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Studies on Type of Gene Action in Some Crosses of Rice (*Oryza Sativa* L.) in Egypt

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ABSTRACT

A field study was performed at the Faculty of Agriculture Experimental Farm, Alexandria University, Egypt, during 1972–1975 to determine the type of gene action through partitioning the genetic variance in two crosses of rice; namely, Nahda × I.R.8 (cross I) and Taichung (N.)1 × Nahda (cross II). Heritability estimates and the expected gain from selection were also determined.

The characters that showed significant additive genetic variance were plant height and number of total tillers per plant in cross I and II, respectively. However, the additive effect was not significant for the other characters in the two crosses. On the other hand, significant dominance genetic variance was obtained for the number of total and ear-bearing tillers per plant in cross I and for plant height, number of total and ear-bearing tillers per plant, and panicle length in cross II.

Heritability values in broad sense, based on F_2 data, were found to be of moderate magnitude with respect to plant height and mean of panicle length in cross I. High estimates of heritability were obtained for the number of total and ear-bearing tillers per plant in cross I and for all characters studied in cross II. Low estimates of heritability percentages were obtained for the characters in the narrow sense in the two crosses. When F_3 data were used, however, all the characters showed moderate heritability magnitude in broad and narrow senses in cross I, but high values were found in cross II. The expected gain from selection was different for each character in the two crosses.

Significantly phenotypic correlation coefficients were obtained among the characters except for the correlation between plant height and panicle length and between number of ear-bearing tillers per plant and panicle length in cross I, and between number of ear-bearing tillers per plant and panicle length in cross II. Different estimates of genotypic and environmental correlation coefficients were obtained among traits studied in the two crosses.

INTRODUCTION

Recently, rice breeders started to apply the concept of an ideal plant type in which short stature habit is being considered a necessary criterion for achieving success in rice breeding programes. Among the ideal 'plant type' cultivars themselves, there are

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cultivars like I.R.8 and Taichung (Native)1 which clearly have higher yield potentialities. The short stature of such cultivars might be combined with other morphological characters in producing a desirable effect on yield, as stated by Chandler (5) and Sastry *et al.* (13).

Generally, the plant breeder is interested in estimating the magnitude of genetic variance and type of gene action due to their importance in determining the most effective selection and breeding procedures for any field crop.

The main objective of the present investigation was to estimate the following parameters in two crosses of rice:

1. Additive and dominance components of genetic variance,
2. Heritability estimates in both broad and narrow senses,
3. Predicted genetic advance from selection for some characters, and,
4. Phenotypic, genotypic, and environmental correlation coefficients between the characters involved in two crosses between an Egyptian tall rice cultivar (Nahda) and two introduced dwarf rice cultivars [I.R.8 and Taichung (N.)1] from the International Rice Research Institute in the Philippines (I.R.R.I.). The introduced cultivars combined the characteristics of an ideal plant type.

MATERIALS AND METHODS

The present study was conducted at the Faculty of Agriculture Experimental Farm, Alexandria University, Egypt, during 1972–1975. The materials used were derived from two crosses between one local and two introduced rice cultivars. These crosses were as follows:

Cross I = Nahda (local) × I.R.8 (introduced), and,

Cross II = Taichung (N.)1 (introduced) × Nahda.

The parental cultivars were chosen from pure genetic stocks previously grown by the Agronomy Department at the Faculty of Agriculture, Alexandria University. Grains of F_1, F_2, and the parents were obtained from 1973 crop and grown in 1974 season. For each cross, thirteen rows of F_2 and three rows of each parent and F_1 were sown. In 1975, 100 F_3 families were randomly chosen from each cross and grown in five sets. Each set included the two parental cultivars and twenty F_3 families. The sets were replicated three times in a randomized complete block design. Fifteen F_3 grains were directly sown in 3 m long rows. At the end of growing season, only the families that had at least four guarded plants in each replicate were considered and used in recording the data.

The following characters were measured: 1) Plant height in centimeters, 2) Number of total tillers per plant, 3) Number of ear-bearing tillers per plant, and 4) Panicle length.

Variance within P_1, P_2, F_1, and F_2 generations was calculated from 1974 data. With respect to 1975 results, the variance component for F_3 families ($V\overline{F}_3$) was computed from the analysis of variance for the F_3-family means [according to Snedecor and Cochran (14)]. The average of variances due to error of the non-segregating generations (VP_1, VP_2, and VF_1) was considered as an estimate of the average environmental variance for the F_2 generation (E_1). Mather (12) derived the expected genetic variance of VF_2 and $V\overline{F}_3$ in terms of additive genetic variance within $F_2(\frac{1}{2}D)$ and dominance within $F_2(\frac{1}{4}H)$ and environmental variance (E_1) in the following manner:

$$V\overline{F}_3 = \tfrac{1}{2}D + \tfrac{1}{16}H + E_2, \text{ and}$$

$$VF_2 = \tfrac{1}{2}D + \tfrac{1}{4}H + E_1.$$

Consequently,

$$\tfrac{1}{2}\mathrm{D} = \tfrac{1}{3}(4\mathrm{V}\bar{\mathrm{F}}_3 - \mathrm{VF}_2 - \mathrm{E}_1 - \mathrm{E}_2), \text{ and}$$

$$\tfrac{1}{4}\mathrm{H} = \tfrac{4}{3}(\mathrm{VF}_2 - \mathrm{E}_1 - \mathrm{V}\bar{\mathrm{F}}_3 - \mathrm{E}_2), \text{ where:}$$

E_1 = the average of environmental variance, E_2 = the environmental variance of F_3 generation estimated as the mean plot error and equals V_p/r. These computations were followed in the present work.

Heritability estimates were calculated as follows:

$$h^2 \text{ (broad sense in } F_2) = \frac{\frac{1}{2}D + \frac{1}{4}H}{\frac{1}{2}D + \frac{1}{4}H + E_1}$$

$$h^2 \text{ (narrow sense in } F_2) = \frac{\frac{1}{2}D}{\frac{1}{2}D + \frac{1}{4}H + E_1}$$

$$h^2 \text{ (broad sense in } F_3) = \frac{\frac{1}{2}D + \frac{1}{16}H}{\frac{1}{2}D + \frac{1}{16}H + E_2}$$

$$h^2 \text{ (narrow sense in } F_3) = \frac{\frac{1}{2}D}{\frac{1}{2}D + \frac{1}{16}H + E_2}$$

The predicted genetic advance from selection was calculated from the following equation:

$\Delta g = Kh^2\sigma ph$, where: K = the selection differential and equals 2.06 upon selecting the highest 5% of the population, h^2 = heritability in narrow sense, and σph = phenotypic standard deviation.

Variance of each of the genetic variance components was estimated as a linear function of the variance of mean squares. The variance of a mean square was calculated as given by Anderson and Bancroft (3). The standard error was computed as the square root of variance.

Simple phenotypic correlation coefficients between all paired combinations of the characters under study were calculated from the following formula:

$$rph = \frac{M_{12}}{\sqrt{M_{11} . M_{22}}},$$

where: M_{12} = covariance of the two variables 1 and 2, M_{11} and M_{22} = variances of the first and second variables, respectively. The environmental correlation coefficient (r_E) was estimated from the following formula:

$$r_E = \frac{M_p(12)}{\sqrt{M_p(11) . M_p(22)}}.$$

The genetic correlation coefficient (r_g) was calculated as follows:

$$r_g = \frac{Mf(12) - M_p(12)}{\sqrt{[Mf(11) - M_p(11)][Mf(22) - M_p(22)]}}$$

where: Mf(12) and $M_p(12)$ = covariance of the variables 1 and 2 between families and between plot means, respectively, Mf(11) and Mf(22) = variances of the variables 1 and 2 between families, respectively, and $M_p(11)$ and $M_p(22)$ = variances of the variables 1 and 2 between plot means, in this order.

RESULTS AND DISCUSSION

Table 1 shows the tests of significance for both parental differences and genetic variances among F_2 plants for all characters studied in the two crosses. Variances and means of the parental cultivars (P_1 and P_2) and F_2 and F_3 generations of each cross for the traits, are presented in Table 2. Table 3 indicates the partitioning of the genetic variance into additive and dominance genetic variance components. Heritability percentages in broad and narrow senses for the characters under study are given in Table 4. Predicted genetic advance (Δg) for all traits, using family selection of the best 5% of the F_3 families, is shown in Table 5.

In general, these data indicate that all characters were quantitatively inherited. There were highly significant differences between parents in the two crosses for all characters except the number of total and ear-bearing tillers per plant and mean panicle length in cross I. The genetic variance was significant among F_2 plants and F_3 family-means in all traits for the two crosses.

1. Plant height

On partitioning the genetic variance for plant height, positive and negative estimates of the additive portion of genetic variance were recorded in crosses I and II, respectively. On the other hand, significant dominance genetic variance was present in cross II, while in cross I, the values were not significant, as shown in Table 3. These results agreed with those reported by Chang (6).

Table 4 shows that heritability estimates in broad sense for plant height were 41.93 and 53.94% in cross I and 74.78 and 74.75% in cross II when F_2 and F_3 data were used, respectively. The low estimates of heritability in cross I might be attributed to the non-heritable effects; i.e., dominance and/or environment. Heritability percentages in narrow sense (due to additive effect only) in the case of cross I were 28.19 and 44.43 as estimated from F_2 and F_3 generations in this respect. So, it was obvious that the heritability values were much lower in narrow than in broad sense, especially in F_2, which indicated that most of the genetic variance was due to dominance effect. Several workers reported high estimates of heritability, such as Ahmed (1), Chang *et al.* (7), Sinha and Patnaik (15), and El-Azizi *et al.* (8). Low estimates of heritability, however, were recorded by Horie *et al.* (10), Latife and Zaman (11), and Aly (2).

Table 1 The t-test for significance between parents and F-test for significance of the genetic variance among F_2 plants, and among F_3-family means for the two crosses of rice.

Crosses	Characters	t-test	F-test	
			F_2^a	F_3
I. Nahda × *I.R.8*	1. Plant height (cm)	**	**	*
	2. No. of total tillers per plant	N.S.[b]	**	*
	3. No. of ear-bearing tillers per plant	N.S.	**	*
	4. Mean panicle length (cm)	N.S.	*	**
II. Taichung (N.)1 × Nahda	1. Plant height (cm)	**	**	**
	2. No. of total tillers per plant	**	**	**
	3. No. of ear-bearing tillers per plant	**	**	**
	4. Mean panicle length (cm)	**	**	**

[a] *, ** = significant at 0.05 and 0.01 levels, respectively.

[b] N.S. = not significant.

Table 2 Variances and means of P_1, P_2, F_2, and F_3 populations for the characters studied.

Characters	Statistics[a]	P_1	P_2	F_2	F_3
Cross I: Nahda × I.R.8:					
1. Plant height (cm)	S^2	27.41	12.60	41.93	14.35
	$\overline{x}$	92.76	76.31	80.20	58.48
	n	42	38	240	100
2. No. of total tillers per plant	S^2	7.70	11.81	28.47	5.50
	$\overline{x}$	7.66	9.08	15.85	14.16
	n	35	40	229	100
3. No. of ear-bearing tillers per plant	S^2	6.10	4.67	26.68	1.83
	$\overline{x}$	4.89	5.90	13.82	7.26
	n	36	39	230	100
4. Mean of panicle length (cm)	S^2	1.24	0.94	1.56	0.22
	$\overline{x}$	14.47	15.21	12.90	8.89
	n	29	29	240	100
Cross II: Taichung (N.)1 × *Nahda*:					
1. Plant height (cm)	S^2	25.75	32.89	116.25	20.49
	$\overline{x}$	68.82	95.07	48.69	59.99
	n	52	52	204	100
2. No of total tillers per plant	S^2	10.53	4.94	35.92	17.27
	$\overline{x}$	10.12	7.65	14.78	12.10
	n	25	35	193	100
3. No. of ear-bearing tillers per plant	S^2	9.27	3.70	25.35	7.39
	$\overline{x}$	10.03	4.73	12.53	8.59
	n	30	33	196	100
4. Mean of panicle length (cm)	S^2	1.02	1.19	3.39	0.51
	$\overline{x}$	13.86	11.15	12.84	9.95
	n	25	24	174	100

[a] S^2 = variance, $\overline{x}$ = mean, and n = number of plants.

Means of the genetic advance from selection (assuming selection of the top 5% of F_3 families) are illustrated in Table 5. The predicted genetic advance was also calculated as percentages of the means. It was found that a gain in plant height of 8.07% would be obtained in the F_4 generation.

2. Number of total tillers per plant

In the two crosses, the additive and dominance genetic variances were positive and significant for this character. However, in cross I, the value of additive genetic variance was not significant because it did not exceed the value of its standard error, as indicated in Table 3.

Heritability estimates for the number of total tillers per plant in broad sense were 65.72 and 36.09% in cross I and 78.45 and 84.94% in cross II, based on F_2 and F_3 data, respectively. In the narrow sense, heritability estimates were low in the two crosses. High estimates were obtained by Ahmed (1).

Data in Table 5 show that a predicted genetic advance of 2.61 and 51.05% in crosses I and II, respectively, would be gained in F_4 by using selection for the highest 5% of the F_3 families.

Table 3 Partitioning of genetic variance into additive and dominance components.

Characters	Statis-tics[a]	$\frac{1}{2}$D[b]	$\frac{1}{4}$H[c]
Cross I. Nahda × I.R.8:			
1. Plant height (cm)	S^2	11.82	10.11
	S.E.	5.74	8.66
2. No. of total tillers per plant	S^2	0.70	18.01
	S.E.	3.60	5.38
3. No. of ear-bearing tillers per plant	S^2	−4.66	25.92
	S.E.	—	3.74
4. Mean of panicle length (cm)	S^2	0.13	0.34
	S.E.	0.11	0.33
Cross II. Taichung (N.)l × Nahda:			
1. Plant height (cm)	S^2	−1.66	88.56
	S.E.	—	13.30
2. No of total tillers per plant	S^2	13.63	14.54
	S.E.	4.12	6.53
3. No. of ear-bearing tillers per plant	S^2	3.57	15.29
	S.E.	1.92	4.09
4. Mean of panicle length (cm)	S^2	−0.05	2.24
	S.E.	—	0.61

[a] S^2 = variance and S.E. = standard error.
[b] $\frac{1}{2}$D = additive genetic variance.
[c] $\frac{1}{4}$H = dominance genetic variance.

3. Number of ear-bearing tillers per plant

Additive genetic variance for this character was negative (−4.66) and positive (3.57) in crosses I and II, respectively, as shown in Table 3. Significant positive values, however, were obtained for dominance genetic variance in the two crosses. Heritability percentages (Table 4) in the broad sense were 79.80 and 37.19 in cross I and 74.40 and 84.94 in cross II, based on F_2 and F_3 data, respectively. Such percentages were relatively low in the narrow sense. Low estimates of heritability were recorded by Horie

Table 4 Heritability percentage in broad and narrow senses for the characters studied in F_2 and F_3 generations.

Characters	F_2		F_3	
	broad	narrow	broad	narrow
Cross I. Nahda × I.R.8:				
1. Plant height (cm)	41.93	28.19	53.94	44.43
2. No of total tillers per plant	65.72	2.46	36.09	4.59
3. No. of ear-bearing tillers per plant	79.80	—	37.19	—
4. Mean of panicle length (cm)	30.12	8.33	55.00	32.50
Cross II. Taichung (N.)l × Nahda:				
1. Plant height (cm)	74.78	—	74.75	—
2. No. of total tillers per plant	78.45	37.95	84.94	67.04
3. No. of ear-bearing tillers per plant	74.40	14.08	84.94	41.03
4. Mean of panicle length (cm).	64.60	—	55.19	—

Table 5 Predicated genetic advance (Δg and $\Delta g\%$) for the characters studied.

Characters	Δg	$\Delta g\%$
Cross I: Nahda × I.R.8:		
1. Plant height (cm)	4.72	8.07
2. No. of total tillers per plant	0.37	2.61
3. No. Of ear-bearing tillers per plant	—	—
4. Mean of panicle length (cm)	0.42	4.72
Cross II: Taichung (N.)1 × Nahda:		
1. Plant height (cm)	—	—
2. No. of total tillers per plant	6.22	51.05
3. No. of ear-bearing tillers per plant	2.49	28.98
4. Mean of panicle length (cm)	—	—

et al. (10) and Aly (2). In other rice crosses, however, high heritability estimates were obtained, as was found by Latife and Zaman (11) and Wang (16). Using selection for the highest 5% of the F_3 families, it was expected that an increase of 28.98% in cross II (Table 5) would be obtained in the F_3 generation for the number of ear-bearing tillers per plant.

4. Mean of panicle length

Partitioning of the genetic variance for this character revealed nonsignificant positive estimates of additive (0.13) and dominance (0.34) components in cross I, as indicated in Table 3. In cross II, the additive genetic variance was nonsignificantly negative (−0.05), while the dominance genetic variance was significantly positive (2.24). Moderate and low heritability estimates in broad and narrow senses were obtained in the two crosses (Table 4). Similar results were recorded by Horie *et al.* (10). On the other hand, high values

Table 6 Phenotypic (rph), genotypic (^{r}g), and environmental (^{r}E) correlation coefficients between characters studied for the two crosses.

Characters correlated[a]	rph[b]	^{r}g	^{r}E
Cross I: Nahda × I.R.8			
H & T	0.270**	0.183	0.347
H & E	0.291**	0.317	0.273
H & P	0.149	0.277	−0.006
T & E	0.518**	−0.732	0.234
T & P	0.247*	−0.272	0.234
E & P	−0.014	−0.658	0.527
Cross II: Taichung (N.)1 × Nahda			
H & T	0.384**	0.330	0.619
H & E	0.297**	0.353	0.078
H & P	0.199*	0.273	0.072
T & E	0.732**	0.768	0.530
T & P	0.316**	0.475	−0.042
E & P	0.035	0.017	0.092

[a] H = plant height (cm), T = no. of total tillers per plant, E = no. of ear-bearing tillers per plant, and P = panicle length (cm).

[b] *,** = significant at 5% and 1% levels of probability, respectively.

of heritability for panicle length were reported by Latife and Zaman (11), Ahmed (1), and Sinha and Patnaik (15). The percentage increase which would be expected in the F_4 generation for panicle length was found to be 4.72% in cross I if family selection was used for the best 5% of the F_3 families.

Generally, several assumptions are considered in derivation of genetic variance components. These assumptions are: no linkage, no epistasis, normal diploid inheritance, no genetic × environment interaction, random choice of materials, and a gene frequency of 0.5. Most of these assumptions were considered in the present investigation. However, linkage and genetic × environment interaction were not tested here because the present data were taken only at one location and in one season. Therefore, it was expected that the genetic × environment interaction would be a significant source of bias. Since the magnitude of bias could not be estimated, the genetic advance from selection would be different from that anticipated. Three of the estimates of additive variance were negative indicating that the additive genetic variance was underestimated in the present work. Gad (9) obtained similar results in this respect.

The expected advance from selection indicated that selection for the characters studied would be successful.

Table 6 shows the phenotypic, genotypic, and environmental correlation coefficients between the characters studied. Significant and highly significant phenotypic correlation coefficients were obtained (by using F_3 family means) between all characters except between plant height and panicle length in cross I and between the number of ear-bearing tillers per plant and panicle length in the two crosses. These results were in general agreement with those obtained by I.R.R.I. (4), Wang (16), and Sastry *et al.* (13). Low estimates of genotypic correlation coefficients were reported between most characters. Such results agreed with those of Wang (16) on plant height and number of ear-bearing tillers per plant. Variable estimates for environmental correlation coefficients were obtained between the studied traits in the two crosses.

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