VARIABILITY, HERITABILITY, CHARACTER ASSOCIATION, AND PATH COEFFICIENT ANALYSIS IN ADVANCED BREEDING LINES OF RICE (*Oryza sativa* L.)

Md. HASAN-UD-DAULA[1], Umakanta SARKER[1*]

[1]Department of Genetics and Plant Breeding, Faculty of Agriculture, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur-1706, Bangladesh.

Hasan-Ud-Daula M. and U. Sarker (2020). *Variability, heritability, character association, and path coefficient analysis in advanced breeding lines of rice (Oryza sativa L.).*- Genetika, Vol 52, No.2, 711-726.

Seven advanced breeding lines developed through hybridization breeding program and a popular cultivar were used to study variability, heritability, character association, and path coefficient analysis in rice for grain yield and its related agronomic traits. The results indicated that genotypes differed significantly in terms of grain yield and its related agronomic traits. Pronounced variations were observed for all the traits except for growth duration and harvest index. High genetic variability was observed for number of filled grains per panicle, number of secondary branches per panicle, plant height, spikelet sterility (%), grain yield per hill, number of primary branches per panicle, 1000-grain weight, duration of flowering and maturity, number of tillers per hill, number of panicles per hill, and panicle length. Based on high heritability and high GA and GAPM along with close values between σ^2_g *vs.* σ^2_p and GCV *vs.* PCV all the traits (except for harvest index, number of primary branches per panicle, days to maturity, and days to flowering) could be selected for improving the grain yield of rice as these traits exhibited less influence of environment. The significant and desirable correlations were observed for number of filled grains per panicle, number of secondary branches per panicle, spikelet sterility (%), days to flowering both at genotypic and phenotypic level. Considering genetic parameters, correlation, and path coefficient analysis, direct selection based on number of filled grains per panicle and spikelet sterility would significantly increase the grain yield of rice. So, direct selection based on these traits would be effective for the improvement of these breeding materials. The residual effect was found 0.1386 which indicated that 86.14% of the variability was accounted for grain yield and yield contributing traits included in the present study. Rest 13.86% variability might be controlled by other yield contributing traits that were not included in the present investigation.

_____

Corresponding authors*:* Umakanta Sarker, Department of Genetics and Plant Breeding, Faculty of Agriculture, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur-1706, Bangladesh. Postal Code 1706. Phone: +880-1716606098, Email: umakanta@bsmrau.edu.bd

Abbreviations
MS = mean sum of square, σ^2g = genotypic variance, σ^2p = phenotypic variance, GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, h^2_b = heritability in broad sense, GA = genetic advance, r_g = genotypic correlation coefficient, r_p = phenotypic correlation coefficient, GAPM = genetic advance in percentage of mean.

INTRODUCTION

Rice (*Oryza sativa* L.) is the staple food for over one-third of the world's people. More than 90% of the world's rice is produced and consumed in Asia (ᴠɪʀᴍᴀɴɪ, 1996). Bangladesh is the fourth-largest producer and consumer of rice in the world. In Bangladesh, the total cultivation area of rice is 64.63 lac ha and total production is 125.55 million M tones (ᴀɴᴏɴʏᴍᴏᴜꜱ, 2005). Rice is one of the most versatile crops cultivated worldwide as it is grown under a wide range of agro-climatic conditions ranging from irrigated, rain-fed lowland, rain-fed, upland, and flooding ecosystems. Among them, transplanted Aman (T. Aman) is most important and occupies about 46.30% of the rice cultivated land and it occupies an area of 54.58 million ha with a production of 108.41 million metric tons (ᴀɴᴏɴʏᴍᴏᴜꜱ, 2007).

Although the world's rice production has more than doubled from 257 million tons in 1966 to 600 million tons in 2000, the increase has not met the demand for rice because of the corresponding increase in the population during this time. Bangladesh agricultural economy predominantly based on rice production. Bangladesh is an overpopulated country and the population is increasing day by day at a rapid rate. The population growth and food grain production are increasing almost at the same rate leaving a static annual deficit of 1-2 million tons. Breeders have to take the necessary breeding program for the improvement of rice yield to meet the demand of the increasing population.

Generally, the success of any crop improvement program largely depends on the magnitude of genetic variability, heritability, genetic advance, and character association (ꜱᴀʀᴋᴇʀ *et al*., 2015a). The creation of variability in rice germplasm is one of the most effective methods to meet the demand of the increasing population. The extent of genetic variability of the existing genotype of a crop plant is an index of its genetic dynamism. Plant breeding revolves around selection which can be effectively practiced only in the presence of variability of desired traits. Hence the success of breeding depends entirely upon the variability (ɢᴀɴᴀᴘᴀᴛʜɪ *et al*., 2014). The variability arises due to genotypic and environmental effects. Variability has two components such as additive and non-additive. For a clear understanding of the pattern of variations, the phenotypic variance has been partitioned into genotypic and environmental variance.

Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based on genetic improvement (ᴋᴀʀɪᴍ *et al*., 2007, 2014). Grain yield in rice is a quantitative character, which is influenced by many yield contributing traits. So, the selection for desirable types should not only

be based on yield, but other yield components should also be considered. Direct selection for yield is often misleading in rice as rice yield is polygenic controlled and also influenced by its component characters. For this reason, selection for grain yield may take consideration of these component characters as well. It is, therefore, necessary to know the correlation of various component characters with yield and among themselves. The correlation coefficients between yield and yield components usually show a complex chain of interacting relationships.

Path coefficient is the direct influence of variable (cause) upon another variable (effect) as measured by standard deviation remaining in the effect after the influence of all other possible paths are estimated except the cause. It measures the cause of the association between two variables based on all possible simple correlations among the various characters and also based on the assumptions of linearity and additively. Path coefficient analysis, correlation coefficients into direct" and indirect effects and illuminates the relationship in a more meaningful way. So it is used to analyze the real contribution of individual complex character to yield. Hence, the present study was undertaken to find out selection criteria for high yielding rice varieties through assessing the magnitude of genetic variability, heritability, genetic advance, association and contribution of characters to yield and path coefficient analysis in selected genotypes.

MATERIALS AND METHODS
Experiment materials, design, layout, and cultural practices

The experiment was carried out at the experimental farm of Bangabandhu Sheikh Mujibur Rahman Agricultural University in a Randomized Complete Block Design (RCBD) with three replications in 2018. The experimental site was located in the center of the Madhupur Tract (AEZ28, about 24°23´N - 90°08´E, with a mean elevation of. 8.4 masl) (SARKER and OBA, 2018a-c, SARKER *et al*., 2018). The experimental field was a high land having silty clay soil. The soil was slightly acidic (pH 6.4) and low in organic matter (0.87%), total N (0.09%) and exchangeable K (0.13 cmol/kg) (SARKER and OBA, 2018d-e). The experiment was conducted using seven breeding lines developed through hybridization breeding program in the Department of Genetics and Plant Breeding and a popular variety. The breeding lines/variety are presented in Table 1.

Table 1. Name, source of origin, and important characters of the lines/variety

Sl. No.	Lines/Variety	Sources	Characters
1.	BUSTR-1	BSMRAU	Salt tolerant HYV line
2.	BUSTR-2	BSMRAU	Salt tolerant HYV line
3.	BR11	BRRI	Most popular variety
4.	BUT-1	BSMRAU	HYV line
5.	BUT-2	BSMRAU	HYV line
6.	BUT-3	BSMRAU	HYV line
7.	BUT-4	BSMRAU	HYV line
8.	BUT-5	BSMRAU	HYV line

The area of each experimental unit was 4 m². Forty days old seedlings were transplanted in each experimental unit by maintaining 20 cm between rows and 20 cm between plants. Treatment was distributed in the experimental unit through randomization by using the IRRISTAT program. Adequate soil fertility was ensured by applying additional quantities of Urea, triple super phosphate (TSP), murate of potash (MP) and Gypsum @ 220-120-90-60 kg/ha, respectively. Total TSP, MP, and Gypsum were applied in final land preparation. Total Urea was applied in three installments, at 15, 30, and 50 days after transplanting (DAT) using the rice production procedure described by the Bangladesh Rice Research Institute (ANONYMOUS, 1999). The necessary intercultural operation was taken during the cropping period for the proper growth and development of the plants.

Data collection on plant traits

Data were collected from ten randomly selected hills of each genotype on individual plant basis and the traits were: plant height, number of tillers per hill, number of panicles per hill, panicle length, number of primary branches per panicle, number of secondary branches per panicle, number of filled grains per panicle, spikelet sterility (%), days to flowering, days to maturity, 1000 grain weight (g) and grain yield per hill (g).

Statistical analysis

The raw data were compiled by taking the means of all the plants taken for each treatment and replication for different traits. Statistix 8 software was used to analyze the data for analysis of variance (ANOVA) (RASHAD and SARKER, 2020; SARKER and OBA, 2020a). The sample data for each replication were averaged and the replication mean values were statistically and biometrically analyzed following the method of SARKER and OBA, (2019a-d). Analysis of variance was done according to SARKER and OBA, (2020b-e) and SARKER *et al.* (2020a, b). Genotypic and phenotypic coefficients of variation were calculated by the formula suggested by RAI *et al.* (2013). Broad sense heritability was estimated following the formula described by HASAN *et al.* (2012a,b). The expected genetic advance for different characters under selection was estimated using the formula of RAHMAN *et al.* (2007a, b). Genetic advance in percentage of mean was calculated from the formula given by AZAM *et al.* (2014). The genotypic and phenotypic correlation coefficients were calculated in all possible combinations through the formula suggested by SARKER and MIAN (2003, 2004). Correlation coefficients were further partitioned into components of direct and indirect effects by path coefficient analysis (SARKER *et al.*, 2001).

RESULTS AND DISCUSSION

Variability and genetic parameters

Mean sum of square, grand mean values, range, genotypic variance and phenotypic variance, heritability in broad sense (h²b), genetic advance (GA) and genetic advance in percent of mean (GAPM), genotypic and phenotypic coefficient of variations (GCV and PCV) for yield and yield-related agronomic traits of are presented in Table 2 and Table 3. In the present study, the mean sum squares of all the traits were highly significant. It indicated that genotypes differed remarkably for all the yield and yield contributing agronomic traits. Pronounced variations were observed for all the traits except for growth duration and harvest index that indicated a wide

range of variations in terms of all the yield and yield contributing agronomic traits among genotypes having the scope of selection of these traits. ALI *et al*. (2014), SIDDIQUE *et al*. (2009), NATH *et al*. (2008) and BISWAS *et al*. (2006) in rice; BISWAS *et al*. (2014) and AZAM *et al*. (2013) in maize TALUKDER *et al*. (2011, 2015) in coconut reported wide range of variability and diversity. Variability plays a vital role for the selection of superior genotypes in crop improvement program (SARKER *et al*., 2014; 2017, 2018a; CHAKRABARTY *et al*., 2018). Pronounced variation in the breeding materials is a prerequisite for the development of varieties for existing demand. The selection of genotypes based on their phenotypic variation (mean and range) is impractical for a breeder (SARKER *et al*., 2015b). Actual genetic variation may be masked by its environmental influence (SARKER *et al*., 2016). Therefore, partitioning the phenotypic variation into genotypic and environmental effects is essential for the selection of suitable genotypes. The genotypic variance was the highest for number of filled grains per panicle (10509.99), followed by number of secondary branches per panicle (605.30), plant height (199.08). Spikelet sterility (%) (55.13), grain yield per hill (22.91), number of primary branches per panicle (15.55), 1000 grain weight (15.19), days to flowering, and days to maturity (14.64 and 10.64) exhibited moderate genotypic variances (Table 2). The results of the genotypic variance of the above traits revealed that more variability was exhibited for these traits, exploring the greater scope of selection based on these traits. On the other hand, the lowest genotypic variance was noticed in harvest index (0.01), number of panicles per hill, (4.09) number of tillers per hill (4.78), and panicles length (7.15). The phenotypic variances for all the traits were a little higher but close to the genotypic variances indicating the preponderance of additive gene effects for these traits. Genotypic coefficient of variation (GCV) considers the best relative amount of genetic variation and it takes into account the mean value as well as the unit of measurement. The genotypic coefficient of variation values ranged from 1.79% (days to maturity) to 28.09% (harvest index). The PCV values showed similar trends as GCV values and ranged from 2.15% (days to maturity) to 30.34% (harvest index) (Table 3). The values of PCV were a little higher but close to the corresponding GCV values for all the traits (Table 2). The small differences between PCV and GCV for all the traits indicated that the variability was predominately due to genotypic differences, i.e. less environmental influences. High values of coefficients of variation were observed for harvest index followed by grain yield per hill, while days to maturity, days to flowering, number of primary branches per panicle, and panicles length exhibited the lowest coefficients of variation (Table 3). The rest of the traits had moderate coefficients of variations (GCV, PCV). Except for number of primary branches per panicle, the heritability estimates were high for all the traits and ranged from 57.70% for number of primary branches per panicle to 89.86% for plant height (Table 3). The high value of heritability for all the traits suggests that all these traits are under genetic control, i.e., less environmental influence. However, it will be relevant to divulge here that the total genotypic variance is made up of additive genetic variance and non-additive or non-fixable variance. High heritability alone is not enough to make sufficient improvement through selection generally in advance generations unless accompanied by a substantial amount of genetic advance (SARKER *et al*., 2015a). The efficacy of heritability is increased with the estimation of genetic advance, which indicates the degree of gain in a trait obtained under particular selection pressure. Thus, the genetic advance is yet another important selection parameter that aids breeders in a selection program (SARKER *et al*., 2014). It has been

emphasized that without genetic advance, the heritability values would not be of practical importance in a selection based on phenotypic appearance. So, the genetic advance should be considered along with heritability in coherent selection breeding programs (SARKER *et al.*, 2016). BAYE and BECKER (2005) obtained comparatively higher phenotypic variance values than the genotypic variance for most of the traits in the crop *Vernonia galamensis*, which was solely due to the involvement of high error variance. So, they narrated that due to a large difference in the phenotypic variation between different traits, the GA was not directly related to heritability. But, in our study, the magnitude of genotypic variance; and phenotypic variances was quit closer due to the lesser role of environmental effect (Ve = Vp - Vg) therefore all the traits were under the control of genotypic variance (additive + non-additive).

Table 2. Mean sum of square (MS), grand mean, range, genotypic variance (σ^2_g), and phenotypic variance (σ^2_p) for yield and its related agronomic traits in rice

Parameters	Plant height (cm)	Number of tillers per hill	Number of panicles per hill	Panicle length (cm)	Number of primary branches per panicle	Number of secondary branches per panicle	Number of filled grains per panicle	Spikelet Sterility (%)	Days to flowering	Days to maturity	1000 grain weight (g)	Harvest Index	Grain yield per hill (g)
Mean sum of square	619.72**	16.08**	12.94**	22.59**	58.04**	1965.85**	36021.57**	174.84**	46.33**	29.79**	48.36**	0.04**	73.71**
Grand mean	126.00	11.45	10.54	27.14	56.63	140.29	546.71	32.78	118.29	164.25	23.58	0.39	17.56
Range	102-150	8-19	8-16	24-34	49-70	72-179	289-731	19-45	113-127	157-169	18-33	0.19-0.55	9-25
Genotypic variance	199.08	4.78	4.09	7.15	15.55	605.30	10509.99	55.13	14.64	10.64	15.19	0.01	22.91
Phenotypic variance	221.56	6.52	4.76	8.28	26.95	755.26	10501.59	57.58	16.04	12.51	17.98	0.01	23.89

**significant at 1% level

Table 3. Heritability (h^2_b), genetic advance (GA), genetic advance in percent of mean (GAPM), genotypic and phenotypic coefficient of variation (GCV and PCV) for yield and its related agronomic traits in rice

Parameters	Plant height (cm)	Number of tillers per hill	Number of panicles per hill	Panicle length (cm)	Number of primary branches per panicle	Number of secondary branches per panicle	Number of filled grains per panicle	Spikelet Sterility (%)	Days to flowering	Days to maturity	1000 grain weight (gm)	Harvest Index	Grain yield per hill (g)
Heritability (%)	89.86	73.39	85.87	86.32	57.70	80.14	70.06	85.38	85.92	69.03	84.50	85.71	82.14
Genetic advance (5%)	27.55	3.86	3.86	5.12	6.17	45.37	176.77	14.13	7.31	5.03	7.38	0.21	8.94
Genetic advance in percent mean (5%)	21.87	33.70	36.63	18.86	10.90	32.34	32.33	43.11	6.18	3.06	31.30	3.57	50.90
Genotypic coefficient of variation	11.20	19.09	19.19	9.85	6.96	17.54	18.75	22.65	3.23	1.79	16.53	28.09	27.26
Phenotypic coefficient of variation	11.81	22.29	20.71	10.60	9.17	19.59	22.40	24.51	3.49	2.15	17.98	30.34	30.08

However, in general, it is considered that if a trait is governed by non-additive gene action, it may give high heritability but low genetic advance, whereas if the trait is governed by additive gene action, heritability and genetic advance both would be high. The traits, which had high heritability along with high expected genetic advance, could be substantially considered for making selections as these traits were mainly influenced by the major effects of additive gene action (SARKER *et al.*, 2014). The expected GAPM varied from 3.06 for days to maturity to 50.90% for grain yield per hill. The highest expected genetic advance was exhibited for number of filled grains per panicle (176.77%), followed by number of secondary branches per panicle (45.37) and plant height (27.55), while the lowest GA was reported for harvest index (0.21) (Table 3). It was revealed that harvest index and number of tillers per panicle had the major role of non-additive gene action in the transmission of this trait from parents to offspring. Except for number of primary branches per panicle, days to maturity and days to flowering all the traits also showed moderate to high coefficient of variation and high heritability values, which indicated a

major role of additive gene action in the inheritance of these traits and their amenability for improvement in the population for grain yield and its component traits. Considering all genetic parameters, except for harvest index, number of primary branches per panicle, days to maturity, and days to flowering, all the traits could be selected for the improvement of rice.

Based on high heritability and high GA and GAPM along with close values between σ^2_g *vs*. σ^2_p and GCV *vs*. PCV all the traits (except for harvest index, number of primary branches per panicle, days to maturity, and days to flowering) could be selected for improving the grain yield of rice as these traits exhibited less influence of environment.

Coefficient of correlation

Yield is a complex product being influenced by several interdependent quantitative characters. Selection for yield may not be effective unless the other yield components influencing it directly or indirectly are taken into consideration. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects many other correlated traits. Hence, knowledge regarding the association of character with yield and among themselves provides a guideline to the plant breeder for improving through selection vis-à-vis provide a clear understanding of the contribution in respect of establishing the association by genetic and non-genetic factors. Genotypic and phenotypic correlation coefficients between pairs of characters of the present study in rice are presented in Table 4. It is evident that in most cases, genotypic correlation coefficients are higher than the corresponding phenotypic correlations might be due to modifying or masking effect of environment in the expression of the character under study (NANDPURI, 1973).

Plant height showed a considerable negative correlation with grain yield per hill both at the genotypic level (-0.575) and the phenotypic (-0.523) level indicating that the increase in plant height progressively decreased the grain yield. So yield could be improved through the selection of short-statured plant. Plant height had considerable negative genotypic and phenotypic correlation with number of filled grains per panicle, number of secondary branches per panicle, days to flowering. Similarly, the significant negative genotypic correlation and considerable phenotypic correlation were reported between plant height *vs*. days to maturity. It indicated that the selection of semidwarf plant could enhance the number of filled grains per panicle, number of secondary branches per panicle, and selection of tall plant reduced the days to flowering and days to maturity. This character had significant positive genotypic and considerable positive phenotypic correlation with spikelet sterility (%) (0.664, 0.572). It signifies that short-statured rice had low spikelet sterility. The correlation of plant height with other characters was insignificant. HAQUE *et al*. (1991) found similar results in rice. Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. GHOLIPOOR *et al*. (1998) found that grain yield had a negative significant genotypic correlation with plant height. Conversely, as biomass is the ultimate yield in vegetable amaranth, SARKER *et al*. (2018b; 2018c) reported a significant positive correlation with foliage yield and plant height. Number of panicles per hill found to display insignificant positive correlation with grain yield per hill and spikelet sterility (%) at phenotypic and genotypic level respectfully. It exhibited a significant negative correlation with 1000-grain weight at the phenotypic level (-0.678) and the genotypic level (-0.822). Therefore, it could be concluded that more panicles in

rice hill reduced the grain size in rice. RAY *et al.* (1993) and BALAN *et al.* (1999) also reported similar types of observations. The trend of the relationship between panicle length with 1000-grain weight (0.709), number of filled grains per panicle (0.609), grain yield per hill (0.439), number of secondary branches per panicle and growth duration were significant or considerable at both levels. These results revealed that long panicle increased 1000-grain weight, number of filled grains per panicle, number of secondary branches per panicle and growth duration of rice. The significant positive correlation between panicle length and days to maturity was also observed by CHAUBCY and SINGH (1994).

Table 4. The genotypic correlation coefficient (r_g) for important yield and its related agronomic traits in rice

Parameters		Plant height (cm)	Panicle length (cm)	Number of secondary branches per panicle	Number of filled grains per panicle	Spikelet Sterility (%)	Days to flowering	Days to maturity	1000 grain weight (g)	Grain yield per hill (g)
Plant height (cm)	r_g	-0.127	0.051	-0.450	-0.516	0.644*	-0.490	-0.696*	-0.150	-0.575
	r_p	-0.095	0.025	-0.410	-0.382	0.572	-0.496	-0.569	-0.184	-0.523
Number of panicles per hill	r_g		-0.334	-0.069	-0.258	0.192	-0.141	-0.327	-0.822*	0.010
	r_p		-0.322	-0.080	-0.212	0.165	-0.142	-0.276	-0.678*	0.081
Panicle length (cm)	r_g			0.285	0.609	-0.222	0.455	0.356	0.709**	0.439
	r_p			0.309	0.549	-0.179	0.380	0.316	0.581	0.420
Number of secondary branches per panicle	r_g				0.884**	-0.248	0.439	0.145	0.221	0.682*
	r_p				0.799*	-0.233	0.320	0.049	0.169	0.637*
Number of filled grains per panicle	r_g					-0.640*	0.807*	0.554	0.461	0.895**
	r_p					-0.598	0.532	0.336	0.333	0.809*
Spikelet Sterility (%)	r_g						-0.777*	-0.894**	-0.249	-0.710*
	r_p						-0.665*	-0.641*	-0.171	-0.707*
Days to flowering	r_g							0.548	0.269	0.878**
	r_p							0.460	0.278	0.715*
Days to maturity	r_g								0.658*	0.454
	r_p								0.533	0.407
1000 grain weight (g)	r_g									0.161
	r_p									0.100

*significant at 5% level, **significant at 1% level

Number of secondary branches per panicle showed a highly significant positive correlation with number of filled grains per panicle (0.799, 0.884) and grain yields per hill (0.637, 0.682) both at the phenotypic and the genotypic level. The trend of interrelationship number of secondary branches per panicle *vs.* days to flowering (0.439) was positive at both levels. It indicated that more secondary branches per panicle would lead to an increase in the number of filled grains per panicle and grain yield as well as long growth duration of rice. A highly significant positive correlation was observed in the number of filled grains per panicle with grain yield per hill and significant and considerable correlation with growth duration both at phenotypic (0.809) and genotypic (0.895) level. This result revealed that grain yield could be improved with the increase in number of filled grains per panicle and growth duration. A highly significant negative correlation was observed in spikelet sterility (%) (0.640) and number of filled grains per panicle at the genotypic level which revealed that spikelet sterility (%) negatively respond to filled grain per panicle. HAQUE *et al.* (1991) found similar results in rice. Association of spikelet sterility (%) with grain yield per hill (-0.707, -0.710), days to flowering (-0.665, -0.777), days to maturity (-0.641, -0.894) was negative and highly significant both at the phenotypic and genotypic level. This feature indicated that a decrease in spikelet sterility (%) results in an increase in grain yield and growth duration of rice. KUMAR *et al.* (1998) observed a

high positive correlation of grain yield with spikelet fertility. MEHETRE *et al*. (1996) also found similar results. Days to flowering represented a highly significant positive correlation with grain yield per hill (0.878, 0.715) at both the genotypic and phenotypic level. It exhibited a considerable positive correlation with days to maturity and 1000 grain weight at phenotypic (0.460, 0.278) and genotypic (0.548, 0.269) level. It indicated that maximum grain yield could be harvested through the selection of long duration and bold grain size in rice. Days to maturity had a significant positive genotypic correlation with 1000-grain weight (0.658), considerable positive phenotypic correlation with 1000-grain weight (0.533), and considerable positive genotypic and phenotypic correlation with grain yield per hill (0.454, 0.407) which indicated that late maturing genotypes furnished higher 1000-grain weight and grain yield per hill. Days to flowering, days to maturity showed a significant positive correlation with grain yield. RAY *et al.* (1993), PAUL and SHARMA (1997) and BALAN *et al.* (1999) reported a highly significant positive correlation between 1000-grain weight and grain yield per hill.

The significant and desirable correlation was observed for number of filled grains per panicle, number of secondary branches per panicle, spikelet sterility (%), days to flowering both at genotypic and phenotypic level. These four traits could be selected for improving the grain yield on rice as these traits exhibited less influence of the environment.

Path coefficient analysis

In the present investigation, grain yield was considered as a resultant variable and plant height, number of panicles per hill, panicle length, number of filled grains per panicle, spikelet sterility (%), 1000-grain weight, number of secondary branches per panicle, days to flowering, and days to maturity were causal (independent) variables. Residual effects of other independent variables, which have influence yield to a small extent, have been presented in Table 5 and Fig. 1.

Table 5. Partitioning of genotypic correlation into direct (bold phase) and indirect components to grain yield per hill (g) in rice

Parameters	Plant height (cm)	Number of panicles per hill	Panicle length (cm)	Number of secondary branches per panicle	Number of filled grains per panicle	Spikelet sterility (%)	Days to flowering	Days to Maturity	1000 grain weight (g)	Genotypic correlation with yield
Plant height (cm)	**-0.816**	0.071	0.045	0.012	-0.123	-0.322	0.002	0.424	0.131	-0.575
Number of panicles per hill	0.103	**-0.563**	-0.296	0.002	-0.061	-0.096	0.000	0.199	0.721	0.010
Panicle length (cm)	-0.041	0.188	**0.885**	-0.008	0.145	0.111	-0.002	-0.217	-0.622	0.439
Number of secondary branches per panicle	0.367	0.039	0.252	**-0.028**	0.210	0.124	-0.001	-0.088	-0.194	0.682*
Number of filled grains per panicle	0.421	0.145	0.539	-0.024	**0.238**	0.321	-0.003	-0.338	-0.404	0.895**
Spikelet sterility (%)	-0.525	-0.108	-0.197	0.007	-0.152	**-0.501**	0.003	0.544	0.219	-0.710*
Days to flowering	0.400	0.080	0.403	-0.012	0.192	0.389	**-0.003**	-0.334	-0.236	0.878**
Days to Maturity	0.568	0.184	0.315	-0.004	0.132	0.447	-0.002	**-0.609**	-0.578	0.454
1000 grain weight(g)	0.122	0.463	0.627	-0.006	0.110	0.125	-0.001	-0.401	**-0.878**	0.161

*significant at 5% level, **significant at 1% level; Residual effect = 0.1386
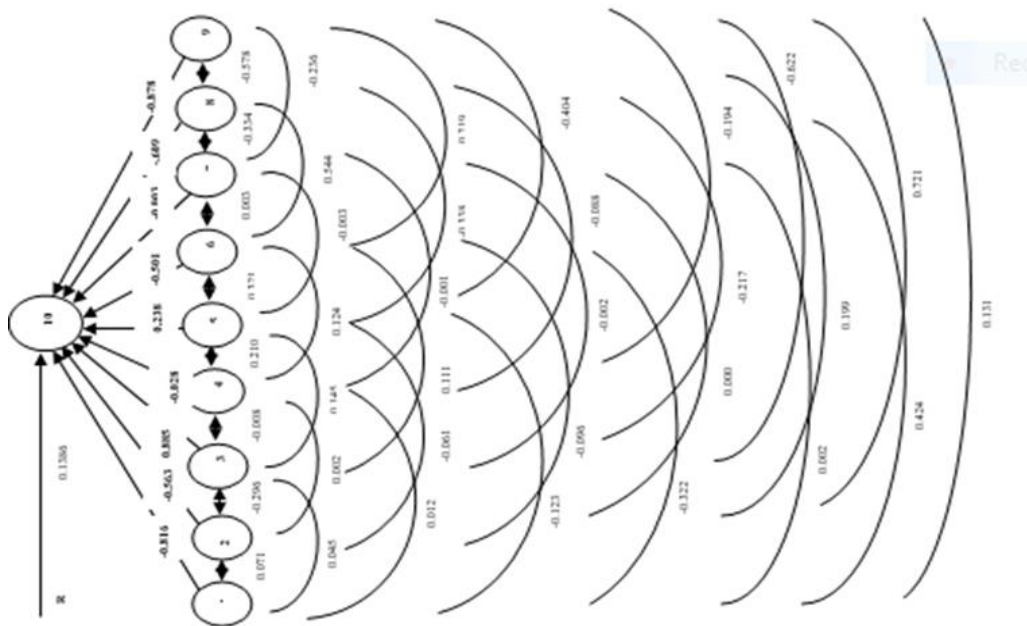
Fig. 1. Path diagram of important yield and yield-related traits in rice, 1 = Plant height, 2 = Number of
panicles per hill, 3 = Panicle length, 4 = Number of secondary branches per panicle, 5 = Number of
filled grains per panicle, 6 = Spikelet sterility %, 7 = Days to flowering, 8 = days to maturity, 9 =
1000 grain weight, 10 = Grain yield per plant, Bold phase, (direct effect)
R = Residual effect

The number of filled grains per panicle showed positive and considerable direct effect
(0.238) on grain yield. A strong positive indirect effect of this trait on grain yield was registered
through plant height (0.421), number of panicles per hill (0.145), panicle length (0.539), and
spikelet sterility % (0.321). Hence, the total correlation was highly significant and positive
(0.8951). Spikelet sterility (%) showed a negative direct effect (-0.501) on grain yield. The
negative indirect effect through plant height (-0.525), number of panicles per hill (-0.108),
panicle length (-0.197), number of filled grains per panicle (-0.152) made the total correlation
highly significant and negative (0.710). So, direct selection based on number of filled grains per
panicle and spikelet sterility (%) would be effective for increasing grain yield. Considerable
positive direct effects of number of filled grains/panicle on yield were also reported by DASH *et
al*. (1996), and PADMAVATHI *et al.* (1996).

Plant height showed the negative high direct effect on grain yield per hill (-0.816).
The positive indirect effect via days to maturity (0.424), 1000 grain weight (0.131) made the
total correlation negative on grain yield (-0.575). The direct effect of number of panicles per hill

was negative (-0.563), while the positive indirect effects of 1000 grain weight, days to maturity and plant height made the total correlation insignificant and positive on grain yield per hill (0.010). Panicle length noticed a high positive direct effect (0.885) on grain yield. The indirect effects via plant height (-0.041), number of secondary branches per panicle (-0.008), days to flowering (-0.002), days to maturity (-0.217) and 1000-grain weight (-0.622) were negative that made the total correlation insignificant and positive (0.439) with grain yield. The direct effect of secondary branches per panicle was negative and negligible (-0.028). The positive indirect effects via plant height (0.367), panicle length (0.252), number of filled grains per panicle (0.210), spikelet sterility % (0.124) made the total correlation positive and significant (0.682) Days to flowering showed negative and negligible direct effect (-0.003) on grain yield. The positive indirect effect of this trait via plant height (0.400), number of panicles per hill (0.080), panicle length (0.403), number of filled grains per panicle (0.192), spikelet sterility (%) (0.389) made the total correlation positive and highly significant (0.878). Days to maturity showed a negative direct effect (-0.609) on grain yield. The positive indirect effect of plant height (0.568), number of panicles per hill (0.184), panicle length (0.315), number of filled grains per panicle (0.132), spikelet sterility (%) (0.447) made the total correlation positive (0.454). Thousands grain weight had the highest negative direct effect (-0.878) on grain yield. The positive indirect effects via plant height (0.122), number of panicles per hill (0.463), panicle length (0.627), number of filled grains per panicle (0.110), spikelet sterility (%) (0.125) made the total correlation positive and insignificant (0.161). So direct selection based on plant height, number of panicles per hill, panicle length, secondary branches per panicle, days to flowering, days to maturity, and 1000 grain weight would not be effective for increasing the grain yield of rice. RAY et al. (1993) and CHOUDHURY and DAS (1998) reported a positive direct effect of plant height on grain yield of rice. KUMAR (1992), RAY et al. (1993), MARWAT et al. (1994), DASH et al. (1996), and KUMAR et al. (1998) reported the high and positive direct effect of panicle length on grain yield of rice.

Path analysis indicated that number of filled grains per panicle and spikelet sterility (%) was the most important character that had the maximum contribution to grain yield per hill as it exhibited a considerable positive direct effects and significant correlation coefficients on yield. The residual effect was found 0.1386 which indicated that there were other contributors which were responsible for yield but not taken into consideration in the present investigation. On the other hand, eighty-seven percent (86.14%) variability was accounted for ten traits included in the present investigation. According to SHANTHAKUMAR et al. (1998), this residual effect towards yield might be due to other characters (which were not studied), environmental factors and sampling errors.

CONCLUSION

Considering genetic parameters, correlation and path coefficient analysis direct selection based on number of filled grains per panicle and spikelet sterility (%) would significantly increase the grain yield of rice. These two traits exhibited less influence on the environment and could be selected for improving the grain yield of rice. The residual effect was found 0.1386 which indicated that 86.14% of the variability was accounted for yield and yield contributing traits included in the present study. Rest 13.86% variability might be controlled by other yield contributing traits that were not included in the present investigation.

So, direct selection based on these traits would be effective for the improvement of these breeding materials.

REFERENCES

ALI, M.A., U., SARKER, M.A.K., MIAN, M.A., ISLAM, F., TUJ-JOHORA (2014): Estimation of genetic divergence in boro rice (*Oryza sativa* L.). Intl. J. BioRes., *16(1)*: 28-36.

ANONYMOUS (1999): Time and requirement of top dressing of urea according to season and variety. Adhunik Dhaner Chash, Bangladesh Rice Research Institute. P.28.

ANONYMOUS (2005): Krishi diary. Krishitathya Service. Farmgate, Dhaka 1215. p. 23.

ANONYMOUS (2007): Yearbook of Agricultural Statistics of Bangladesh. The Ministry of Planning. The Government of the People Republic of Bangladesh. p. 129.

AZAM, M.G., U., SARKER, J.A., MAHMUD, M., MANIRUZZAMAN, B.R., BANIK (2014): Genetic variability of yield and its contributing characters of CIMMYT maize inbreds in stress condition. Bangladesh J. Agri. Res., *39(3)*: 419-426.

AZAM, M.G., U., SARKER, M.A.K., MIAN, B.R., BANIK, M.Z.A., TALUKDER (2013): Genetic divergence on quantitative characters of exotic maize inbreds (*Zea mays* L.). Bangladesh J. Plant Breed. Genet., *26(2)*: 09-14

BALAN, A., A.R., MUTHIAH, S.N.M.R., BOOPATHI (1999): Genetic variability, correlation and path coefficient analysis in upland early rice genotypes. Madras Agril. J., *86*: 7-9.

BAYE, T., H.C., BECKER (2005): Genetic variability and interrelationship of traits in the industrial oil crop *Vernonia galamensis*. Euphytica, *142*:119–129.

BISAWAS, A., U., SARKER, B.R., BANIK, M.M., RAHMAN, M.A.K., MIAN (2014): Genotic divergence study in salinity stress tolerance maize (*zea mays* L.). Bangladesh J. Agril. Res., *39(4)*: 621-630.

BISWAS, P.S., U., SARKER, M.A.R., BHUIYAN, S., KHATUN (2006): Genetic divergence in cold tolerant irrigated rice (*Oryza sativa* L.). The Agriculturists, *4(1 & 2)*: 15-20.

CHAKRABARTY, T., U., SARKER, M., HASAN, M.M., RAHMAN (2018): Variability in mineral compositions, yield and yield contributing traits of stem amaranth *(Amaranthus lividus).* Genetika, *50*: 995-1010.

CHAUBEY, P.K., R.P., SINGH (1994): Genetic variability, correlation and path analysis of yield components of rice. Madras Agril. J., *81*: 468-470.

CHOUDHURY, P.K.D., P.K., DAS (1998): Genetic variability, correlation and path coefficient analysis in deep-water rice. Ann. Agril. Res., *19*: 120-124.

DASH, S.K., J., SINGH, M., TRIPATHY, D., MISHRA (1996): Association of quantitative traits and path analysis in medium land rice. Environ. Ecol., *14*: 99-102.

GANAPATI, R.K., M.G., RASUL, M.A.K., MIAN, U., SARKER (2014): Genetic variability and character association of T-Aman rice (*Oryza Sativa* L) Intl. J. Plant Biol. Res., *2*: 1013.

GHOLIPOOR, M., H., ZEINALI, M.A., ROSTAMI (1998): Study of correlation between yield and some important agronomic traits using path analysis in rice. Iranian J. Agric. Sci., *29*: 627–638.

HASAN, M.R., U., SARKER, M.A.K., MIAN, T., HOSSAIN, M.N.H., MAHMUD (2012a): Genetic variation in micronutrient dense rice and its implication in breeding for higher yield. Eco-friendly Agril. J., *5(9)*: 75-182.

HASAN, M.R., U., SARKER, M.R., HASAN, M.R. ISLAM, M.N.H., MAHMUD (2012b): Genetic diversity in micronutrient dense rice and its implication in breeding program. Eco-friendly Agril. J., *5(9)*: 183-185.

HAQUE, M.E. (2001): Genetic variability and path analysis in rice genotypes. Bangladesh J. Pl. Breed. Genet., *16*: 33-37.

KARIM, D., M.N.A., SIDDIQUE, U., SARKER, M.Z., HASNAT, J., SULTANA (2014): Phenotypic and genotypic correlation co-efficient of quantitative characters and character association of aromatic rice J. Biosci. Agric. Res., *1*: 34-46.

KARIM, D., U., SARKER, M.N.A., SIDDIQUE, M.A.K., MIAN, M.Z., HASNAT (2007): Variability and genetic parameter analysis in aromatic rice. Intl. J. Sustain. Crop Prod., *2*: 15-18.

KUMAR, B., R., THAKUR, S.B., MISHRA, D.N., SINGH (1992): Variability studies in segregating population of rice (*Oryza sativa* L.). Ann. Biol., *17*: 43-45.

KUMAR, G.S., M., MAHADEVAPPA, M., RUDRARADHYA (1998): Studies on genetic variability, correlation and path analysis in rice during winter across the locations. Karnataka J. Agril. Sci., *11*: 73-77.

MARWAT, K.B., M.,TAHIR, D.R., KHAN, M.S., SWATI (1994): Path coefficient analysis in rice (*Oryza sativa* L.). Sarhad J. Agril., *10*: 547-551.

MEHETRE, S.S., C.R., MAHAJAN, P.A., PATIL, P.M., DHUMAL (1996): Variability, heritability, correlation, path analysis, and genetic divergence studies in M_2 generation of gamma-irradiated upland rice. Int. Rice Res. Notes., *21*: 56-58.

NATH, J.K., U., SARKER, M.A.K., MIAN, T., HOSSAIN (2008): Genetic divergence in T. Aman rice. Ann. Bangladesh Agric., *12(1)*: 51-60.

NANDAPURI, P.J.S. (1994): Path analysis of yield and yield components and construction of selection indices of direct-seeded rice: first season. Annual review conference proceedings, 20-23 October 1992, National Agricultural Research Institute, Caribbean Agril. Res. and Development Inst. Guyana. pp. 63-71.

PADMAVATHI, N., M., MAHADEVAPPA, O.U.K., REDDY (1996): Association of various yield components in rice (*Oryza sativa* L.). Crop Res. Hisar., *12*: 353-357.

PAUL, S.K., A.K., SARMAH (1997): Interrelationship of yield and yield contributing characters in upland aus rice. J. Agril. Sci. Soc., *10*: 164-167.

RAHMAN, M.H., U., SARKER, M.A.K., MAIN (2007a): Assessment of variability of floral and yield traits; II maintainer lines of rice. Ann. Bangladesh Agric., *11(1)*: 95-102.

RAHMAN, M.H., U., SARKER, M.A.K., MAIN (2007b): Assessment of variability of floral and yield traits; I restorer lines of rice. Ann. Bangladesh Agric., *11(1)*: 87-94.

RAI, P.K., U., SARKER, P.C., ROY, A.K.M.S., ISLAM (2013): Character Association in F_4 generation of rice (*Oryza sativa* L.). Bangladesh J. Pl. Breed. Genet., *26(2)*: 39-44.

RASHAD, M.M.I., U., SARKER (2020): Genetic variations in yield and yield contributing traits of green amaranth. Genetika, *52*: 391-404.

RAY, S.A., M.A., KHAN, T., MCNEILLY, A.A., KHAN (1993): Cause and effect relations of yield and yield components in rice (*Oryza sativa* L.). J. Genet. Breed., *51*: 1-5.

SARKER, U., M.T., ISLAM, M.G., RABBANI, S., OBA (2015a): Variability, heritability and genetic association in green amaranth (*Amaranthus tricolor*). Span. J. Agric. Res., *13*: 1-8.

SARKER, U., S., OBA (2018a): Drought stress enhances nutritional and bioactive compounds, phenolic acids, and antioxidant capacity of *Amaranthus* leafy vegetable. BMC Plant Biol., *18*: 258.

SARKER, U., S., OBA (2018b): Response of nutrients, minerals, antioxidant leaf pigments, vitamins, polyphenol, flavonoid and antioxidant activity in selected green amaranth under four soil water content. Food Chem., *252*: 72-83.

SARKER, U., S., OBA (2018c): Augmentation of leaf color parameters, pigments, vitamins, phenolic acids, flavonoids and antioxidant activity in selected *Amaranthus tricolor* under salinity stress. Sci. Rep., *8*: 12349.

SARKER, U., M.T., ISLAM, S., OBA (2018): Salinity stress accelerates nutrients, dietary fiber, minerals, phytochemicals and antioxidant activity in *Amaranthus tricolor* leaves. PLOS One, *13*(11)**:** 0206388.

SARKER, U., S., OBA (2018d): Drought stress effects on growth, ROS markers, compatible solutes, phenolics, flavonoids, and antioxidant activity in *Amaranthus tricolor*. Appl. Biochem. Biotechnol., *186*: 999-1016.

SARKER, U., S., OBA (2018e): Catalase, superoxide dismutase and ascorbate-glutathione cycle enzymes confer drought tolerance of *Amaranthus tricolor*. Sci. Rep., *8*: 16496.

SARKER, U., S., OBA (2019a): Nutraceuticals, antioxidant pigments, and phytochemicals in the leaves of *Amaranthus spinosus* and *Amaranthus viridis* weedy species. Sci. Rep., *9*: 20413.

SARKER, U., S., OBA (2019b): Protein, dietary fiber, minerals, antioxidant pigments and phytochemicals, and antioxidant activity in selected red morph *Amaranthus* leafy vegetable. PLoS One, *14*: 0222517.

SARKER, U., S., OBA (2019c): Antioxidant constituents of three selected red and green color *Amaranthus* leafy vegetable. Sci. Rep., *9*: 18233.

SARKER, U., S., OBA (2019d): Salinity stress enhances color parameters, bioactive leaf pigments, vitamins, polyphenols, flavonoids and antioxidant activity in selected Amaranthus leafy vegetables. J. Sci. Food Agric., *99*: 2275-2284.

SARKER, U., S., OBA, M.A., DARAMY (2020a): Nutrients, minerals, antioxidant pigments and phytochemicals, and antioxidant capacity of the leaves of stem amaranth. Sci. Rep., *10*: 3892.

SARKER, U., M.M., HOSSAIN, S., OBA (2020b): Nutritional and antioxidant components and antioxidant capacity in green morph *Amaranthus* leafy vegetable. Sci. Rep., *10*: 1336.

SARKER, U., S., OBA (2020a): The response of salinity stress-induced *A. tricolor* to growth, anatomy, physiology, non-enzymatic and enzymatic antioxidants. Front. Plant Sci., (accepted)

SARKER, U., S., OBA (2020b): Nutrients, minerals, pigments, phytochemical, and radical scavenging activity in *Amaranthus blitum* leafy vegetable. Sci. Rep., *10*: 3868.

SARKER, U., S., OBA (2020c): Leaf pigmentation, its profiles and radical scavenging activity in selected *Amaranthus tricolor* leafy vegetables. Sci. Rep., (accepted).

SARKER, U., S., OBA (2020d): Phenolic profiles and antioxidant activities in selected drought-tolerant leafy vegetable amaranth. Sci. Rep., (accepted).

SARKER, U., S., OBA (2020e): Nutritional and bioactive constituents and scavenging capacity of radicals in *Amaranthus hypochondriacus*. Sci. Rep., (accepted).

SARKER, U., M.T., ISLAM, M.G., RABBANI, S., OBA (2014): Genotypic variability for nutrient, antioxidant, yield and yield contributing traits in green amaranth. J. Food Agri. Environ., *12*: 168-174.

SARKER, U., M.T., ISLAM, M.G., RABBANI, S., OBA (2017): Genotypic diversity in green amaranth for antioxidant, nutrient and agronomic traits. Indian J. Genet. Pl. Breed., *77*: 173-176.

SARKER, U., M.T., ISLAM, M.G., RABBANI, S., OBA (2018a): Variability in total antioxidant capacity, antioxidant leaf pigments and foliage yield of green amaranth. J. Integrative Agric., *17*: 1145-1153.

SARKER, U., M.T., ISLAM, M.G., RABBANI, S., OBA (2015b): Genotype variability in composition of antioxidant vitamins and minerals in green amaranth. Genetika, *47*: 85-96.

SARKER, U., M.T., ISLAM, M.G., RABBANI, S., OBA (2016): Genetic variation and interrelationship among antioxidant, quality and agronomic traits in green amaranth. Turk. J. Agric. For., *40*: 526-535.

SARKER, U., M.T., ISLAM, M.G., RABBANI, S., OBA (2018b): Antioxidant leaf pigments and variability in green amaranth. Genetika, *50*: 209-220.

SARKER, U., M.T., ISLAM, M.G., RABBANI, S., OBA (2018c): Phenotypic divergence in green amaranth for total antioxidant capacity, antioxidant profile, dietary fiber, nutritional and agronomic traits. Acta Agric. Scand. Section B-Plant and Soil Sci., *68*: 67-76.

SARKER, U., M.A.K., MIAN (2003): Genetic variability, character association and path analysis for yield and its components in rice. J. Asiat. Soc. Bangladesh Sci., *29(2)*: 47-54.

SARKER, U., M.A.K., MIAN (2004): Genetic variations and correlations between floral traits in rice. Bangladesh J. Agril. Res., *29(4)*: 553-558.

SARKER, U., P.S., BISWAS, B., PRASAD, M.A.K., MIAN (2001): Correlated response, relative selection efficiency and path analysis in cold tolerant rice. Bangladesh J. Pl. Breed. Genet., *14* (2): 33-36.

SHANTHAKUMAR, G., M., MAHADEVAPPA, M., RUDRARADHYA (1998): Studies on genetic variability, correlation and path analysis in rice (*Oryza saliva* L.) over seasons. Karnataka J. Agril. Sci., *11*: 67-72.

SIDDIQUE, M.N.A, U., SARKER, M.A.K., MIAN (2009): Genetic diversity in restorer line of rice In: *Proceedings of the international conference on plant breeding and seed for food security*. M.S.R. Bhuiyan, L. Rahman, ed. Plant Breeding and Genetics Society of Bangladesh. pp. 137-142.

TALUKDER, M.Z.A., U., SARKER, A.B.M.M.M., KHAN, M., MONIRUZZAMAN, M.M., ZAMAN (2011): Genetic variability and correlation coefficient of coconut (*Cocos nacifera* L.) in Barisal region. Intl. J. BioRes., *11(1)*: 15-21.

TALUKDER, M.Z.A., U., SARKER, HARUN-OR-RASHID, M.A.K., MIAN, M., ZAKARIA (2015): Genetic diversity of coconut (*Cocos nucifera* L.) in Barisal Region. Ann Bangladesh Agric., *19*: 13-21.

VIRMANI, S.S. (1996): Hybrid rice. Adv. Agron., *57*: 379.

PROMENLJIVOST, HERITABILNOST, POVEZANOST OSOBINA I ANALIZA KOEFICIJENTA PUTA U LINIJAMA PIRINČA (*Oriza sativa* L.)

G. HASAN-UD-DAULA[1], Umakanta SARKER[1*]

[1]Odeljenje za genetiku i oplemenjivanje biljaka, Poljoprivredni fakultet, Poljoprivredni Univerzitet u Bangabandhuu Sheikh Mujibur Rahman, Gazipur-1706, Bangladeš.

Izvod

Sedam inbred linija razvijenih putem oplemenjivačkog programa hibridizacije i popularni kultivar korišćeno je za proučavanje varijabilnosti, heritabilnosti, povezanosti osobina i analize koeficijenta puta kod pirinča za prinos zrna i srodne agronomske osobine. Rezultati su pokazali da se genotipovi značajno razlikuju u pogledu prinosa zrna i srodnih agronomskih karakteristika. Izuzetne varijacije primećene su za sve osobine osim dužine trajanja rasta i žetvenog indeksa. Primećena je velika genetička varijabilnost za broj nalivenih zrna po klasu, broj sekundarnih grana po klasu, visinu biljke, sterilnost klasića (%), prinos zrna po kućici, broj primarnih grana po klasu, težinu 1000 zrna, trajanje cvetanja i zrelost, broj stabala po kućici, i dužinu klasića. Na osnovu visoke heritabilnosti i visokog GA i GAPM-a, uz bliske vrednosti između σ^2_g *vs.* σ^2_p i GCV u odnosu na PCV, sve osobine (osim žetvenog indeksa, broja primarnih grana po klasu, dana do zrelosti i dana do cvetanja) mogu biti izabrane za poboljšanje prinosa zrna pirinča, jer su ove osobine bile pod manjim uticajem spoljašnje sredine. Primećene su značajne i poželjne korelacije za broj nalivenih zrna po klasu, broj sekundarnih grana po klasu, sterilnost klasića (%), broj dana do cvetanja i na genotipskom i na fenotipskom nivou. Uzimajući u obzir genetske parametre, korelaciju i analizu koeficijenta puta, direktna selekcija na osnovu broja nalivenih zrna po klasu, i sterilnosti klasića, značajno bi povećala prinos zrna pirinča. Rezidualni efekat od 0.1386, ukazuje da je 86.14% varijabilnosti utvrđeno za prinos zrna i osobine koje doprinose prinosu koje su bile uključene u ovu studiju. Ostala varijabilnost od 13.86% može se kontrolisati drugim osobinama koje doprinose prinosu, a koje nisu bile obuhvaćene ovim istraživanjem. Dakle, direktan izbor na osnovu ovih osobina bio bi efikasan za poboljšanje ovih oplemenjivačkih materijala.

.