

## GENETICAL ANALYSIS OF YIELD AND YIELD COMPONENTS IN FLAX (*Linum usitatissimum* L.) .

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### Abstract

Genetical architecture of yield per plant as well as yield component traits in flax (*Linum usitatissimum* L.) from F<sub>1</sub> and F<sub>2</sub> data of a 6 x 6 diallel cross using Hayman's method was investigated during the period from 1999 to 2002. Mean squares due to genotypes were significant for all traits except number of basal branches per plant in both F<sub>1</sub> and F<sub>2</sub> generations.

Estimates of the average degree of dominance  $(H1/D)^{1/2}$  revealed that over dominance or epistasis is important in the inheritance of yield per plant and yield component characters in both generations except seed yield per plant and 1000-seed weight in F<sub>1</sub>, where partial dominance was detected. Concerning gene distribution, positive and negative genes exhibiting dominance were unequally distributed among the parents in most cases. The results showed that at least one group of genes is involved in controlling yield per plant and yield component characters. Heritability estimates (narrow sense) were low for biological yield, straw yield and number of capsules per plant; moderate for seed per plant and number of seeds/capsules; whereas high heritability estimates were obtained for plant height and 1000-seed weight, revealing that additive genes had a major role in the inheritance of such traits and that improvements could be done through selection programs. Graphical analysis showed that the parent S.2465/1 contains dominant genes for biological yield per plant and plant height. The parent Giza8 appeared to possess dominant genes for plant height, whereas the parent Giza7 appeared to contain recessive genes for the same trait. The results showed clearly that accumulation of recessive genes induce maximization for seed yield per plant as well as plant height and technical stem length.

### INTRODUCTION

Information on genetical architecture of quantitative traits in flax has been derived initially from crosses among lines and cultivars of *Linum usitatissimum* L. The method of diallel cross analysis suggested by Jinks and Hayman (1953) has been used to study type of gene action through accurate estimation of the relative magnitudes of each possible source of genetic variability among a given set of parents under certain

assumptions (Jinks, 1954 and Hayman, 1953). This method which involves the study of the variances and co-variances among the progeny from all possible matings between a given number of parental lines, has been applied by Rao and Singh (1985) and Ashry (1991) to get more information about the genetical basis of flax seed and straw yields in addition to related yield component characters. However, none of the previous studies in this respect has tackled the genetical analysis of biological yield which has become the current form for marketing flax crop in Egypt. In this paper an attempt has been made to investigate the genetical architecture of biological yield well as yield contributing traits in flax.

## MATERIAL AND METHODS

The materials used for the present study consisted of 6 parents (two commercial varieties viz.,  $P_1$ (Giza 7) and  $P_2$ (Giza 8) and four promising strains of flax :  $P_3$  (S.2465/1/3),  $P_4$ (S.402/3/5/10),  $P_5$ (S.282/37/14/8) and  $P_6$ (S.533/39/5)}. In 1999/2000 season, the six parents were crossed in a diallel mating design excluding reciprocals to obtain 15  $F_1$  crosses. In 2000/2001 season, parents were re-crossed to obtain more hybrid seeds, and  $F_1$  seed were sown to obtain  $F_2$  seeds. In 2001/2002 seasons, the parents, their 15  $F_1$ s and 15  $F_2$  seeds were evaluated in the breeding nursery of Fiber Crops Res. Section, ARC at Giza .

The experiment was laid out in a randomized complete block design with four replications with restricted randomization where each plot consisted of single  $F_1$  row and two  $F_2$  rows which were guarded by their two respective parents of the cross. Rows were 2 m long, spaced 20 cm apart. Single seeds were hand drilled in 5 cm spacing within rows. At harvest, individual guarded plants were taken at random from each row ; 5 plants for each parent and  $F_1$  and 10 plants for each  $F_2$  per each replication. These plants were used for recording: biological yield/plant, straw yield, plant height, technical stem length, No. of basal branches, seed yield, 1000-seed weight , No. of capsules / plant, and No. of seeds / capsule.

### Statistical analysis

Plot means were used for statistical analysis .The genetic parameters were estimated as described by Hayman (1954) for diallel crosses. The (Vr.Wr) graphs for each character were developed according to Jinks (1954) after computation of covariance – variance regressions. The genetic variance components D,F,H1,H2,h<sup>2</sup> and E were calculated, where: D: The additive genetic variance., F: The covariance of additive and domi-

nance gene effects, which evaluate gene symmetry.; H1: variation due to the dominance effect of genes.; H2: dominance variance adjusted for symmetric positive and negative gene distribution among parents.;  $h_2$ : dominance variance over all heterozygous loci. and E: expected environmental variance .To test the significance of these components,  $t_2$  and b were made according to Singh and Chaudhary (1985). Heritability in narrow sense was estimated by the method described by Mather and Jinks (1971).

**Estimates of genetic ratios:** Variance components estimates were used to calculate the following:  $(H1/D)^{1/2}$ , the mean degree of dominance;  $H_1/4H_1$ ; the proportion of genes with negative and positive effect in the parents and had a maximum value of 0.25;  $KD/KR: \{(4DH1)^{1/2}+F/(4DH1)^{1/2}-F\}$  ,the proportion of both dominant and recessive alleles in the parents and  $h^2/H_2$ : an estimator of number group of genes controlling the performance of the trait and exhibited dominance to certain degree.

## RESULTS AND DISCUSSION

Analysis of variance showed highly significant differences among genotypes for yield/plant and yield component characters in both sets of analyses ( $F_1$  and  $F_2$ ), indicating the presence of genetic variability for these traits except number of basal branches/plant and therefore no further genetic analysis could be conducted for such trait (Table 1).

To test the validity of the assumptions for this type of diallel analysis (homozygous parents, normal diploid segregation, no reciprocal differences, no genotype – environmental interaction, no epistasis, no multiple alleles and uncorrelated gene distribution),  $t^2$  (the uniformity of  $W_r - V_r$ ) was used. Insignificant  $t^2$  values, revealing the validity of all assumptions, were obtained for all traits except 1000-seed weight in  $F_2$  (Tables 2, 3 and 4). Partial failure of the assumptions indicated a more complex genetic system than that described by the theoretical additive dominance model (Hayman, 1954). However, Hayman (1954) stated that it is possible to make estimates of the population parameters for genetic components in case of partial failure of the assumptions, but it must be realized that such estimates are less reliable than would have been had if all the assumptions have been satisfied.

The results of  $F_1$  (Tables 2 , 3 and 4 ) revealed that both additive and non-additive gene action were involved in the inheritance of biological yield/plant, seed yield/plant, 1000-seed weight and number of seeds/capsule as indicated by significant estimates of D (additive components of variation) and  $H_1$  and  $H_2$  (dominance compo-

nents of variation). Moreover, the same pattern of gene action was detected for plant height, technical length, number of capsules/plant and 1000-seed weight in F<sub>2</sub> generation. However, additive genetic component D was significant for plant height, technical length and 1000-seed weight in both F<sub>1</sub> and F<sub>2</sub> suggesting the importance of additive genetic variance for these traits. On the other hand, additive genetic component D was insignificant whereas H<sub>1</sub> and H<sub>2</sub> (dominance components of variation) were significant and larger in magnitude than (D) component for straw yield/plant in both F<sub>1</sub> and F<sub>2</sub> generations, indicating the importance of dominant gene action in the inheritance of this character. The smaller H<sub>2</sub> than H<sub>1</sub> for yield/plant and yield component characters in most cases of this study suggests that the positive U and negative V allelic frequencies are not equal in proportion in the parents. Sign (F) value had a positive sign for all traits in F<sub>1</sub> and F<sub>2</sub> generations except straw yield/plant it is concluded that there is an excess of dominant alleles in the parents. The negative sign of (F) for straw yield/plant in each of F<sub>1</sub> and F<sub>2</sub> generations indicates an excess of recessive genes in the parents. Estimates of h<sup>2</sup> were found to be positive and insignificant in most cases indicating the absence of dominance effect over all loci in heterozygous state.

The average degree of dominance  $(H_1/D)^{1/2}$  was more than unity for yield/plant and yield component characters in F<sub>1</sub> and F<sub>2</sub> suggesting over dominance except for seed yield/plant and 1000-seed weight in F<sub>1</sub> where the average degree of dominance was less than unity indicating partial dominance. Disparity between F<sub>1</sub> and F<sub>2</sub> analyses for these two characters may be due to certain linkages (Hayman, 1954, 1958) or due to sampling error. The ratio  $(H_2/4H_1)$  was less than 0.25 in most cases. This showed that the positive and negative genes exhibiting dominance were unequally distributed among the parents.

The genetic ratio KD/KR was less than unity in both F<sub>1</sub> and F<sub>2</sub> for straw yield/plant indicating that recessive genes were in excess in the parents for this character. However, this genetic ratio was found to be more than unity for almost all other yield/plant and yield component characters suggesting an excess of dominant genes. Number of gene groups controlling each of the studied traits and exhibit dominance to certain degree  $(h^2/H_2)$  suggested that at least one group of genes is involved in controlling biological yield and yield component characters.

Heritability estimates (narrow sense) were low for biological yield/plant, straw yield /plant and number of capsules/plant. This is mainly due to non-additive type of gene action and these traits are more affected by environmental conditions. These selection may not be effective in improving such traits, therefore some form of recurrent

selection program is suggested. Technical stem length and number of seeds /capsule showed moderate heritability, while seed yield/plant was moderate to high. High heritability was indicated for plant height and 1000-seed weight . Improvement of those two traits through selection is expected to be rapid. Similar findings for straw and seed yields/plant as well as their component characters were reported by Rao and Singh (1985) and Ashry (1991). It should be noted that analysis of  $F_1$  diallel table for seed yield/plant was not completed by Ashry (1991) where  $t^2$  value was significant indicating that additive-dominance model with independent gene distribution is not adequate for such trait.

### Graphical analysis

Figures 1,2 and 3 demonstrate the graphical analysis of  $W_r$  (parent/offspring covariance) on  $V_r$  (parental array variance) and their limiting parabola from  $F_1$  and  $F_2$  diallel analyses for yield/plant, straw and seed yield component characters. Emphasis will be directed only to the significant correlation estimates between parental mean performance ( $Y_r$ ) and order of dominance expressed as  $(W_r+V_r)$ . The correlation coefficient ( $r$ ) between the parental means and their order of dominance was negative and significant for biological yield /plant and straw yield /plant in  $F_2$ , indicating that most of increaser genes are dominant (Table 2). None of the coefficient of determinations ( $r^2$ ) presented in Tables (2,3 and 4) is close to unity , therefore it may be stated that none of the tested genotypes contains all of possible recessive or dominant genes. The regression lines cut below the origin for biological yield and straw yield/plant (Figure1) suggesting the presence of over-dominance controlling these two characters. These results are in agreement with those obtained from the ratio  $(H_1/D)^{1/2}$  in Table 2. On the other hand, the regression line intersects the  $(W_r)$  axis above the origin for seed yield / plant , plant height and technical length (Figures1 and 2) . However, the results obtained from the parameter  $(H_1/D)^{1/2}$  indicated the presence of over-dominance for these characters. This contradiction between the two types of analysis may be due to the presence of complementary type of non-allelic interaction which inflated the ratios of  $H_1/D$  and distorted the  $(V_r,W_r)$  graphs (Hayman,1954 and Mather and Jinks, 1971). Parent 3(S.2465/1/3) contained the dominant genes responsible for biological yield and straw yield/plant (Figure1). On the other hand, significant positive correlation coefficient ( $r$ ) between  $(Y_r)$  and  $(W_r+V_r)$  was detected for plant height in both  $F_1$  and  $F_2$  sets of analyses, seed yield/plant in  $F_2$  and technical length in  $F_2$ , suggesting that these characters are controlled by recessive genes. In other words, accumulation of recessive genes induce maximization for seed yield /plant as well as plant height and technical length. These findings might reveal that the larger number of seeds was domi-

nant over a small number where parent 6(S.533/9/5) was located close to the Wr intercept, whereas the parent2 (Giza 8) and 3 (S.2465/1/3) were farthest from the origin (Figure1). Regarding plant height the parents 2(Giza 8) and 3(S.2465/1/3) had dominant genes, whereas parent1(Giza7) had an excess of recessive genes (Figure2). The two parents 6(S.533/9/5) and 4(402/3/5/10) were in the middle of the regression line, therefore, these two parents had dominant and recessive genes in almost equal proportion.

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Table 1. Mean squares from ANOVA of the nine studied characters of 21 genotypes ( parents and crosses ) in flax.

S.O.V.	F1									F2																
	Biological yield /plant (g)	Straw yield/plant (g)	Seed yield/plant (g)	plant height (cm)	Technical length (cm)	No. of basal branches/plant	No. of capsules/plant	1000-seed weight (g)	No. of seeds/ capsule	Replications	Genotypes	Error	Biological yield /plant (g)	Straw yield/plant (g)	Seed yield/plant (g)	plant height (cm)	Technical length (cm)	No. of basal branches/plant	No. of capsules/plant	1000-seed weight (g)	No. of seeds/ capsule	Replications	Genotypes	Error		
	1.876 ns	0.283 ns	0.055 ns	44.551 ns	27.023 ns	0.177 ns	67.993 ns	0.482 ns	0.361 ns	5.714 **	1.226 ns	0.208 *	7.641 ns	1.103 ns	0.290 **	116.442 *	0.216 ns	0.009 ns								
	10.423 **	4.999 **	1.218 **	509.483 **	229.723 **	1.055 ns	319.097 **	6.818 **	2.821 **	6.134 **	3.480 **	1.633 **	377.284 **	196.133 **	0.364 ns	201.237 **	8.419 **	2.529 **								
	1.864	1.106	0.1	23.285	11.136	0.113	41.142	0.196	0.422	1.170	0.897	0.063	9.400	10.983	0.063	29.005	0.099	0.304								

ns, \*, \*\* Nonsignificant at 0.05 and 0.01 levels of probability, respectively.

Table ( 2 ): Estimates of genetic variances components and genetic ratios for yield traits of flax per plant .

Components	Biological yield/plant(g)			Straw yield/plant (g)			Seed yield/plant (g)					
	F <sub>1</sub>											
D	1.316	±	0.386	*	0.213	±	0.403	ns	0.545	±	0.045	**
F	2.151	±	0.932	*	-0.255	±	0.974	ns	0.158	±	0.108	ns
H <sub>1</sub>	11.338	±	0.979	**	4.848	±	1.023	**	0.352	±	0.113	*
H <sub>2</sub>	9.748	±	0.875	**	5.008	±	0.914	**	0.328	±	0.101	*
h <sup>2</sup>	0.963	±	0.589	ns	-0.095	±	0.615	ns	0.160	±	0.068	*
E	0.466	±	0.146	*	0.267	±	0.152	ns	0.024	±	0.017	ns
(H1/D) <sup>0.5</sup>	2.935				4.771				0.804			
H2/4H1	0.215				0.258				0.233			
KD/KR	1.772				0.777				1.441			
h <sup>2</sup> /H2	0.099				-0.019				0.486			
h <sup>2</sup> narrow	0.115				0.092				0.658			
t <sup>2</sup>	1.150	ns			2.230	ns			1.800	ns		
r	-0.192	ns			-0.023	ns			0.322	ns		
r <sup>2</sup>	0.037				0.001				0.104			
OR1	231546				123654				234156			
OR2	165432				513246				123456			
bwr/vr±S.E.	0.611	±	0.227	#	0.319	±	0.251	@	0.634	±	0.193	ns
a±S.E.	-1.573	±	2.296	ns	-0.258	±	0.956	ns	0.111	±	0.169	ns
F <sub>2</sub>												
D	1.435	±	0.752	ns	0.251	±	0.505	ns	0.552	±	0.418	ns
F	5.614	±	3.315	ns	-0.394	±	1.558	ns	0.601	±	0.480	ns
H <sub>1</sub>	28.736	±	3.490	**	10.482	±	2.685	**	3.625	±	2.435	ns
H <sub>2</sub>	22.396	±	6.191	*	9.810	±	2.910	*	3.123	±	0.896	*
h <sup>2</sup>	0.050	±	4.226	ns	0.025	±	2.142	ns	1.255	±	1.086	ns
E	0.347	±	0.258	ns	0.228	±	0.121	ns	0.018	±	0.037	ns
(H1/D) <sup>0.5</sup>	4.474				6.457				2.563			
H2/4H1	0.195				0.234				0.215			
KD/KR	2.553				0.784				1.539			
h <sup>2</sup> /H2	0.002				0.003				0.402			
h <sup>2</sup> narrow	0.058				0.268				0.470			
t <sup>2</sup>	0.240	ns			0.110	ns			3.220	ns		
r	-0.717	**			-0.635	*			0.767	**		
r <sup>2</sup>	0.514				0.403				0.588			
OR1	231546				123654				234156			
OR2	642531				152463				321456			
bwr/vr±S.E.	0.413	±	0.362	ns	0.238	±	0.564	#	0.193	±	0.237	@
a±S.E.	-0.610	±	1.594	ns	-0.002	±	1.097	ns	0.146	±	0.169	ns

ns,\*,\*\*Nonsignificant, Significant at 0.05 and 0.01 levels of probability, respectively.

r= Correlation coefficient between( W<sub>r</sub>+V<sub>r</sub>) and observed parental means(Y<sub>r</sub>).

OR1 Order of the parents based on their mean performance, high to low performance.

OR2 Order of dominance of the parents,dominant-recessive.

# , @ Significant from zero and significant from unity, respectively.



Table ( 3 ): Estimates of genetic variances components and genetic ratios for flax straw yield components

Components	plant height (cm)			Technical length (cm)				
	F <sub>1</sub>							
D	156.067	±	41.999	*	96.452	±	27.383	*
F	1.750	±	101.505	ns	59.287	±	66.181	ns
H <sub>1</sub>	198.037	±	106.617	ns	121.710	±	69.514	ns
H <sub>2</sub>	163.233	±	95.244	ns	94.637	±	62.099	ns
h <sup>2</sup>	75.625	±	64.106	ns	50.687	±	41.796	ns
E	6.075	±	15.874	ns	2.973	±	10.350	ns
(H1/D) <sup>0.5</sup>	1.126				1.123			
H2/4H1	0.206				0.194			
KD/KR	1.010				1.753			
h <sup>2</sup> /H2	0.463				0.536			
h <sup>2</sup> narrow	0.669				0.547			
t <sup>2</sup>	4.690	ns			4.410	ns		
r	0.603	*			0.684	**		
r <sup>2</sup>	0.364				0.468			
OR1	615423				615243			
OR2	154623				156423			
bwr/vr±S.E.	0.172	±	0.211	@	-0.106	±	0.219	@
a±S.E.	62.839	±	49.743	ns	38.299	±	23.101	ns
F <sub>2</sub>								
D	159.812	±	9.722	**	96.797	±	12.837	**
F	88.881	±	50.964	ns	168.865	±	67.318	*
H <sub>1</sub>	498.931	±	38.929	**	500.275	±	51.378	**
H <sub>2</sub>	365.983	±	95.173	**	355.910	±	125.712	*
h <sup>2</sup>	-1.136	±	63.455	ns	12.137	±	83.813	ns
E	2.329	±	3.966	ns	2.628	±	5.238	ns
(H1/D) <sup>0.5</sup>	1.767				2.273			
H2/4H1	0.183				0.178			
KD/KR	1.374				2.245			
h <sup>2</sup> /H2	-0.003				0.034			
h <sup>2</sup> narrow	0.747				0.493			
t <sup>2</sup>	0.150	ns			1.420	ns		
r	0.537	*			-0.031	ns		
r <sup>2</sup>	0.288				0.001			
OR1	615423				615243			
OR2	146532				341562			
bwr/vr±S.E.	0.992	±	0.188	ns	1.055	±	0.454	ns
a±S.E.	8.295	±	75.780	ns	-10.122	±	57.146	ns

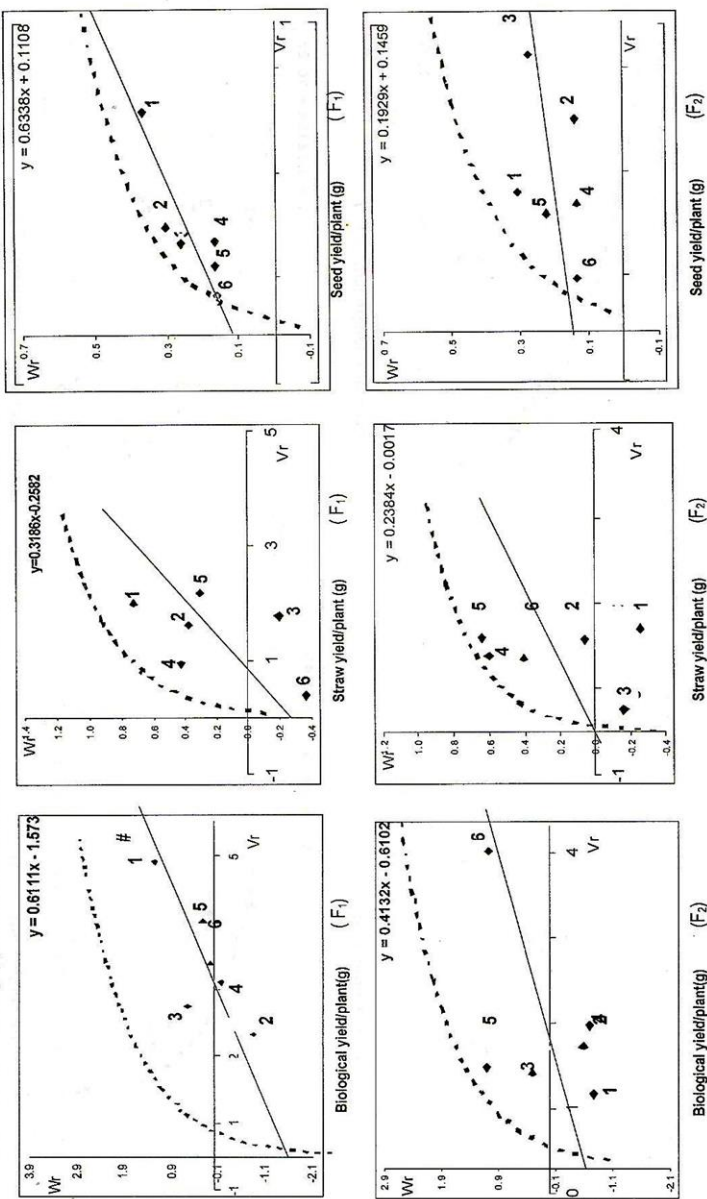
For explanation see Table 2 .

Table( 4 ): Estimates of genetic variances components and genetic ratios for flax seed yield components

Components	No.of capsules/plant				1000- seed weight(g)				No.of seeds/capsule			
	F <sub>1</sub>											
D	42.211	±	25.389	ns	3.081	±	0.109	**	0.736	±	0.187	* *
F	16.929	±	61.361	ns	0.184	±	0.263	ns	0.079	±	0.453	ns
H <sub>1</sub>	248.336	±	64.451	**	0.982	±	0.276	*	1.372	±	0.475	*
H <sub>2</sub>	198.326	±	57.576	*	0.959	±	0.246	**	1.235	±	0.425	*
h <sup>2</sup>	70.297	±	38.752	ns	0.332	±	0.166	ns	0.518	±	0.286	ns
E	10.605	±	9.596	ns	0.052	±	0.041	ns	0.105	±	0.071	ns
(H1/D) <sup>0.5</sup>	2.426				0.565				1.365			
H2/4H1	0.200				0.244				0.225			
KD/KR	1.180				1.112				1.081			
h <sup>2</sup> /H2	0.354				0.346				0.419			
h <sup>2</sup> narrow	0.385				0.833				0.490			
t <sup>2</sup>	1.960	ns			0.340	ns			0.030	ns		
r	-0.325	ns			-0.444	ns			0.366	ns		
r <sup>2</sup>	0.106				0.197				0.134			
OR1	536214				324156				635241			
OR2	526431				563412				521643			
bwr/vrtS.E.	0.054	±	0.281	@	0.848	±	0.168	ns	0.676	±	0.407	ns
a±S.E.	14.649	±	45.410	ns	0.655	±	0.978	ns	-0.018	±	0.670	ns
F <sub>2</sub>												
D	44.524	±	15.145	*	3.108	±	0.442	**	0.768	±	0.428	ns
F	64.923	±	79.431	ns	-1.341	±	0.885	ns	0.579	±	0.667	ns
H <sub>1</sub>	644.019	±	60.605	**	5.499	±	2.500	*	5.905	±	2.461	*
H <sub>2</sub>	587.301	±	148.334	**	5.143	±	1.653	*	5.180	±	1.246	* *
h <sup>2</sup>	63.552	±	98.894	ns	0.262	±	1.427	ns	-0.018	±	1.230	ns
E	8.292	±	6.181	ns	0.026	±	0.069	ns	0.073	±	0.052	ns
(H1/D) <sup>0.5</sup>	3.803				1.330				2.773			
H2/4H1	0.228				0.234				0.219			
KD/KR	1.474				0.721				1.315			
h <sup>2</sup> /H2	0.108				0.050				-0.003			
h <sup>2</sup> narrow	0.226				0.848				0.454			
t <sup>2</sup>	0.780	ns			7.660	*			0.620	ns		
r	-0.237	ns			-0.365	ns			0.449	ns		
r <sup>2</sup>												
OR1	536214				324156				635241			
OR2	436251				563412				346521			
bwr/vrtS.E.	0.139	±	0.722	ns	0.750	±	0.085	@	0.848	±	0.485	ns
a±S.E.	8.835	±	72.203	ns	0.748	±	1.172	ns	-0.127	±	0.724	ns

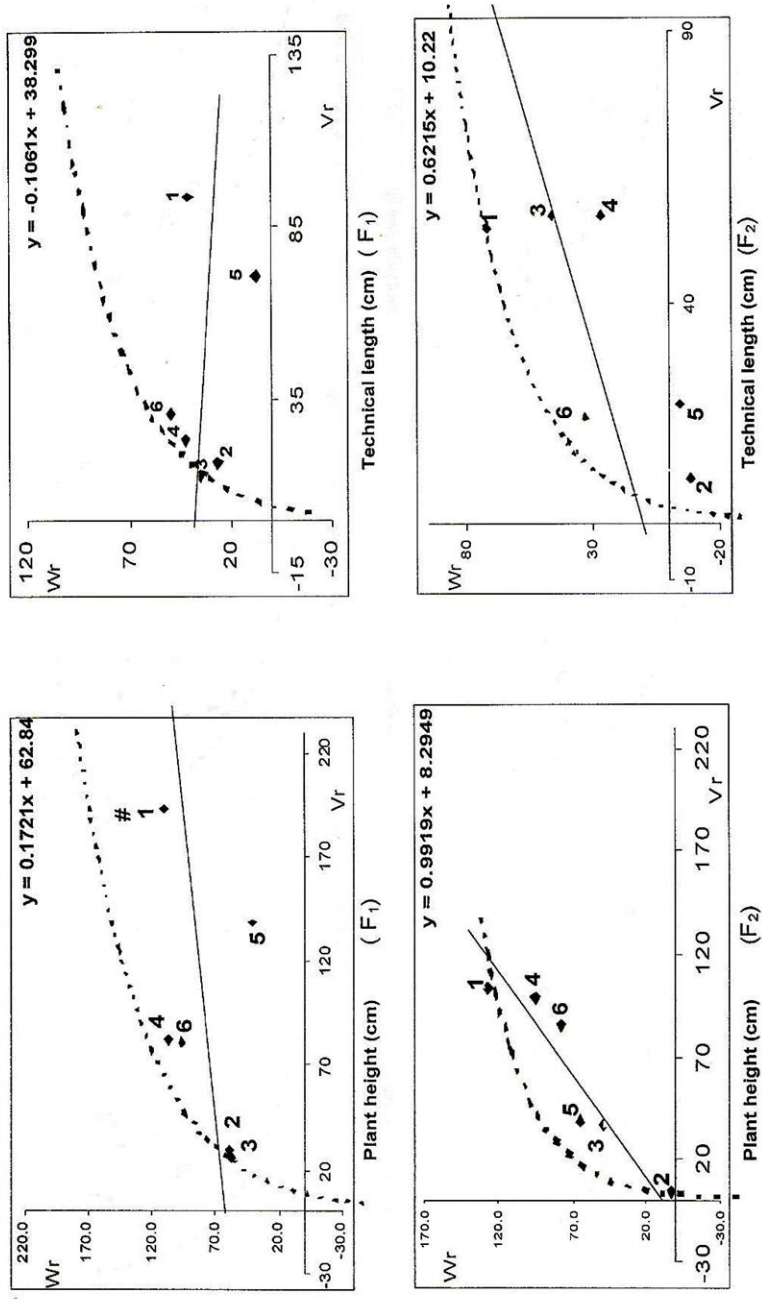
For explanation see Table 2 .

Fig. (1) Parabola graph for flax biological yield/plant and its components in F<sub>1</sub> and F<sub>2</sub> generations

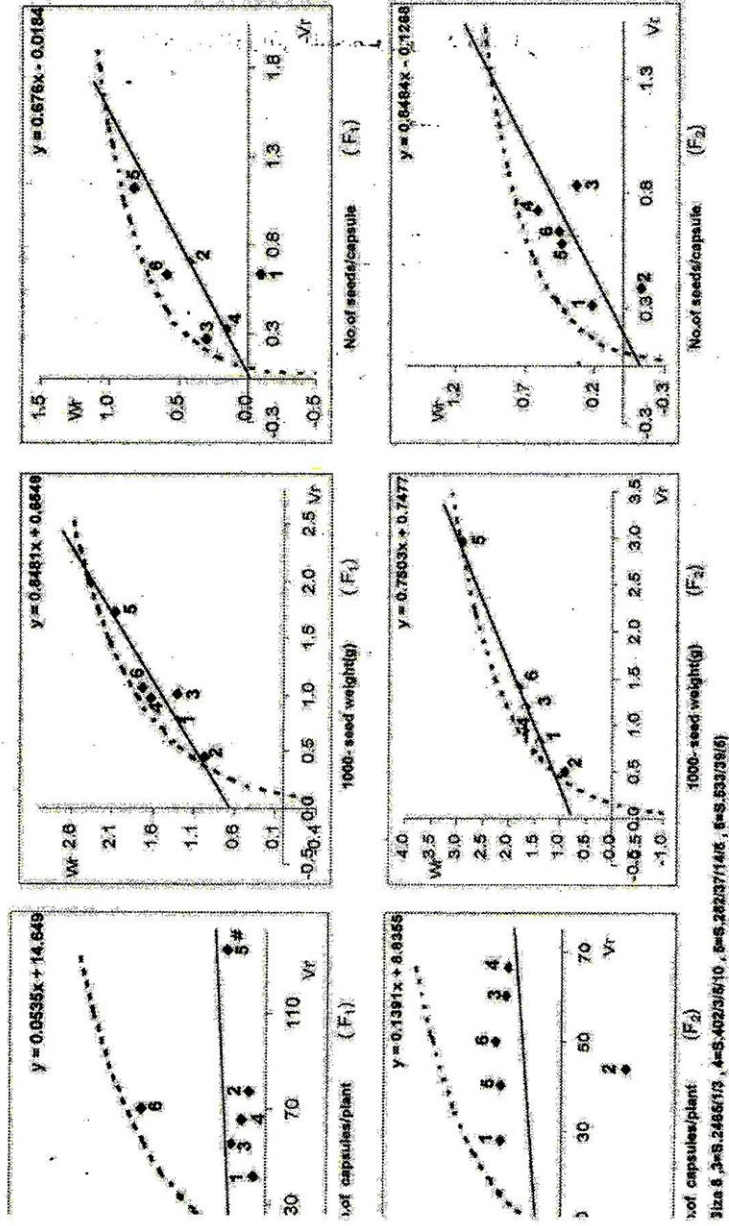


#(1=Giza 7, 2=Giza 8, 3=S.2465/113, 4=S.4023/5/10, 5=S.28237/148, 6=S.5333/9/5)

Fig. (2) Parabola graph for flax straw yield components in F<sub>1</sub> and F<sub>2</sub> generations



#1=Giza 7, 2=Giza 8, 3=S.2465/1/3, 4=S.402/3/5/10, 5=S.282/3/7/14/8, 6=S.533/3/9/5



## التحليل الوراثي للمحصول و مكوناته في الكتان

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يهدف البحث إلى دراسة البناء الوراثي للمحصول ومكوناته في الكتان في الجيلين الأول والثاني لـ ٦ أباء تحت نظام التزاوج الدائري وباستخدام طريقة Hayman في التحليل ، وأجريت الدراسة خلال الفترة من ١٩٩٩ إلى ٢٠٠٢ م. تشير النتائج إلى أن التباينات الراجعة إلى التراكيب الوراثية ( الآباء والهجن ) كانت معنوية في كل الصفات المدروسة ، حدا عدد الأفراد القاعدية - نبات في الجيلين الأول والثاني . كانت تقديرات درجة السيادة  $(H_1/D)^{1/2}$  تقع في نطاق السيادة الفائقة والتفوق والذي كان له أهمية كبيرة في توريث صفة المحصول ومكوناته / نبات في كلا الجيلين ماعدا محصول البذور / نبات ووزن الألف بذرة في الجيل الأول الذي كان في نطاق السيادة الجزئية ، وكان التأثير السالب والموجب للجينات السائدة غير متساوي بين الآباء في معظم الحالات كما أظهرت النتائج أن مجموعة واحدة من الجينات تتحكم في توريث صفة المحصول ومكوناته. كانت درجات التوريث في المعنى الضيق منخفضة للمحصول البيولوجي ومحصول القش وعدد الكبسولات / نبات ، بينما كانت متوسطة في صفة محصول البذور / نبات وعدد البذور / كبسولة ، في حين كانت عالية في صفتي الطول الكلي ووزن الألف بذرة مما يفيد بان هاتين الصفتين يتحكم في توريثها جينات ذات تأثير مضعف ، وأنه يمكن إجراء التحسين لها عن طريق الانتخاب بطريقة مختلفة ، أظهرت التحليلات البيانية إلى أن الأب س ١ / ٢٤٩٩ يحتوى على جينات سائدة تتحكم في توريث صفة المحصول البيولوجي / نبات ومحصول القش والطول الكلي ، كما تشير النتائج إلى أن الأب جيزة ٨ يحتوى على جينات سائدة لصفة الطول الكلي ، بينما الأب جيزة ٧ احتوى على جينات متنحية لنفس الصف . أوضحت النتائج أن تجمع الجينات المتنحية أدى إلى زيادة كبيرة في صفة محصول البذور / نبات بالإضافة إلى الطول الكلي والطول الفعال للساق .