GENETIC VARIABILITY OF RICE GENOTYPES (*Oryza sativa* L.)

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ABSTRACT

An attempt was made to study genotypic variance, phenotypic variance, environmental variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2_b) and genetic advance (GA) for some rice genotypes during July 2007 to January 2009 at BSMRAU campus, Gazipur 1706. Significant variations were obtained among the genotypes for all the characters studied. Considering genetic parameters high genotypic coefficient of variation (GCV) value was observed for harvest index followed by yield per hill, number of tillers per hill, number of filled grain per panicle, whereas days to maturity showed very low GCV. High heritability with high genetic advance (GA) observed for yield per hill followed by number of tillers per hill, number of filled grains per panicle indicated that these characters were under additive gene control and selection for genetic improvement for these traits might be effective.

Key words: Rice, genotypic variance, phenotypic variance, heritability (h^2_b) and genetic advance (GA)

INTRODUCTION

Rice contributes about 50% dietary energy (Juliano, 1985). In Bangladesh it is major source of calorie, which covers almost 80% of the required calorie for the people in the country (MOA, 2001). Rice is also considered as a source of protein, which is comprised of albumins, globulins, prolamins and glutamins, these proteins have also highly digestible energy, which are necessary for growth and development of the body. So grain yield and quality improvement of rice are essentially required. Projected demand of the next 30 years clearly indicates the need for sustainable increase in production of rice cultivation. The present population of 145 million will increase to 233 million by 2030 requiring 48 million tons of extra food grain (Karim *et al.,* 1990). Under such conditions, all the additional production must come from higher yield due to non-availability of lands for expansion of rice. It is not possible to increase the production of rice horizontally due to lack of land. So we can increase the production of rice vertically utilizing every resources and opportunity judiciously. Considering these aspects and importance of rice, this piece of work has been initiated to estimate heritability, genetic advance of yield and yield related characteristics in order to design a meaningful breeding strategy and to develop selection criteria for improving yield potentiality of rice.

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MATERIALS AND METHODS

The experiment was carried out at the experimental farm of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur during July 2007 to January 2009. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. The whole experimental area was divided into three blocks, representing three replications. Five rows of 4m each constituted the experimental unit. Twenty five genotypes were distributed in the experimental unit through randomization by using the IRRISTAT programme. Thirty days old healthy seedlings were transplanted at a spacing of 20 cm x 20 cm spacing between plant to plant and row to row, respectively were maintained. Proper control measures were taken against rice stem borer during tillering and heading stage of rice. Furadan 5G @ lg per square meter were applied at active tillering stage and panicle initiation stage of rice for controlling the stem borer. Adequate soil fertility was ensured by applying additional quantities of Urea, TSP, MP and Gypsum @ 180-100-70-60 kg/ha, respectively. Total TSP, MP and Gypsum were applied in final land preparation. Total Urea was applied in three installments, at 15 days after transplanting (DAT), 30 DAT and 50 DAT. Data were collected from five randomly selected hills of each genotype on individual plant basis. All data obtained for each character were subjected to the analysis of variance following the RCB design. Mean ($\bar{x}$), range and standard deviation (σ) for each character were also estimated. The mean sum of square (MS) of error and phenotypic variances were estimated followed by Johnson *et al.* (1955). The error mean sum of square was considered as error variance ($\sigma^2 e$). Genotypic variances ($\sigma^2 g$) were derived from the ratio of difference between error mean sum of square and the mean sum of square to number of replications.

RESULTS AND DISCUSSION

Analysis of variance for all the characters showed highly significant mean sum of square due to genotypes (Table 1) indicating the existence of considerable variation among the genotypes. The mean value for days to maturity ranged from 137 to 160 days. The genotypic and phenotypic variances were 38.38 and 114.46, respectively (Table 2). The phenotypic variance was high and differed considerably from its corresponding genotypic variance. This pronounced variation for days to maturity was mostly due to environmental effect. The values of GCV (4.13) and PCV (7.137) were low (Table 2) and had the least difference. Similar findings were reported by Balan *et al.* (1999). Low heritability (33.53) with low genetic advance (4.03) was observed for days to maturity. Selection for such trait may not be effective. High heritability with low genetic advance was also reported by Gomathinayagam *et al.* (1990) for days to maturity. The phenotypic and genotypic variances for the plant height were high (256.14 and 222.23, respectively). The phenotypic variance appeared to be close to genotypic variance, suggested less influence of environment on the expression of the genes controlling this trait. Here environmental variance was also high (33.92). Heritability was high (86.75) with moderate genetic advance (21.91). So, selection based on this trait would be effective. The phenotypic variance for number of tillers per hill (16.51) was close to genotypic variance (14.94) as presented in Table 2. This feature indicated higher influence of genotype on the expression of the trait rather than the environment factor for numbers of panicles per hill. The numbers of panicles per hill showed high phenotypic and genotypic coefficient of variation (36.83 and 38.81, respectively). The phenotypic coefficient of variation (38.71) was also similar to genotypic coefficient of variation (36.83) indicating the variation was only due to genotypes with very less influence of environment.

Table 1. Analysis of variance for yield and its component characters in rice

Varieties	d.f.	Days to 50% flowering	Days to maturity	Plant height(cm)	No. of tiller/hill	Panicle length (cm)	Primary branch	Secondary branch	Spikelet sterility	Wt. of 100 grain (g)	No. of filled grain/panicle	Yield/hill (g)	Harvest index
Genotype	24	151.83**	191.24**	700.61**	46.41**	12.41**	5.00**	132.91**	3624.4**	1.18**	3791.30**	67.31**	3.51**
Replication	2	87.64	56.37	90.90	0.39	0.015*	0.026	5.93*	155.22	0.097	45.94	1.95	0.0014
CV%		1.21	5.82	4.46	11.91	2.02	3.50	5.45	8.55	10.71	7.05	7.81	12.31

*indicates significant at 5% level and **indicates significant at 1% level

Table 2. Estimates of genetic parameter for yield and its component characters in 25 rice genotypes

Varieties	Days to 50% flowering	Days to maturity	Plant height(cm)	No. of tiller/hill	Panicle length(cm)	Primary branch	Secondary branch	Spikelet sterility	Wt. of 100 grain (g)	No. of filled grain/panicle	Yield/hill (g)	Harvest index
Range	94-113.66	137-160	98.8-160.6	6.06-17.9	21.54-29.7	6.92-11.8	5.86-41.53	6.93-76.66	1.9-4	40.56-160.6	4.59-22.18	0.14-.40
Mean	102.07	149.91	130.54	10.50	27.20	10.12	24.19	135.45	2.91	99.34	11.09	0.23
v^2g	50.10	38.38	222.23	14.94	4.03	1.62	43.72	1163.403	0.36	1247.39	22.18	1.16
v^2p	51.62	114.46	256.14	16.51	4.33	1.75	45.46	1297.619	0.45	1296.51	22.93	1.17
v^2e	1.51	76.08	33.92	1.56	0.30	0.13	1.74	134.22	0.10	49.12	0.75	0.01
PCV	7.03	7.13	12.26	38.71	7.65	13.07	27.871	26.594	23.22	36.24	43.17	148.05
GCV	6.935	4.13	11.42	36.83	7.38	12.59	27.33	25.18	20.61	35.55	42.46	147.54
h^2b	97.06	33.53	86.75	90.53	93.03	92.82	96.17	89.65	78.75	96.21	96.72	99.31
GA	14.07	4.93	21.91	72.20	14.67	24.99	55.21	49.11	37.68	71.83	86.028	302.88

The estimates of heritability (90.53) for no. of tillers/hill was high with high genetic advance (72.20). Gomathinayagam *et al.* (1990) also reported similar result. The minimum difference between PCV (7.65) and GCV (7.38) revealed less influence of environment on the expression of panicle length (Table 2). This character showed high heritability (93.03) together with moderate genetic advance (14.67). 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. The character showed low phenotypic (1.75) and genotypic (1.62) variance indicating less effect of environment for the expression of the trait (Table 2). The PCV (13.07) was close to the GCV (12.59) for this character. Number of primary branches per panicle showed high heritability (92.82) with moderate genetic advance (24.99). Therefore selection based on this trait would be effective. These results matched with the findings of Reddy and Kumar (1996). The value of PCV and GCV presented in Table 2, were moderate and the difference was very close (23.22 and 20.61). Heritability value (78.75) was very high. This character also represented very high genetic advance (37.68). This feature suggested 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. Choudhury and Das (1997) reported high heritability and high genetic advance in percent of mean for this character which agreed with the present findings. The mean values ranged from 40.56 to 160.6. The phenotypic variance (1296.51) was much higher than genotypic variance (1247.39 indicating that environment had been playing a significant role for the expressing of the character (Table 2). The PCV (36.24) and GCV (35.55) were very close (Table 2). High heritability (96.21) with high genetic advance (71.83).as seen in this character indicated existence of additive gene action and selection should be effective. De and Suriya (1988) reported higher estimates of coefficient of variation and genetic advance in percent of mean for filled grain per panicle (%). The mean values for yield per hill ranged from 4.59 to 22.18 g. The components of variance showed least difference between phenotypic variance (22.93) and genotypic variance (22.18) indicating least influence of environment for comparison of this trait (Table 2). The phenotypic coefficient of variation (43.17) and genotypic coefficient of variation (42.46) were high in magnitude but very close to each other. Reddy and Kumar (1996) reported higher PCV than GCV for grain yield per plant, whereas Choudhury and Das (1997) reported higher values of PCV and GCV. In case of heritability estimates this character showed high heritability (96.72) with high genetic advance (86.02). These findings were 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.

The highest mean value was observed for days to maturity (149.91). This character exhibited the range of variation (137-160) indicated that all the genotypes showed wide range of variation in respect of this character. The phenotypic variance was higher than the corresponding genotypic variance for the characters. However, these differences were also higher in case of spikelet sterility (%), number of filled grains per panicle and plant height indicating greater influence on environment for expression of these characters. All the characters showed moderate phenotypic and genotypic coefficient of variation except days to maturity (4.133 and 7.137) days to 50% flowering (6.9 and 7.0) and panicle length (7.3 and 7.6). Among the characters the highest genotypic coefficient of variation was recorded for harvest index (147.54) followed by

yield per hill (42.46), number of tiller per hill (36.83), number of filled grains per panicle (35.55), number of secondary branches per panicle (27.33), number of primary branches per panicle (12.59), plant height (11.42), panicle length (7.30) and days to maturity (4.12) in order of merit. The highest heritability value was observed for harvest index (99.30) and the lowest for number of days to maturity (33.53). The highest genetic advance was observed for harvest index (302.88), followed by yield per hill (86.02), number of tiller per hill (72.20), number of filled grains per panicle (71.83) and grain yield per hill (49.11), where as the lowest for days to maturity (4.93). The parameter harvest index showed both the highest heritability and genetic advance, indicated additive gene action for expression of the character and selection for such trait might be rewarding. The highest genotypic coefficient of variation was observed for harvest index whereas days to maturity showed very low genotypic coefficient of variation. The highest heritability coupled with the highest genetic advance was observed in harvest index. Days to maturity showed the lowest heritability and genetic advance.

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