Research Article

Genetic Variability and Character Association of T-Aman Rice (*Oryza Sativa* L)

Ganapati RK[1]*, Rasul MG [2], Mian MAK[2] and Sarker U[2]

[1]*Breeding Division, Bangladesh Sugarcane Research Institute, Bangladesh*
[2]*Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Bangladesh*

Abstract

Twenty five genotypes were evaluated for yield and yield contributing characters to observe their variability, associations and direct and indirect effect on yield during Amon season, 2010. Grain panicle-1 and filled grain panicle-1 had high genotypic variance, high heritability, high genetic advance and high genotypic coefficient of variation. Tiller hill-1, plant height and thousand grain weights showed significant positive association with grain yield. Path coefficient analysis also revealed that, tiller hill-1, thousand grain weight and grain panicle-1 had higher direct effects on yield. Genetic variability, correlation and path analysis revealed that tiller hill-1, plant height and thousand grain weights are the most important yield components in rice. Therefore, from the present study it could be suggested that emphasize should be given on these characters for the selection of genotypes for higher grain yield in transplanted Amon rice.

INTRODUCTION

Rice is a semi aquatic plant. It is required for the rainy season but flood or submergence condition can hampered the expected production. Sometimes, rice plants may be damaged due to submergence for long time which affects the production of rice. So, we should improve the production of rice vertically utilizing every resources and opportunity judiciously. Rice yield is dependent on many yield contributing characters as well as on the environmental influence. Association of different characters is essential to determine their contribution towards yield. Yield component analysis is of fundamental importance to determine the direct and indirect contributions towards yield. As the yield is polygenic ally controlled and also influenced by its component characters, direct selection for yield is often misleading. Knowledge about genetic variability of yield contributing characters, interrelationship among them and their relation with yield are necessary for a successful breeding program. As the yield potential of modern varieties has reached to a certain level, selection based on related characters to yield can help to get progenies having high yield potential. Therefore, the present study was conducted to explore the characters highly responsible for high yield potential of transplanted amonrice.

MATERIALS AND METHODS

Twenty five genotypes including nine parents, eight crosses and their reciprocal crosses are evaluated. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Thirty days old seedlings were transplanted low land area using single seedling hill^{-1}. Fertilizer doses were 180:100:70:60 kg Urea, TSP, MP and Gypsum per hectare. Except urea all other fertilizers were used as basal dose and urea fertilizer was top dressed in three equal splits at 15, 30 and 45 days after transplant. Standard crop management practices were done as and when necessary. All data were taken from randomly selected ten plants from each plot. Yields were taken from whole plot crop cutting and converted it to ton hectare^{-1}. Genotypic variance ($\sigma^2 g$), phenotypic variance ($\sigma^2 p$), genotypic coefficient of variation (GCV %), phenotypic coefficient of variation (PCV %), heritability ($h^2 b$ %) and Genetic Advance (GA) were estimated by the formula suggested by [1]. Genotypic and phenotypic correlation coefficient and path coefficient analysis were done through Basica stat. The estimate of GCV and PCV were classified as low, medium and high [2]. The heritability was categorized as suggested by [3]. Again, genetic advance was classified by adopting the method [4].

RESULTS AND DISCUSSION

Genetic variability

Mean sum of square, range, variance components, coefficient of genotypic and phenotypic variations, heritability estimates and genetic advance are presented in Table 1. Mean sum of square for all the characters were highly significant except harvest index

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Email: rkganapati@hotmail.com

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due to genotypes indicated wide range of variability among the genotypes for these traits. The Genotypic variance (σ^2g), phenotypic variance (σ^2p), Genotypic Coefficient of Variation (GCV %), Phenotypic Coefficient of Variation (PCV %) were close to each other for the traits plant height (cm), panicle length (cm), thousand grain weight (g), filled grain panicle[-1] and yield (g/hill) which indicated less environmental influence and additive gene action for these traits.

But some differences were found for effective tillers hill[-1], panicle length (cm) and unfilled grain panicle[-1] indicating that environment had more influence on the expression of these characters. The highest GCV was found in harvest index (70.22), unfilled grain panicle[-1] (46.67) and grain yield plant[-1] (45.69 gm) indicated wide range of variability for these traits. Very little GCV was found in days to maturity (5.54) followed by panicle length (6.09 cm), fifty percent flowering (7.64) and internode length (10.90 cm) indicating lack of inherent variability and limited scope for improvement through selection for these traits among the tested genotypes. High h²b values were observed in all the characters except effective thousand grain weight. Broad sense heritability (h²b) indicates the effectiveness of selection is not always accompanied by high GA [5]. High h²b estimate with high GA for grain yield plant[-1], harvest index, unfilled grain plant[-1], grain panicle[-1] and tiller hill[-1] suggested that they were simply inherited traits governed by a few major genes or additive gene effects. While high h²b estimates with low GA for panicle length, fifty percent flowering, thousand grain weight, days to maturity, plant height, internode length and number of filled grain panicle[-1] indicated non additive type of gene action and genotype x environment (g x e) interaction plays a significant role in the expression of the trait. Harvest index and grain yield plant[-1] showed high GCV and h²b suggesting better scope for selection. Characters with high values of GCV and heritability indicating that they might transmit to their progenies and therefore, phenotypic selection based on these characters would be effective [6].

Character associations

Character association analysis among grain yield and yield contributing characters (Table 2) revealed that in most of the cases the genotypic correlation coefficient were higher than the respective phenotypic correlation coefficients. This indicated that the suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. Grain yield was found positively and significantly associated with tiller hill[-1], plant height both at genotypic and phenotypic levels and, harvest index, thousand grain weight had positive and significant association at only genotypic level and days to fifty percent flowering, days to maturity show negatively and highly significant both at genotypic and phenotypic levels. Similar associations in rice were also reported by [7]. Plant height showed significant and positive correlation with internode length, panicle length and show highly negative correlation with harvest index at both genotypic and phenotypic level. Similar associations in rice were also reported by [8]. Days to fifty percent flowering showed highly significant positive correlation with days to maturity and significant and negative correlation with tiller hill[-1], plant height, inter node length. Days to maturity showed highly significant negative correlation with tillers hill[-1] and plant height and positively significant correlation with harvest index. Tiller hill[-1] show highly significant and positive correlation with plant height at both genotypic and phenotypic level and exhibited significant positive and negative correlation with inter node length and harvest index respectively at genotypic level only. Panicle length had highly significant and positive association with grain panicle[-1] and unfilled grain panicle[-1] and highly significant positive association with filled grain panicle[-1] at genotypic level. Grain panicle[-1] showed highly significant positive association with unfilled grain per panicle and filled grain per panicle at genotypic level. However, the correlation study revealed that plant height, tiller hill[-1], harvest

Table 1: Estimation of statistical and genetic parameters of yield and its contributing traits of 25 rice genotypes.

Parameters	MSS	Range	σ^2g	σ^2e	σ^2p	GCV	PCV	h²b	GA
FF	96.67**	66-89	31.60	1.87	33.47	7.64	7.86	94.41	15.29
DM	102.21**	94-115	32.89	3.55	36.43	5.54	5.83	90.27	21.84
TH	10.38**	5 -13.8	2.87	1.79	4.65	18.10	23.06	61.61	29.26
PH	731.061**	95.4-158.6	233.81	29.62	263.44	11.31	12.01	88.76	21.96
INL	22.21**	18.8-30.3	7.34	0.23	7.57	10.90	11.07	96.93	22.10
PL	9.22**	1.2-31.5	2.62	1.36	3.98	6.09	7.51	65.76	10.17
GP	1863.58**	67-190.4	589.48	95.13	684.61	17.70	19.08	86.10	33.84
UFGP	677.11**	6.8-52.4	218.94	20.29	239.23	46.67	48.79	91.52	91.98
FGP	717.21**	71.4-137.4	202.55	109.57	312.12	13.50	16.75	64.89	22.40
HI	0.17	0.14-0.4	0.06	0.01	0.06	70.22	71.92	98.31	141.22
TGW	72.37**	19-42	18.18	17.83	36.01	14.42	20.29	50.49	21.11
GYP	**246.024****	**4.66-34.5**	**78.88**	**9.38**	**88.26**	**45.69**	**48.33**	**89.37**	**88.97**

*and **indicates significant at 5% and 1% level of significance.
(Fifty percent flowering=FF, Days to Maturity=DM, Plant height = PH, Number of tiller per hill = TH, Inter node length = INL, Panicle length = PL, Grain per panicle=GP, Unfilled grain per panicle =UFGP, Harvest Index = HI, filled grains per panicle= FGP, Thousand Grain weight=TGW, Grain yield per plant= GYP)

Table 2: Genotypic (rg) and phenotypic (rp) correlation coefficient among yield and its contributing traits of 25 rice genotypes.

Parameters		DM	TH	PH	INL	PL	GP	UFGP	FGP	HI	TGW	GYP
F F	rg	0.666**	-0.808**	-0.585**	-0.427*	-0.393	-0.225	-0.089	-0.291	0.33739	-0.403	-0.732**
	rp	0.623**	-0.611**	-0.534**	-0.416*	-0.303	-0.194	-0.083	-0.214	0.317	-0.279	-0.662**
DM	rg		-0.680**	-0.746**	-0.217	-0.369	-0.25	-0.102	-0.32	0.451*	-0.448	-0.839**
	rp		-0.534**	-0.668**	-0.203	-0.251	-0.207	-0.093	-0.225	0.425*	-0.332	-0.749**
TH	rg			0.710**	0.404*	0.212	0.076	-0.045	0.176	-0.467*	0.332	0.913**
	rp			0.458**	0.309	0.037	0.055	-0.059	0.133	-0.369	0.159	0.747**
PH	rg				0.529**	0.479*	0.217	0.153	0.211	-0.446*	0.359	0.807**
	rp				0.492*	0.364	0.177	0.139	0.141	-0.403*	0.219	0.719**
INL	rg					0.165	-0.044	0.02	-0.095	0.054	-0.003	0.388
	rp					0.155	-0.041	0.039	-0.095	0.051	-0.014	0.372
PL	rg						0.716**	0.688**	0.506**	-0.32	0.095	0.297
	rp						0.549**	0.562**	0.321	-0.236	-0.004	0.274
GP	rg							0.843**	0.829**	-0.35	-0.075	0.215
	rp							0.756	0.819	-0.328	-0.034	0.217
UFGP	rg								0.399*	-0.281	-0.107	0.044
	rp								0.244	-0.261	-0.127	0.051
FGP	rg									-0.305	-0.017	0.32
	rp									-0.258	0.061	0.277
HI	rg										0.086	0.421*
	rp										0.045	0.369
TGW	rg											0.453*
	rp											0.268

* and**indicates significant at 5% and 1% level of significance, rg and rp indicates genotypic and phenotypic correlation coefficient.

Table 3: Partitioning of genotypic correlation with grain yield into direct (bold) and indirect effect of yield contributing traits in 25 rice genotypes.

Parameters	FF	DM	T/H	PH	INL	PL	GP	UFGP	NFGP	HI	TGW	GYP
F F	0.3	-0.243	-0.652	-0.022	-0.048	0.018	0.12	-0.035	-0.142	0.025	-0.055	-0.73**
DM	0.2	-0.364	-0.549	-0.028	-0.024	0.017	0.133	-0.04	-0.156	0.033	-0.061	-0.84**
TH	-0.242	0.248	0.807	0.027	0.045	-0.01	-0.04	-0.017	0.086	-0.035	0.045	0.93**
PH	-0.175	0.272	0.573	0.038	0.06	-0.022	-0.115	0.059	0.103	-0.033	0.049	0.87**
INL	-0.128	0.079	0.326	0.02	0.113	-0.008	0.023	0.008	-0.046	0.004	0	0.38
PL	-0.118	0.134	0.171	0.018	0.019	-0.046	-0.381	0.267	0.247	-0.024	0.013	0.29
GP	-0.068	0.091	0.061	0.008	-0.005	-0.033	0.532	0.327	0.405	-0.026	-0.01	0.22
UFGP	-0.027	0.037	-0.036	0.006	0.002	-0.032	-0.449	0.388	-0.195	-0.021	-0.015	0.04
NFGP	-0.087	0.116	0.142	0.008	-0.011	-0.023	-0.441	0.155	0.488	-0.023	-0.002	0.32
HI	0.101	-0.164	0.377	-0.017	0.006	0.015	0.186	-0.109	-0.149	0.074	0.012	-0.42*
TGW	-0.121	0.163	0.268	0.014	0	-0.004	0.04	-0.041	-0.008	0.006	0.137	0.45*

Residual Effect= 0.164

index and thousand grain weights were the important characters to be considered in the selection for improvement of T-aman rice genotypes.

Path coefficient analysis

In correlation studies, with the increasing number of variables, the indirect association becomes complex and important. In such situation, path coefficient analysis is useful to find out direct and indirect causes of associations. Path coefficient analysis permits a critical examination to specific factors acting to produce a given correlation and measures the relative importance of each factor. From the results of path analysis (Table 3) it was evident that direct positive effects contributed by tiller hill[-1], number of filled grain panicle[-1] and thousand grain weight were high indicating that

among the component traits, these four characters contributed maximum for grain yield in rice. These four characters also showed significantly positive genotypic correlation with yield which indicates that selection based on these characters would to be effective. plant height showed negligible direct effect (0.038) but indirect positive effect via tiller per hill, days to maturity and number of filled grain panicle[-1] made highly positive significant genotypic correlation with yield (0.807). On the other hand unfilled grain panicle[-1] had also positive (negligible) direct effect but its indirect effect through other characters was mostly negative. Grain panicle[-1] showed insignificant positive direct effect (0.532) and insignificant positive genotypic correlation with yield which indicated that indirect causal factors are to be considered. Fifty percent flowering and harvest index show

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positive direct correlation and days to maturity showed negative direct correlation but all three are negatively significant to grain yield. The residual effect of the present study was 0.164, indicating that 15 percent of the variability in grain yield was contributed by the twelve component characters studied in this path analysis. Similar findings (R=0.766) was found by [9].This gave an impression that a more other characters than those involved in the present study might also contributed to yield. The genetic variability, correlation and path analysis showed that tiller per hill, plant height and thousand grain weights are the most important yield components in rice. Therefore, emphasis should be given on these characters for the selection of genotypes for higher grain yield in rice.

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