GENETIC ANALYSIS FOR PANICLE CHARACTERS IN DIALLEL CROSS OF RICE

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Abstract

An experiment was carried out to study the genetic components for eight panicle characters in rice using an 8-parent half diallel cross excluding reciprocals during Transplant Aman season, 2003. The parental genotypes used in the study were BRRI dhan29, BR4828-54-4-l-4-9, BRR1 dhan28, 1R8, Amol3, 1R65610-38-2-4-2-6-3, Minikit and ZhongYu7, which were chosen for their diversity in panicle characters. Hayman's analysis of variance (ANOVA) indicated importance of both additive and non-additive genetic components for all the panicle characters except dominance component for filled grains/secondary branches. The ANOVA showed unidirectional dominance for the characters viz, primary branch length, secondary branch length, primary branches/panicle, secondary branches/panicle and filled grains/primary branch, asymmetrical gene distribution for all the panicle traits except filled grains/secondary branch and residual dominance effects for all the panicle characters studied. Two out of eight panicle characters viz., primary branches/panicle and unfilled grains/ secondary branch followed the simple additive-dominance genetic model. The rest of the panicle characters showed nonallelic gene interaction or epistasis. According to Vr-Wr graph, partial dominance was involved in the action of genes governing the inheritance of primary branches/panicle, while complete dominance was involved in the inheritance of unfilled grains/secondary branch. Most of the dominant genes for primary branches/panicle belonged to other hand, 1R8 possessed most of the dominant genes, while 1R65610-38-2-4-2-6-3 possessed most of the recessive genes for unfilled grains/secondary branch. The estimates of components of variance demonstrated involvement of both additive and dominant components in the inheritance of primary branches/panicle and unfilled grains/secondary branch. The distribution of dominant and recessive genes was unequal in the parents for these two characters also. There was drastic influence of environment on these two panicle characters following simple additive-dominance genetic model. Heritability in narrow sense (h^2 ns) was very high for primary branches/panicle and unfilled grains/secondary branch.

Key Words: Genetic analysis, diallel cross, panicle characters, rice.

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Introduction

Rice, the major crop of Bangladesh, constitutes 94.38% of the total food grain (rice and wheat) production accounting for 26.7 million metric tons (Anonymous, 2004). Rice is the staple food and ranks first position by production among cereals in Bangladesh. Bangladesh is the fourth largest producer and consumer of rice in the world with an annual production ranging from *25* to 26 million metric tons (Bhuiyan *et al.,* 2002). The yield potential of current modem rice varieties in the tropics of Asia has stagnated recently. It is essential to improve the yield potential of modem rice varieties which can be accomplished through improving genetic potentiality of the genotypes. For another quantum jump in rice yield potential, we need to modify the present high yielding plant type. Panicle characters represent the most important part of rice plant type in respect of yield improvement. Bangladesh Rice Research Institute (BRRI) has so far developed a number of modem rice varieties suitable for different ecosystems. The yield potentials of these rice varieties vary due to the architecture of panicle. Yield increase in modem rice was possible through improvement of panicle characters viz, long panicles, high number of filled grains, more primary and secondary rachis, etc. (Seetharaman *et al.,* 1973). Hence, apart from yield and its component characters, emphasis should be given on panicle characters. But improvement of panicle characters requires investigation on their genetic system. Information on mode of inheritance and nature of genetic components of panicle characters in rice are very scanty (Mahmood *et al.,* 2004; Chang *et al.,* 1998; Kim, 1987). More information is required on these aspects. The mode of inheritance of different characters can be investigated following Hayman's (I 954a and 1954b) variance component analysis in diallel crosses. The present investigation has been undertaken with an attempt to study the mode of inheritance and nature of genetic components of eight panicle characters in an eight-parent half-diallel cross of rice.

Materials and Method

Eight genotypes of rice viz., BRRI dhan29, BR4828-54-4-1-4-9, BRRI dhan28, 1R8, Amol3, 1R65610-38-2-4-2-6-3, Minikit and ZhongYu7 with different panicle characters were crossed in diallel fashion excluding reciprocals. Twenty-eight F_1s and their parents were grown in a randomized complete block design with three replications at the experimental farm of Bangladesh Rice Research Institute, Gazipur in Transplant Aman season, 2003. Twenty five days old seedlings were transplanted with single seedling/hill at the spacing of 25cm $\times$ 20cm. The unit plot size was 2m $\times$ 2 rows. The recommended crop management for Transplant Aman season was followed. Observations on eight panicle traits were recorded from each replication. The lengths of primary and secondary branches of panicle were measured in cm from randomly selected panicles and

average data were used. Similarly, number of primary and secondary branches per panicle, filled and unfilled grains per primary and secondary branches of the panicles were determined. The data were analyzed for analysis of variance and Vr-Wr graph following Hayman (1 954a) and Hayman (1 954b). Components of genetic parameters were calculated following numerical approach of Jinks and Hayman (1953) based on Mather's notation (Mather and Jinks, 1982).

Results and Discussion

Preliminary ANOVA

The mean squares due **to** genotypes for all the panicle traits under present study were highly significant as shown by the preliminary ANOVA. The results indicated significant differences among 36 genotypes of the present diallel study, which was necessary for further analysis (Table 1). Genotypes were partitioned into parents (P), crosses (F_1) and parents vs. crosses (P vs. F_1) items. All the panicle traits showed significant mean squares due to parents and crosses from which significant differences among parents and crosses separately were obtained. The parents vs. crosses item was significant for primary branch length, secondary branch length, primary branches per panicle, secondary branches per panicle and filled grains per primary branch which detected the presence of significant overall heterosis in cross combination for the concerned characters.

Table 1. Preliminary analysis of variance (MS) for different panicle traits in an 8-parent diallel cross of rice

Item	df	Primary branch length (cm)	Secondary branch length (cm)	Primary branches/ panicle	Secondary branches/ panicle	Filled grains/ primary branch	Unfille grains/ primary branch	Filled grains/ secondary branch	Unfilled grains/ secondary branch
Replication	2	0.698	0.034	0.203	3.06	2.83	0.243	0.249	0.024
Genotype	35	3.336***	0.248***	4.573***	168.55***	16.20***	1.640***	0.225**	0.086***
P (Parent)	7	2.877***	0.187***	8.884***	87.70***	6.88*	1.926*	0.229*	0.099***
F_1	27	3.012***	0.231***	3.479***	177.48***	18.08***	1.609***	0.224**	0.86***
P vs. F_1	1	15.30***	1.134***	3.937**	493.60***	30.87**	0.467	0.240	0.000
Error	70	0.316	0.030	0.416	19.20	3.08	0.243	0.104	0.019

*p<0.05; **p<0.01; ***p<0.001

Morley Jones ANOVA

Highly significant mean squares due to the item a (additive component) and b (dominance component) were found for all the characters except for mean square due to 'b' for filled grains per secondary branch (Table 2). Hence, both additive and dominance genetic components were important in the inheritance of all the panicle traits except dominance component for filled grains/secondary branch. Significant item 'b' established the validity of further analysis of Vr-Wr graph.

Table 2. Hayman analysis of variances (MS) following Morley Jones modification for different panicle traits in an 8-parent diallel cross of rice.

Item	df	Primary branch length (cm)	Secondary branch length (cm)	Primary branches/ panicle	Secondary branches/ panicle	Filled grains/ primary branch	Unfille grains/ primary branch	Filled grains/ secondary branch	Unfilled grains/ secondary branch
a	7	2.622***	0.222***	4.937***	114.04***	12.97***	1.037***	0.174***	0.055***
b	28	0.734***	0.048***	0.671***	41.72***	3.51***	0.24***	0.050	0.022***
B_1	1	5.100***	0.378***	1.312**	164.53***	2.98**	0.156	0.080	0.000
B_2	7	0.608*	0.049***	0.446**	28.38***	2.98*	0.555***	0.058	0.033***
B_3	20	0.560***	0.031***	0.718***	40.25***	3.36***	0.391***	0.046	0.019***
Error	70	0.105	0.010	0.139	6.40	1.03	0.081	0.035	0.006

*p<0.05; **p<0.01; ***p<0.001

Item b_1 was highly significant for primary branch length, secondary branch length, primary branches per panicle, secondary branches per panicle and filled grains per primary branch, which detected unidirectional dominance and significant differences between parental and hybrid grand mean for these five characters. Again, asymmetrical gene distribution was obtained for all the panicle traits expect filled grains per secondary branch as item b_2 was significant for the respective characters. Finally, item b_3, representing residual dominance effects, was significant for all the studied panicle traits indicating the involvement of the part of dominance deviation which did not belong to b_1 and b_2. The significant b_3 also showed dominance effects specific to individual crosses (Mather and Jinks, 1982).

Vr-Wr graph

Statistics related to Vr-Wr analysis showed that out of eight panicle traits, only two traits (primary branches per panicle and unfilled grains per secondary branch) satisfied the assumptions related to the simple additive-dominance genetic model (Table 3). The rest of the panicle traits exhibited nonallelic gene interaction or epistasis. Kim (1987) obtained nonallelic gene interactions for all

the panicle traits he studied. While Chang *et al.* (1998) reported epistasis for number of primary branches per panicle and number of spikelets per panicle, but they explained the inheritance of primary branch length using the additive-dominance genetic model. The Vr-Wr graph and Hayman's numerical approach have been, therefore, subjected for primary branches per panicle and unfilled grains per secondary branch only.

Tabele 3. Statistics related to Vr-Wr analysis for different panicle traits in an 8-parent diallel cross of rice.

Character	a	b	SE (b)	b=1	b=0	t^2	Significance of t^2
Primary branch length (cm)	0.114	0.313	0.200	*	ns	2.72	ns
Secondary branch length (cm)	0.015	0.248	0.258	*	ns	1.093	ns
Primary branch/ panicle	0.1912	0.845	0.262	ns	*	0.058	ns
Secondary branch/ panicle	-3.728	0.361	0.146	**	ns	6.45	*
Filled grains/ primary branch	2.665	-0.250	0.155	**	ns	6.57	*
Unfilled grains/primary branch	-0.111	0.530	0.268	ns	ns	0.288	ns
Filled grains/ secocondary	-0.0010	0.411	0.278	ns	ns	0.435	ns
Unfilled grains/ secondary branch	-0.012	0.733	0.275	ns	*	0.000	ns

The regression line for primary branches per panicle intercepted Wr-axis above the origin with the 'a' value of 0.1912 indicates partial dominance in the inheritance of primary branches per panicle (Fig. 1). For unfilled grains per secondary branch, the regression line seemed to intercept below the origin (Fig. 2). This was because of too smaller values of Vr and Wr. Actually, on the basis of the value 'a' for this character (—0.012), more or less complete dominance could be considered for unfilled grains per secondary branch. The position of the array point for BRRI dhan29 was nearest to the origin, which implicated that most of the dominant genes for primary branches per panicle belonged to BRRI dhan29. On the other hand, Amol3 contained most of the recessive genes for the same character as array point for Amol3 was placed farthest from the origin. On the same background, 1R8 possessed the most of the dominant genes, while 1R65610-38-2-4-2-6-3 possessed most of the recessive genes for unfilled grains per secondary branch.

Components of variance

The estimates of components of variance reflected that both additive (D) and dominance variance (H_1 and h_2) were all highly significant (Table 4) for primary

branches per panicle and unfilled grains/secondary branch. The results indicated the importance of both additive and non-additive genetic variance in the inheritance of these two characters. Mahmood *et al.* (2004) reported that additive genetic effects were important for the expression of variation of number of primary branches per panicle in an 8-parent diallel cross of rice.
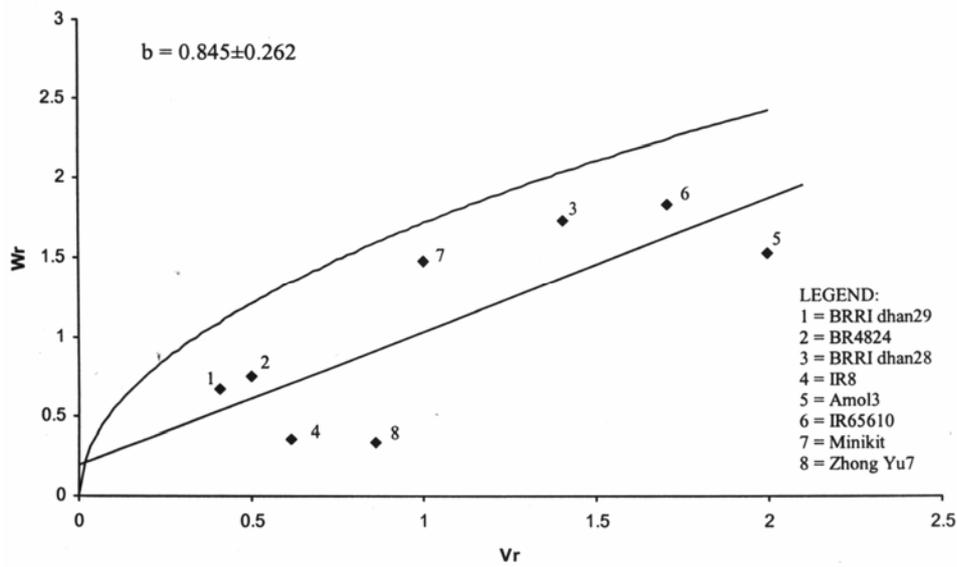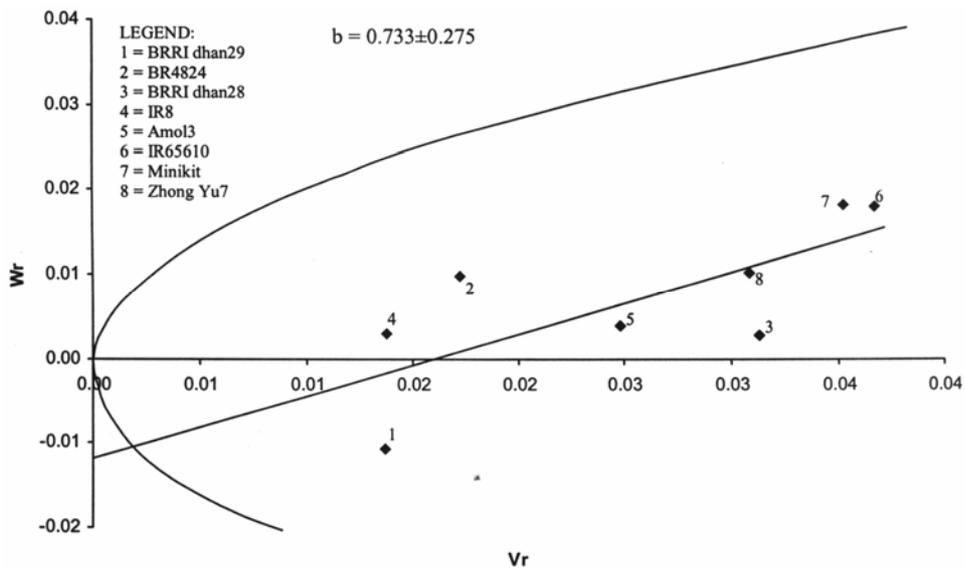

Fig 1. Vr-Wr graph for primary branch/ panicle

Fig 2. Vr-Wr graoh for unfilled grains/ secondary branch

Table 4. Components of variance and genetic parameters for panicle characters in an 8-parent diallel cross of rice.

Components	Primary branch number	Unfilled grains/ secondary branch
E	$0.137^{***}\pm0.0005$	$0.00065^{***}\pm0.00001$
D	$2.82^{***}\pm0.0016$	$0.0266^{***}\pm0.00003$
F	$1.36^{***}\pm0.0038$	$0.0290^{***}\pm0.00007$
H_1	$2.13^{***}\pm0.0032$	$0.0631^{***}\pm0.00007$
H_2	$2.16^{***}\pm0.0032$	$0.0631^{***}\pm0.00006$
h^2	$1.55^{***}\pm0.0021$	$-0.0202^{***}\pm0.00004$
$\sqrt{D/H_1}$	0.121	0.707
$H_2/4H_1$	12.99	1.18
$\dfrac{\sqrt{4DH_1+F}}{\sqrt{4DH_1-F}}$	3.03	7.69
r_{xy}	-0.858^{**}	0.118
r^2	0.737	0.014
h^2/H_2	0.716	0.320
h^2_{nn}	0.978	0.18

*p<0.05; **p<0.01; ***p<0.001

Inequality of the two components H_1 and H_2 for primary branches per panicle and unfilled grains per secondary branch indicated unequal distribution of positive and negative alleles in the parents for these two characters. These findings were further established by the $H_2/4H_1$ ratio being highly deviated from 0.25. Significant h_2 indicated net dominance effect for all loci which was 1.55 and -0.0202 for primary branches per panicle and unfilled grains per secondary branch, respectively. The mean degree of dominance ($\sqrt{H_1/D}$) was less than unity for primary branches per panicle indicating partial dominance. The same value for unfilled grains per secondary branch could be taken as unity indicating complete dominance.

The influence of environment on two panicle traits was drastic as the component E was significant for these two characters. Primary branches per panicle and unfilled grains per secondary branch showed positive sign for the

component F which meant that dominant alleles were more frequent than recessive alleles in the parents for the two characters. The results were confirmed by the ratio $(\sqrt{4DH_1} + F) (\sqrt{4DH_1} - F)$ which were greater than unity for the respective traits.

The correlation coefficient (r) between parental measurement (Yr) and parental order of dominance (Wr + Vr) was highly significant and negative indicating recessive alleles to have positive effects for primary branches per panicle. Again, positive correlation coefficient for unfilled grains per secondary branch in the present study revealed that the parents containing most decreasing genes had the lowest values of Wr, + Vr, and thus decreasing genes were prevalent in them (Singh and Chaudhary, 1985). The prediction of completely dominant and recessive parents were not possible, which was revealed from less than unity r^2 estimates for the two panicle traits in rice.

Number of blocks of dominant genes was estimated from h^2/H_2 ratios, which were 0.716 and 0.320 for primary branches per panicle and unfilled grains per secondary branch, respectively. The narrow sense heritability was very high for these two characters.

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