Published with Open Access at Journal BiNET
Vol. 09, Issue 01: 768-774
Journal of Bioscience and Agriculture Research
Home page: www.journalbinet.com/jbar-journal.html

Genetic study and selection in F_4 generation of rice (*Oryza sativa* L.)

Pangkaj Kumar Rai[a], Uma Kanta Sarker[a], A. K. M. Sajjadul Islam[b], Md. Asif Rahman[a] and Monjur Hasan[c]

[a]Dept. of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur
[b]Hybrid Rice Division, BRAC Agricultural Research and Development Centre, Gazipur
[c]Vegetable Division, BRAC Agricultural Research and Development Centre, Gazipur, Bangladesh

✉ akmsajjad@yahoo.com (Islam, A. K. M. S.), ✆ +88-017-12 779142, Published: 25 May 2016.

ABSTRACT

An attempt was made to study the variability in 25 F_4 generation of T. Aman rice. Highly significant variations were obtained for all the characters studied. The highest mean and range value was observed for grain yield per meter square followed by number of filled grains per panicle, spikelet sterility (%) and 1000-grain weight. Highest genotypic variance was observed for grain yield per meter square followed by plant height, number of filled grains per panicle and spikelet sterility (%) whereas the highest genotypic coefficient of variation was recorded for spikelet sterility (%) followed by grain yield per meter square, panicle weight and plant height. Phenotypic variance was close to the corresponding genotypic variance for all the traits studied except plant height, panicle size, weight and branching habit. On the other hand, all the characters showed close phenotypic and genotypic coefficient of variation except panicle weight and spikelet sterility (%) which indicated additive gene action for expression of the characters. Considering mean, range and all genetic parameters selection could be performed on the basis of number of tillers per hill, number of panicles per hill, panicle length, number of filled grains per panicle, spikelet sterility (%), 1000-grain weight and grain yield per square meter for significantly improvement of rice yield.

Key Words: *Heritability, Variability, Selection, F_4 Generation and Rice (Oryza sativa L.)*

Cite article: Rai, P. K., Sarker, U. K., Islam, A. K. M. S., Rahman, M. A. & Hasan, M. (2016). Genetic study and selection in F_4 generation of rice (*Oryza sativa* L.). *Journal of Bioscience and Agriculture Research,* 09(01), 768-774.

Article distributed under terms of a Creative Common Attribution 4.0 International License.

I. Introduction

Compared to mid sixties rice production in Bangladesh has almost doubled during the past three decades. This increased rice production has been possible largely due to the adoption of modern rice varieties on around 66% of the rice land which contributes to about 73% of the country's total rice production. T. Aman rice covers about 50.92% of the rice areas of Bangladesh (BBS, 2013) of which modern T.Aman varieties covers 60% (BBS, 2013). In Ganges Tidal Floodplain belongs under the Agroecological zone-13 T. Aman is the main crop. Agro ecological condition of this area favours the large-scale cultivation of T. Aman rice.

Published with open access at journalbinet.com
EISSN: 2312-7945, © Rai et al. (2016), Research paper

Bangladesh needs to increase rice production from 2.74 to 3.74 t/ha per year due to increasing population. The total rice area has also been continuously declining at about 1.00% per annum (Bhuiyan *et al.,* 2002). Among Aus, Aman and Boro seasons, Aman occupied the highest area coverage (34% of gross cropped area) (Anonymous, 2005). So, we have to give more attention on the improvement of T. Aman rice varieties to increase rice production in order to satisfy our population's need of food.

The quantitative measurement of individual character provides the basis for an interpretation of analysis of variance. The available variability in a population can be partitioned into heritable and non heritable parts with the aid of genetic parameters such as genetic coefficient of variation, heritability and genetic advance (Miller *et al.,* 1958). Therefore, this experiment was conducted to study the variability among the F_4 generation of rice genotypes and to find out the genetic parameters in the selected genotypes.

II. Materials and Methods

Previously produced twenty five F_4 generation materials (Table 01) from 8 x 8 diallel cross were grown in randomized complete block design (RCBD) with three replications during Aman season in 2011. Plot size was 1 m x 2 m. Twenty cm plant to plant and row to row spacing respectively were maintained. Urea, TSP, MP and gypsum were applied @ 150-100-70-60 kg/ha, as recommended for rice cultivation. Thirty days old seedlings were transplanted in the experimental units. Normal intercultural practices and plant protection measures were followed to raise the crop successfully. One m^2 area was harvested for measuring grain yield. Data were collected from 10 randomly selected hills of each genotype. Data were recorded on plant height at maturity (cm), number of tillers per hill, number of panicles per hill, panicle length (cm), panicle weight (g), number of primary branches per panicle, number of secondary branches per panicle, number of filled grains per panicle, spikelet sterility (%), 1000-grain weight (g), days to flowering, days to maturity and grain yield per meter square (g). All the data obtained from each trait were statistically analyzed. The analysis of variance was done according to Goulden's methods (1959). Genotypic coefficient of variation was computed using the formula suggested by Burton (1952). Heritability in broad sense and genetic advance was calculated according to the methods given by Allard (1960).

Table 01. 25 rice genotypes of F_4 generation of T. Aman rice

Sl. No.	Name of Genotypes	Sl. No.	Name of Genotypes
01	Rajashail x Pokkali	14.	BRRI dhan 10 x BRRI dhan 33
02.	Pokkali x BR 10	15.	BRRI dhan 33 x BRRI dhan 32
03.	Pokkali x BRRI dhan33	16.	BRRI dhan 44 x BRRI dhan 10
04.	BRRI dhan44 x pokkali	17.	Rajashail x BRRI dhan30
05.	BRRI dhan39 x pokkali	18.	BRRI dhan 33 x BRRI dhan 10
06.	Pokkali x BR 11	19.	BRRI dhan 39 x BRRI dhan 32
07.	Rajashail x BRRI dhan39	20.	BRRI dhan 32 x BRRI dhan 44
08.	Rajashail x BRRI dhan44	21.	BRRI dhan 33 x BRRI dhan 39
09.	BR 11 x Rajashail	22.	BRRI dhan 39 x BRRI dhan 11
10.	BR 11 x BRRI dhan 33	23.	BRRI dhan 44 x BRRI dhan 39
11.	BR 11 x BRRI dhan 32	24.	BRRI dhan39 x BR 10
12.	BR 10 x Rajashail	25.	BR10 x BRRI dhan32
13.	Rajashail x BRRI dhan 33		

III. Results and Discussion

Variability and genetic parameters

The genotypes differed significantly for all the characters (Table 02). The extent of variation among the genotypes in respect of 13 characters were studied and mean value, range, genotypic variance (σ^2_g), phenotypic variance (σ^2_P), environmental variance (σ^2_e), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2b), genetic advance (GA) and genetic advanced (GA) in percent of mean have been presented in Table 03 and Table 04. Performance of the genotypes is described below for each character.

Published with open access at journalbinet.com
EISSN: 2312-7945, © Rai et al. (2016), Research paper

Table 02. Analysis of variance for 11 yield and its related characters in 25 genotypes of T. Aman rice

Sources of variation	df	Mean sum of squares										
		Plant height (cm)	Tillars/hill	Panicle/ hill	Panicle length (cm)	Panicle weight (cm)	Primary branches per panicle	Secondary branches per Panicle	Filled grain per panicle	Spikelet sterility (%)	1000 grain weight (gm.)	Grain yield/m^2 (g)
Genotype	24	1528.75**	4.42**	4.52**	9.36**	3.92**	4.77**	60.69**	1279.25**	131.5**	36.63**	14506.47**
Replication	2	81.908	5.57*	6.09*	11.032	1.245	43.066	74.751	1234.258	44.489	5.45*	178923
Error	*48*	*48.246*	*0.758*	*0.76*	*1.063*	*1.245*	*1.44*	*12.047*	*171.977*	*26.504*	*3.217*	*12087.931*
CV%		*12.13*	*9.21*	*9.36*	*3.92*	*11.3*	*8.97*	*9.56*	*8.90*	*28.54*	*6.3*	*20.95*

Plant height (cm)

Analysis of variance for plant height showed significant mean sum of square due to genotypes (Table 02). The highly significant genotypic difference indicated that there was a wide range of variation among the varieties for plant height. The mean value ranged from 108.80 to 188.37 cm, whereas mean performance was 139.46 cm (Table 03). The phenotypic and genotypic variances for this trait were (541.75 and 493.50 respectively). The phenotypic variance appeared to be higher than genotypic variance, suggested considerable influence of environment on the expression of the genes controlling this trait. Here environmental variance was also high (192.98). The difference between phenotypic coefficient of variation (2166.99) and genotypic coefficient of variation (1974.01) was minimum (Table 04). Heritability estimation was high (91.09) with high genetic advance (1.88) and genetic advance in percent of mean (1.35) was considerable for this trait indicating apparent variation was due to genotype. So, selection based on this trait would be effective. These results confirmed the finding of Biswas *et al.* (2000).

Number of panicles per hill

Number of panicles per hill showed a highly significant mean sum of square due to genotypes, which indicated considerable range of variation for this character (Table 03). The mean value ranged from 7.13 to 12.00. The phenotypic variance (2.01) was higher than genotypic variance (1.25) as presented in Table 03. This feature indicated higher influence of environment on the expression of the trait and genetic factor had low expressivity on the number of panicles per hill. The character showed high phenotypic and genotypic coefficient of variation (8.05 and 5.01 respectively) (Table 04). Here the phenotypic coefficient of variation (8.05) was higher than genotypic coefficient of variation (5.01) indicating the apparent variation not only due to genotypes but also due to the influence of environment. Estimation of heritability (62.25) for this trait was the low among the characters studied. However, the genetic advance was very low (1.28) with high genetic advance in percent of mean (13.74). Gomathinayagam *el al.* (1990) and Biswas *et al.* (2000) also reported similar result.

Panicle length (cm)

Significant mean sum of square due to genotypes for panicle length (9.36**) indicated considerable differences among the varieties studied (Table 02). The mean value of the genotypes showed small range of variation from 23.77 to 29.43 cm. (Table 03). Phenotypic variance (3.83) appeared to be slightly higher than genotypic variance (2.77). The minimum difference between PCV (15.32) and GCV (11.06) revealed less influence of environment on the expression of the character (Table 3). This character showed high heritability (72.24) estimation together with high genetic advance in percent of mean (5.65) (Table 04). Therefore selection based upon phenotypic expression of this character would be effective for the improvement of this crop. Sadhukhan and Chattopadhyay (2000) in their study with 26 aromatic rice genotypes reported similar results.

Number of primary branches per panicle

Analysis of variance for number of primary branches per panicle showed significant mean sum of square (4.77**) due to genotypic difference (Table 02). The mean value with respect to this trait ranged from 10.50 to 15.70. The character showed low phenotypic (2.55) and genotypic (1.11) variance. The considerable difference between genotypic and phenotypic variance indicating effect of environment for the expression of the trait was high (Table 03). The PCV (10.19) was higher than the GCV (4.45) for this character. Number of primary branches per panicle showed moderately heritability (43.65) with low genetic advance (0.89)

Published with open access at journalbinet.com
EISSN: 2312-7945, © Rai et al. (2016), Research paper

and genetic advance in percent of mean (6.75) (Table 04). Therefore selection based on this trait will not be effective. These results matched with the findings of Reddy and Kumar (1996).

Number of secondary branches per panicle

Analysis of variance for number of secondary branches per panicle showed significant mean sum of square (60.69** due to genotypic difference (Table 02). The mean value with respect to this trait ranged from 28.20 to 45.07. The character showed phenotypic and genotypic variance was (28.26 and 16.21 respectively). The considerable difference between genotypic and phenotypic variance indicating effect of environment for the expression of the trait was high (Table 03). The PCV (113.05) was higher than the GCV (64.86) for this character. Number of secondary branches per panicle showed moderately heritability (57.37) with low genetic advance (1.18) and genetic advance in percent of mean (3.25) (Table 04). Therefore selection based on this trait will not be effective. These results matched with the findings of Reddy and Kumar (1996).

Number of filled grains per panicle

Mean square for number of filled grains per panicle was highly significant (Table 02). The mean values ranged from 103.30 to 192.77. The phenotypic variance (541.07) was little higher than genotypic variance (529.09) indicating that environment had not been playing a significant role for the expressing of the character (Table 03). The PCV (2164.27) and GCV (2116.36) had a little variation (Table 04). High heritability (88.22) with high genetic advance (13.41) and genetic advance in percent of mean (9.09) were reported for number of filled grains per panicle that confirmed the findings of Choudhury and Das (1998) and Iftekharuddaula *et al.* (2005).

Spikelet sterility (%)

Analysis of variance showed that spikelet sterility (%) varied significantly among the genotypes used (Table 02). The mean value ranged from 5.59 to 30.91. The components of variation for spikelet sterility (%) showed considerable phenotypic variation (61.50) in comparison to genotypic variation (34.99) indicating the influence of environment to a great extent for this trait (Table 03). Phenotypic and genotypic coefficients of variance (246.01 and 139.99) were comparatively high (Table 04). In the present investigation spikelet sterility (%) represented moderate heritability (56.91) and genetic advance (1.17) but high genetic advance in percent of mean (6.49). De and Suriya (1988) and Akanda *et al.* (1997) also reported higher estimation of coefficient of variation and genetic advance in percent of mean for spikelet sterility (%).

Table 03. Mean, range, phenotypic variance (Vp), genotypic variance (Vg) and environmental variance (Ve) for 13 yield and yield contributing traits in F_4 generation of rice

Traits	Mean	Range	Vp	Vg	Ve
Days to flowering	76.82	70.00-85.00	18.62	16.86	1.76
Days to maturity	111.82	109.00-115.00	5.60	5.08	0.52
Plant height (cm)	139.46	108.80-188.37	541.75	493.50	48.25
Tillers/hill	9.46	7.20-12.10	1.98	1.22	0.76
Panicles/hill	9.34	7.13-12.00	2.01	1.25	0.76
Panicle length (cm)	26.33	23.77-29.43	3.83	2.77	1.06
Panicle weight (g)	4.45	3.30-5.65	2.14	0.89	1.25
Primary branches/panicle	13.33	10.50-15.70	2.55	1.11	1.44
secondary branches/panicle	36.32	28.20-45.07	28.26	16.21	12.05
Filled grains/panicle	147.37	103.03-192.77	541.07	529.09	11.98
Spikelet sterility %	18.05	5.59-30.91	61.50	34.99	26.50
1000 grain weight (g)	28.54	23.00-36.00	14.36	13.14	1.22
Grain yield/m^2 (g)	523.58	383.33-633.33	12894.11	12854.18	39.93

1000-grain weight (g)

Mean sum of square for 1000-grain weight was highly significant (Table 02). The mean value ranged from 23.00 to 36.00 g. The genotypic variance (13.14) and phenotypic variance (14.36) were almost same indicating least environmental effect for the expression of the character (Table 03). The value of PCV and GCV presented in Table 04, were high and the difference was very close (57.42 and 54.55).

Published with open access at journalbinet.com
EISSN: 2312-7945, © Rai et al. (2016), Research paper

Heritability value for 1000-grain weight (78.59) was very high. This character also represented very high genetic advance in percent of mean (40.64). This feature suggesting that the environmental influence on the phenotypic expression of this character was not considerable and the phenotypic expression of this character was true representation of the genetic makeup. Therefore selection based on this character would be effective. Akanda et al. (1997) found high value but narrow difference between PCV and GCV for 1000-grain weight, where Choudhury and Das (1997) reported high heritability and high genetic advance in percent of mean for this character which agreed with the present findings.

Days to maturity

Analysis of variance for days to maturity showed highly significant mean sum of square due to genotypes (Table 02). The mean value ranged from 109.00 to 115.00 days. The genotypic variance and phenotypic variance were 5.08 and 5.60 respectively (Table 03). The value of phenotypic variance was close to its corresponding genotypic variance. There was a pronounced variation for the character days to maturity and this variability was conserved by genetic constituent rather than environment. The values of GCV (20.33) and PCV (22.41) were low (Table 04) and had least difference. Similar findings were reported by Balan *et al.* (1999). Very high heritability (90.72) but low genetic advance in percent of mean (1.67 %) was observed for the character of days to maturity. It revealed non-additive gene action was involved for expression of this character. The high heritability was exhibited due to influenced of favorable environment rather than genotype and selection for such trait may not be rewarding. High heritability with low genetic advance was also reported by Gomathinayagam *et al.* (1990) for days to maturity.

Panicle weight (g)

Significant mean sum of square due to genotypes for panicle weight indicated considerable differences among the genotypes studied (Table 02). The mean value of the genotypes showed less variation from 3.30 to 5.65 cm. (Table 03). Phenotypic variance (2.14) appeared to be slightly higher than genotypic variance (0.89). The minimum difference between PCV (8.55) and GCV (3.57) revealed less influence of environment on the expression of the character (Table 04). This character showed moderately heritability (41.73) estimation together with moderate genetic advance (0.86). Therefore selection based upon phenotypic expression of this character would be effective for the improvement of this crop. Sadhukhan and Chattopadhyay (2000) in their study with 26 rice genotypes reported similar results.

Number of tillers per hill

Number of tillers per hill showed a highly significant mean sum of square due to genotypes, which indicated considerable range of variation for this character (Table 02). The mean value ranged from 7.20 to 12.10. The phenotypic variance (1.98) was close to genotypic variance (1.22) as presented in Table 02. This feature indicated higher influence of genotype on the expression of the trait and environment factor had low expressivity on the number of panicles per hill. The character showed moderate phenotypic and genotypic coefficient of variation (7.92 and 4.88 respectively). Here the phenotypic coefficient of variation (7.92) was although similar to genotypic coefficient of variation (4.88) indicating the variation only due to genotypes with very less influence of environment. Estimation of heritability (61.69) for this trait high with high percent mean genetic advance (13.43). Gomalhinayagam *et al. (*1990) and Biswas *et al.* (2000) also reported similar result.

Grain yield per m^2 (g)

Mean sum of square for yield per hill was highly significant due to genotypes. The highly significant difference indicated that there was a wide range of variation among the genotypes for grain yield (Table 01). The mean values ranged from 383.33 to 633.33 g. The components of variance for grain yield per m^2 showed least phenotypic variance (12894.11) close to genotypic variance (12854.18) indicating the least influence of environment for comparison of this trait (Table 03). The phenotypic coefficient of variation (51576) and genotypic coefficient of variation (51486.72) were high in magnitude but very close to each other. Reddy and Kumar (1996) reported higher PCV than GCV for grain yield per m^2, whereas Choudhury and Das (1997) reported higher values of PCV and GCV. In case of heritability estimation this character showed high heritability (82.50) with high genetic advance

Published with open access at journalbinet.com
EISSN: 2312-7945, © Rai et al. (2016), Research paper

(22.29). These findings showed agreement with that of Kumar *et al.* (1998) and Shanthakumar *et al.* (1998). It is therefore, apparent from the present findings that selection for this trait could bring about satisfactory improvement over the population mean.

Table 04. Genotypic and phenotypic coefficient of variation (GCV and PCV), heritability (h^2_b), genetic advance (GA) and genetic advance in percent of mean (GAMP) for 13 yield and yield contributing traits in F_4 generation of rice

Traits	PCV	GCV	ECV	h^2b	GA	% GAMP
Days to flowering	74.47	67.43	7.04	90.55	1.87	2.43
Days to maturity	22.41	20.33	2.08	90.72	1.87	1.67
Plant height (cm)	2166.99	1974.01	192.98	91.09	1.88	1.35
Tillers/hill	7.92	4.88	3.03	61.69	1.27	13.43
Panicles/hill	8.05	5.01	3.04	62.25	1.28	13.74
Panicle length (cm)	15.32	11.06	4.25	72.24	1.49	5.65
Panicle weight (g)	8.55	3.57	4.98	41.73	0.86	19.31
Primary branches/panicle	10.19	4.45	5.74	43.65	0.89	6.75
secondary branches/panicle	113.05	64.86	48.14	57.37	1.18	3.25
Filled grains/panicle	2164.27	2116.36	47.91	88.22	13.41	9.09
Spikelet sterility %	246.01	139.99	106.02	56.91	1.17	6.49
1000 grain weight (g)	57.42	54.55	2.87	78.59	11.60	40.64
Grain yield/m^2 (g)	51576.44	51486.72	89.72	82.50	22.29	4.26

IV. Summary and Conclusion

Highest mean value was observed for grain yield per m^2 (523.58). This character also exhibited the highest range of variation (383.33-633.33) indicated that all the genotypes showed wide range of variation in respect of this character. Phenotypic variance was more or less higher than the corresponding genotypic variance for the characters. However, these differences were in case of plant height, number of secondary branches per panicle, number of filled grains per panicle, and spikelet sterility (%) indicating greater influence on environment for expression of these characters. Among the characters, days to maturity, tillars per hill, number of panicles per hill, panicle length, panicle weight, number of primary branches per panicle, 1000-grain weight showed least difference between phenotypic and genotypic variance, which indicated additive gene action for expression of the characters. All the characters showed moderate to high phenotypic and genotypic coefficient of variation except days to maturity (22.41 and 20.33). Amongst the characters the highest genotypic coefficient of variation was recorded for grain yield per m^2 (51576.44) followed by filled grain per panicle (2116.36), plant height (1974.01), spikelet sterility (%) (139.99), days to flowering (67.43), number of secondary branches per panicle (64.86), 1000-grain weight (57.42), panicle length (11.06), in order to merit. The highest heritability value was observed for plant height (91.09) and the lowest for panicle weight (41.73). Highest genetic advance in percent of mean was observed for 1000-grain weight (40.64), followed by panicle weight (19.31), panicle per hill (13.74), tillers per hill (13.43), number of filled grains per panicle (9.09), where the lowest for plant height (1.35). The parameter 1000-grain weight showed both the moderate heritability and highest genetic advance in percent of mean, indicated additive gene action for expression of the character and selection for such trait might be rewarding. Plant height showed high heritability but low genetic advance in percent of mean. It revealed non-additive gene action for expression of the character. High heritability was exhibited due to favorable environment rather than genotype.

V. References

[1]. Akanda, M. A. L., Alam, M. S. & Uddin, M. M. (1997). Genetic Variability, Correlation and Path Analysis in Maice (Zea mays L.) inbreds. *Bangladesh J. Plant Bre. Gene.* 10(2), 57-61.
[2]. Allard, R. W. (1960). Principles of Plant Breeding. John Wiley and sons, Inc., New York.
[3]. Anonymous (2005). Krishi Diary. Krishi Tathy Service. Farmgate, Dhaka 1215. p. 23.
[4]. Balan, A., Mulhiah, A. R. & Bhoopathi, M. R. (1999), Genetic variability, character association and path coefficient analysis in rainfed rice, under alkaline condition. *Madras Agril. J*. 86, 122-124.
[5]. BBS (Bangladesh Bureau of Statistics) 2013. Monthly Statistical Bulletin, Bangladesh.

Published with open access at journalbinet.com
EISSN: 2312-7945, © Rai et al. (2016), Research paper

[6]. Bhuiyan, N. I., Paul, D. N. R. & Jabbar, M. A. (2002). Feeding the extra millions by 2025 challenges for rice research and extension in Bangladesh. A keynote paper presented on national workshop on rice research and extension held on 29-31 January 2002 at BRR1, Gazipur. p. 9.
[7]. Burton, G. W. (1952). Quantitaive inheritance in grasses. Proc. 6lh Intercropping. Grassland Cong. 1, 277-283.
[8]. Biswas, P. S., Prasad, Bishwajit & Dawan, S. B. A. (2000). Variability, character association and path analysis in rice (*Orysa Sariva* L.). *Bangladesh J. Plant Bre. Gene.* 13(1), 19-25.
[9]. Choudhury, P. K. D. & Das, P. K. (1997). Genetic variability, correlation and path analysis in deep water rice. *J. Agril. Sci. Soc.* 10(1), 155-157.
[10]. Choudhury, P. K. L. & Das, P. K. (1998). Genetic variability, correlation and path analysis in deep water rice. *Ann. Agrie. Res.* 19(2), 120-124.
[11]. De, R. N. & Suriya Rao, A. V. (1988). Genetic variability and correlation studies in rice under semi-deep waterlogged situation. *Oryza*, 25, 360-364.
[12]. Gomathinayagam, P., Nataranjan, S. & Subramanian, M. (1990). Genetic Variability in drought tolerant genotypes in rice. *Oryza*, 27, 328-330.
[13]. Goulden, C. H. (1959). Methods of Statistical Analysis.
[14]. Iftekharuddaula, K. M., Badshah, M. A., Hassan, M. S., Bashar, M. K. & Akter, K. (2005). Genetic variability, character association and path analysis of yield components in irrigated rice (*Orya saliva* L.). *Bangladesh J. Plant Breed*. *Genet.* 43(3), 193-200.
[15]. Kumar, G. S., Mahadevappa, M. & Rudraradhya, M. (1998). Studies on genetic variability, correlation and path analysis in rice during winter across the locations. *Karnataka J. Agril. Sci.* 11(1), 73-77.
[16]. Milller, P. J., Williams, J. C., Robinson, H. F. & Comstock, R. E. (1958). Estimates of genotypic and environmental variances and covarianccs in upland cotton and their implications in selection. *Agron. J.* 50, 126-131. http://dx.doi.org/10.2134/agronj1958.00021962005000030004x
[17]. Reddy, Y. S. & Kumar, P. V. R. (1996). Studies on genetic variability, correlation and path analysis in rice. *New Botanist.* 23, 129-133.
[18]. Sadhukhan, R. N. & Chattopadhyay, P. (2002). Variability and character association between yield attributes and grain quality in aromatic rice. *J. Interacademicia.* 4(4), 494-497.
[19]. Shanthakumar, G., Mahadevappa, M. & Radraradhya, M. (1998). Variability, correlation and path analysis in rice (*Oryza saliva* L.) over seasons. *Karnataka J. Agril. Sci.* 11(1), 67-72.

Published with open access at journalbinet.com
EISSN: 2312-7945, © Rai et al. (2016), Research paper