ANALYSIS OF A SIX PARENT DIALLEL CROSS IN MUTANTS OF BASMATI RICE

AKBAR ALI CHEEMA AND M.AFSAR AWAN

Nuclear Institute for Agriculture and Biology,
Faisalabad, Pakistan.

Abstract

Nature of genetic control and gene action of yield and yield components in induced mutants of Basmati rice was investigated in a six parent diallel cross (including reciprocals) involving 5 mutants and the parent variety Basmati 370. The resulting 36 F_1's alongwith the six parents were grown in randomly arranged replicated plots. Analysis of variance for all the traits revealed significant differences. Additive genetic variance was observed for the expression of tillers per plant whereas the influence of both additive and non additive genetic variance was noted for the expression of panicle length, secondary branches per panicle and spikelets per panicle. Yield per plant was influenced by non additive type of genetic variance. The number of effective factors estimated ranged from 1 for tillers per plant to 2 for the other yield components. Heritability estimates varied from low (0.16%) for grain yield to high (0.63%) for tillers per plant. The results suggest a desired response to selection for tillers per plant, panicle length, secondary branches per panicle and total spikelets per panicle.

Introduction

Gene action on quantitative traits in rice has been studied by Shaalan & Aly (1977) who observed that additive gene effects were significant for grain yield. For grain yield Li (1975) concluded that both additive and dominance inheritance were important in determining higher panicle length. Although studies on qualitative inheritance in basmati rices are available (Cheema & Awan, 1986; Awan *et al*, 1984), yet complete genetic information in this direction on quantitative inheritance are meagre (Cheema & Awan,1985).

The present study was initiated to find out the genetic mechanism of the induced mutants of Basmati rice for yield and yield components.

Materials and Methods

The material consisted of six basmati varieties/mutants viz., Basmati 370, EF (Early flowering)-27-73-2, DM(Dwarf mutant)-179-1, DM-178-1, DM-15-11 and DM-15-4. All the 6 genotypes were crossed in all possible combinations. Thirty hybrids alongwith their parents were planted in a randomized complete block design with three replications. There was one row each of F_1's and their parents having ten plants 20 cm apart each. The crop was fertilized with 70-35-0, NPK kg/ha.

At maturity data were recorded on 8 competitive plants for the following characters:

Table 1. Mean performance of parents and F_1's for different characters in rice.

Crosses/ parents	Tillers/ plant	Panicle length (cm)	Secondary branches/ panicle	Total fertile spikelets per panicle	Grain yield/ plant (gm)
Basmati 370	7.86	30.85	34.32	151.39	14.07
EF27-73-2	8.85	30.73	22.28	112.68	15.52
DM178-1	7.18	26.49	25.51	106.17	10.47
DM179-1	7.04	26.76	19.76	109.01	9.15
DM15-11	11.95	23.12	9.76	70.99	7.92
DM15-4	12.21	21.75	7.82	64.06	7.08
Basmati 370x EF27-73-2	8.8	32.06	29.17	147.69	15.03
Basmati 370 x DM178-1	7.92	30.14	35.06	147.63	13.12
Basmati 370 x DM179-1	7.48	30.48	31.28	147.42	13.75
Basmati 370 x DM15-11	9.57	30.14	30.53	137.34	17.21
Basmati 370 x DM15-4	8.15	31.28	31.98	146.50	15.57
EF27-73-2 x DM178-1	9.63	31.47	34.02	163.98	21.27
EF27-73-2 x DM179-1	8.96	31.80	32.35	151.60	16.44
EF27-73-2 x DM15-11	9.74	29.18	23.73	122.69	17.13
EF27-73-2 x DM15-4	11.15	30.42	24.71	115.48	18.10
DM178-1 x DM15-11	8.23	29.73	31.79	137.60	14.71
DM178-1 x DM15-11	10.79	29.11	33.39	147.06	17.75
DM178-1 x DM15-4	10.49	29.77	33.90	150.13	17.54
DM179-1 x DM15-11	9.00	29.90	32.91	140.69	16.10
DM179-1 x DM15-4	9.59	31.42	33.24	152.35	18.69
DM15-11 x DM15-4	13.55	22.02	9.19	67.18	8.74
CD_1	2.47	1.30	4.01	17.33	4.95
CD_2	3.28	1.73	5.32	23.01	6.57

1. No. of productive tillers per plant.
2. Panicle length (cm).
3. No.of secondary branches per panicle.
4. Total fertile spikelets per panicle.
5. Grain yield per plant (gms).

The data were analysed by the method proposed by Mather & Jinks (1971) & Hayman (1954).

Result and Discussion

The analysis of variance for tillers/plant, panicle length, secondary branches /panicle, fertile spikelets/ panicle and grain yield/plant revealed significant differences (Table 1). V_r, W_r values and genetic components of variations are presented in Table 2 and 3 respectively.

Tiller per plant: In the covariance-variance graph for tillers/ plant (Fig.1) the regression value (b) was not significantly different from UNITY indicating absence of non-allelic interaction. The regression line intercepted the W_r axis above the origin, suggesting partial dominance. Array 6 and 1 possess maximum number of recessive and dominant genes respectively. The genetic component D was significant (Table 3), indicating additive type of gene action. The estimated value of $(H_1/D)^{1/2}$ revealed partial dominance effect of this trait. This was further supported by the value of 0.92 for K_D/K_R. The ratio of h^2/H_2, which is the estimate of a group of dominant genes; was negative showing cancelling effect of positive and negative genes; which might have resulted in under estimation of this value (-0.08). Heritability in the present study is high suggesting that most of phenotypic variability would be due to genetic variation.

Table 2. Vr, Wr for different characters in rice.

Array variety	Tillers/ plant		Panicle length (cm)		Secondary branches/ panicle		Total fertile spikelets per panicle		Grain yield/ plant	
	V_r	W_r	V_r	W_r	V_r	W_r	V_r	W_r	V_r	W_r
Basmati 370	1.07	1.21	0.93	2.19	5.96	15.00	59.31	135.23	2.27	-2.19
EF27-73-2	0.16	-0.65	0.43	1.21	26.43	23.79	594.45	329.31	7.01	-1.56
DM-178-1	2.29	3.38	2.62	2.01	11.27	-4.86	327.62	-33.30	16.88	1.07
DM-179-1	2.38	3.22	3.84	-0.40	29.02	-5.66	323.31	-143.81	19.48	-4.03
DM-15-11	3.38	3.65	13.23	10.87	124.87	92.59	1286.06	975.87	23.19	11.20
DM-15-4	5.85	4.30	21.02	15.76	153.55	107.66	1581.35	1052.73	26.33	15.36

Table 3. Genetic parameters for different characters in rice.

	Tillers/ plant	Panicle length	Secondary branches/ panicle	Total fertile spikelets/ panicle	Grain yield/ plant
	**	**	**	**	NS
D	4.60	13.95	96.72	967.24	8.26
	NS	NS	NS	NS	NS
F	-0.31	6.96	42.45	414.96	5.49
	ns	**	**	**	**
H_1	3.15	20.56	175.01	2143.21	52.93
	ns	**	**	**	**
H_2	2.76	16.58	166.77	1856.51	49.81
	NS	**	**	**	**
h_2	-0.21	30.50	272.71	3575.36	78.45
	**	NS	NS	·NS	NS
E	0.86	0.21	2.06	36.79	3.32
$(H_1/D)^{1/2}$	0.83	1.21	1.35	1.49	2.53
$H_2/4H_1$	0.22	0.20	0.24	0.22	0.24
KD/KR	0.92	1.52	1.39	1.34	1.30
h_2/H_2	-0.08	1.84	1.64	1.93	1.58
h_2(n.s)	0.63	0.56	0.42	0.46	0.16
$(Y_r, V_r + W_r)$	0.55	-0.88	-0.88	-0.86	-0.49

|	
D	Additive component of variation.
F	Relative frequency of dominant and recessive alleles.
H_1	Component of variation due to the dominance effect of the genes.
H_2	Mesure of gene frequency.
h_2	Dominance effect.
E	Variation due to environment (non-heritable component).
$(H_1/D)^{1/2}$	Mean degree of dominance.
$H_2/4H_1$	Average frequency of positive and negative alleles in parents.
KD/KR	Ratio of dominant to recessive genes.
h^2/H_2	Number of groups of genes which control the character and exhibit dominance.
h^2_r(n.s.)	Heritability in narrow sense.
$(Y_r, V_r + W_r)$	The coefficient of correlation between the parental order of dominance and parental measurement.
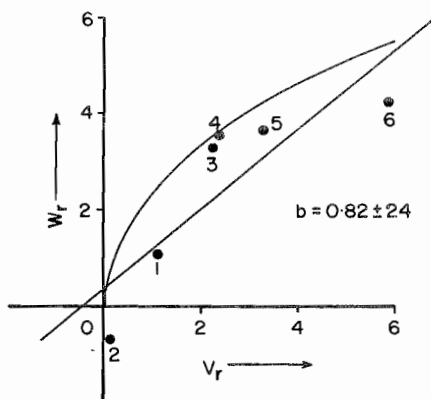
Fig.1. V_r, W_r graph for tillers per plant in induced mutants of rice in 6x6 diallel. The points of intercepts refer to (1) Basmati 370, (2) EF-27-73-2, (3) DM-178-1. (4) DM-179-1, (5) DM-15-11. (6) DM-15-4.

Panicle length: In the W_r-V_r graph (Fig.2) the regression coefficient (b) did not differ significantly from unity, showing thereby absence of non-allelic interaction and the regression line passes through the origin, indicating complete dominant type of gene action. Arrays 1 and 2 being nearer to the origin possessed the dominant genes, whereas array point 6 possessed the recessive genes being farthest from the origin. Among the genetic components, H_1, H_2 and h^2 (Table 3) are significant suggesting thereby dominant genes. This was confirmed by the ratio of KD/KR which is greater than 1. h_2/H_2 indicates that two sets of genes are exhibiting dominance.
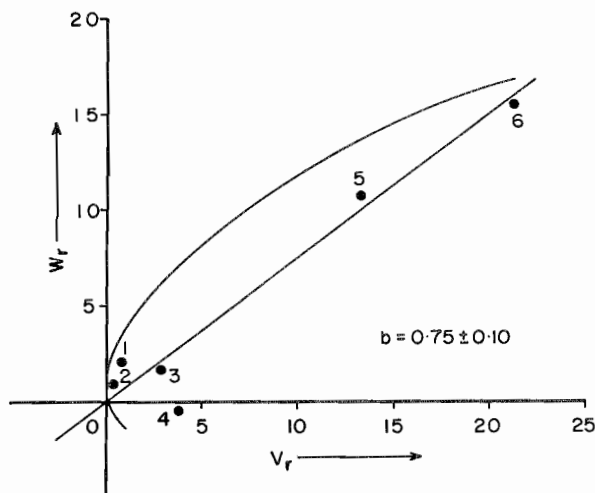

Fig.2. V_r W_r graph for panicle length in induced mutants of rice in 6x6 diallel. The points of intercepts refer to (1) Basmati 370, (2) EF-27-73-2, (3) DM-178-1. (4) DM-179-1, (5) DM-15-11. (6) DM-15-4.
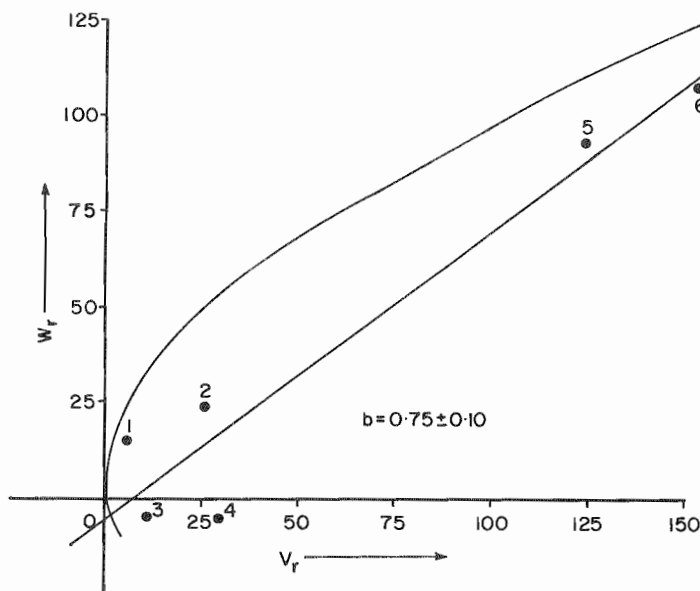
Fig.3. V_r, W_r. graph for number of secondary branches per panicle in induced mutants of rice in 6x6 diallel. The points of intercepts refer (1). Basmati 370, (2) EF-27-73-2, (3) DM-178-1. (4) DM-179-1 (5) DM-15-11, (6) DM-15-4.

Secondary branches/panicle: The position of regression line indicated the over dominance type of gene action as it passes below the origin (Fig.3). The spread of array points along the regression line was wide, showing genetic diversity among the parents. Parent 1 and 3 have dominant genes whereas array 6 has recessive genes (Fig.3). Among the various genetic components (Table 3),D, H_1, H_2, h^2 are significant. There was preponderance of dominant alleles as the F value is positive. This was further confirmed by the KD/KR value, which was more than unity. The estimates of $(H_1/D)^{1/2}$, indicated over dominance effect. The value 0.24 for $H_2/4H_1$ showed symmetric distribution of the genes with positive and negative effects.

Total fertile spikelets/panicle: The regression line cuts the ordinate much below the origin, indicating over dominance (Fig.4) which is further confirmed by the genetic components of variation where $D < H_1$. Array 1 being nearer to the point of the origin possessed dominant genes. Array 6 possessed recessive alleles. D, H_1, H_2 and h^2 are significant (Table 3). $(H_1/D)^2$ is greater than one showing thereby overdominance type of gene action. $H_2/4H_1$ shows asymmetry of positive and negative alleles. KD/KR indicates excess of dominant genes. Heritability is moderate.

Yield/plant: Non-allelic interaction was absent as indicated by the regression coefficient which did not differ significantly from 1, over dominance effect was evident as the regression line intercepted the W_r axis much below the origin (Fig.5). Arrays 1 and 2 possessed dominant alleles being nearer to the origin. The array points 5 and 6 possessed recessive genes being away from the origin.. The array point 4 is away from the regression, showing thereby genetic diversity from the rest of the parents.
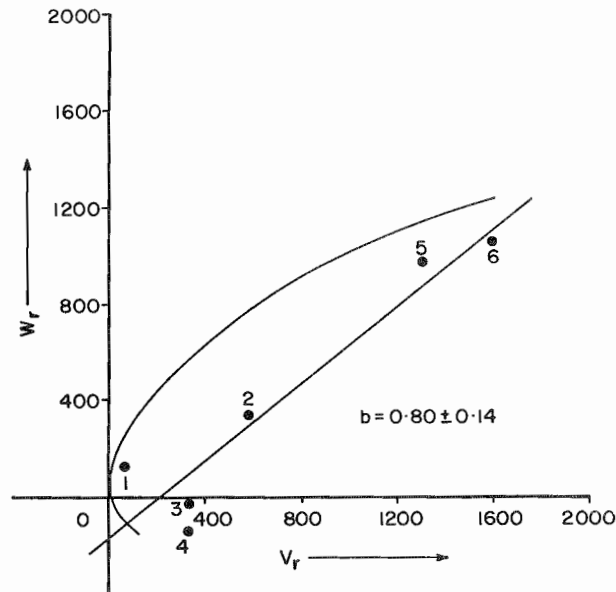
Fig.4. V_r, W_r, graph for total spikelets per panicle in induced mutants of rice in 6x6 diallel. The points of intercepts refer to (1) Basmati 370, (2) EF-27-73-2, (3) DM-178-1, (4) DM-179-1, (5) DM-15-11, (6) DM1-15-4.

Genetic components of variation H_1, H_2 and h^2 are significant (Table 3), indicating excess of dominant genes. The array points are scattered along the regression line, indicating wide genetic diversity among the parents. The value of $(H_1/D)^{1/2}$ showed over dominance effects. Estimate, of $H_2/4H_1$ was below 0.25, showing that plus alleles were present in greater frequency. The value of KD/KR (1.30) also indicated excess of dominant genes in the parents. The estimates of heritability was very low perhaps due to non significant D component. Hence there is limited scope for selection in the segregating generation.
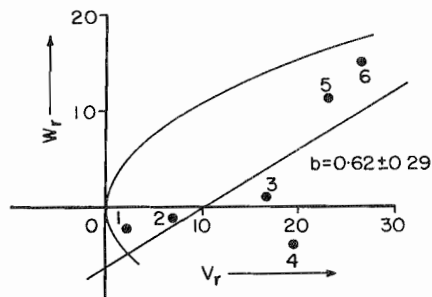

Fig.5. $_r$, W_r graph for grain yield per plant in induced mutants for rice in 6x6 diallel. The points of intercepts refer to (1) Basmati 370, (2) EF-27-73-2, (3) Dm-178-1, (4) DM-179-1, (5) DM-15-11, (6) DM-15-4.

The results of the study have revealed the nature of gene action in characters related to the productivity and development in rice crosses. The genetic analysis indicated that the characters except tillers/plant were predominantly under the control of over dominance. gene action. Tillers/plant is controlled by partial dominance. Heritability is low to moderate. Khaleque & Eunus (1975) while studying the inheritance of some quantitative characters reported overdominance for the panicle length, number of secondary branches/panicle and total spikelets/panicle. Singh & Nanda (1976) reported overdominance for yield/plant and panicle length and partial dominance for panicle numbers/plant.

References

Awan, M.A., A.A. Cheema and G.R. Tahir. 1984. Evaluation and genetic analysis of semi dwarf mutants in rice (*Oryza sativa* L.).In: *Semidwarf cereal mutants and their use in cross breeding* 11,IAEA TECDOC 307 (Proc. Meeting, Davis,1982).

Cheema, A.A and M.A. Awan. 1985. Heterosis, gene action and combiningability study of yield and yield components of four parent diallel in rice. *Pak. J. Sci. Ind. Res.*, 28:175-178.

Cheema, A.A. and M.A. Awan. 1986. Linkage and inheritance studies of heading date and plant height in induced mutants of Basmati rice. *Egypt J. Genet. Cytol.*, 15:307-312.

Hayman, B.I. 1954. The theory and analysis of diallel crosses. *Genetics,* 39:789-809.

Khaleque, M.A. and A.M. Eunus. 1975. Inheritance of some quantitative characters in a diallel experiment of six rice strains. *SABRAO*, 7:217-224.

Li, C.C. 1975. Diallel analysis of yield and its component traits in rice (*Oryza sativa* L.). *J. Agri. Assoc. China.*, 92:41-56.

Mather, K and J.L. Jinks. 1971. *Biometrical genetics,* 2nd ed. Chapman and Hall, London, pp 382.

Shaalan, M.I. and A.E. Aly. 1977. Studies on type of gene effects in some crosses of rice (*Oryza sativa* L.). *Libyan J. Agric.*, 6:229-233.

Singh, D.P. and J.S. Nanda. 1976. Inheritance of yield and yield contributing characters. *Ind. J.Agri. Sci.,* 46:323-326.