GENETIC COMPONENTS OF GRAIN CHARACTERS IN RICE (*Oryza sativa* L.)

K. M. Iftekharuddaula[1], M. A. Newaz[2], P. S. Biswas[1] and M. K. Bashar[3]

[1]Plant Breeding Division, [3]Genetic Resources & Seed Division,
Bangladesh Rice Research Institute, Gazipur-1701
[2]Dept of Genetics and Plant Breeding, Bangladesh Agricultural University,
Mymensingh-2202
Corresponding author's email: kiftekhar03@yahoo.com

ABSTRACT

Hayman's analysis of variance (ANOVA) indicated importance of both additive and non-additive genetic components for all the grain characters. The ANOVA showed unidirectional dominance for the characters viz. kernel breadth, upper empty glume length and endosperm-embryo ratio, asymmetrical gene distribution for the characters viz. grain length, grain breadth, kernel length, kernel breadth and kernel thickness and residual dominance effects for all the grain characters studied. Five out of nine grain characters viz. grain breadth, grain thickness, kernel breadth, kernel thickness and upper empty glume length followed the simple additive-dominance genetic model. The rest of the grain 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 grain breadth, grain thickness, kernel breadth and kernel thickness while complete dominance was involved in the inheritance of upper empty glume length. BR4828-54-4-1-4-9 contained the most of the recessive genes for four characters except upper empty glume length while Amol3 appeared to possess most of the recessive genes. On the other hand, Minikit for grain breadth, Amol3 for grain thickness and BRRI dhan29 for kernel breadth, kernel thickness and upper empty glume length possessed most of the dominant genes for the respective characters. The components of variance demonstrated involvement of both additive and dominant components in the inheritance of grain breadth, grain thickness, kernel breadth, kernel thickness and endosperm-embryo ratio. The distribution of dominant and recessive genes was unequal in the parents for grain breadth, kernel breadth, grain thickness, kernel thickness and upper empty glume length. Again, net dominance effects were in the negative direction for all the grain characters. There was drastic influence of environment on all the five grain characters following simple additive-dominance genetic model. Heritability in narrow sense (h^2_n) was very high for grain breadth, grain thickness, kernel breadth and kernel thickness. However, h^2_n for upper empty glume length was moderate.

Key words: Rice (*Oryza sativa* L.), variance-covariance analysis, genetic components, diallel cross, grain character

INTRODUCTION

Development of modern rice varieties was concentrated on increasing yield potential of the genotypes without much considering grain characters. But the acceptability of modern rice varieties depends largely on grain characters. Even the breeding program with the target of improving yield potential of the genotypes also depends on grain character because it is possible to increase the yield potential of genotypes by increasing grain characters like weight of each grain keeping all other yield contributing parameters unchanged. There are considerable variations among rice

consumers in respect of size and shape of the grains. For example, bold grains are preferred by people in the southern districts while fine grains are preferred in the northern region of Bangladesh. Interestingly, daily laborers prefers bold grain as they claim that bold rice remain in their stomach comparatively longer period. Furthermore, there is demand of long slender grain in the export market. So, proper emphasis should be given on the grain characters in addition to yield potential of the genotypes. But improvement of grain characters requires investigation on their genetic system. Information on mode of inheritance and components of genetic variances of grain characters in rice are very scanty (Verma *et al*., 1994 and Kuo *et al.*, 1988). More information is required on these aspects. One of the popular methods to study the mode of inheritance of the different characters is the diallel analysis following Hayman's (1954a and 1954b) variance component analysis. In the present investigation, attempt has been made to study the mode of inheritance and nature of genetic components of nine grain characters in an eight parent half-diallel cross of rice (*Oryza sativa* L.).

MATERIALS AND METHODS

Eight genotypes of rice viz. BRRI dhan29, BR4828-54-4-1-4-9 (BR4828), BRRI dhan28, IR8, Amol3, IR65610-38-2-4-2-6-3 (IR65610), Minikit and ZhongYu7 with different grain characters were crossed in an 8 X 8 diallel fashion excluding reciprocals. Eight parents with their twenty eight F_1s 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 day old seedlings were transplanted @ single seedling/hill in a spacing of 25 X 20cm. The unit plot size was 2m X 2 rows. Data of 10 grains from 10 random panicles were recorded on grain length (mm), grain breadth (mm), grain thickness (mm), kernel length (mm), kernel breadth (mm), kernel thickness (mm), upper empty glume length (mm), lower empty glume length (mm) and endosperm weight (g) and embryo weight (mg). Grain and kernel length, breadth and thickness were measured by a digital slide caliper while micrometer was used for the measurement of upper and lower empty glume length. Endosperm and embryo weight were taken using sensitive electronic balance and later on converted into endosperm-embryo ratio. Moisture content of endosperm was measured by moisture meter and adjusted at 14% moisture content. The data were analyzed for analysis of variance and Vr-Wr graph following Hayman (1954a) and Hayman (1954b). 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
Hayman analysis of variance

Significant mean squares due to additive (a) and dominant (b) components were obtained for all the grain characters studied (Table 1). The results indicated that both the additive and dominance components were involved in the inheritance of all the grain characters. Moreover, significance of b permits for advancing towards the further analysis of Vr-Wr graph. Dominant component (b_1) detects the difference between mean of F_1 and parent and also unidirectionality of dominance assuming that there is no epistasis. In the present study of grain characters, b_1 was significant for kernel breadth, upper empty glume length and endosperm-embryo ratio which indicated unidirectional dominance and significant difference between parental and hybrid mean for these three characters. Asymmetrical gene distribution was found for grain length, grain breadth, kernel length, kernel breadth and kernel thickness as b_2 was significant for these characters.

Table 1. Hayman analysis of variances (MS) following Morley Jones modification for grain characters in an eight parent diallel cross of rice

Item	df	Grain length (mm)	Grain breadth (mm)	Grain thickness (mm)	Kernel length (mm)	Kernel breadth (mm)	Kernel thickness (mm)	Upper empty glume length (mm)	Lower empty glume length (mm)	Endosperm-embryo ratio
a	7	1.119**	0.287**	0.033**	0.672**	0.226**	0.031**	0.094**	0.157**	116.88**
b	28	0.048**	0.006**	0.001*	0.029**	0.005**	0.001**	0.014*	0.013*	32.47**
b_1	1	0.016	0.006	0.001	0.020	0.008**	0.002	0.076**	0.012	58.65*
b_2	7	0.062**	0.006*	0.001	0.054**	0.005**	0.002*	0.010	0.013	19.29
b_3	20	0.045**	0.006**	0.001*	0.021**	0.005**	0.001**	0.013*	0.013*	35.77**
Error	70	0.010	0.002	0.001	0.007	0.001	0.001	0.006	0.007	9.08

*p <0.05; **p <0.01

Table 2. Statistics related to Vr-Wr analysis for nine grain characters in an eight parent diallel cross of rice

Characters	a	b	SE (b)	Significance level (b=1)	Significance level (b=0)	t^2	Significance of t^2
Grain length (mm)	0.082	0.642	0.142	*	**	2.70	ns
Grain breadth (mm)	0.028	0.923	0.083	ns	**	0.421	ns
Grain thickness (mm)	0.0028	0.826	0.098	ns	**	1.758	ns
Kernel length (mm)	0.045	0.600	0.095	**	**	9.40	**
Kernel breadth (mm)	0.022	0.909	0.094	ns	**	0.40	ns
Kernel thickness (mm)	0.002	0.808	0.126	ns	**	1.002	ns
Upper empty glume length (mm)	-0.0016	0.805	0.172	ns	**	0.260	ns
Lower empty glume length (mm)	0.005	0.621	0.136	*	**	3.425	ns
Endosperm-Embryo ratio	0.658	0.414	0.224	*	ns	1.385	ns

ns-nonsignificant; *p <0.05; **p <0.01

Component b_3, representing residual dominance effects, was significant for all the characters studied which detected the involvement of the part of dominance deviation which were not attributable to b_1 and b_2. The significant b_3 also showed that there were dominance effects specific to individual crosses (Mather and Jinks, 1982).

**Table 3. Genetic variance components and allied genetic parameters for grain characters in an eight parent diallel cross of rice**

Components	Grain breadth (mm)	Grain thickness (mm)	Kernel breadth (mm)	Kernel thickness (mm)	Upper empty glume length(mm)
E	0.0019*** ±0.00001	0.0007*** ±0.000001	0.0008*** ±0.000001	0.0006*** ±0.000001	0.0073*** ±0.00001
D	0.1263*** ±0.00002	0.0125*** ±0.000002	0.1013*** ±0.00002	0.0122*** ±0.000003	0.0272*** ±0.00002
F	0.0183*** ±0.00004	-0.0006*** ±0.000005	0.0170*** ±0.00004	0.0008*** ±0.000008	-0.0072*** ±0.00005
H_1	0.0005*** ±0.00004	-0.0008*** ±0.000005	0.0023*** ±0.00004	-0.0002*** ±0.000008	-0.0104*** ±0.00005
H_2	0.0167*** ±0.00003	0.0025*** ±0.000005	0.0174*** ±0.00003	0.0039*** ±0.000007	0.0336*** ±0.00005
h^2	-0.1142*** ±0.00002	-0.0497*** ±0.000003	-0.1293*** ±0.00002	-0.0575*** ±0.000005	-0.3905*** ±0.00003
$\sqrt{H_1/D}$	0.064	0.253	0.150	0.13	0.619
$H_2/4H_1$	8.015	0.751	1.90	4.781	0.808
$\dfrac{\sqrt{4DH_1}+F}{\sqrt{4DH_1}-F}$	16.30	0.838	3.53	1.71	0.65
r_{xy}	0.795*	0.352	0.816*	0.41	0.774*
r^2	0.632	0.124	0.666	0.168	0.598
h^2/H_2	6.847	19.805	7.411	14.73	11.634
h^2_n	0.961	0.842	0.978	0.905	0.510

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

Vr-Wr graph

Vr-Wr analysis showed that five out of nine grain characters viz. grain breadth, grain thickness, kernel breadth, kernel thickness and upper empty glume length followed the simple additive- dominance genetic model (Table 2). The rest of the grain characters showed nonallelic interaction or epistasis. Verma *et al*. (1994) reported nonallelic interaction for grain length in rice.
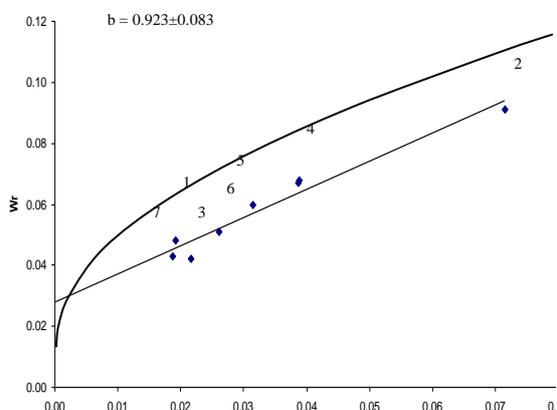
Fig 1. Vr-Wr graph for grain breadth [1 = BRRI dhan29, 2 = BR4828, 3 = BRRI dhan28. 4 = IR8. 5 = Amol3. 6 = IR65610. 7 = Minikit. 8 = Zhong Yu7]
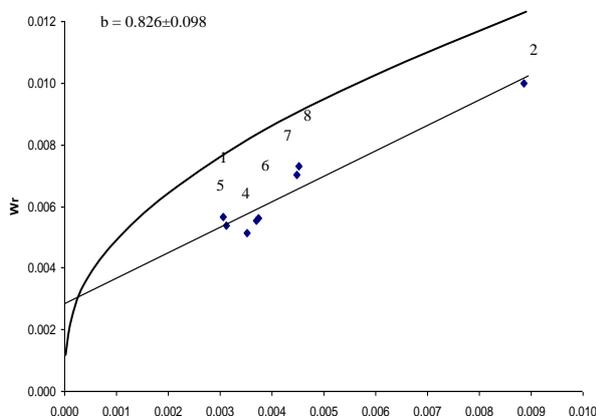
Fig 2. Vr-Wr graph for grain thickness [1 = BRRI dhan29, 2 = BR4828, 3 = BRRI dhan28, 4 = IR8, 5 = Amol3, 6 = IR65610, 7 = Minikit, 8 = Zhong Yu7]
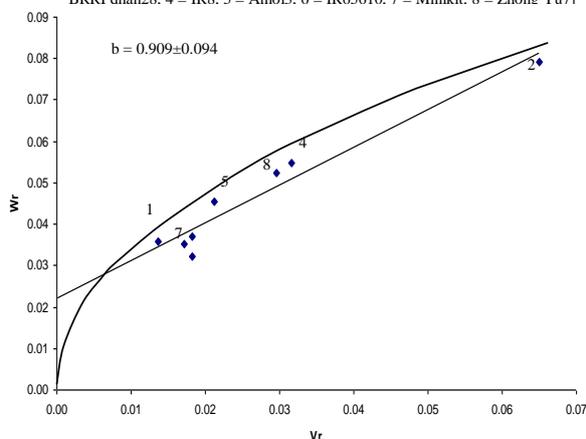
Fig 3. Vr-Wr graph for kernel breadth [1 = BRRI dhan29, 2 = BR4828, 3 = BRRI dhan28, 4 = IR8, 5 = Amol3, 6 = IR65610, 7 = Minikit, 8 = Zhong Yu7]
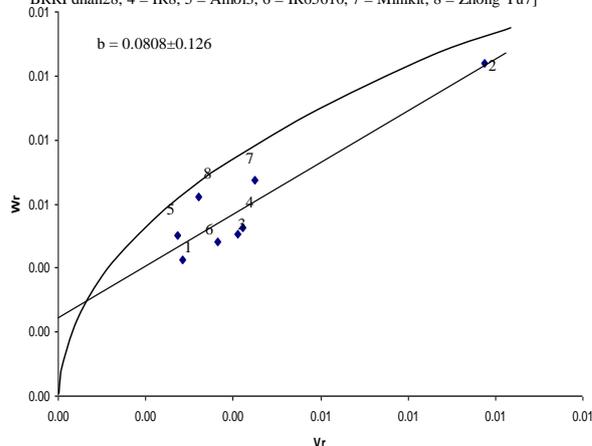
Fig 4. Vr-Wr graph for kernel thickness [1 = BRRI dhan29, 2 = BR4828, 3 = BRRI dhan28, 4 = IR8, 5 = Amol3, 6 = IR65610, 7 = Minikit, 8 = Zhong Yu7]
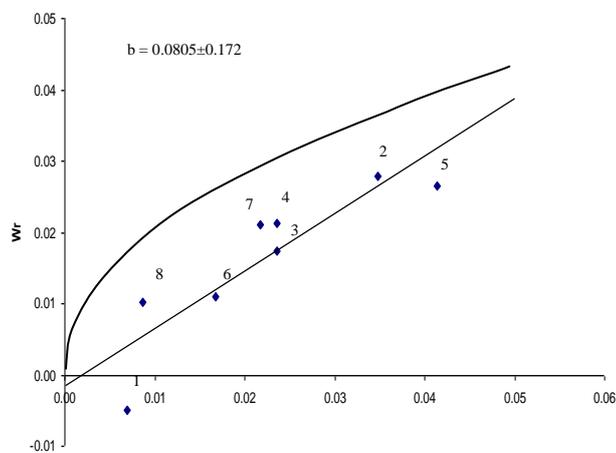

Fig 5. Vr-Wr graph for upper empty glume length [1 = BRRI dhan29, 2 = BR4828, 3 = BRRI dhan28, 4 = IR8, 5 = Amol3, 6 = IR65610, 7 = Minikit, 8 = Zhong Yu7]

The regression line for grain breadth, grain thickness, kernel breadth and kernel thickness intercepted Wr-axis above the origin with the 'a' values of 0.028, 0.0028, 0.022 and 0.002, respectively (Fig. 1-4). Hence, partial dominance was involved in the inheritance of these four characters. For upper empty glume length, regression line intercepted more or less near the origin with the 'a' value −0.0016 indicating complete dominance for the concerned character (Fig. 5). Kuo *et al.* (1988) reported partial dominance for grain breadth and grain thickness in rice.

The relative proportion of dominant and recessive alleles present in the common parent of each array determines the position of array points along the regression line. Vr-Wr graph for grain breadth (Fig. 1) showed that the array point for BR4828-54-4-1-4-9 was far away from rest of the array points indicating BR4828-54-4-1-4-9 was genetically diversed from the rest of the parents for grain breadth. BR4828-54-4-1-4-9 was also genetically diversed than other parents for grain thickness, kernel breadth and kernel thickness. Sharma (1998) stated that array points scattered all along the regression line in Vr-Wr graph would indicate genetic diversity among parents. Not only that, out of five characters BR4828-54-4-1-4-9 contained the most of the recessive genes taking the farthest position from origin for four characters except upper empty glume length whereas Amol3 appeared to possess maximum amount of recessive genes. On the other hand, Minikit for grain breadth, Amol3 for grain thickness and BRRIdhan29 for kernel breadth, kernel thickness and upper empty glume length possessed the most of the dominant genes for the respective characters as they took the nearest position from the origin.

Genetic variance components

The estimates of components of variance indicated that both additive variance (D) and dominance variance (H_1 and h^2) were all highly significant (Table 3) for grain breadth, grain thickness, kernel breadth, kernel thickness and endosperm:embryo ratio. The results detected the importance of both additive and dominance variance for the inheritance of all these characters. However, additive component (D) was much higher than the dominant component (H_1) for grain breadth, grain thickness, kernel breadth and kernel thickness indicating preponderance of additive components in the inheritance of all the traits. It is expected from the result that their genetic advance through single plant selection would be quite rewarding.

The component H_1 and H_2 were unequal for grain breadth, kernel breadth, grain thickness, kernel thickness and upper empty glume length indicating unequal distribution of positive and negative alleles in the parents for all of those characters. The ratios $H_2/4H_1$ were deviated from 0.25 which also established these findings. Again net dominance effects were in the negative direction for all the traits. Direction of dominance components was also negative for all the characters except grain and kernel breadth in which the amount of dominance components were too smaller. Drastic influence of environment on all the five grain characters was obtained since the component E was significant for all the respective characters.

The ratio $\sqrt{H_1/D}$ representing mean degree of dominance over all loci was less than one for all the characters except upper empty glume length indicating partial dominance for these four characters which were supported by the positive Y-intercept in Vr-Wr graph for all of these characters.

For grain breadth, kernel breadth and kernel thickness the sign of F was positive which meant that dominant alleles were more frequent than recessive alleles for the concerned character. The results were confirmed by the ratio ($\sqrt{4DH_1}$ + F) / ($\sqrt{4DH_1}$ −

F) which were greater than unity for the respective traits. On the contrary, F value showed negative sign for grain thickness and upper empty glume length indicating more frequencies of recessive alleles for the respective traits. The findings were accordingly confirmed by the less than unity ratio for ($\sqrt{4DH_1}$ + F) / ($\sqrt{4DH_1}$ − F). Number of blocks of dominant genes was 6.847, 19.81, 7.41, 14.73 and 11.63 for grain breadth, grain thickness, kernel breadth, kernel thickness and upper empty glume length, respectively, which were estimated by h^2/H_2 ratio.

Significant positive correlation coefficients were found for grain breadth, kernel breadth and upper empty glume length which reflected that most of the dominant alleles for these characters acted in one direction and recessive alleles in the other direction. The r^2 estimates were deviated from unity which made impossible to predict completely dominant and recessive parent for all of these five grain characters.

Heritability in narrow sense (h^2_n) was very high for grain breadth, grain thickness, kernel breadth and kernel thickness. The high narrow sense heritability also indicated the preponderance of additive components for these characters which confirmed the previous similar findings of D and H_1 components. However, h^2_n for upper empty glume length was moderate. High narrow sense heritability for grain length and grain breadth were also reported by Fu *et al.* (1994) and Kuo and Liu (1986) in rice.

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