

DIALLEL ANALYSIS OF SOME QUANTITATIVE CHARACTERS IN F₁, AND F₂ GENERATIONS IN RICE (*ORYZA SATIVA* L.)

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Abstract

Eight rice cultivars (*Oryza sativa* L.) having diverse morphological and agronomical character were crossed in all possible combinations (excluding reciprocals) to determine nature of gene action and inheritance of some quantitative characters in F₁ and F₂ generations. Data were collected on days to heading, plant height, panicle length, number of panicles per plant, spikelet sterility, number of spikelets per panicle, biological yield per plant, grain yield per plant, harvest index, 1000 grain weight, grain length and grain width. The results of variance analysis of diallel tables (Hayman 1954a, and Jones, 1965) indicated that the additive genetic variance (a) was significant and larger than non-additive (B) for all characters except grain yield per plant in both generations.

Additive (D) as well as dominance estimates (H₁) and (H₂) were significant for nine characters, whereas only the non-additive component was significant for biological yield per plant, grain yield per plant and harvest index.

Mean degree of dominance (H₁/D)^{1/2} was less than unity (<1) indicating partial dominance for plant height, but panicle length, spikelet sterility, 1000 grain weight and grain length in both F₁ and F₂ generations, but it was equal or near unity suggesting complete dominance for days to heading. However, it was greater than unity (>1) indicating over-dominance for the number of panicles per plant, the number of spikelets per panicle, biological yield per plant, grain yield per plant, harvest index, and grain width in both generations. The significance levels of the parameters estimated in F₁ and F₂ generally were in agreement. In this case, the results obtained applying one of these biometrical analysis methods, either in F₁ or in F₂ generation, may be used in making decisions concerning the type of breeding system and in selecting breeding material.

Estimates of narrow sense heritability were high for days to heading, plant height, panicle length, spikelet weight and grain length in F₂ generation. Moderate heritability estimates were observed for the number of spikelets per panicle and low for the number of panicles per plant, biological yield per plant, grain yield per plant, harvest index, and grain width in both generations.

Key words: Additive variance, non-additive variance, diallel analysis heritability, quantitative characters, rice (*Oryza sativa* L.)

INTRODUCTION

In any plant breeding programs, the aim of selection is to identify superior genotypes which will transfer their desirable characteristics to next generations. In respect to quantitative characters, the difficulty is that they tend to be continuous in their variation. This means indistinguishable phenotypic classes and difficult or impossible applicability of classical Mendelian analysis. In the middle of the 20th century, the diallel cross technique was used by plant breeders for the genetic study of continuous variation. The application of diallel-cross technique for evaluation of quantitative variability in self-pollinated crops was developed by Hayman (1954 a and b), Jinks (1954), Kempthorne (1956), and Crumpacker and Allard (1962).

The diallel analysis provides very useful information to plant breeders in making decisions concerning the type of breeding system and in selecting breeding materials that show the greatest promise for successful selection (Gardener, 1966). It has been used successfully by quantitative geneticists attempting to gain a better understanding of the nature of gene action involved in determining quantitative traits.

Diallel analysis in rice has been applied by many workers, Li (1975) reported that both additive and dominance inheritance were important in determining plant height, panicle number, panicle length and weight, and spikelet number, but not grain yield. Sbramanian and Rathinam (1984) examined gene action of yield per plant and ten of its components. They found out that dominance gene effects were important for grain and straw yields, while most of the other traits were controlled by additive gene action, and heritability was moderate for grain and straw yield but high for many other traits. Kaushik and Sharma (1988) reported that additive gene action was probably most important for plant height, panicle length and spikelets per panicle, whilst non-additive effects were likely to be more important for 1000 grain weight, spikelet sterility and yield per plant. Kou and Liu (1987) observed that additive and dominance gene effects were important for grain and biological yields, and harvest index. Narrow-sense heritability values were 61, 27, and 67% for grain yield, biological yield and harvest index, respectively. Kou and Liu (1986) also pointed out that additive effects were more important than dominance effects for grain length and width. Nematzadeh (1987) reported that both additive (D) and non-additive (H1) components were involved in the inheritance of plant height, tillers per panicle, spikelets per panicle, days to flower and 1000-grain weight, whereas only non-additive component was involved in panicle length, sterility percent and grain

yield per plant. Narayan and Rangasamy (1990) observed that additive and dominance gene effects were significant for days to flowering, plant height, tiller number, panicle length, number of spikelets per panicle, 1000 grain weight, and dry matter accumulation under both normal and salinized conditions. However, the additive effect was significant for grain yield only in the salinized situation.

This study was undertaken to determine nature of gene action and inheritance of some quantitative characters in rice (*Oryza sativa* L.) in F1 and F2 generations.

MATERIALS AND METHODS

Eight elite and diverse rice cultivars, Delta, Baldo, Balilla, Titanio, Rodina, Krasnodarsky-424, H-33, and K-78-13 having diverse morphological and agronomical characters were crossed in all possible combinations (excluding reciprocals) in 1988. Seeds from each of the 28 F1's were sown in 1989 to produce F2 seeds. Twenty eight F1 hybrids, and 28 F2 populations with their parents, were grown at the experimental farm of Thrace Agricultural Research Institute in a randomized complete block design with four replications in 1990. A single row of twenty plants constituted the experimental plot. Seedlings grown in seedbed were transplanted to the paddy field with single plant per hill spaced at 30x20 cm. The amount of fertilizers applied was 130 kg N and 80 kg P per ha.

Data were collected for days to heading, plant height, panicle length, number of panicles per plant, spikelets sterility, number of spikelets per panicle, biological yield per plant, grain yield per plant, harvest index, 1000 grain weight, grain length and width. Observations were recorded on twelve random plants in each plot and plot means were used in the statistical analysis.

The variance analyses of diallel tables were carried out based on the method of Hayman (1954a) and on its modification for a half set of data by Jones (1965). Estimates of the genetic components of variation were made according to Hayman (1954b) and Mather and Jinks (1971). Narrow sense heritability was estimated according to Mather and Jinks (1971).

RESULTS AND DISCUSSION

Test of Assumptions

It was necessary for advanced analysis to ascertain that each character sat-

ified the six assumptions made by Hayman (1954b). "Diploid segregation" and Homozygous parents were satisfied judging from the nature of the materials. Also, it was believed no Reciprocal difference. Two kinds of tests, one by the heterogeneity of W_r - V_r and the other by the regression coefficient of W_r on V_r , were conducted to ascertain the other three assumptions i.e. No multiple allelism, Independent distribution of genes among the parents and especially Independent action of non-allelic genes.

The heterogeneity among the eight arrays was not significant in any character (Table 1). Regression coefficients were significant only for two characters in F1 generation, the number of spikelets per panicle and harvest index. Therefore, these two traits failed to satisfy some of the assumptions. Therefore, the arrays 5 and 7 and arrays 3 and 4 were eliminated for the number of spikelets per panicle and harvest index, respectively and the data, were reanalyzed as a 6x6 diallel set. The results of analysis showed that the hypotheses were satisfied. Thus, the additive-dominance model may be used for genetic component interpretation for all characters studied.

Analysis of Variance:

The variance analyses of diallel tables (Hayman, 1954a, and Jones, 1965) for F1 and F2 generations are presented in Table-2. The results of variance analysis indicated that the additive genetic variance (a) was significant and larger than non-additive variance (b) for all characters, except grain yield per plant in both generations. Smaller, but nevertheless significant, effects due to non-additive variance were also detected for days to heading, plant height, panicle length, number of spikelets per panicle, biological yield per plant, grain yield per plant, harvest index, 1000 grain weight and grain length in F1 generation and for days to heading, plant height, the number of spikelets per panicle, 1000 grain, grain length and grain width in F2 generation. The magnitude of non-additive variance for grain yield per plant was larger than additive variance in both generations. Similarly, Li (1975), Subramanian and Rathinam (1984), Kaushik and Sharma (1988) reported larger non-additive gene effect for grain yield. On the other hand, Murai and Kinoshita (1986) pointed out that additive gene action predominated over-dominance action (b) for number of panicles per plant, number of spikelets per panicle, the mean straw weight and culm length.

Analysis by Components of Variation

The estimated genetic components of variation for all traits studied in F1 and

Table 1. Test of assumptions.

Character	Heterogeneity of W_r-V_r F-value)		b, Regression Coefficient of W_r on V_r		T = test of b on the null- hypothesis $b = 1$	
	F1	F2	F1	F2	F1	F2
Days to heading	1.85	1.75	0.595	0.650	2.36	2.01
Plant height	0.92	1.93	0.687	0.460	0.98	1.67
Panicle length	3.60	1.91	0.140	0.673	2.43	2.45
No. of panicles/plant	0.95	0.95	0.741	0.748	1.16	2.34
Spikelets sterility	3.59	0.97	0.408	0.500	1.82	1.65
No. of spikelets/panicle	1.85	0.75	0.246	0.378	4.20**	2.37
	(a) 1.46	---	0.402	---	2.69	---
Biological yield/ plant	0.19	2.54	0.584	0.145	1.66	2.46
Harvest index	1.23	1.76	0.491	0.304	2.22	2.08
	3.84	1.47	0.217	0.359	24.78**	1.88
1000 grain weight	(a) 0.64	---	0.409	---	2.18	---
Grain length	0.82	1.73	0.364	1.074	2.36	0.39
Grain width	2.38	1.98	0.939	1.067	0.94	1.07
	0.59	0.71	0.382	0.882	2.44	0.99

(a): The values determined from 6 x 6 diallel set.

(**) : Significant at 1% level.

F2 generations are presented in Table-3. Additive (D) as well as dominance estimates (H1) and (H2) were significant for nine characters, days to heading, plant height, panicle length, the number of panicles per plant, spikelet sterility, the number of spikelets per panicle, 1000 grain weight, grain length, and grain width in both F1 and F2 generations. Whereas, only the non-additive component was significant for biological yield per plant, grain yield per plant and harvest index. Similar results for different traits were reported by Kaushik and Sharma (1988), Kuo and Liu (1986 and 1987) Subramanian and Rathinam (1984), Nematzadeh (1987), Agrawi and Sharma (1987), and Sardana and Borthakur (1987).

The additive effect was considerably stable in both the F1 and F2 generations which was confirmed by the results obtained from other studies of agronomic traits in rice (Li, 1975 and Li and Rutger, 1980).

Although the additive component (D) was larger than the dominance components for some characters in the F1, the dominance components (H1 and H2) were generally larger than the additive component (D) in the F2 generation. This is non-add. Variance is associated with the heterozygous loci, these, it is expected to decrease in F2 as a result of decrease in of heterozyg loci. Therefore other seasons should be found for the decrease in additive var. in F2 because the number of heterozygous loci should be halved due to elfing in F2 generation. The results agreed with Sampson and Tarumoto (1976).

Breeding/selection strategy to be followed for the improvement of a trait is based on the basis of gene action controlling that trait. On the basis of gene action obtained in the present study, conventional breeding methods like pedigree breeding which exploits additive or additive x additive i.e. fixable gene effects could be advantageous for the improvement of days to heading, plant height, panicle length, spikelet sterility, number of spikelets per panicle, 1000 grain weight, and grain length. On the other hand, non-additive gene effects were more important for the number of panicles per plant, biological and grain yield per plant, harvest index and grain width. Therefore, if genes having non-additive action are predominant in the population, direct selection would be ineffective. Results obtained in the present study suggest that direct selection for yield would not be very effective. Many workers emphasized the importance of yield components like panicle number, panicle weight, number of grains per panicle and 1000 grain weight in selection for yield. Use of a component trait in indirect selection for yield is dependent on its heritability or relative magnitude of the additive to total genetic variance (Falconer, 1989)

Table 2. Mean squares from the Variance Analysis of diallel tables .

Character	F1 Generation					F2 Generation					Error	
	a	b	b1	b2	b3	a	b	b1	b2	b3		
Days to heading	363.83*	26.98*	77.00**	44.28**	18.78**	243.20**	19.78**	86.33**	21.30**	21.30**	15.82**	5.22
Plant height	2150.88**	60.04**	205.09**	78.72**	46.25*	1639.4**	50.92**	216.59**	42.48*	45.59**	17.51	22.95
Panicle length	101.75**	2.74**	9.71**	4.15**	1.90	86.24**	2.53	0.59	4.37**	1.98	1.21	0.91
No. of panicles/plant	42.36**	7.36	64.36**	3.38	4.15	29.02**	5.28	7.90	1.99	6.30	5.02	4.86
Spikelets sterility	523.56**	18.03	12.48	12.73	20.16	380.76**	8.84	12.19	15.89	6.20	14.07	13.01
No. of spikelets/panicle	9904.98**	1060.59**	6662.07**	1333.05**	685.15**	5395.80**	441.20**	1838.11**	579.53*	322.93*	201.24	248.73
Biological yield/plant	708.75*	541.04**	5744.26**	291.64	368.17	587.18*	383.67	977.36	144.99	437.52	244.78	242.50
Grain yield/plant	116.51	182.50*	2195.83**	79.50	117.88	96.21	103.93	178.10	23.66	127.47	77.42	78.49
Harvest index	40.32**	13.04**	29.30**	12.30**	12.49**	20.78**	4.73	0.45	6.47	4.33	4.64	3.13
1000 grain weight	156.70**	2.42**	1.21	3.99**	1.93*	126.88**	3.91**	0.12	5.25**	3.63**	0.96	0.89
Grain length	10.59**	0.16*	0.02	0.11	0.19**	8.93**	0.19**	0.04	0.27**	0.18**	0.05	0.06
Grain width	0.22**	0.03	0.02	0.03	0.03	20.1**	0.02	0.0003	0.025*	0.02	0.01	0.02

Table 3. Components of variation and estimates of genetic parameters in F1 and F2 generations of 6x6 diallel cross.

Character	D	H1	H2	F	h2	Error	(H1/D) ^{1/2}	(H2/4H1)	KD/RR	r(Yr, wr+Vr)	(H) a	
Days to heading	F1	34.91**	33.71**	24.06**	5.06	8.27	5.22	0.98	0.18	1.16	0.283	0.64
	F2	33.13**	150.79**	113.87**	43.75*	72.04**	7.12	1.06	0.19	1.90	0.553	0.27
Plant height	F1	151.55**	85.21*	66.49*	-64.13*	20.95	22.95	0.75	0.19	0.62	0.480	0.75
	F2	157.57**	376.65**	300.36*	39.44	96.07	17.38	0.77	0.20	1.18	-0.378	0.51
Panicle length	F1	8.35**	3.63**	2.74**	-1.62	1.45*	0.91	0.66	0.19	0.74	0.778*	0.63
	F2	8.31**	22.12**	17.13**	2.82	1.27	1.12	0.82	0.19	1.23	0.300	0.49
No. of panicles/plant	F1	0.62*	2.4*	3.08*	-3.93	11.86**	4.86**	1.97	0.32	0.23	-0.306	0.26
	F2	1.81**	63.90**	60.38**	3.65	0.31	5.00	4.35	0.25	1.70	0.488	0.04
Spikelets sterility	F1	46.38**	25.14*	26.03*	-17.67	5.64	13.01	0.74	0.26	0.59	0.427	0.62
	F2	45.33**	167.98**	125.41**	23.05	15.36	14.52*	0.96	0.19	1.37	0.696*	0.42
No. of spikelets/panicle	F1	398.75**	1216.67**	948.75**	-550.64	993.80**	248.73	1.75	0.20	0.43	-0.083	0.56
	F2	504.22**	969.67*	1064.67**	-779.56	386.14*	237.35	1.38	0.27	0.28	0.342	0.54
Biological yield/plant	F1	446.07**	410.12**	2844.03**	589.78	116.21	242.51**	4.51	0.29	0.37	-0.542	0.01
	F2	18.22	3700.00**	3300.98	-73.43	710.99	244.80*	6.91	0.22	5.75	-0.515	0.01
Grain yield/plant	F1	5.46	206.14**	198.70**	-4.85	254.09**	78.49*	6.155	0.24	0.87	-0.843**	0.06
	F2	15.68	1120.32**	997.65**	126.74	103.06	77.36*	4.22	0.22	106.15	-0.318	0.02
Harvest index	F1	1.65	15.60*	12.88**	-1.13	2.83	3.13	3.07	0.21	0.80	-0.556	0.30
	F2	1.82	7.45*	5.86*	2.66	1.97	2.01	2.02	0.18	2.14	-0.207	0.11
1000 grain weight	F1	0.24	47.80**	6.95	6.95	5.40	4.64	7.92	0.20	2.66	-0.250	0.16
	F2	18.50**	3.62**	2.58**	4.34**	0.12	0.88	0.44	0.18	1.72	-0.071	0.86
Grain length	F1	18.42**	24.87**	21.10**	18.49**	1.34	0.96	0.58	0.21	2.52	0.621	0.23
	F2	1.29**	0.24*	0.19*	0.29**	0.01	0.06	0.44	0.22	1.78	-0.474	0.78
Grain width	F1	1.34**	1.10**	0.99**	1.18**	0.34**	0.08	0.91	0.22	1.59	0.083	0.29
	F2	0.03**	0.04**	0.04**	0.01	0.01	0.02	1.29	0.23	1.25	-0.170	0.29
	F2	0.03**	0.16**	0.13	0.04*	0.04*	0.04	1.11	0.23	1.87	0.662	0.12

and its degree of genetic association to yield. Similar results were observed by Mandal (1982) for plant height, grain weight, panicles per plant, grain yield and grains per panicle, and by Kuo and Liu (1986) of grain length and 1000 grain weight.

In this study, the number of spikelets per panicle and 1000 grain weight having considerable high additive gene effects and narrow sense heritabilities appear to be relatively more important in selection for grain yield.

Mean degree of dominance, $(H1/D)1/2$, was less than unity (<1) indicating partial dominance for plant height, panicle length, spikelet sterility, 1000 grain weight and grain length in both F1 and F2 generations. Whereas it was equal or near unity suggesting complete dominance for days to heading. However, it was greater than unity (>1) indicating over-dominance for per plant number of panicles, number of spikelets per panicle, biological yield and grain yield, harvest index and grain width in both generations. The results of generations were in harmony for all characters in terms of dominance levels.

Proportion of genes with positive and negative effects in the parents, $H2/4H1$ reached the maximum value of 0.25 (0.5×0.5) in the case of the symmetrical of both kinds of genes. It showed asymmetrical distribution for all traits in both generations, except the number of panicles per plant. However this ratio was very close to 0.25 for some characters either in F1 or in F2. Generally, these ratios were in agreement with b2 items.

As indicated by KD/KR and F values, the eight parents may contain more recessive genes than dominant ones for plant height, panicle length, the number of panicles per plant, spikelet sterility, the number of spikelets per panical length, the number of panicles per plant, and harvest index in F1 generation. But it showed excessive of dominant genes in parents for all characters in F2 generation and for days to heading, 1000 grain weight, grain length, and grain width in F1 generation.

The correlations between the values of the parents (yr) and $Wr+Vr$ were positively significant for panicle length in F1 and for spikelet sterility in F2 generation indicating that dominance decreases the values of these traits. It was negatively significant for grain yield per plant in F1 generation suggesting dominance increases grain yield per plant. Although the correlation coefficient values were negative for most characters, they were not significant indicating unidirectional dominance.

Estimates of narrow sense heritability were high for days to heading, plant

height, panicle length, spikelet sterility, 1000 grain weight and grain length in F1 generation, whereas, it was lower for days to heading, 1000 grain weight and grain length in F2 generation. Narrow sense heritabilities were moderate for the number of spikelets per panicle, and low for the number of panicles per plant, biological yield per plant, grain yield per plant, harvest index, and grain width in both generations. Kuo and Liu (1986) reported similar results for grain length and 1000 grain weight. However, Subramanian and Rathinam (1984) observed moderate heritabilities for grain and straw yield, but high for other traits and Kuo and Liu (1986) found out 61, 27, and 67% narrow-sense heritabilities for grain yield, biological yield and harvest index, respectively.

When we compare the results obtained from the variance analysis of diallel tables (Hayman 1954a and Jones 1965). It indicated that the significance levels of the components estimated in F1 and F2 generations generally were in agreement. On the other hand, the parameters (D, H1, and H2) and ratios $[H1/D]^{1/2}$, $H2/4H1$, and KD/KR estimated using diallel cross analysis (Hayman, 1954b, and Mather and Jinks, 1971) were in agreement in both generations as well. In this case the results obtained applying one of the biometrical analysis methods mentioned above to the F1 or F2, may be used in making decisions concerning the type of breeding system and in selecting breeding materials.

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تحليل الهجن الدورية (Diallel) لبعض الصفات الكمية في الجيل الأول والثاني للأرز

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تم إجراء كل الهجن الممكنة (عدا العكسية) بين ثمانية أصناف منزرعة من الأرز متباينة في الصفات المورفولوجية والزراعة لتحديد كل من طبيعة التفاعل الجيني ودرجة التوريث في كل من الجيل الأول والثاني، لصفات :

عدد الأيام من الزراعة للأزهار، إرتفاع النبات، طول السنبله - عدد السنابل للنبات، نسبة السنبلات العقيمة، عدد السنبلات الكلى بالسنبله، المحصول الحيوى (الكلى) للنبات، محصول الحبوب للنبات، معامل الحصاد، وزن الألف حبه وطول وعرض الحبة.

وقد أظهرت نتائج تحليل التباين أن التباين الوراثى المضيف كان معنوياً وأكبر من التباين الوراثى غير المضيف لكل الصفات ماعدا محصول الحبوب بالنبات في كلا الجيلين .

كانت تقديرات الإضافة (D) والسيادة (H1 & H2) معنوية في تسع صفات بينما كان المكون غير المضيف معنوي في المحصول الكلى للنبات، محصول الحبوب للنبات، ومعامل الحصاد.

كان متوسط درجة السيادة (H1/D) أقل من الوحدة دلالة على وجود السيادة الجزئية لكل من إرتفاع النبات، طول السنبله، نسبة السنبلات العقيمة، وزن الألف حبة، وطول الحبة في كل من الجيل الأول والثاني بينما كان متوسط درجة السيادة قريب من أو مساوي للوحدة دلالة على تواجد السيادة التامة لصفة عدد الأيام للازهار في حين كانت أعلى من الوحدة دلالة على تواجد السيادة الفائقة لكل من عدد السنابل بالنبات، عدد السنبلات بالسنبله، المحصول الكلى للنبات في كلا الجيلين. وكان مستوى المعنوية للمكونات المقدرة في كل من الجيل الأول والثاني متوافقة وبناءً عليه فإن النتائج المتحصل عليها يمكن تطبيقها لأي من الجيل الأول أو الثاني مستخدمين طرق تحليل الإحصاء البيرومترى لأخذ القرار في تقدير طبيعة نظام التربية وكذلك اختبار مواد التربية. كانت تقديرات درجة التوريث بالمعنى الضيق عالية لكل من عدد الأيام للازهار، إرتفاع النبات، طول السنبله، نسبة السنبلات العقيمة، وزن الألف حبه وطول الحبة في الجيل الأول، بينما كانت منخفضة لعدد الأيام للازهار، وزن الألف حبة وطول الحبة في الجيل الثاني.

كما كانت درجة التوريث متوسطة لصفة عدد السنبلات بالسنبله ومنخفضة لكل من عدد السنابل للنبات، المحصول الكلى للنبات، محصول الحبوب للنبات معامل الحصاد وعرض الحبة في كلا الجيلين.