect (0.685) and tillers number plant^{-1} (−0.364) showed maximum negative direct effect towards yield plant^{-1} as revealed from path analyses. The multiple linear regression analyses showed that the change of 1 cm of plant height could influence about 0.19 g rice yield plant^{-1} as per Model 1 and 0.16 g rice yield plant^{-1} as per Model 2. Measured plant height, active tillers number plant^{-1} and days to first flowering could be more influencing traits for selecting breeding lines in segregating generations to develop high yielding of rice genotypes.

Keywords: Characters relationship, path coefficient, regression analyses, rice

Cite this article: Talukder J, Bari MAA, Islam MM, Islam M, Jewel R, Jahan I. 2019. Traits association, path analyses and multiple linear regression estimates in rice (*Oryza sativa* L.). Fundamental and Applied Agriculture 4(4): 1019–1024. doi: 10.5455/faa.60679

1 Introduction

Rice is the major food crop of Bangladesh and in terms of rice production and consumption the country holds fourth position worldwide (FAO, 2011; Baral, 2016). Almost half of the world's population consumed rice (Ravikumar et al., 2015) which is predicted to be 4.6 billion by 2050 (Ashok et al., 2016). It is the cheapest source of food, energy and protein in the developing countries and fulfills the nutritional requirements of not only 90 per cent population of Asian countries but also almost half population of the world (Ashok et al., 2016; Kumar, 2013). Rice is also a good source of dietary energy supplying around 20% dietary energy in the world of food (Laxuman et al., 2011) and in Asia more than 30% calories consumed from rice (Narciso and Hossain, 2002). The arable land of the country is occupied by rice covering more than 74.85% area of Bangladesh (BBS, 2016).

Bangladesh produces huge amount of rice in every year to meet the need of the country. The rice production was 34.71 million MT in 2014-15 from 28.20 million acres of land and it produced the same by using 28.12 million acres of land in 2015-16 (BBS, 2016). But the production is merely adequate to satisfy the requirement of our people. As a consequence, Bangladesh imports rice in every year from other countries. The import was 900 thousand mt. in 2015 and increased to 1300 thousands MT due to severe flooding in 12 districts in 2016 (Lagos and Hossain, 2016). Lately the amount of imported rice reached the pick of 1690.6 thousand MT till November 2017 (MoF, 2017). So it is clear that rice production to be increased in Bangladesh to minimize the import and fulfill the demand of the citizens.

Yield is a complex character (Chandra et al., 2009), influenced by several other characters which could regulate yield jointly may be directly and/or even indirectly through other related characters. As a result, screening of segregating breeding lines based on only yield may misguide selection in the breeding programs. Information on plant traits association, direct influence and indirect influence via different other traits contributed towards yield would generate valuable message to perform successful selection. The study of traits association among component characters along with yield is very important (Ravikumar et al., 2015). The measurement of direct influence on yield and also indirect effects via different characters on yield estimated through path coefficient analyses enables the breeders to select better plant by accommodating most suitable component characters (Laxuman et al., 2011). In addition, it assists in identifying criteria for better selection in order to improve yield of crop plants (Chandra et al., 2009). Multiple linear regression analyses has been used to predict yield on other traits to identify few predominantly responsible secondary traits having considerable influence on yield to be used in selection process to boost yield of rice for improving genotypes (Augustina et al., 2013). The present research work, is therefore, framed to measure the association between yield and yield attributing traits, dissect effects of yield contributing traits on yield that influence directly/or indirectly and also estimate the influence of yield attributing traits in determining yield of rice genotypes through statistical means in an aim to decide the selection criteria for breeding programs in progress to improve yield.

2 Materials and Methods

The two donor parents *i.e.* high yielding aman rice variety BINA dhan17 and drought tolerant NERICA mutant (N10-350-P-5-4) and a recipient parent as high yielding rice variety BINA dhan10 were collected from Bangladesh Institute of Nuclear Agriculture (BINA) for generating desired genetic materials. For developing two F1 populations using collected parents, staggered planting of the parental genotypes was executed for achieving synchronization of flowering at plant breeding research field of BINA from 16 July 2015 to 06 August 2015. After emerging the panicle towards flowering of recurrent/recipient parent, emasculated the selected part of recurrent/recipient parent for removing anther and covered by poly bag to check unwanted fertilization *i.e.* contamination at afternoon. Then The panicle of donor parents were collected keeping in water jar at around 10 AM for flowering and dusted the anther of donor parents BINA dhan17 and NERICA mutant (N10-350-P-5-4) to recurrent parent BINA dhan10 for obtaining F1 seeds through successful cross. The seedlings of F1 populations and BINA dhan10 using as recurrent parent were raised at plant breeding research field of BINA following staggered planting from 20 January 2016 to 18 February 2016 to develop two BC1 and forty F2 populations by phenotypic selection. Finally during 28 August, 2016 all the seedlings of developed generations *i.e.*, two F1, two BC1, forty F2 populations, one mutant line and two popular rice verities were transplanted following RCBD with three replicates following recommended standard agronomic practices. Data were recorded on nine quantitative traits *viz.*, plant height (cm), tillers number plant^{-1}, active tillers number plant^{-1}, panicle length (cm), days to first flowering, days to maturity, number of filled grains panicle^{-1}, number of unfilled grains panicle^{-1} and yield plant^{-1} (g).

The statistical program MSTAT-C was used for analysis of variance and the genotypic and phenotypic correlations. The measure of direct effect and indirect effect on grain yield via other traits were analyzed by path coefficient analyses were carried out using statistical program BASICA. Stepwise multiple linear regression analyses were done by using two models. The first model was considered as:

$$Y = a + \sum_{i=1}^{n} b_i X_i + \varepsilon \tag{1}$$

where, Y = rice yield, a = intercept, X = (independent variables) different plant characteristics (n = 1...7), *viz.*, plant height, tillers number plant^{-1}, effective tiller number plant^{-1}, days to first flowering, days to maturity, panicle length, number of filled grains panicle^{-1}, and number of unfilled grains panicle^{-1}; a = intercept, ε = error term, and b_i = slopes associated with respective independent variables X_i.

Improved model was also used with the assumption that significantly correlated variables with yield would better fit the model. The second model is:

$$Y = a + b_1X_1 + b_2X_2 + b_3X_3 + \varepsilon \tag{2}$$

where, a is intercept, ε is error term, independent variables X_1, X_2, X_3 refer plant height, tillers number plant^{-1} and active tillers number plant^{-1}, respectively. b_1, b_2 and b_3 are slopes respectively or regression coefficient that implies rate of change. Both the models were executed in R software (R, 2017).

3 Results and Discussion

The estimated variance analysis (Table 1) exhibited significant variations for the studied traits viz., plant height, tillers number plant^{-1}, active tillers number plant^{-1}, days to first flowering, panicle length, days to maturity, number of filled grains panicle^{-1}, number of unfilled grains panicle^{-1} and yield plant^{-1}. It indicates the considerable genetic variability existed among the genotypes of this study.

The association analyses among different traits of the genotypes helps the plant breeder to determine priority component traits on which selection need to be proceed for genetic advancement leading to genetic gain. Trait association reveals the strength of relationships in determining traits on which selection could be executed for enhancing rice genotypes. The traits association of existing research using 9 selective traits of 47 genotypes presented in Table 2. Out of 72 phenotypic and genotypic associations, 33 associations were positive and rests of the associations were negative. The associations that are statistically significant and non significant with yield plant^{-1} were 31 and 41, respectively. Among the statistically significant associations (31), the 20 associations were positive so, possibly less affected by the environment and rest 11 associations were negatively significant. The 25 associations between the traits were positive both in genotypic and phenotypic situations, however, non significant associations indicating inherent relationship among the pairs of combination. In contrast, 27 relationship were negative and non- significant both at genotypic and phenotypic level. Again 16 genotypic associations and 15 phenotypic associations were found significant. Our research found 11 associations where genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients, such observation might results if environmental effects get masked or modified as Singh (1980) reported in rice.

Plant traits association analyses among yield and yield influencing traits of rice genotypes depicted that yield plant^{-1} was significant and positively correlated with plant height (r_p = 0.577, r_g = 0.591) indicating the yield plant^{-1} will increase if height of plants increases which is in agreement with Kole et al. (2010), however, different results were found by Sala et al. (2015) and Shet et al. (2012). The tillers number plant^{-1} and active tillers number plant^{-1} will be increased due to increase of plant height whereas the days to maturity will increase and the panicle length will decrease due to increase plant height. The tillers number plant^{-1} showed significant genotypic and phenotypic positive correlation with yield plant^{-1} (r_p = 0.337, r_g = 0.342) mentioning the increase of yield plant^{-1} due to the increase tillers number plant^{-1} which is coincide with Kahani and Hittalmani (2015). The active tillers number plant^{-1} will increase with the increase of total tillers number plant^{-1} but the number of filled and unfilled grains panicle^{-1} will decrease due to increase of total tillers number plant^{-1}.

Active tillers number plant^{-1} showed significant genotypic and phenotypic positive correlation with yield plant^{-1} (r_p = 0.372, r_g = 0.364) indicating that yield plant^{-1} will increase with the increase active tillers number plant^{-1} as suggested earlier by Chandra et al. (2009), Ashok et al. (2016), Kahani and Hittalmani (2015) and Chandra et al. (2009). Yield plant^{-1} showed significantly negative correlation with days to first flowering (r_p = -0.095, r_g = -0.094) at both genotypic and phenotypic level mentioning the yield plant^{-1} will decrease if more days required for flowering, the findings were supported by Haradari and Hittalmani (2017) and Sala et al. (2015). Although no significant relationship was found among days to maturity and yield plant^{-1}, however, previous studies by Haradari and Hittalmani (2017) claimed to found significant negative association between these traits. Panicle length exhibited positive and significant phenotypic as well as genotypic correlation with number of filled grains panicle^{-1} (r_p = 0.368, r_g = 0.366) mentioning the maximum filled grains panicle^{-1} due to maximum panicle length. Besides, no significant relationship among panicle length and yield plant^{-1} was observed in this study, however, Laxuman et al. (2011) found significant positive correlation between panicle length and yield plant^{-1}.

As per path coefficient (Table 3) analyses, plant height, active tillers number plant^{-1}, panicle length and number of filled grains panicle^{-1} had direct positive effect towards yield plant^{-1}. Similar findings

Table 1. Analysis of variance for different morphological plant characters of 47 rice genotypes

	df	PH (cm)	TT plant^{-1}	ET plant^{-1}	DFF (d)	DFM (d)	PL (cm)	FG pan.$^{-1}$	UG pan.$^{-1}$	Yield (g plant^{-1})
R	2	50.77	1.1	0.13	0.03	17.45	0.4	5.21	0.93	5.98
G	46	404.54**	26.53**	13.36**	157.31**	89.24**	40.68**	425.51**	125.09**	33.34**
E	92	19.11	1.96	2.02	4.84	29.2	3.47	20.9	8.78	2.34

R = replication, G = genotype, E = error, PH = plant height, ET = number of effective tillers, PL = panicle length, FG = number of filled grains, UG = number of unfilled grains; *, ** and *** refer the level of significance at 5%, 1% and 0.1%, df = degree of freedom

Table 2. Phenotypic and genotypic traits association among different yield components of 47 genotypes

Characters	Cor.	TT plant^{-1}	ET plant^{-1}	DFF (d)	DFM (d)	PL (cm)	FG pan.$^{-1}$	UG pan.$^{-1}$	Yield (g plant^{-1})
PH	r_p	0.437**	0.341*	−0.11	−0.558**	−0.467**	−0.271	−0.035	0.577**
	r_g	0.443**	0.357*	−0.109*	−0.610**	−0.476**	−0.279	−0.034	0.591**
TT plant^{-1}	r_p		0.919**	−0.066	−0.248	−0.082	−0.308*	−0.337*	0.337*
	r_g		0.946**	−0.068	−0.262	−0.088	−0.314*	−0.336*	0.342*
ET plant^{-1}	r_p			−0.022	−0.063	0.001	−0.12	−0.233	0.372**
	r_g			−0.024	−0.084	−0.001	−0.134	−0.221	0.364*
DFF	r_p				0.159	0.105	0.111	−0.045	−0.0948**
	r_g				0.17	0.105	0.114	−0.046	−0.0944**
DFM	r_p					0.590**	0.496**	0.117	−0.191
	r_g					0.652**	0.533**	0.123	−0.205
PL (cm)	r_p						0.368*	−0.186	0.001
	r_g						0.366*	−0.206	0.023
FG pan.$^{-1}$	r_p							0.515**	0.084
	r_g							0.517**	0.08
UG pan.$^{-1}$	r_p								−0.046
	r_g								−0.03

Cor. = correlation, TT= number of total tillers plant^{-1}, ET = number of effective tillers, PL = panicle length, FG = number of filled grains, UG = number of unfilled grains; r_p = phenotypic association, r_g = genotypic association, *, ** and *** refer the level of significance at 5%, 1% and 0.1%.

Table 3. Phenotypic path coefficient analysis showing direct and indirect effects of different characters on yield per plant of rice genotype

Char.	PH (cm)	TT plant^{-1}	ET plant^{-1}	DFF (d)	DFM (d)	PL (cm)	FG pan.$^{-1}$	UG pan.$^{-1}$	Yield (g plant^{-1})
PH (cm)	0.685	−0.159	0.165	0.0066	0.0674	−0.1411	−0.0474	0.0008	0.577**
TT	0.299	−0.364	0.444	0.0039	0.0299	−0.0248	−0.0539	0.0028	0.337*
ET	0.233	−0.335	0.483	0.0013	0.0076	0.0003	−0.021	0.0019	0.372**
DFF (d)	−0.07	0.024	−0.0106	−0.0598	−0.024	0.032	0.0194	−0.0004	−0.0948**
DFM (d)	−0.4	0.09	−0.0304	−0.012	−0.1208	0.1783	0.0868	−0.001	−0.191
PL (cm)	−0.32	0.0298	0.0005	−0.0063	−0.0713	0.3023	0.0644	0.0015	0.001
UG pan.$^{-1}$	−0.18	0.112	−0.0579	−0.0066	−0.0599	0.1112	0.1749	−0.0042	0.084
UG pan.$^{-1}$	−0.06	0.12	−0.113	−0.0027	−0.014	−0.056	0.0901	−0.008	−0.046

TT= number of total tillers plant^{-1}, ET = number of effective tillers plant^{-1}, PL = panicle length, FG = number of filled grains, UG = number of unfilled grains

Table 4. Multiple linear regression based rate of change of yield on yield components (Model 1)

	Estimates	Stad. Error	t Value	Pr (>∣t∣)
Intercepts	−0.32	12.93	−0.02	0.98
Plant height	0.19 ***	0.04	4.37	0.00009
No. of tillers per plant	−0.43	0.41	-1.04	0.305
No. active tillers per plant	0.77	0.54	1.41	0.165
Days to first flowering	−0.008	0.07	−0.1	0.915
Days to maturity	−0.07	0.11	−0.65	0.519
Panicle length	0.24	0.15	1.63	0.111
No. of filled grains per panicle	0.06	0.04	1.28	0.206
No. of unfilled grains per panicle	−0.04	0.08	−0.54	0.589

R^2 = 0.49, *** refer significance at 0.1% level of probability

Table 5. Multiple linear regression based rate of change of yield on yield components (Model 1)

	Estimates	Stad. Error	t Value	Pr (>∣t∣)
Intercepts	5.85	3.98	1.47	0.14
Plant height	0.16 ***	0.03	4.33	0.00008
No. of tillers per plant	−0.55	0.35	−1.55	0.12
No. active tillers per plant	0.99 *	0.48	2.07	0.04

R^2 = 0.40, *, ** and *** refers significance at 5%, 1%, and 0.1% level of probability

were reported in rice by Ashok et al. (2016), Haradari and Hittalmani (2017) and Musila (2015). Among the yield and yield related traits plant height and active tillers number plant^{-1} had significant positive correlation with yield plant^{-1} indicating direct selection would be effective for improving yield plant^{-1}. Days to first flowering showed negative direct effect on yield plant^{-1} (−0.0598) and highly significant negative association with yield plant^{-1} however different findings were reported by Haradari and Hittalmani (2017) which was positive direct effect on yield plant^{-1}. Musila (2015) was reported negative indirect effects of days to maturity on yield plant^{-1} which is corroborating the research findings but Ashok et al. (2016) observed positive direct effect of days to maturity on yield plant^{-1}. The result of multiple linear regression model 1 (Table 4) exhibited all the traits contributed towards yield plant^{-1} but only plant height contributed significantly whereas others contribution towards yield plant^{-1} was negligible. For this situation the multiple linear regression model 2 was constructed to predict the yield plant^{-1} by using positively correlated significant traits (Table 5). Among the traits height of plant and active tillers number plant^{-1} were contributed significantly towards yield which is agreed to the result of Musila (2015) (Table 5).

4 Conclusions

Yield, the ultimate desire of breeders as well as growers, is a complex trait affected by yield influential traits directly or indirectly and perfect selection of breeding lines through plant breeders becomes more accurate by considering yield influential traits. Our research findings suggests that plant height, active tillers number plant^{-1} and days to first flowering could be considered as valuable traits for selecting better genotypes.

Acknowledgements

We acknowledge Bangladesh Institute of Nuclear Agriculture (BINA) for providing the materials and access to conduct research in BINA research field and all associates who are inspired and assist to complete the research.

Conflict of Interest

The authors declare that there is no conflict of interests regarding the publication of this paper.

References

Ashok S, Jyothula D, Ratnababu D. 2016. Character association and path analysis for yield components and grain quality parameters of rice (*Oryza sativa* L.). International Journal of Agricultural Science and Research 6:253–258.

Augustina UA, Iwunor OP, Ijeoma OR. 2013. Heritability and character correlation among some rice genotypes for yield and yield components. Journal of Plant Breeding and Genetics 1:73–84.

Baral B. 2016. Agriculture Market Information System (AMIS) in Bangladesh. Twenty-sixth Session on Asia and Pacific Commission on Agriculture Statistics, 15-19 February 2016, Thimphu, Bhutan.

BBS. 2016. Yearbook of Agricultural Statistics. Statistics and Information Division, Ministry of Planning, Government of the People's Republic of Bangladesh.

Chandra BS, Reddy TD, Ansari N, Kumar SS. 2009. Correlation and path analysis for yield and yield components in rice (*Oryza sativa* L.). Agricultural Science Digest 29:45–47.

FAO. 2011. Food and Agricultural Commodities Production. Food and Agriculture Organization of The United Nations, Rome, Italy.

Haradari C, Hittalmani S. 2017. Character association and path coefficient analysis for yield component traits in rice (*Oryza safiva* L.) under moisture stress condition at vegetative stage. Current Trends in Biomedical Engineering and Biosciences 2:555–597. doi: 10.19080/CTBEB.2017.02.555597.

Kahani F, Hittalmani S. 2015. Genetic analysis and traits association in F2 intervarietal populations in rice under aerobic condition. Rice Research: Open Access doi: 10.4172/2375-4338.1000152.

Kole P, Chakraborty N, Bhat J. 2010. Analysis of variability, correlation and path coefficients in induced mutants of aromatic non-basmati rice. Tropical Agricultural Research and Extension 11. doi: 10.4038/tare.v11i0.1791.

Kumar K. 2013. Studies on character association and genetic divergence in upland rice (*Oryza Sativa* L.). MS Thesis, College of Agriculture, Kolhapur, Mahatma Phule Krishi Vidyapeeth, Rahuri, India.

Lagos J, Hossain T. 2016. BANGLADESH: Grain and Feed annual 2016. Global Agricultural Information Network, USDA foreign Agricultural Service (BG6005).

Laxuman PM, Salimath HE, Shashidhar HD, Mohankumar SS, Patil HM, Vamadevaiah M, Janagoudar BS. 2011. Character association and path coefficient analysis among the backcross inbred lines derived from indica × NERICA cross for productivity traits in rice (*Oryza sativa* L.). Karnataka Journal of Agricultural Science 24:97–112.

MoF. 2017. Fortnightly Foodgrain Outlook. Food Planning and Monitoring Unit, Issue no. 241. Ministry of Food, Government of the People's Republic of Bangladesh.

Musila R. 2015. Genetic analysis for drought tolerance and yield stability in interspecific and *Oryza sativa* L. rice germplasm. African Centre for Crop Improvement, School of Agricultural, Earth, and Environmental Sciences, College of Agriculture, Engineering and Science, University of KwaZulu-Natal, Republic of South Africa.

Narciso J, Hossain M. 2002. In: IRRI World Rice Statistics. http://www.irri.org/science/ricestat.

R. 2017. R: a Language and Environment for Statistical Computing. Version 3.3. R Foundation for Statistical Computing, Vienna, Austria.

Ravikumar B, Kumari PN, Rao PVR, Rani MG, Satyanarayana P, Chamundeswari N, Vishnuvardhan KM, Suryanarayana Y, Bharathalakshmi M, Reddy AV. 2015. Principal component analysis and character association for yield components in rice (*Oryza sativa* L.) cultivars suitable for irrigated ecosystem. Current Biotica 9:25–35.

Sala M, Kumar CA, Geetha S. 2015. Variability studies for quality traits in rice with high iron and zinc content in segregating population. Rice Genomics and Genetics 6:1–5.

Shet RM, Rajanna M, Ramesh S, Sheshshayee M, Mahadevu P. 2012. Genetic variability, correlation and path coefficient studies in F2 generation of aerobic rice (*Orzya sativa* L.). Electronic Journal of Plant Breeding 3:925–931.

Singh R. 1980. Association of grain yield and its components in F1 and F2 populations of rice. Oryza 17:200–204.

The Official Journal of the
Farm to Fork Foundation
ISSN: 2518–2021 (print)
ISSN: 2415–4474 (electronic)
http://www.f2ffoundation.org/faa