

GENE ACTION OF AGRONOMIC TRAITS IN RICE (*Oryza sativa* L.)

P. S. Biswas and M. Enamul Haque

Plant Breeding Division
Bangladesh Rice Research Institute
Gazipur-1701, Bangladesh

ABSTRACT

Six parent diallel cross without reciprocal was studied to investigate the genetic behavior of different agronomic traits in rice. The analysis of W_r-V_r graph showed that panicle length, thousand grain weight and grain yield per plant did not follow the additive-dominance model indicating epistatic gene action responsible for the expression of these traits. All other traits under the study were conditioned by overdominance gene action except grains per panicle, which was controlled by partial dominance. The $Y_r' - (V_r + W_r)'$ graph revealed random distribution of dominant and recessive gene in expressing different traits in different parent, while correlation between parental mean and parental order of dominance indicated increasing effect of dominant gene for all the traits except days to heading and % spikelet sterility.

Key words: Rice (*Oryza sativa* L), $V_r - W_r$, gene action, agronomic traits, yield.

INTRODUCTION

Since the green revolution of 1960s semi-dwarf rice varieties are mostly cultivated elsewhere in the world and the yield of such varieties has arrived at plateau. To ensure food security to the poor people in the developing countries, the productivity of rice must be increased in unit area. Exploitation of hybrid vigor, development of new plant type, introgression of foreign genes related to biotic and abiotic stresses may be some of the alternatives to have a breakthrough in this regard. Improvement of rice variety through the above techniques requires perfect knowledge of genetic background of the economic traits in rice plant. Therefore, an attempt has been undertaken to investigate the genetic behavior of different agronomic traits in rice.

MATERIALS AND METHODS

A 6×6 diallel (without reciprocal) cross was made using six advanced breeding lines (IR55166-4R-215-1 (P_1), DWC-B-14-X-1-6 (P_2), IR64588-47-2B-12-1-2-3 (P_3), IR11141-6-R-1-4 (P_4), IR60436-B-65-2 (P_5) and BR683-65-4-1-1 (P_6)). Fifteen F_1 hybrids along with their parents were grown following randomized complete block design with two replications in the net house of Bangladesh Rice Research Institute in T. Aman 2004. The unit plot size was $2.5m \times 2$ rows. Thirty days old single seedling was transplanted with a spacing of 20×15 cm. Data from each entry on different agronomic traits viz., days to heading, plant height (cm), leaf area index, panicles per plant, filled grains per panicle, % spikelet sterility, 1000 grain weight (g) and grain yield per plant (g) were collected from 10 randomly selected plants. The collected data were analysed following graphical approach of Hayman (1954). Standardized values were calculated as suggested by Johnson and Askel

(1959). The interpretations was made as per Dhabolkar (1992), Sharma (1998) and Mather and Jinks (1949).

RESULTS AND DISCUSSION

The analysis of variance revealed significant variations among the entries for all the traits under study (Table 1). The analysis of all arrays for Wr-Vr graph showed that regression coefficients did not differ significantly from unity except days to heading and panicles per plant. But exclusion of array(s) satisfied the simple additive-dominance model for days to heading and panicles per plant (Table 2). Panicle length, thousand grain weight and yield per plant did not satisfy the simple additive-dominance model even after excluding one or more array(s). This indicated that thousand grain weight and grain yield per plant might be conditioned by epistatic gene action. Iftekharuddaula (2003) also observed similar finding in grain yield of rice.

Table 1. Analysis of variance in 6 × 6 diallel for ten characters in rice

Source of variation	df	Days to heading	Plant height	Flag leaf area	Leaf area index	Panicles/plant	Panicle length	Filled grain/panicle	% spikelet sterility	1000 grain weight	Yield/plant
Replication	1	0.381	71.188	20.22	5.13	0.086	0.236	4.56	6.19	0.283	0.754
Treatment	20	96.45**	1606.29**	237.18**	9.47**	8.05**	27.66**	2395.14**	191.48**	9.71**	131.81**
Parent (P)	5	81.55**	2294.47**	410.47**	2.5	8.56**	20.54**	1940.67**	221.26**	6.65**	67.93*
Cross (C)	14	86.98**	1464.36**	183.76**	9.89**	7.19**	31.57**	2387.9**	139.36**	11.33**	249.9**
P vs C	1	303.45**	152.33*	118.62*	38.5**	17.67**	8.59*	4768.82**	772.27**	2.36*	35.13**
Error	20	2.33	29.34	24.59	2.84	0.698	1.06	49.8	42.3	0.528	5.91

*, ** significance level of probability at 5% and 1%, respectively

Table 2. Statistic required for adequacy of simple additive dominance model

Parameter	Days to heading	Plant height	Flag leaf area	Leaf area index	Panicles/plant	Panicle length	Filled grain/panicle	% spikelet sterility	1000 grain weight	Yield/plant
Vr	49.05	528.34	81.20	4.29	5.07	9.96	897.78	67.75	3.49	101.58
Wr	29.38	483.38	74.03	0.80	2.95	7.84	591.81	44.19	2.53	16.96
t _(b=0)	3.33*	4.55*	6.09**	3.36*	9.80**	5.84**	4.41*	3.29*	2.04 ^{ns}	0.24 ^{ns}
t _(b=1)	0.78 ^{ns}	0.34 ^{ns}	-0.39 ^{ns}	0.33 ^{ns}	0.81 ^{ns}	2.89*	2.58 ^{ns}	0.16 ^{ns}	2.04 ^{ns}	3.52*
r	0.779	-0.35	-0.064	-0.294	-0.747	0.208	-0.842*	0.646	0.05	0.035

*, ** significance level of probability at 5% and 1%, respectively; ns = not significant

Regression coefficient ($b=0.685\pm 0.291$) for days to heading was neither significantly different from unity nor zero. However, elimination of array 1 for P₁ gave a regression coefficient, $b=0.811\pm 0.243$ (Fig.1a), which was significantly different from zero but not from unity, suggested additive genetic system and the parent P₁ contained the epistatic genes. The regression line intercepted Wr axis below the origin ($a = -10.39$) indicating overdominance gene action for the trait. In the Wr-Vr graph, P₂ occupied the closest position to the point of origin indicating preponderance of dominant gene, while P₄ possessed the farthest from the origin followed by P₆ suggested recessive gene action for expressing the trait. The parents P₃ and P₅ were at the intermediate position in the Wr-Vr graph indicating almost equal control of dominant and recessive gene. The Y' - (Vr + Wr)' graph (Fig.1b) suggested similar predominance of dominant alleles in P₂ with positive effect and recessive

alleles in P_4 with negative effect. However, the positive correlation ($r = 0.779$) between parental mean and parental order of dominance revealed decreasing effect of dominant gene i.e. early heading was apparently dominant over late heading.

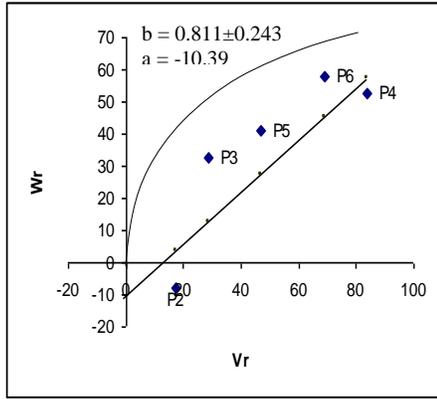


Fig. 1a. W_r - V_r graph for days to heading (array 1

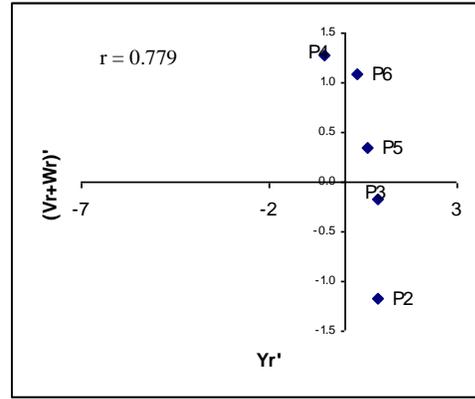


Fig. 1b. $Y_r'-(V_r+W_r)'$ graph for days to

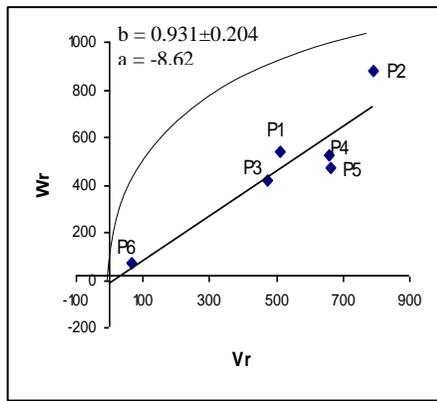


Fig. 2a. W_r - V_r graph for plant

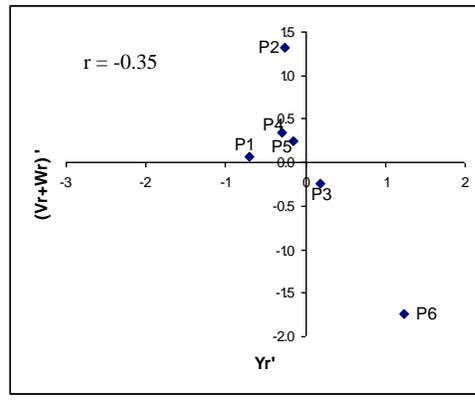


Fig. 2b. $Y_r'-(V_r+W_r)'$ graph for

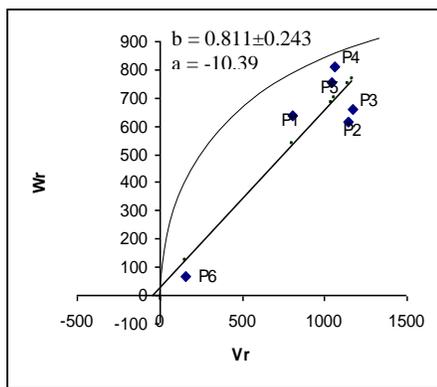


Fig. 3a. W_r - V_r graph for flag leaf area

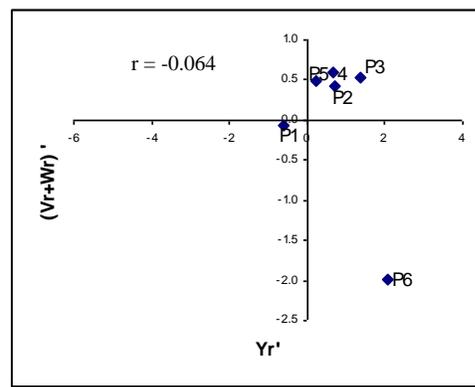


Fig. 3b. $Y_r'-(V_r+W_r)'$ graph for flag leaf

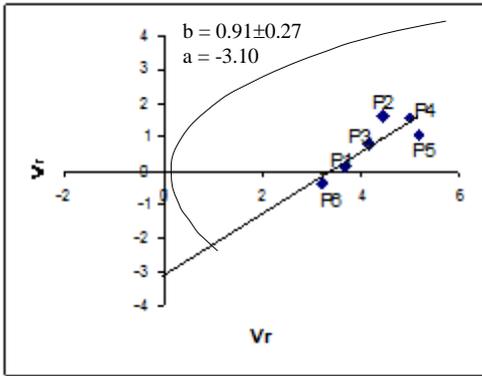


Fig. 4a. W_r - V_r graph for leaf area index

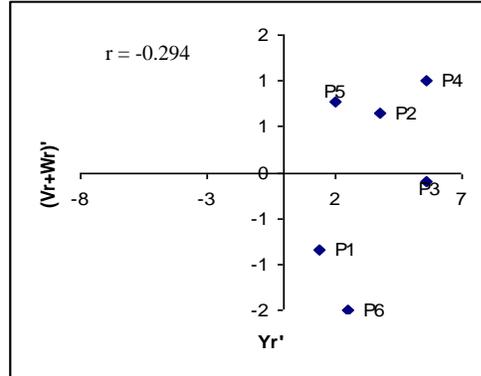


Fig. 4b. $Y_r'-(V_r+W_r)'$ graph for leaf area

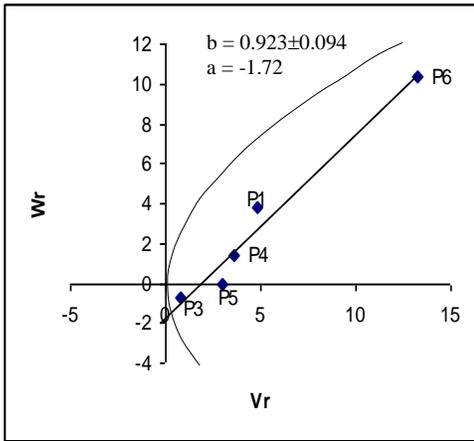


Fig. 5a. W_r - V_r graph for panicles/plant

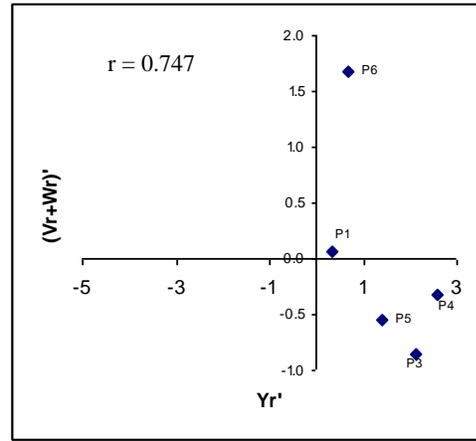


Fig. 5b. $Y_r'-(V_r+W_r)'$ graph for panicles/plant

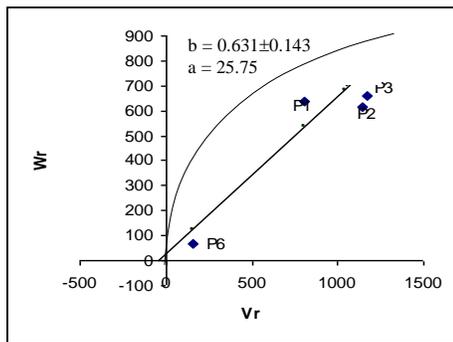


Fig. 6a. W_r - V_r graph for filled grains/panicle

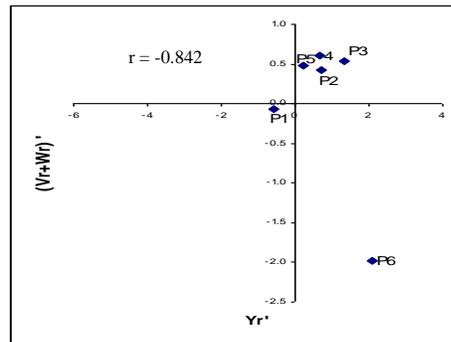


Fig. 6b. $Y_r'-(V_r+W_r)'$ graph for filled grains/panicle

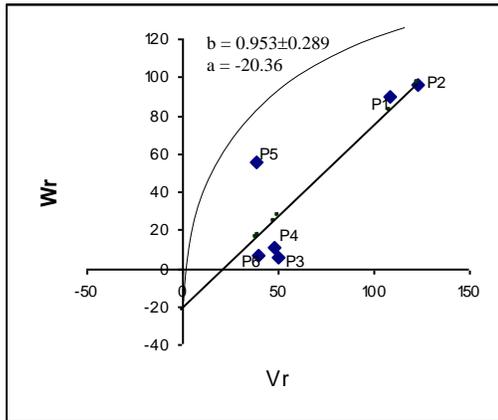


Fig.7a. W_r - V_r graph for % spikelet sterility

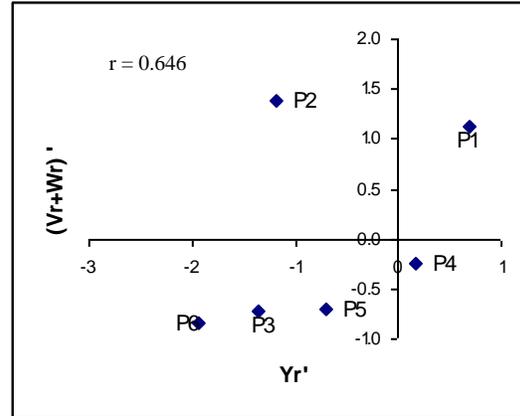


Fig.7b. $Y_r' - (V_r + W_r)'$ for % spikelet sterility

The simple additive dominance model was found adequate as the regression coefficient ($b = 0.931 \pm 0.204$) for plant height was significantly different from zero but not from unity. In W_r - V_r graph (Fig.2a), the regression line intercepted W_r axis below the origin at -8.62 , indicating overdominance gene action for the trait. The relative distribution of array points in graph showed that P_6 occupied the closest and P_2 the farthest position from the origin, while other parents occupied more or less intermediate position. These indicated that P_6 and P_2 possessed maximum frequency of dominant and recessive alleles, respectively, while other parents were conditioned by almost equal frequencies of dominant and recessive alleles. The array points in $Y_r' - (V_r + W_r)'$ graph (Fig. 2b) also indicated preponderance of dominant alleles with positive effect in P_6 and recessive alleles with negative effect in P_2 . Furthermore, the correlation coefficient ($r = -0.35$) between Y_r' and $(V_r + W_r)'$ was negative indicating increasing effect of dominant gene i.e. longer plant height was barely dominant over shorter plant height.

The W_r - V_r graph for flag leaf area is shown in Fig. 3a. The analysis of all arrays showed a regression coefficient ($b=1.068 \pm 0.75$) significantly different from zero but not from unity, which indicated that the data was adequately fit for additive dominance model. The regression line in W_r - V_r graph intercepted W_r axis below the origin ($a = -12.74$) indicating overdominance gene action for the trait. Occupying the nearest and furthest position to and from the origin in W_r - V_r graph P_3 and P_1 were highly influenced by dominant and recessive alleles, respectively. The $Y_r' - (V_r + W_r)'$ graph (Fig.3b) also confirmed the above findings.

The analysis of all arrays for leaf area index was found adequate for simple additive dominance model as the regression coefficient ($b=1.068 \pm 0.75$) differed significantly from zero but not from unity. The regression line intercepted W_r axis in W_r - V_r graph (Fig.4a) below the origin ($a = -3.10$) indicating overdominance gene action for this trait. The relative position of the array points of respective parents suggested predominance of dominant alleles in P_6 and recessive alleles in P_4 , while P_3 was conditioned equally by dominant and recessive alleles. The $Y_r' - (V_r + W_r)'$ graph (Fig. 4b) also confirmed the results of above findings. The non-significant negative correlation ($r = -0.294$) between Y_r' and $(V_r + W_r)'$ indicated that higher leaf area index was barely dominant over lower leaf area index.

In case of panicles per plant, the regression coefficient ($b=0.654\pm 0.266$) for all arrays was neither significantly different from unity nor zero. However, elimination of array 2 (P_2) from the analysis gave a regression coefficient, $b=0.923\pm 0.094$ (Fig. 5a) significantly different from zero but not from unity. This suggested that the parent P_2 contained some sorts of the epistatic genes and the trait appeared to be conditioned by additive-dominance gene action. The regression line passed below the origin intercepting W_r axis at -1.72 , which indicated overdominance gene action for the expression of panicles per plant. The W_r - V_r graph showed that P_3 was closest and P_6 was farthest from the origin, which implied preponderance of dominant alleles in P_3 and recessive alleles in P_6 for expressing this trait. The $Y' - (V_r + W_r)'$ graph (Fig. 5b) also confirmed the above findings. The negative correlation ($r = -0.747$) between parental mean and parental order of dominance revealed increasing gene action, i.e. higher number of panicles per plant was dominant over lower number.

The regression coefficient ($b=0.631\pm 0.143$) for filled grains per panicle was significantly different from zero but not from unity. This revealed the adequacy of simple additive dominance model. In the W_r - V_r graph (Fig. 6a), the regression line intercepted W_r axis at 25.75 indicating partial dominance gene action for the trait. The relative position of array points for respective parent in the graph showed that P_6 was the closest to the origin and other parents were the farthest from the origin occupying a cluster. These indicated that P_6 possessed maximum frequency of dominant, whereas recessive alleles were predominant in the rest five parents for this trait. The $Y' - (V_r + W_r)'$ graph (Fig. 6b) also revealed preponderance of dominant alleles with positive effect in P_6 and recessive alleles with more or less equal positive and negative effect in other parents. Furthermore, the correlation coefficient ($r = -0.842$) between Y_r' and $(V_r + W_r)'$ was negative indicating increasing effect of dominant genes for filled grains per panicle. The regression coefficient for spikelet sterility was also significantly different from zero but not from unity, i.e. the data was adequate for simple additive dominance model. The regression line in W_r - V_r graph (Fig. 7a) intercepted W_r axis at -20.36 , indicating overdominance gene action for the character. The relative position of array points indicated that P_6 , P_4 and P_3 possessed maximum frequency of dominant and P_1 and P_2 were predominated with recessive alleles, while P_5 was conditioned by equal frequencies of dominant and recessive alleles for this trait. The $Y' - (V_r + W_r)'$ graph (Fig. 7b) also revealed preponderance of dominant alleles in P_6 , P_4 and P_3 and recessive alleles in P_1 and P_2 . The correlation coefficient (0.646) between Y_r' and $(V_r + W_r)'$ was positive indicating decreasing effect of dominant gene for spikelet sterility.

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