Results and Discussion

RESULTS AND DISCUSSION

This investigation was carried out to through some light on the inheritance of some morphological characters and to study the cytological devision of some Oenothera species. Therefore, the results and discussion will be handled under two headings i.e. genetic variance components of morphological characters and cytological studies.

A- Genetic variance components :

A complete dialled cross analysis as proposed by Hayman (1958) was used to get useful genetic parameter estimates. The genetic variances were obtained for the morphological characters such as :

Earliness (flowering time), plant height number of fruits per plant, number of seeds per fruit, weight of seeds per plant and weight of 1000 seeds in the F_1 and F_2 generations. However, the complete valiolity of the diallel cross analysis is based on the fulfillment of several assumptions. Herein, the regular type of analysis of variance wich included blocks, genotypes, and error variance (Blocks x genotypes) was conducted and the significance of mean squares of genotypes were highly significant when tested againest error mean square for all the forementioned characters in both F_1 and F_2 generations.

Moreover, two general tests were used, Mather and Jinks (1971) to test the valiability of the diallel assumptions. These tests were :

1- The anaysis of variance for the quantity (W_r- V_r); where, W_r is the parent- offspring covariances, and V_r is the array variances. This test was conducted for 4 arrays in each of 4 blockes for F_1 and F_2 generations , Table (2). The value of W_r- V_r was constant over arrays for all the studied character except those for earliness, number of fruits per plant, and weight of 1000 seeds in the F_1 generation; weight of seeds per plant and weight of 1000 seed in the F_2 generation. Therlefore, all the assumptions of the diallel cross analysis were valid for the rest of the characters where insignificant mean squares were obtained. Accordingly, the additive-dominance model with independent gene distribution is adequate and epistatic gene effects are absent for characters which showed insignificant mean squares.

2- The regression coefficient (b) of (W_r, V_r) is expected to be significantly different from zero, but not significantly different from unity if all assumptions are valid. The regression coefficients (b) of all the studied

characters in F_1 generation, (Table (3)) were either significant or highly significant. Moreover, the values were significant or highly significant for number of fruits per plant and number of seeds per fruits. However, the values of (b) were not significantly differed from unity except that of weight of 1000 seeds in the F_1 and F_2 generations, Table (3). Accordingly, most of the traits have satisfied the test while the others were partially fulfilled. It should be noted that the estimation of population parameters are possible with partial fulfillment (Hayman 1954), but these estimates will be less reliable than those traits which completely satisfy the assumption 1.b.o.

1- Earliness (flowering time) :

The estimates of genetic variance components are given, in Table (4). The results showed that the additive gene effect (D) value was positive and highly significant. The value of (H_2) was highly significant with positive value, which indicate asymmetry of positive and negative gene effect. The values of (H_1) and (F) were highly significant. The (h^2) value was significant, suggesting that the effect of dominance was due to heterozygosity.

The proportion of the genetic components and heritability estimates are shown in Table (5). The estimate of degree of dominance $(H_1/D)^{1/2}$ was (0.667), denoting partial dominanee, which was also expressed by regression line (Figs. 9 and 10). The ratio of $(H_2/_4H_1)$ was (0.193), therefore, the frequency of positive alleles was not equal to the frequency of negative ones at loci exhibiting dominance in the parents. The ratio of (K_D/ K_R) was (1.020), suggesting that recessive genes were in excess, a conclusions which was reported by positive (F) value. The (K) value was (3.06), suggesting that there were four groups of genes exhibiting dominance for this trait. Narrow sense heritability was high (30.31 %).Table (5) .

Perhaps, more meaningful estimate of the direction of dominance is obtained by $(V_r - W_r)$ correlations with parental means. This estimate is obtained by computing a linear correlation coefficient between the mean values of $(V_r + W_r)$ of each array averaged over blocks. A high correlation indicates that most dominant alleles act in one direction and most recessive alleles act in the opposite direction (Hyman 1954). The correlation coefficient for time of flowering with number of fruits / plant was the only significant one. However, positive"r" values, though failed to reach the level of significance

was obtained for earliness indicating that most of dominant genes had negative effects. Table (5).

The values of prediction (r^2) were 0.521 and 0.032 in F_1 and F_2, respectively, Table (5).

Similar results have been reported by Kupyanskaya (1987), who found that dominance gene has affected earliness in flax.

The regression line intersects W_r axis below the origin indicates over dominance in the F_1 for earliness, which is in accordance with result detected from the parameter $(H_1 / D)^{1/2}$. As indicated by the distribution of the points representing the different arrays along the regression species O. coronifera possesses and excess of recessive genes for earliness.

The graphical analysis is shown in Figures (9, 10). The distribution of parents on the diallel graph places parent O. nissensis at the recessive side and parent O. biennis at the dominant side. Parents O. coronifera and O. odorata have positions nearly at the middle of regression line, indicating that these parents possess different proportions of genes exhibiting dominance. The regression line, intersected the W_r axis above the origin suggesting partial dominance, which is in accordance with the result

1- O. nissensis
2- O. biennis
3- O. coronifora
4- O. odorata.

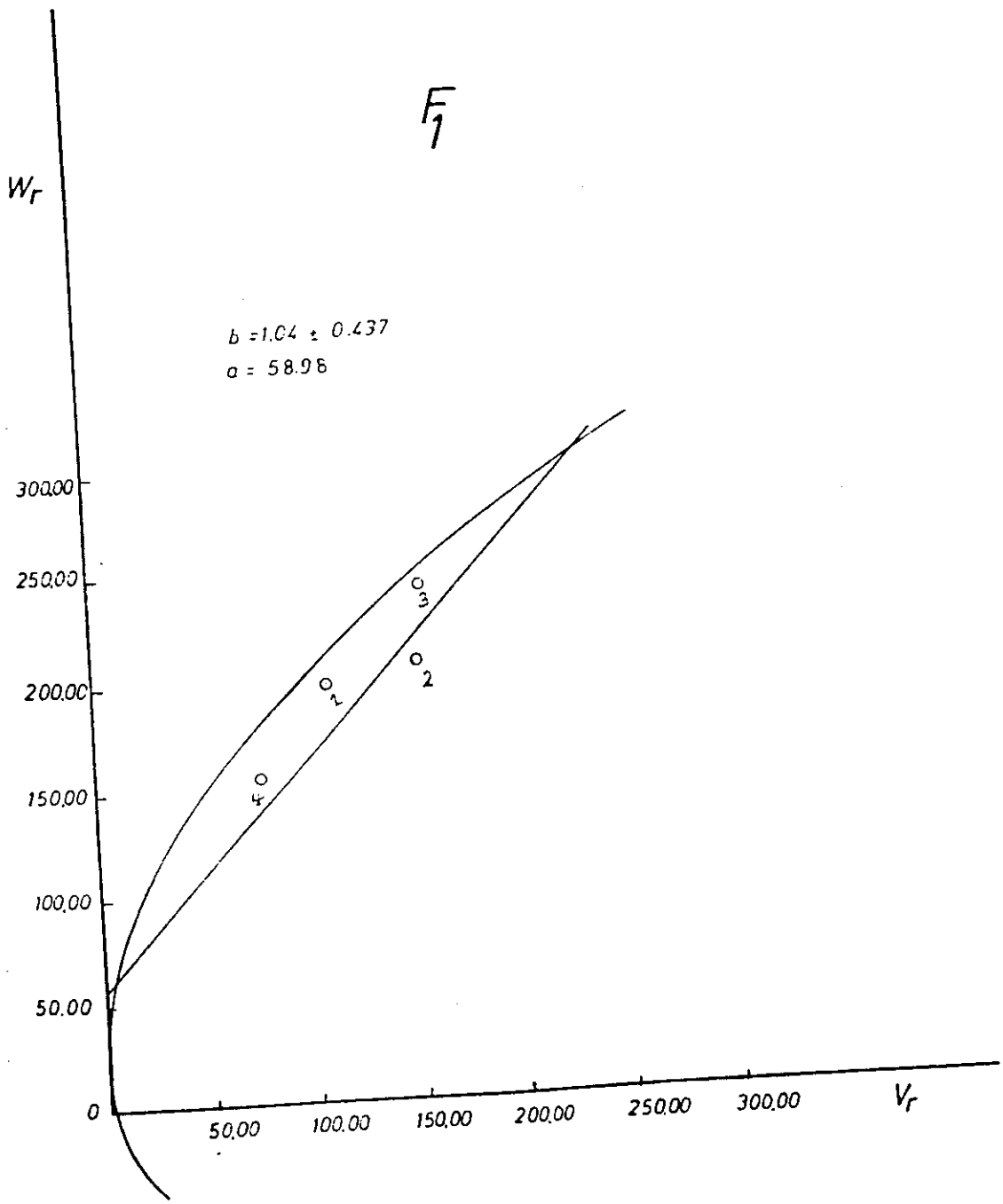

Fig. (9): W_r, V_r regression for earliness of F_1.

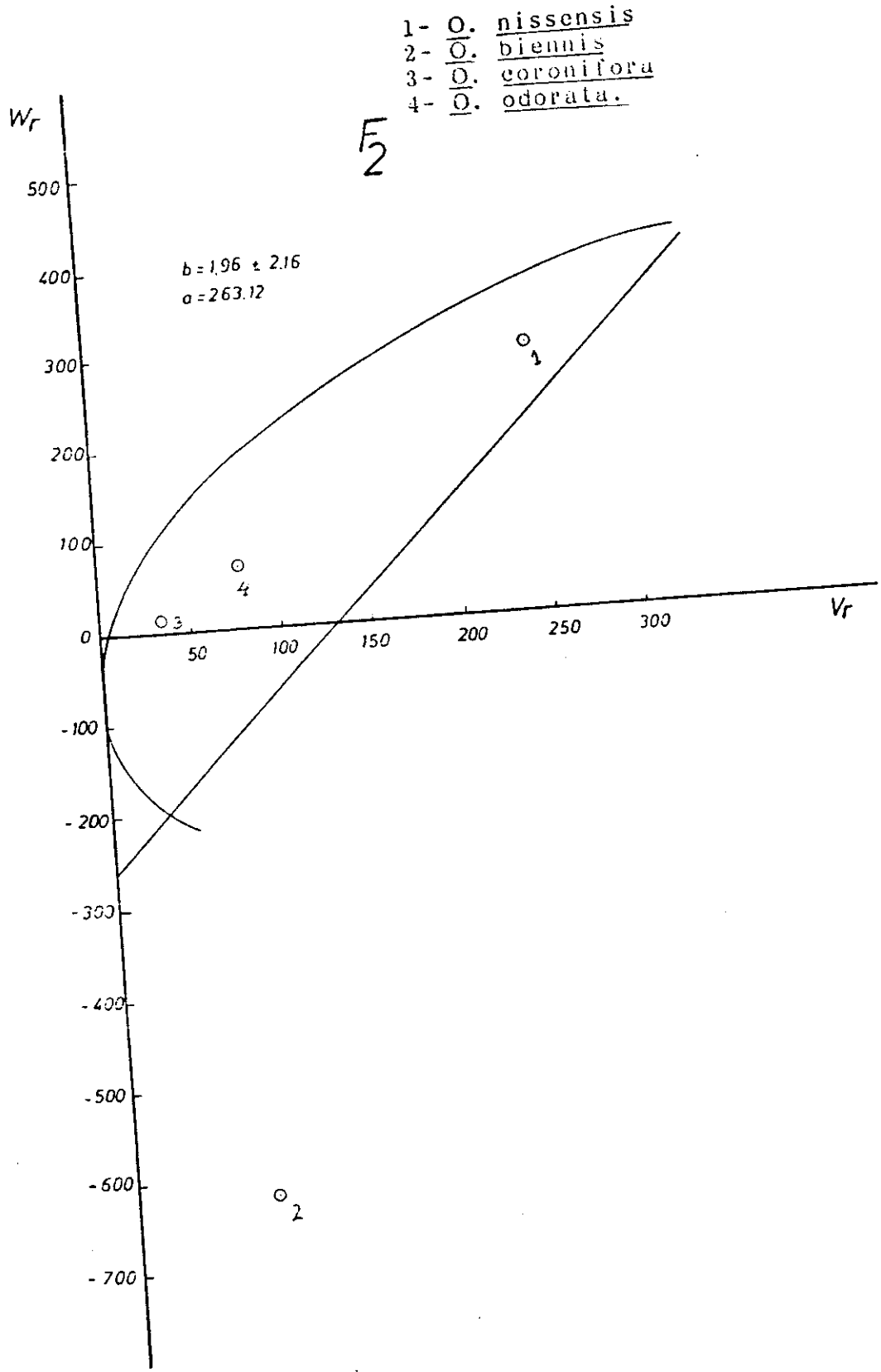

Fig. (16): W_r, V_r regression for earliness in F_2.

detected from the parameter $(H_1 / D)^{1/2}$ = (0.667) in F_1 and 0.770 in F_2 generations.

2- Plant height :

The analysis of variance of $(W_r - V_r)$ for plant height is presented in Table (2). It showed that the differences between arrays were insignificant, indicating a constancy of $(W_r - V_r)$ and the environmental effects were considered to be equal zero. Moreover, the value of regression coefficient (b) of (W_r, V_r) in F_1 was highly significant differing from zero. Meanwhile, value of (b) was insignificantly different from unity, Table (3). But in F_2 the value of regression coefficient (b) of (W_r, V_r) was insignificantly different from both zero and unity.

Estimates of the components of genetic variance are given in, Table (4). The results showed that the (D) value was positive and highly significant, in F_1 and F_2 while (H_2) was highly significant with positive values in F_1 and F_2. The value of (H_1) was highly significant in two generations F_1 and F_2. In the F_1 and F_2 the (F)was highly significant with positive values. The (h_2) values were insignificant in both F_1 and F_2 generations, suggesting that the effect of dominance was due to heterozygosity.

The proportion of the genetic components and heritability estimate are shown in Table (5). The estimate of

degree of dominance $(H_1/D)^{1/2}$ was (0.630) in F_1 and (-0.351) in F_2 denoting partial dominance. This was also expressed by regression line in Figs. (11, 12). The ratios of $(H_2/_4H_1)$ were (0.143) in F_1 and (0.138) in F_2, therefore, the frequency of positive alleles was not equal to the frequency of negative ones at loci exhibiting dominance in the parents. The ratios of (K_D/K_R) were (0.538) in F_1 and (0.315) in F_2, suggesting that recessive genes were in excess, a conclusion which was reported by the positive (F) value. The (K) values were (0.055) in F_1 and(-0.102), suggesting that there was one group of genes exhibiting dominance for this trait. Narrow sense heritability was high (93.13 %) in F_1 and (91.75 %) in F_2. The values of correlation (r) were (0.540) and (0.815) in F_1 and F_2, respectively. In both generations F_1 and F_2 the values of prediction (r^2) were (0.292) and (0.664), respectively.

These results are in agreement with those of Chung, (1976) who showed high ratio of heritability for plant height, Doucet, (1978), who observed partial dominance for stem length and strong negative correlation between seed yield and stem length, Doucet, (1980) who found higher dominance and partial dominance for stem length and Parelek, (1980) found partial dominance for stem length

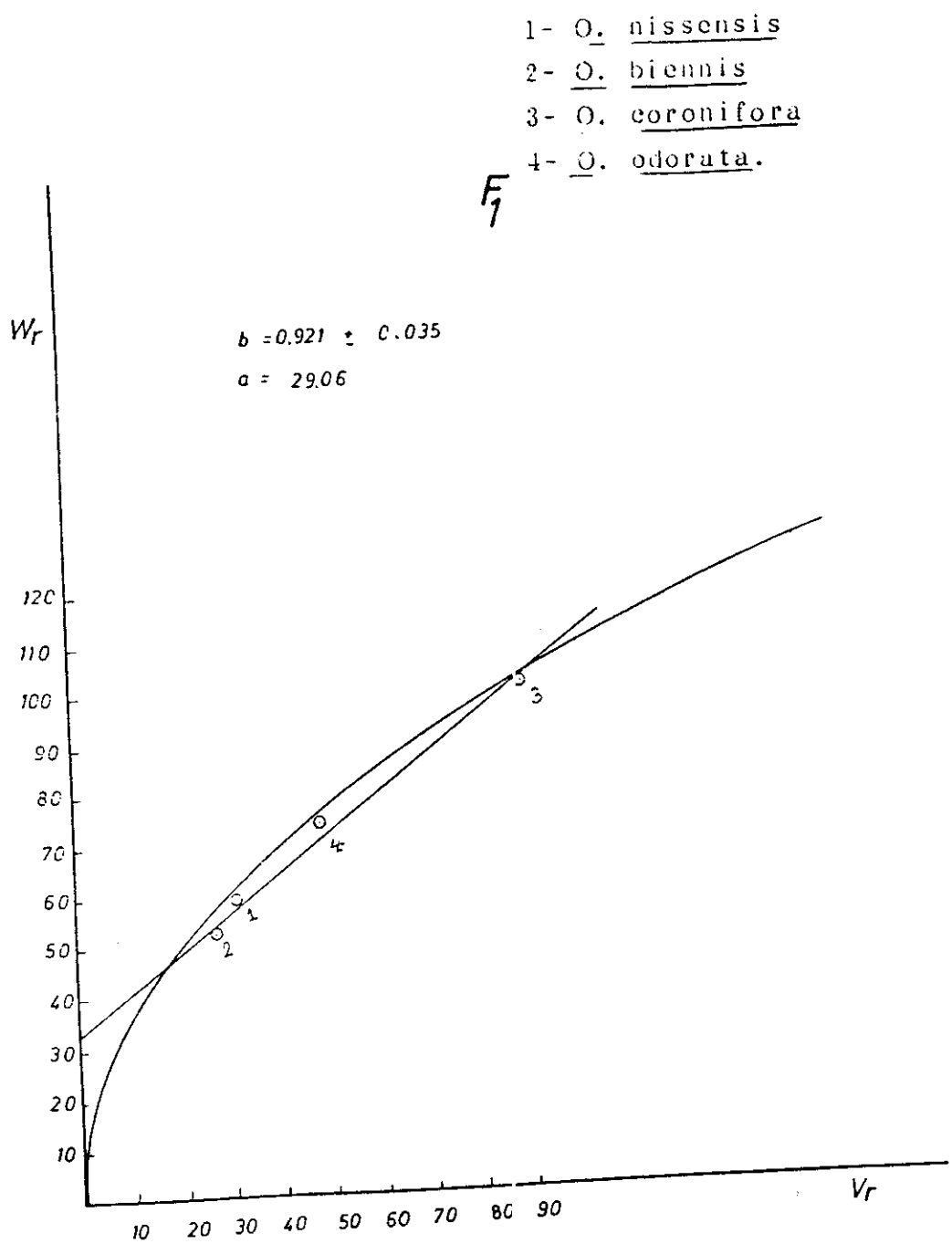

Fig. (11): W_r, V_r regression for plant height of F_1.

1- O. nissensis
2- O. biennis
3- O. coronifora
4- O. odorata.

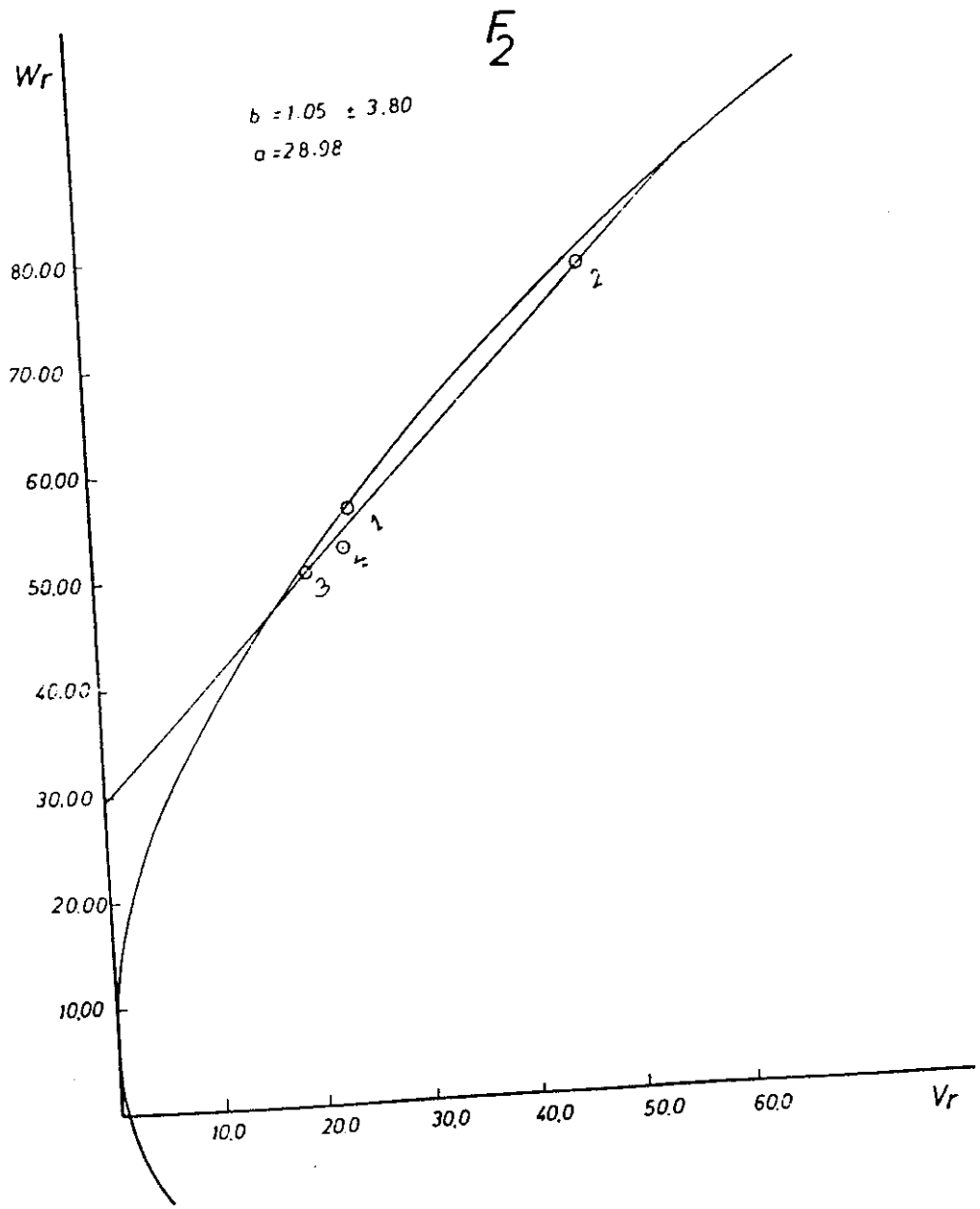

Fig. (12): W_r, V_r regression for plant height of F_2.

3- Number of fruits per plant :

Data in Table (3), indicate a constancy of (W_r,V_r) and the environmental effects were considered to be equal zero in F_1 and F_2 generation. Moreover, the value of regression coefficient (b) of (W_r, V_r) was highly significant different from zero in F_1 and F_2. But it was insignificantly different from unity in F_1 and significantly different from unity in F_2.

The components of genetic variation in, Table (4) showed that the component of additive gene effects (D) as well as the other components were highly significant in both F_1 and F_2 generations. The values of (F) effect were insignificant in F_1 and highly significant in F_2. The values of (H_1) were highly significant in both F_1 and F_2 generations. The values of (H_2) were significant in F_1 and insignificant in F_2. The values of (h^2) were insignificant in both F_1 and F_2 generations. The values of (E) were insignificant in F_1 and highly significant in F_2 generation.

The proportion of genetic components and heritability values were listed in, Table (5). The average degree of dominance $(H_1/D)^{1/2}$ was (0.41) in F_1 and (0.350) in F_2 generation indicating the presence of over dominance .

The proportion of the genes with positive and negative effects in the parents ($H_2/_4\ H_1$) was (0.200) in F_1 and (0.22) in F_2 generation. This indicated a symmetrical distributions of positive and negative alleles at loci exhibiting dominance in the parents. The proportion of dominant and recessive genes in the parents ($K_D/\ K_R$)was (1.220) in F_1 and (1.480) in F_2 generation. This revealed that the proportion of dominant alleles was higher than the recessive alleles in the parents. The ratio of $(h^2/H_2)(K)$ was (0.500) in F_1 generation, suggesting that one group of genes exhibiting dominance was involved. Narrow sense heritability was (90.39 %) and (95.32 %) in F_1 and F_2 generations. The values of correlation (r) were (2.556) and (0.79) in F_1 and F_2 generations and the(r^2) values were (0.531) and (0.626) in F_1 and F_2.

The examination of the distribution of arrays on the graph Fig (13)in F_1 shows that O.coronifera occupies position near the end of the regression line, and O. odorata have the recessive side. Meanwhile, the parents O. odorata. and O. nissensis have intermediate position on the regression line, on the other hand the parent of O. biennis have dominant, side, which was supported by the value of $(H_1/\ D)^{1/2}$) (0.410). Table (5), Figure (10) shows the regression line of F_2 has fallen at approximatly the origin, indicating the presence of complete dominance the parent O . odorata have

1- O. nissensis
2- O. biennis
3- O. coronifora
4- O. odorata.

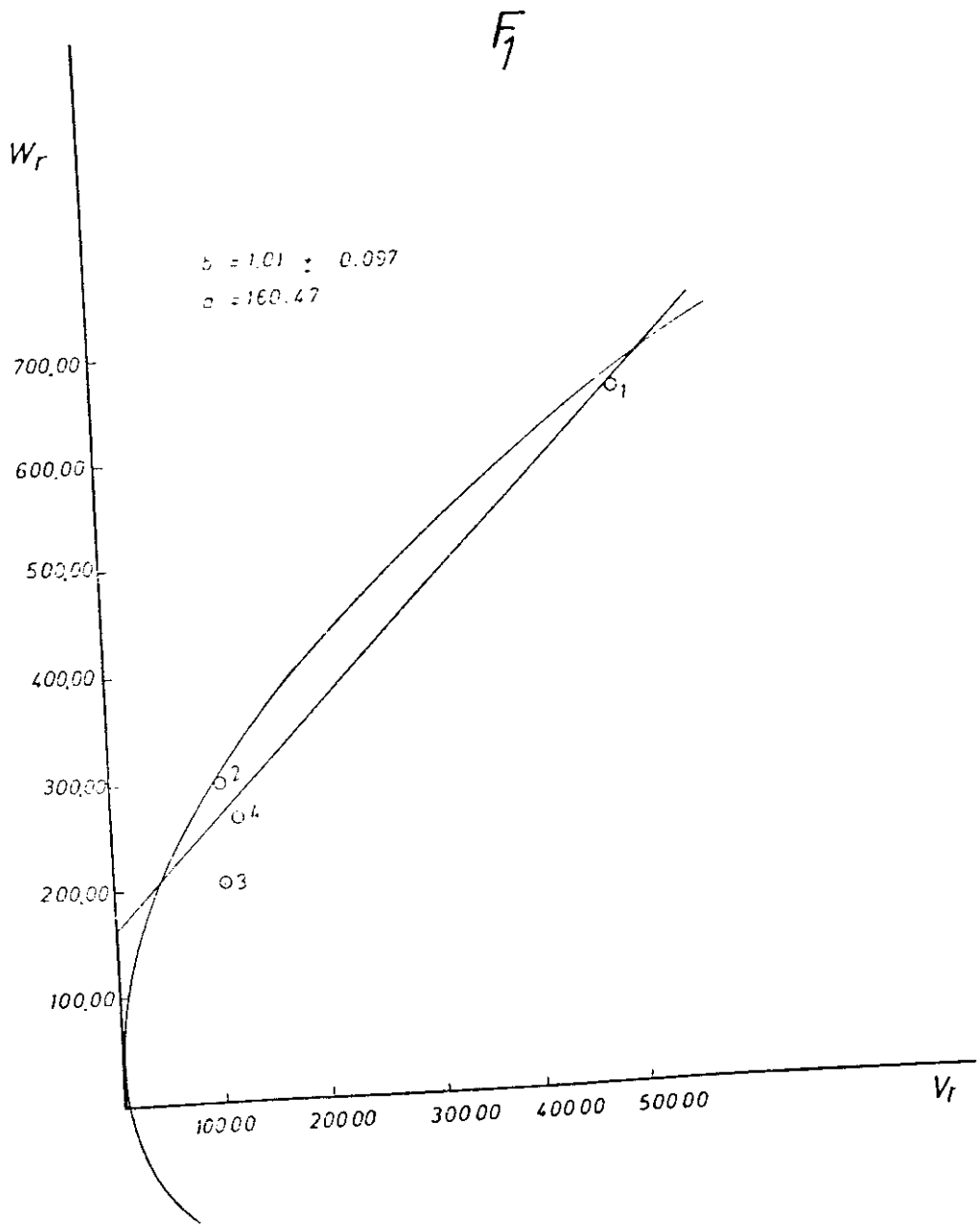

Fig. (13): W_r, V_r regression for number of fruits/ plant of F_1.

1- O. nissensis
2- O. biennis
3- O. coronifora
4- O. odorata.

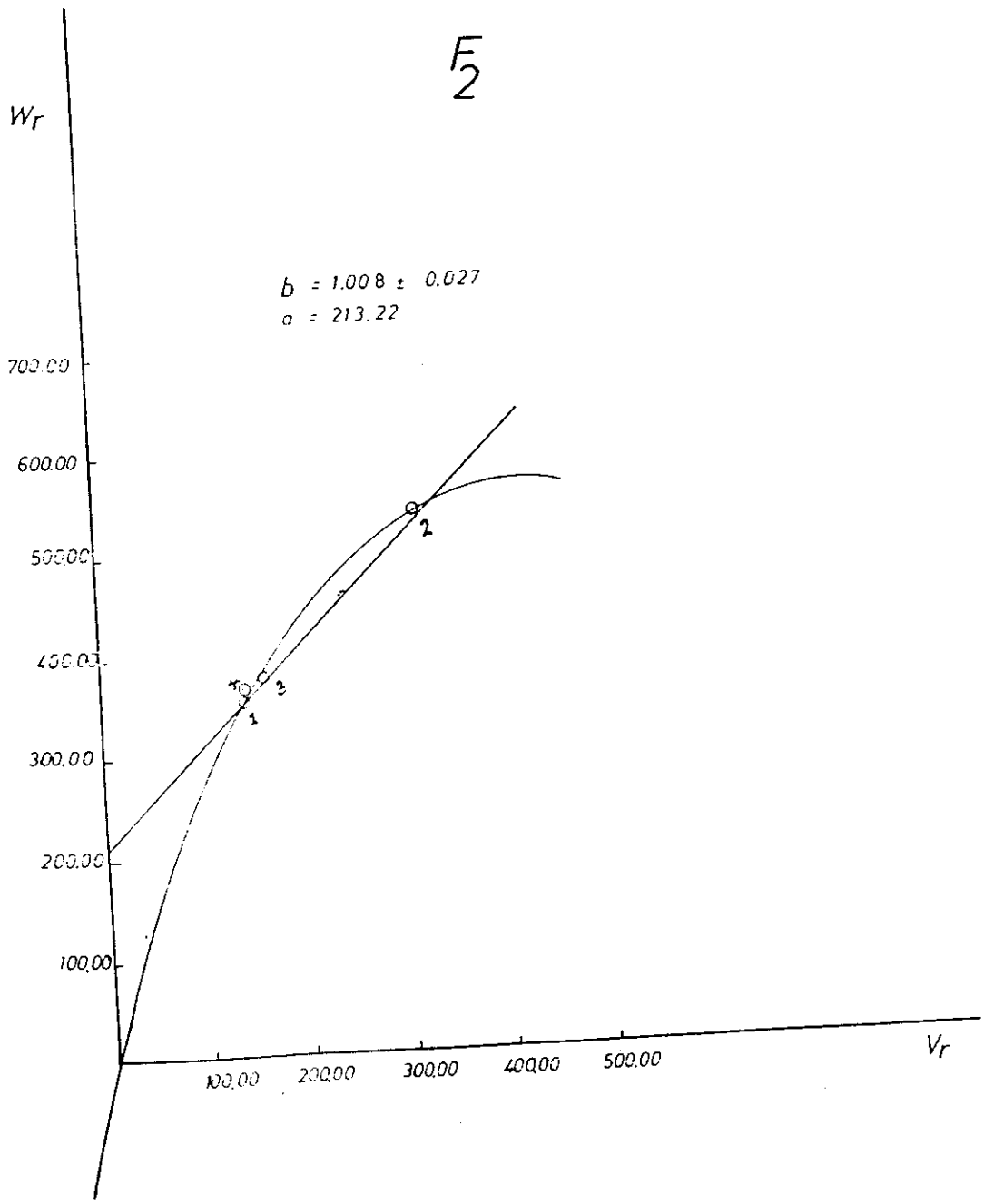

Fig. (14): W_r, V_r regression for number of fruits/ plant of F_2.

a recessive gene side while the parent O. biennis had a dominant allel. Both the parents O. coronifera and O. odorata have a middle position, where the value $(H_1/D)^{1/2}$ = (0.350) Table (5)

These results are in agreement with those of Omran and Alkins (1973) who found highly positive correlation between number of fruits and seed yield, Kupyanskaya (1975), indicating that the F_1 hybrids exceeded their parent and in F_2 most hybrids were intermediate between their parents. Nikandrova (1979), Parelek (1930), also found dominance or over dominance effects for number of fruits and Prygun and Polonetskaya, (1985) found that coefficients of heritability in the broad sense were high.

4- Number of seeds per fruit :

The analysis of variance of $(W_1 - V_r)$ for number of seeds per fruit revealed that the differences between arrays were insignificant in both F_1 and F_2 generation indicating inconstancy of $(W_r - V_r)$ over arrays and the environmental effects were considered to be zero , Table (2). Moreover, the value of regression coefficient (b) of $(W_r - V_r)$ was highly significant different from zero in both F_1 and F_2 generations. Meanwhile, values of (b) were insignificantly different from unity in both F_1 and F_2 generations., Table (3).

The components of genetic variation are presented in Table (4). The results showed that the (D) value was highly significant in both F_1 and F_2 generation and the (H_2) value was highly significant in F_1 and insignificant in F_2 generation. The components of (H_1) were highly significant in F_1 and insignificant in F_2. The (F) values were highly significant in both F_1 and F_2 generations . The (h^2) values were insignificant in F_1 and F_2 and the (E) values were insignificant in F_1 and highly significant in F_2 generation .

The proportion of the genetic components, heritability, r and r^2 are listed in Table (5). The average degree of dominance $(H_1/D)^{1/2}$ was (0.77) in F_1 and (0.153) in F_2, denoting partial dominance, which was also shown by the regression line in Figs. (15 ,16). The ratio of $(H_2/_4H_1)$, was (0.081), (0.149) in both F_1 and F_2 generations. Therefore, the frequency of positive genes was not equal with the frequency of negative alleles at loci exhibiting dominance in the parents. The ratio of dominant to recessive alleles (K_D/ K_R) was (2.688), (2.860) in both F_1 and F_2 generation, The proportion of dominant recessive genes nearly equal in the parents. The ratio of (h^2/H_2) was -0.540 in F_2 generation .

Narrow sense heritability was high giving the values 87.66% and 95.81% in F_1 and F_2, respectively. The correlation values between number of seeds/ fruits and weight of seeds were (0.837) and (2.48) in F_1 and F_2, the values of prediction (r^2) were (0.887) and (6.152) F_1 and F_2 generations

The graphical analysis in F_1 shown in Fig. (15) indicates the distribution of parents on the diallel graph places O. nissensis at the recessive side and O. coronifera at the dominant side, while the parent O. odorata and O. biennis have positions nearly at the middle regression line, which is in agreement with the result detected from the parameter $(H_1/D)^{1/2}$ = (0.772). Table (5 .

The graphical analysis of F_2 the F_2 showd that the parent O. nissensis have a recessive genes, while, the parent O. coronifera have a dominant genes. These results are in accordance with the result detected from the parameter $(H_1/D)^{1/2}$ (0.153) Table(5)Fig(16) The obtained results are in the same line with those found by Allen (1976) who reported that environment had no effect on heritability, Rubes (1976) who found non allelic interactions in the wheritance of seed number, Shehata and Comstock (1976) who found that seed size was negatively correlated with number of seeds/ fruit, Doucet (1978), who observed complete dominance

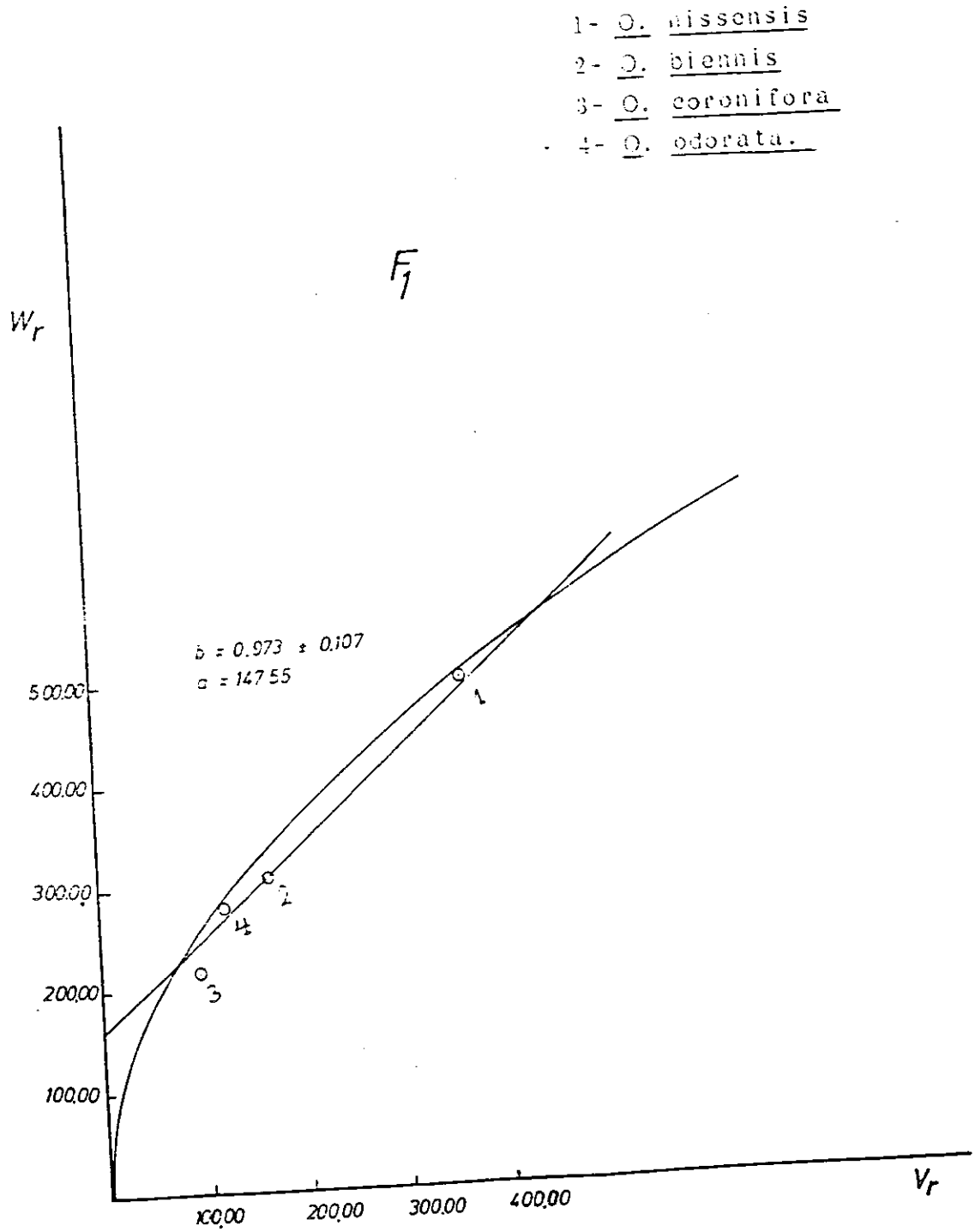

Fig. (15): W_r, V_r regression for number of seed / furit in F_1.

1- O. nissensis
2- O. biennis
3- O. coronifora
4- O. odorata.

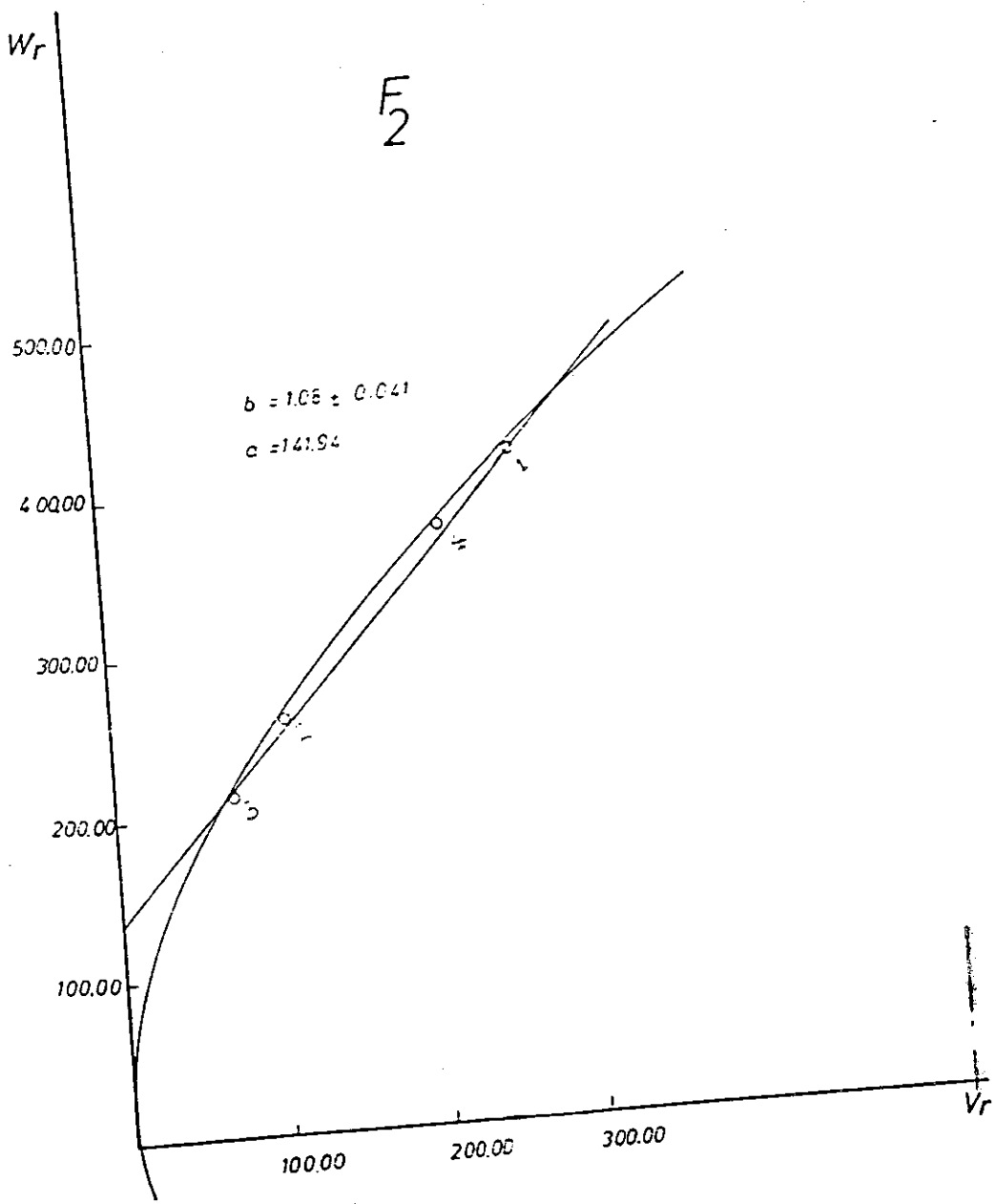

Fig. (16): W_r, V_r regression for number of seeds / fruit of F_2 .

for seed number and found strong positive correlation between seed yield and number of seeds/ fruit.

5- Weight of seeds per plant :

Data in Table (2) showed that the analysis of variance of arrays mean square was insignificant in F_1 and highly significant in F_2 generation indicating a constancy of $(W_r - V_r)$ and the environmental effects were considered to be equal zero in F_1 and was not considered to be equal zero in F_2. Moreover, the value of regression coefficient, (b) of (W_r, V_r) was highly significant in F_1 and insignificant in F_2 generation but it was insignificantly different from unity in both F_1 and F_2 generation, Table (3).

The components of genetic variation in Table (4) showed that the component of addtive gene effects (D) , were highly significant in both F_1 and F_2 generation, the value of (F) was insignificant in F_1 and highly significant in F_2 while the (H_1) value was insignificant in F_1 and highly significant in F_2. Moreover, the values of (H_2), (h^2) and (E) were insignificant in both F_1 and F_2 generations .

The proportion of genetic components and heritability are listed in Table (5). The average degree of dominance $(H_1/D)^{1/2}$ were (0.15) and (0.751) in both F_1 and F_2 generations denoting over dominance. The proportion of the genes with positive and negative effects in the parents $(H_2/_4H_1)$ were (0.170) and (0.02) in both F_1 and F_2 generatd ion; This indicated asymmentrical distributions of positive and negative alleles at loci exhibiting dominance in the parents. The proportion of dominant and recessive genes in the parents (K_D/ K_R) were (0.770) and (1.520) in both F_1 and F_2. This revealed that the proportion of dominant alleles was higher than the recessive alleles in the parents. The ratio of (h^2/H_2) was (0.130) and (0.132) in the two generations , suggesting that one group of genes exhibiting dominance was involved. Narrow sense heritability values were higher (95.95 %) and (95.89 %) in both generations . Values of (r) were (0.158) and (1.269) in both generation and the prediction values (r^2) were (0.025) and (1.610) in the F_1 and F_2 .

The regression line intersects W_r axis below the origin indicating dominance in the F_1 which is in accordance with result detected from the parameter $(H_1/ D)^{1/2} = (0.150)$ Table (5). As indicated by the distribution of the points representing the different arrays along the regression line, O. odorata possesses as excess of dominant over

recessive genes for weight of seed/ plant, while O. coronifera possesses an excess of dominant genes Fig. (17).

The graphical analysis in F_2 for weight of seed/ plant is shown in Fig. (18). The distribution of parents on the diallel graph places the parent of O. biennis at the recessive side and parent O. odorata at the over dominant side, while parents O. coronifera and O. nissensis have positions nearly at the middle regression line, indicating that these parrents possess different proportions of genes exhibiting dominance. The regression line, intercepted the W_r axis below the origin suggesting over dominance, which is in accordance with the result detected from the pramater $(H_1/D)^{1/2} = (0.721)$. Table (5).

These results are in accordance with those reported by Omran and Atkins, (1973), who found that seed yield was highly positively correlated with number of fruits in flax, Allen (1976) who found no effect for environment on heritability of seed yield, Rubes, (1976) observed non-allelic and additive interaction for seed yield with over dominance, Shehata and Comstock, (1976) found that seed yield was positively associated with number of bolls, Doucet (1978) reported that partial dominance for seed yield and epistasis was significant for yield and stem length, Doucet, (1980), found higher values of dominance,

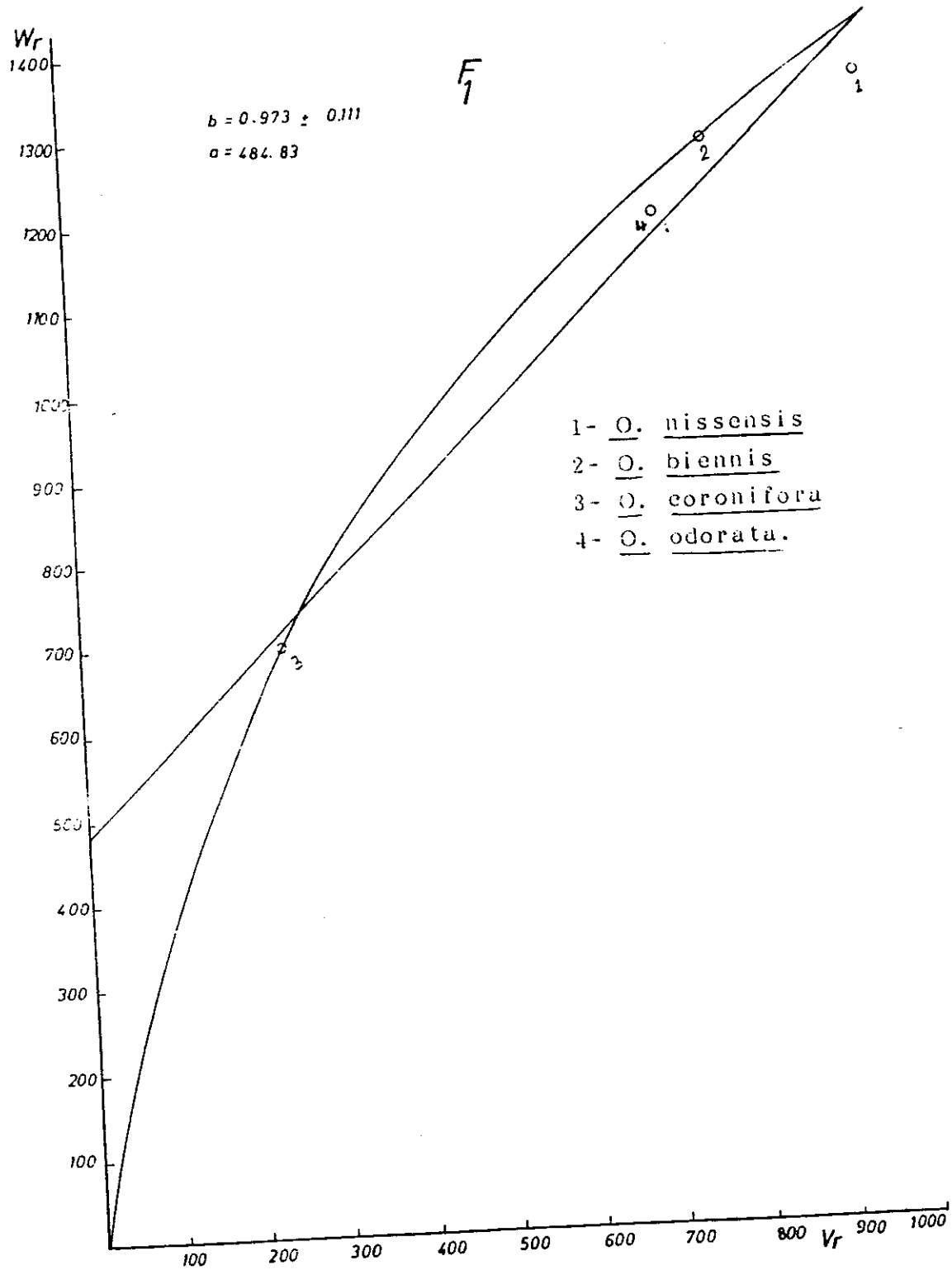

Fig. (17): W_r, V_r regression for wichgt of seeds per plant. of F_1.

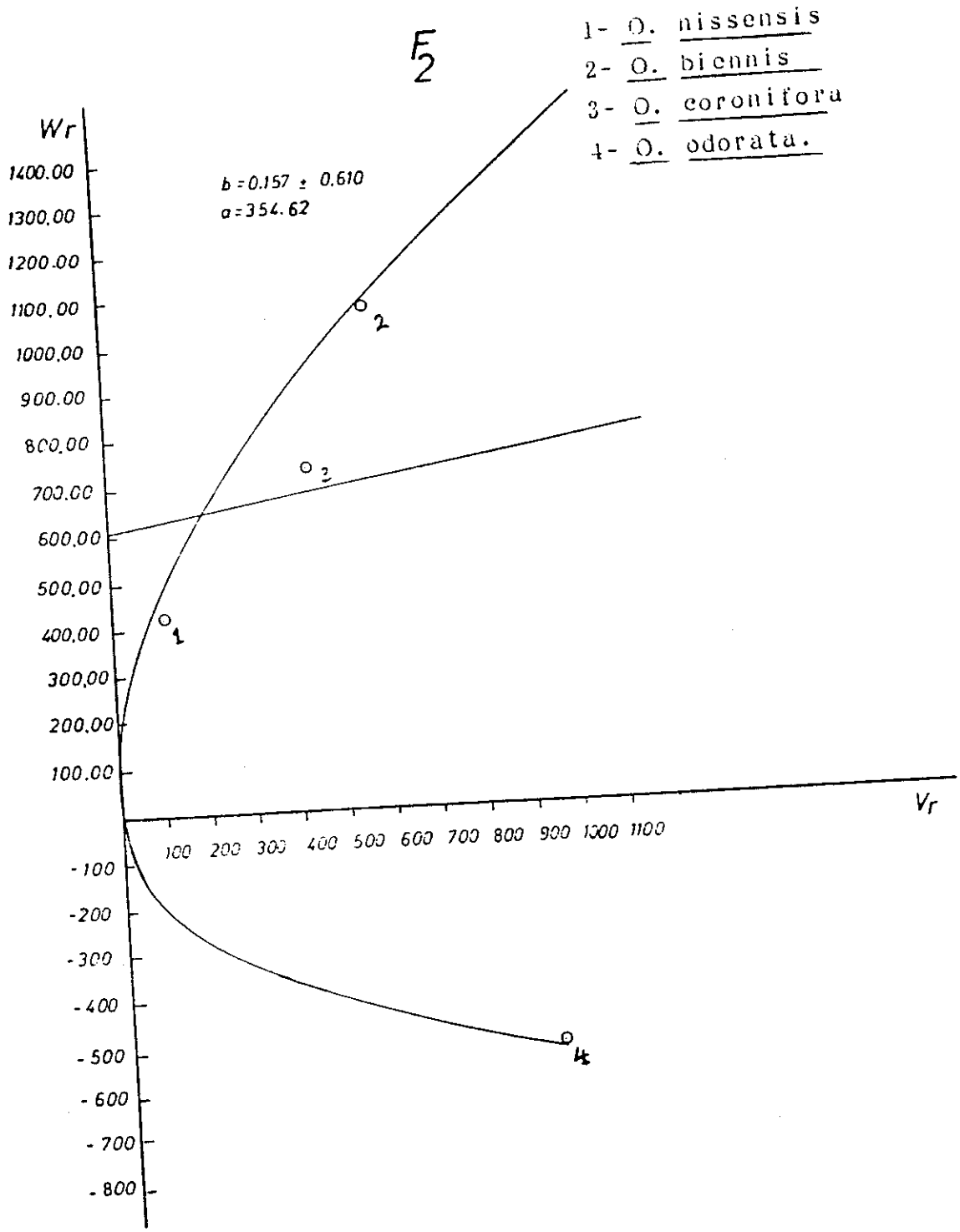

Fig. (18): W_r, V_r regression for weight of seeds / plant of F_2.

seed weight- and Erminov and Dynnik, (1981) who observed that coefficient of heritability for seed size was high (78 %) .

6- 1000- seeds weight :

The anova of (W_r- V_r) for weight of 1000 seeds showed that the differences between arrays mean of squares were highly significant in F_1 generation. This indicated a constancy of (W_r - V_r) over arrays and environmental effects were not consedered to be zero. But in F_2 generation differences were insignificant indicating a constancy of (W_r- V_r) over arrays and environmental effects were considered to be zero Table (2). Moreover, the regression significantly different from zero in F_1 and insignificantly different from zero in F_2. Regression coefficient of (W_r, V_r) was negative and highly significant in F_2 (Table 3).

The components of genetic parameters in Table (4) showed that the values of (D) were highly significan and differ from zero in both F_1 and F_2 generations. However, the values of (F) were insignificantly in F_1 and highly significant in F_2, but the values of (H_1) were highly significant in both F_1 and F_2 generations. The H_2 values were highly significant in F_1 and insignificant in F_2 , but the values of (h_2) and (E) were insignificantly in F_1

and highly significant in F_2 generation.

The proportion of the genetic components and heritability are given in Table (5). The estimate of degree of dominance $(H_1/D)^{1/2}$ was (1.170) in F_1 and (0.470) in F_2 generation denoting partial dominance. The ratio of $(H_2/4\ H_1)$ was (0.190) and (0.600) in both F_1 and F_2 generations. This indicated asymmetrical distribution of positive and negative alleles at loci exhibited dominance in parents. The ratio of $(K_D/\ K_R)$ was (1.530) and (0.220) in F_1 and F_2 generations, showing that the proportion of dominant alleles was greater than the recessive alleles in the parents. The ratio of (h^2/H_2) (K) was (0.100), (-1.500) in both F_1 and F_2 generations suggesting that one group of genes exhibiting dominance was involved. Narrow sense heritability was (62.69 %) in F_1 and (92.00 %) in F_2 generations. The values of (r) were (0.640) and (0.148) in F_1 and F_2. The prediction values, (r^2) were (0.140) and (0.022) in both F_1 and F_2 generation,respectively.

The examination of the distribution of arrays on the graph in F_1 shows that parent O. nissensis have recessive side while the parent of O. odorata possess dominant genes. Both parents of O. coronifera and O. biennis have a positions nearly middle regression line which is in accordance with result detected from the parameter $(H_1/D)^{1/2}$ Fig. (19).

In the graphical analysis Fig.(20)The distribution of arrays in F_2 of the parent of O. nissensis have recessive genes side while the parent of O. coronifera have dominant genes this result was in accordance with the result detected from the parameter $(H_1/D)^{1/2}$ = (0.470) Table (5).

In this connection similar results were reported by Omran and Atkins (1973) who found high negative correlation between seed yield and 1000 seeds weight, Douet , (1978) noted that partial dominance was observed for 1000 seeds weight while, additive gene effects were significant for 1000 seeds weight and greater number of dominance genes for 1000 seeds weight and found strong positive correlation between seed yield and 1000 seeds weight.

1- O. nissensis
2- O. biennis
3- O. coronifora
4- O. odorata.

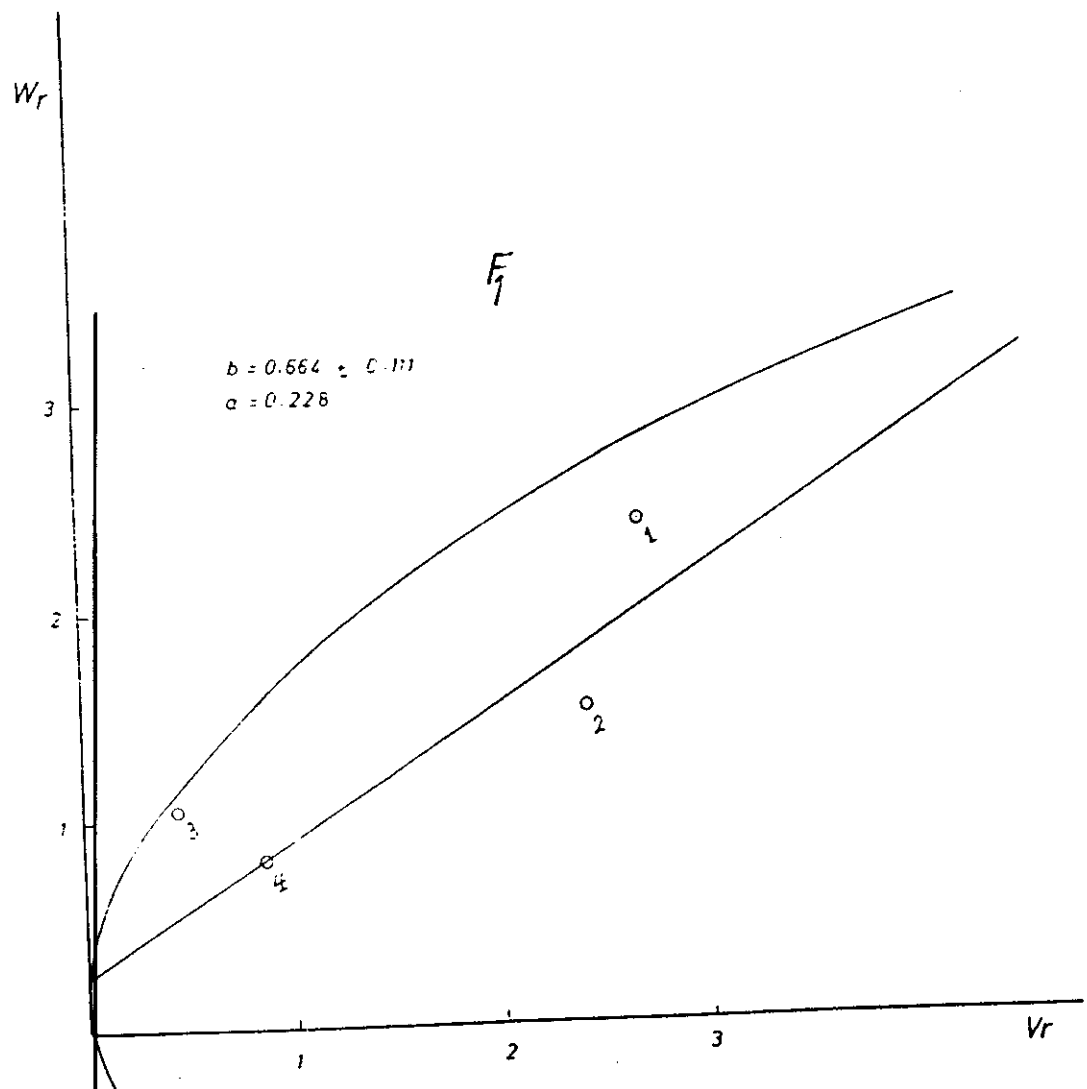

Fig. (19): W_r, V_r regression for weight of 1000- seed of F_1

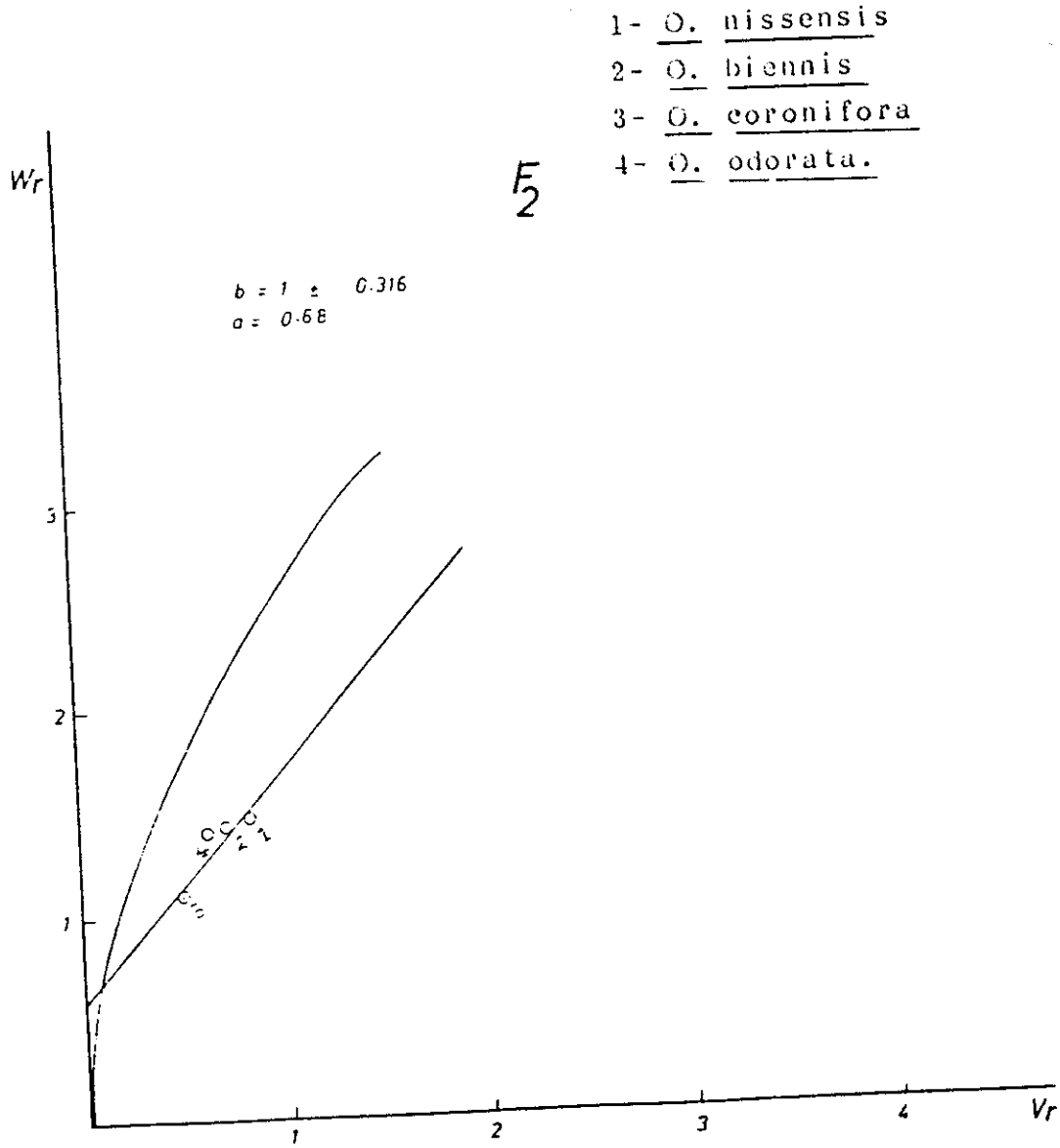

Fig. (20): W_r, V_r regression for wichgt of 1000 seeds/ of F_2.

Table (1): Analysis of variance for earliness , plant height, number of fruits/ plant, number of seeds/ fruit of weight of seeds/plant and weight of 1000 seeds. of *O. oenothera* sp.

S.V	D.F.	Mean squares (M. S.)											
		Earliness		Plant height		Number of fruits / plant		Number of seeds /fruit		Weight of seeds / plant		Weight of 1000 seeds	
		F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Blocks	3	734.19**	5032.12**	160.42**	46.84	5.02**	1401.57**	1769.71**	22.62	1894.90**	10917.01**	0.090**	0.12**
Genotypes	15	10041.67**	13066.95**	5023.76**	3201.40**	20947.67**	18169.37**	19579.69**	21941.59**	81931.78**	1791.61**	109.32**	0.003
Geno. x Blockss	45	127.52	17.30	37.90**	35.10	5.71	228.15*	49.53**	135.96	97.65**	17444.44**	0.073**	0.009
Error	1088	181.25	102.77	00.765	33.33	0.786	256.90	14.38	202.69	7.28	578.74	0.010	0.030

* Significant.

** Highly significant.

Table (2):Analysis of variance of ($W_r - V_r$) values for F_1 and F_2 generations of O. oenothera sp.

S.V.	D.f.	Earliness	Plant height	Number of fruit /plant	Number of seeds/fruit	Weight of seeds / plant	Weight of 1000- seeds
				F_1 generations			
Replications	3	1722.630	3731.180	45.640	158250.410	1217751.97	1.680
Arrays	3	10786.080**	3164.150	3832.930**	162645.100	1106099.54	4.100**
Error	9	1515.150	15123.760	305.050	588059.000	5028266.00	1.100
				F_2 generations			
Replications	3	6157.090	1048.750	2210.270	14005.820	20959.98**	0.360**
Arrays	3	157035.110	373.170	2278.150	5435.280	24410.650**	0.010
Error	9	301188.690	3129.540	3551.250	9123/170	9258/870	0.080

* Significant. , ** Highly significant.

Table (3): (W_r, V_r) regression coefficients in F_1 and F_2 generations of O. oenothera sp.

No.	Character measurement	Genera-ration	b	sb	b-0 / sb	b-1 / sb
1	Floring time (Earliness)	F_1	1.04	± 0.44	2.36**	0.09
		F_2	1.95	± 3.16	0.62	0.30
2	Plant height	F_1	0.92	± 0.04	23.00**	-1.00
		F_2	1.05	± 3.80	0.27	0.01
3	Number of fruits/plant	F_1	0.97	± 0.11	8.81**	-0.27
		F_2	1.08	± 0.04	27.00**	2.00*
4	Number of seeds/fruit	F_1	1.01	± 0.10	10.10	0.10
		F_2	1.01	± 0.03	23.66**	0.33
5	Weight of seeds yield / plant	F_1	0.97	± 0.11	8.81**	-0.27
		F_2	0.16	± 0.61	0.26	-1.37
6	Weight of 1000 seed	F_1	0.67	± 0.11	6.09**	-3.00**
		F_2	0.04	± 0.32	0.12	-3.00**

*, ** Significant at 0.5 and 0.1 level of probability, respectively.

Table (4): Mean estimates of genetic and environmental components from F_1 and F_2 in 4 x 4 diallel crosses of *Oenothera* sp.

Variables		D ± S.E.	F ± S.E.	H_1 ± S.E.	H_2 ± S.E.	h_2 ± S.E.	E ± S.E.
Earliness	F_1	396.77** ± 17.60	58.85** ± 47.34	176.48** ± 45.32	153.89** ± 51.28	50.24** ± 32.11	5.71 ± 7.89
	F_2	487.55** ±258.98	274.59** ±694.92	284.86 ±665.33	141.16 ±751.74	102.46 ±471.32	10.07 ±115.62
Plant height	F_1	131.29** ± 1.98	49.48** ± 5.32	51.33** ± 5.09	29.39** ± 5.76	1.60 ± 3.61	0.43 ± 0.89
	F_2	129.46** ± 0.87	9.27** ± 2.34	150.94** ± 2.24	8.87** ± 2.54	0.90 ± 1.59	1.85** ± 0.39
Number of fruit ʃ /plant	F_1	689.57** ± 15.05	56.36 ± 40.36	115.45** ± 38.64	92.72* ± 43.72	46.27 ± 27.38	0.044 ± 6.73
	F_2	657.49** ± 13.68	89.69** ± 36.70	80.13** ± 35.14	68.51 ± 39.75	35.56 ± 24.89	14.27** ± 6.12
Number of seeds/ / fruit	F_1	896.59** ± 21.67	633.66** ± 58.15	534.51** ± 55.67	172.46** ± 62.98	68.30 ± 39.44	0.799 ± 9.69
	F_2	869.67** ± 5.52	127.81** ± 14.81	20.26 ± 14.18	12.05 ± 16.04	6.47 ± 10.05	16.89** ± 2.47
Weight of seeds / plant	F_1	2143.70** ± 82.26	215.66 ±220.72	312.72 ±211.33	206.20 ±239.09	27.19 ±149.70	0.405 ± 17.27
		2113.16** ± 38.02	1037.01** ±103.64	1099.68** ± 99.23	116.83 ±112.26	15.45 ± 70.29	32.152 ± 36.79
Weight of 1000 seeds	F_1	2.91** ± 0.30	1.13 ± 0.79	3.98** ± 0.76	2.93** ± 0.86	0.29 ± 0.54	0.089 ± 0.13
	F_2	3.02** ± 0.05	0.48** ± 0.14	0.65** ± 0.13	0.16 ± 0.15	0.24** ± 0.09	0.064** ± 0.02

* Significant ** Highly significant.

Table (5): Mean ratios estimating genetic characteristics of the populations of F_1 and F_2 generations in O. oenothera sp.

	Genera-tion	Earleness	Plant height	Number of fruit/ plant	Number of seed/ frut	Weight of seed / plant	Weight of 1000 seeds
$(H1/D)^{1/2}$	F_1	0.667	0.630	0.410	0.772	0.150	1.170
	F_2	0.770	-0.351	0.350	0.153	0.721	0.470
$H_2/4H_1)$	F_1	0.193	0.143	0.200	0.081	0.170	0.190
(UV)	F_2	0.124	0.138	0.220	0.149	0.027	0.600
(K_D/K_R)	F_1	1.020	0.538	1.220	2.688	0.770	1.530
	F_2	4.780	0.815	1.480	2.860	1.520	0.220
K	F_1	3.060	0.055	0.500	0.396	0.130	0.100
	F_2	0.726	-0.102	6.070	-0.540	0.132	-1.500
Heritability	F_1	80.310	93.19 %	93.39 %	87.66 %	95.95 %	62.69 %
	F_2	91.090	91.75 %	95.32 %	95.81 %	95.89 %	92.00 %
r	F_1	0.722	0.540	2.556	0.837	0.158	0.640
	F_2	-0.177	0.815	0.791	2.480	1.269	0.148
r^2	F_1	0.521	0.292	6.531	0.887	0.025	0.410
	F_2	0.032	0.664	0.626	6.152	1.610	0.022

II- Cytological studies :

A- Karyotype studies :

The main features of the individual chromosomes in the haploid complement, of the different species of Oenothera, O. nissensis, O. biennis, V. grandiflora, O. coronifera and O. odoratea are found in tables (6, 8 , 10, 12 ,respectively.

Considerable differences in stainability of proximal and distal regions of the chromosomes were observed. Region near the centromere is always more dense and strongly stained, whereas the distal parts of the chromosomes are very slightly stained as a rule. Similar observations were performed earlier by Cleland 1972. According to this observation the distal region of chromosomes of Oenothera is euchromatic, whereas the proximal one is heterochromatic.

The number, size and shape of arrested metaphase chromosomes in the mitotic division provide the most reliable information for a comparative study of the concerned karyotypes. Arrested metaphase chromosome of the four species of Oenothera were studied, The number of examined cells were five for each species studied. The microscopic examination, conclusively , confirmed that the somatic chromosome number in all taxa is 2 n = 14.

The characteristics used to identify the karyotypes included: Length of chromosomes (in μ) of short arm, long

arm, total length of the haploid complement and length and distance from centromere to any secondary constrictioin in any particular chromosome, as well as their mean values. Tables 6, 8, 10 and 12 show the calculated short to long arm ratios (S: L), centromeric indicies (C.I.) and chromosome type for the previous taxa respectively. Photomicrographs of somatic cells and drawings are included in the data of each taxon.

A: Parents :

1- O. nissensis var fiedleri :

The main characteristics of the haploid complement are presented in Table (6, 7) The total length of the chromosomes as average of 5 cells, ranged from 29.85 to 46.35 μ with a mean value of 29.10 ± 0.41. The average length of chromosome I (the longest) is 5.84 μ contributing about 20.03 % of the total length of the haploid complement. The chromosomes I, II, and III are metacentric, the chromosomes IV and V are akrocentric and the chromosomes VI and VII are subacrocentric. The average length of these chromosomes (II to VII) are 5.54, 5.24, 4.89, 4.09, 2.55 and 0.95 μ, respectively. The centromeric index values of chromosomes IV and V are low (0.10- 0.12). Meanwhile those of chromosomes I, II, III and VI were high (0.55, 0.55, 0.50 and 0.40, respectively).

Photomicrographs of five well spread mitotic cells are shown in Figure (21) (a, b, c, d and e), showing six metacentric, four acrocentric and four submetacentric, chromosomes.

2- O. biennis L. var. grandiflora :

The main characteristics of the haploid complement of this species are found in Table (8, 9) The similarity between the karyotype of this species and that of the previous one was obvious. The total length of the chromosomes, (average of five cells) ranged from 22.02 to 33.39 µ with a mean value of 25.45 ± 0.12. The average length of chromosome I (the longest) is 7.06 µ contributing 23.42 % of the total the length of the haploid complement. Chromosomes I and II were metacentric, meanwhile the chromosomes II, IV and V are acrocentric . Chromosome III is characterized by the presence of sattelite. Chromosomes VI and VII are subacrocentric. The centromeric index reached 0.50 in the chromosomes I and II, and ranged from 0.12 to 0.31 in the other five chromosomes (II to VII).

Photomicrographs of five well- spread mitotic cells are shown in figure, (22) a, b, c, d and e, showing four metacertric, six acrocentric with a sattelite in the third chromosome and four subacrocentric.

3- O. cornifera Renner :

The main features of the haploid complement of this species are shown in Table (10, 11) The total length of the chromosomes ranged from 26.80- 39.44 µ, with a mean value of 30.22 ± 0.06. Chromosome I and II are metacentric with the

centromeric index values 0.48 and 0.50, respectively. Chromosome III is submetacentric with the centromeric index value 0.41. Chromosomes IV and V are characterized as acrocentric with centromeric index 0.12 and 0.11, respectively . Meanwhile chromosome VI and VII are subacrocentric with centromeric index 0.36 and 0.27, respectively.

Photomicrographs of five well- spread mitotic cells are shown in Fig.(23), a, b, c, d and e, showing four metacentric; two submetacentric, four acrocentric and four subacrocentric.

4- O. odorata jacy :

Data concerning the haploid complement of this species are shown in Table(12,13)where the total length of the chromosomes, ranged from 16.82- 29.58 μ with a mean value of 19.00 ± 0.08. The average length of chromosome I (the longest) is 4.49 μ which contributes 23.96 % of the total length of the haploid complement. The chromosomes I,II and III are metacentric and the chromosomes V,VI, and VII are acrocentric . The centromeric index of chromosomes I, II and III are the same giving the value 0.49, while that for the chromosome IV is 0.44. For the chromosomes V, VI and VII the index values are 0.07; 0.10 and 0.10, respectively.

Five photomicrographs of well spread mitotic metaphase plates of O. odorata showing six metacentric, two submetacentric and six acrocentric (Fig.24).

The main features of the karyotypes of the different species outlined in Table (14) indicate that all these species have 2n = 14. The data obtained in this study confirm those reported by stinson(1953);Ary- Avand (1976), Pogan et al. (1982) and Nishikawa (1985).

There are marked variations in the karyotypes of the available species of Oenothera as indicated Table (19). O. biennis has the longest chromosome (7.06 µ) compared with any chromosome of the other species. O. coronifera has the total length of the haploid complement, i.e. 30.21 µ, while the O. odorata has shortest haploid complement giving the value (19.00 µ).

Three chromosomes (a, b and c). Fig. (5) were metacentric and two (d, e) were acrocentric and the last two (f, g) were subacrocentric in O. nissensis .

For O. biennis, two chromosomes were metacentric (a,b), three chromosomes were acrocentric (c, d, e) and two chromosomes (f, g) were subacrocentric. It is worthy to mention that chromosome "c" possess satellite. The obtained data on O. biennis were different from those recorded on the other studied species. The incidence of one satellite on the chromosome "c" of O. biennis is in agreement with that of Steiner and Stubbe (1979).

For O. coronifera, two chromosomes were metacentric (a, b),one submetacentric (c), and two were acrocentric (d,e) and two as subacrocentric (f, g).

Table (6): Characteristics of the chromosome complement of O. nissensis.

Chromosome No.		Mean length and range of variation in microns			R.L. %	S : L	C.I.	Chromosome type
		Short arm	Long arm	Total				
I	$\bar{X}$	2.62±0.06	3.22±0.05	5.84± 0.12	20.03	1:1.23	0.55	m
	range	2.10–3.40	3.10–3.80	5.10– 8.50				
II	$\bar{X}$	2.54±0.15	3.00±0.15	5.54± 0.34	19.00	1:1.18	0.50	m
	range	2.30–3.25	3.05–3.15	5.00– 7.60				
III	$\bar{X}$	2.50±0.02	3.74±0.02	5.24± 0.04	17.97	1:1.50	0.50	m
	range	2.25–3.15	3.50–4.50	5.20– 7.90				
IV	$\bar{X}$	0.50±0.02	4.43±0.06	4.89± 0.03	16.77	1:8.86	0.10	t
	range	0.40–5.20	3.20–5.40	5.60– 7.90				
V	$\bar{X}$	0.49±0.02	3.61±0.04	4.09± 0.04	14.05	1:7.37	0.12	t
	range	0.32–4.80	3.20–4.20	6.30– 8.20				
VI	$\bar{X}$	1.00±0.01	1.55± 0.06	2.55± 0.14	8.74	1:1.53	0.40	st
	range.	0.85–3.22	1.45–3.20	1.65– 4.25				
VII	$\bar{X}$	0.27±0.01	0.68±0.01	0.95± 0.01	3.44	1:2.77	0.27	st
	range	0.18–0.78	0.68–1.20	1.00– 2.00				
Total	$\bar{X}$			29.10± 0.41				
	range			29.85–46.35				

R.L. = Relative length of chromosome.

C.I. = Centromeric index.

t = acrocentric.

S.L. = Short to long arm ratio.

m = metacentric.

st = sub-acrocentric.

Table 7: Length in microns of short arm, long arm and total of each two homologus chromosome (a and b) of chromosome complement ment of O. nissensis and their average as measurement in mitotic metaphase plates (x. 2083). Relative length (R.L.) is calculated as percent of total length of the haploid complement (H.C L.). Secondary constriction located in the short arm of chromosome V located.

Cell No.	Chromo.	I			II			III			VI			V			VI			VII			Total
		Short	Long	Total	Short	Long	Total	Short	Long	Total	Short	Long	Total	Short	Long	Total	Short	Long	Total	Short	Long	Total	
1	a	2.80	3.20	6.00	2.60	2.90	5.50	2.60	2.70	5.30	0.40	4.60	5.00	0.35	3.65	4.00	1.00	1.50	2.50	0.25	0.75	1.00	29.30
	b	3.40	3.60	7.00	2.70	3.10	5.80	2.55	2.65	5.20	0.50	4.40	4.90	0.40	3.60	4.00	1.00	1.80	2.80	0.30	0.80	1.10	30.80
	a+b/2	3.00	3.50	6.50	2.85	3.00	5785	2.50	2.65	5.15	0.55	4.45	4.95	0.60	3.40	4.00	1.15	1.50	2.65	0.15	0.80	1.05	30.15
2	a	3.00	3.40	6.40	2.70	2.90	5.60	2.60	2.70	5.30	0.50	4.30	4.80	0.60	3.60	4.20	1.00	1.40	2.40	0.25	0.75	1.00	29.80
	b	3.05	3.15	6.20	2.60	2.86	5.40	2.50	2.70	5.20	0.40	4.60	4.90	0.50	3.60	4.10	1.00	1.80	2.80	0.25	0.75	1.00	28.90
	a+b/2	3.10	3.20	6.30	2.70	2.80	5.50	2.50	2.65	5.05	0.35	4.50	4.85	0.55	3.60	4.15	1.00	1.60	2.60	0.25	0.75	1.00	29.55
3	a	3.00	3.30	6.30	2.50	2.70	5.20	2.65	2.75	5.40	0.45	4.35	4.80	0.45	3.95	4.40	1.00	1.30	2.30	0.20	0.80	1.00	29.40
	b	3.10	3.20	6.30	2.70	2.90	5.60	2.55	2.65	5.20	0.55	4.45	5.00	0.50	3.60	4.10	1.00	1.50	2.50	0.25	0.75	1.00	29.70
	a+b/2	3.05	3.25	6.30	2.60	2.80	5.40	2.60	2.70	5.30	0.45	4.45	4.90	0.55	3.70	4.25	1.00	1.40	2.40	0.20	0.80	1.00	29.55
4	a	2.80	3.20	6.00	2.70	2.90	5.60	2.55	2.65	5.20	0.50	4.40	4.90	0.55	3.45	4.00	1.00	1.50	2.50	0.25	0.75	1.00	29.20
	b	3.40	3.60	7.00	2.60	2.80	5.40	2.40	2.60	5.00	0.55	4.35	4.80	0.60	3.50	4.10	1.00	1.80	2.80	0.35	0.65	1.00	30.10
	a+b/2	3.10	3.40	6.50	2.70	2.80	5.50	2.50	2.60	5.10	0.45	4.40	4.85	0.50	3.55	4.05	1.15	1.50	2.65	0.26	0.75	1.00	29.60
5	a	3.20	3.60	3.80	2.70	2.80	5.50	2.65	2.75	5.40	0.55	4.45	5.00	0.45	3.55	4.00	1.05	1.55	2.60	0.25	0.75	1.00	27.30
	b	3:10	3.30	3.40	2.55	2.15	5.80	2.55	2.65	5.20	0.60	4.20	4.80	0.45	3.55	4.00	1.60	1.30	2.30	0.30	0.70	1.00	26.50
	a+b/2	3.10	3.50	6.60	2.60	2.80	5.65	2.55	2.75	5.30	0.50	4.40	4.90	0.45	3.55	4.00	1.00	1.45	2.45	0.30	0.70	1.00	30.10
Total		32.20	32.20	58.40	27.70	27.70	55.40	26.20	26.20	52.40	5.00	44.30	48.90	4.85	36.05	40.90	10.05	15.45	25.50	2.65	7.45	10.05	291.00
X		3.22	3.22	5.94	2.77	2.77	5.54	2.62	2.62	5.24	0.50	4.43	4.89	0,485	3.605	4.09	1.005	1.55	2.55	0.27	0.75	1.01	29.10
SX		0.06	0.059	0.12	0.152	0.15	0.31	0.02	0.29	0.04	0.02	0.06	0.078	0.017	0.043	0.05	0.0006	0.07	0.14	0.013	0.02	0.01	00.41
R.L.		11.05	11.05	20.10	9.500	9.50	19.00	8.99	8.99	17.98	1 72	15.22	16.94	1.67	12.30	13.97	3.45	5.30	8.75	0.93	2.57	3.45	99.31

Table (8): Characteristics of the chromosome complement of O. biennis.

Chromosome No.		Mean length and range of variation in microns			R.L. %	S : L	C.I	Chromosome type
		Short arm	Long arm	Total				
I	$\bar{X}$	3.43±0.03	3.63±0.03	7.06± 0.06	28.42	1:2.01	0.50	m
	range	3.20–4.20	2.50–6.20	6.03– 8.20				
II	$\bar{X}$	3.02±0.02	3.23±0.02	6.25± 0.04	25.16	1:2.0	0.50	m
	range	3.01–5.12	3.00–4.50	5.80– 7.20				
III	$\bar{X}$	0.42±0.15	3.50±0.01	3.92± 0.01	14.09	1:8.33	0.12	t
	range	0.31–0.56	3.20–5.20	3.10– 4.72				
IV	$\bar{X}$	0.53±0.18	2.08±0.04	2.61± 0.03	10.39	1:4.87	0.21	t
	range	0.31–0.73	2.00–3.50	2.32– 3.78				
V	$\bar{X}$	0.15±0.05	2.19±0.02	2.34± 0.02	8.92	1:14.60	0.10	t
	range	0.12–0.35	2.00–3.50	1.90– 3.82				
VI	$\bar{X}$	0.63±0.02	1.39±0.03	2.02± 0.03	8.09	1:221	0.31	st
	range	0.51–0.85	1.20–2.37	1.87– 3.20				
VII	$\bar{X}$	0.25±0.02	1.00±0.03	1.25± 0.02	5.03	1:400	0.20	st
	range	0.15–0.42	0.95–2.20	1.00– 2.47				
Total	$\bar{X}$			25.45± 0.12				
	range			22.02–33.39				

R.L. = Relative length of chromosome.
S.L. = Short to long arm ratio.
C.I. = Centromeric index.
m = metacentric.
t = acrocentric.
st = sub-acrometric.

Table 9 Length in microns of short arm, long arm and total of each two homologus chromosomes (a and b) of chromosome complement of Q. beinnes and their average as measurement in mitotic metaphase plates (x 2083). Relative length (R.L.) is calculated as percent of total length of the haploid complement (H.C.L.). Secondary constriction (S.C.) located in the short arm of chromosome V located.

Cell No.	Chromo	II			II			III			IV			V			VI			VII			Total
		Short	Long	Total	Short	Long	Total	Short	Long	Total	Short	Long	Total	Short	Long	Total	Short	Long	Total	Short	Long	Total	
1	a	3.70	3.60	7.00	3.00	3.10	6.10	0.40	3.10	3.60	0.50	2.00	2.50	0.10	2.10	2.20	0.60	1.40	2.00	0.20	1.00	1.20	24.40
	b	3.50	3.70	7.20	3.00	3.12	6.12	0.50	3.10	3.60	0.50	2.10	2.60	0.20	2.10	2.30	0.70	1.30	2.00	0.30	0.80	1.20	25.02
	a+b/2	3.50	3.60	7.20	3.00	3.11	6.11	0.55	3.00	3.55	0.40	2.15	2.55	0.10	2.15	2.25	0.65	1.35	2.00	0.30	1.00	1.30	24.96
2	a	3.40	3.60	7.00	3.00	3.20	6.20	0.30	3.30	3.60	0.70	2.00	2.70	0.10	2.60	2.10	0.70	1.30	2.00	0.30	1.00	1.30	24.90
	b	3.90	3.60	7.00	3.00	3.40	6.40	0.40	3.00	3.40	0.60	2.10	2.60	0.20	2.00	2.20	0.60	1.40	2.00	0.20	1.10	1.30	24.90
	a+b/2	3.45	3.55	7.00	3.00	3.30	6.30	0.50	3.00	3.50	0.55	2.00	2.85	0.15	2.00	2.15	0.65	1.35	2.00	0.25	1.05	1.20	24.85
3	a	3.65	3.75	7.40	3.00	3.40	6.40	0.10	3.20	3.30	0.40	2.00	2.40	0.10	2.05	2.15	0.50	1.50	2.00	0.20	1.00	1.20	24.85
	b	3.30	3.50	6.80	3.00	3.40	6.40	0.60	3.00	3.60	0.70	2.00	2.70	0.15	2.00	2.15	0.60	1.60	2.10	0.30	0.90	1.20	24.95
	a+b/2	3.45	3.65	7.10	3.00	3.40	6.40	0.45	3.00	3.45	0.55	2.00	2.55	0.15	2.00	2.15	0.55	1.55	2.10	0.30	1.00	1.30	25.05
4	a	3.40	3.60	7.00	3.05	3.15	6.20	0.60	3.00	3.60	0.20	2.20	2.45	0.05	2.15	2.20	0.70	1.30	2.00	0.20	1.10	1.30	24.70
	b	3.50	3.70	7.20	3.15	3.25	6.40	0.20	3.20	3.40	0.50	2.10	2.60	0.10	2.00	2.10	0.60	1.40	2.00	1.10	1.10	1.40	25.10
	a+b/2	3.45	3.65	7.20	3.10	3.20	6.30	0.50	3.00	3.50	0.50	2.00	2.50	0.15	2.00	2.15	0.65	1.35	2.00	0.25	1.10	1.35	25.00
5	a	3.20	3.60	6.80	3.00	3.10	6.10	0.50	3.00	3.50	0.70	2.00	2.70	0.20	2.00	2.20	0.60	1.40	2.00	0.20	1.00	2.00	24.50
	b	3.55	3.65	7.70	3.00	3.12	6.12	0.60	2.90	3.50	0.60	2.00	2.60	0.30	2.00	2.30	0.70	1.30	2.00	0.30	0.90	1.20	23.92
	a+b/2	3.40	3.60	7.00	3.00	3.10	6.10	0.50	3.00	3.50	0.65	2.00	2.65	0.25	2.00	2.25	0.65	1.35	2.30	0.30	1.00	1.30	25.00
Total		34.30	36.30	70.60	30.20	32.24	62.44	4.20	30.80	3.50	5.30	20.50	25.80	1.50	20.00	21.30	6.30	13.90	20.10	2.50	10.00	12.50	246.24
X		3.43	3.63	7.06	3.02	3.23	16.25	0.42	3.08	3.50	0.53	2.05	2.58	0.15	2.00	2.19	0.63	1.39	2.01	0.25	1.00	1.25	24.63
SX		0.015	0.045	0.060	0.015	0.027	0.042	0.152	0.226	0.378	0.182	0.247	0.329	0.055	0.663	0.318	0.021	0.032	0.003	0.017	0.026	0.022	0.121
R.L. %		14.21	14.21	28.42	12.26	12.86	25.12	1.58	12.51	14.09	2.07	8.32	10.39	0.770	8.120	8.890	2.54	5.60	8.14	1.01	4.03	5.04	99.83

Table (10): Characteristics of the chromosome complement of O. coronifera.

Chromosome No.		Mean length and range of variation in microns			R.L. %	S: L	C.I	Chromosome type
		Short arm	Long arm	Total				
I	$\bar{X}$	3.33±0.01	3.67±0.02	7.00± 0.02	30.03	1:1.10	0.48	m
	range	3.12-4.50	3.00-5.21	6.2 - 8.50				
II	$\bar{X}$	3.14±0.01	3.17±0.02	6.31± 0.03	20.86	1:1.01	0.50	m
	range	3.05-4.21	2.81-4.19	5.20- 7.32				
III	$\bar{X}$	2.14±0.02	3.08±0.01	5.17± 0.02	17.11	1:1.42	0.41	sm
	range	2.00-3.15	2.80-4.20	5.00- 6.80				
IV	$\bar{X}$	0.48±0.09	3.50±1.24	3.98± 0.05	13.18	1:7.29	0.12	t
	range	0.32-1.20	3.20-4.50	3.20- 5.22				
V	$\bar{X}$	0.34±0.05	2.80±0.24	3.14± 0.03	10.39	1:8.23	0.11	t
	range	0.21-1.28	2.70-3.95	3.00- 4.50				
VI	$\bar{X}$	0.93±0.03	1.63±0.03	2.56± 0.02	8.48	1:1.75	0.36	st
	range	0.82-1.33	1.23-3.21	2.20- 3.50				
VII	$\bar{X}$	0.56±0.02	1.51±0.05	2.06± 0.02	6.82	1:2.68	0.27	st
	range	0.32-2.10	1.32-2.32	2.00- 3.60				
Total	$\bar{X}$			30.22± 0.06				
	range			26.80-39.44				

R.L. = Relative length of chromosome.

C.I. = Centromeric index.

sm = sub-metacentric.

st = sub-acrometric.

S.L. = Short to long arm ratio.

m = metacentric.

t = acrocentric.

Table 11 Length in microns of short arm, long arm and total of each two homologus chromosomes (a and b) of chromosome complement of O. coronifera and their average as measurement in mitotic metaphase plates (x. 2083). Relative length (R.L.) is calculated as percent of total length of the haploid complement (H.C.L.), Secondary constriction (S.C.) located is the short arm of chromosome V located.

Cell No.	Chromo.	I			II			III			IV			V		VI			VII			Total
		Short	Long	Total	Short	Long	Total	Short	Long	Total	Short	Long	Total	Short	Long	Short	Long	Total	Short	Long	Total	
1	a	3.60	3.40	7.00	3.20	3.10	6.30	2.20	3.50	5.20	0.20	3.60	4.00	0.10	3.10	1.00	1.50	2.50	0.50	1.50	2.00	30.10
	b	3.50	3.50	7.00	3.15	3.15	6.30	2.10	3.10	5.20	0.30	3.50	3.80	0.20	3.20	1.00	1.50	2.50	0.60	1.40	2.00	29.80
	a+b/2	3.55	3.55	7.10	3.15	3.15	6.30	2.15	3.05	5.20	0.30	3.60	3.90	0.15	3.15	1.00	1.50	2.50	0.55	1.45	2.00	30.15
2	a	3.45	3.45	6.90	3.10	3.20	6.30	2.15	3.05	5.20	0.30	3.90	4.20	0.10	3.10	0.80	1.80	2.60	0.55	1.55	2.10	30.50
	b	3.50	3.50	7.00	3.15	3.15	6.30	2.20	3.00	5.20	0.20	3.80	4.00	0.20	2.80	0.90	1.70	2.60	0.65	1.50	2.15	30.25
	a+b/2	3.45	3.45	6.90	3.12	3.18	6.30	2.17	3.03	5.20	0.30	3.80	4.10	0.10	3.00	0.85	1.75	2.60	0.60	1.52	2.13	30.33
3	a	3.60	3.40	7.00	3.15	3.15	6.30	2.20	3.00	5.20	0.30	3.70	4.00	0.20	3.10	1.00	1.60	2.60	0.50	1.50	2.00	30.40
	b	3.50	3.50	7.00	3.15	3.15	6.30	2.10	3.10	5.20	0.30	3.50	3.80	0.20	3.00	1.00	1.70	2.70	0.60	1.40	2.00	30.20
	a+b/2	3.55	3.55	7.10	3.15	3.15	6.30	2.17	3.05	5.20	0.20	3.70	3.90	0.20	3.05	1.00	1.65	2.65	0.55	1.45	2.00	30.30
4	a	3.50	3.50	7.00	3.10	3.20	6.30	2.00	3.00	5.00	0.20	4.00	4.20	0.05	3.05	1.00	1.50	2.50	0.55	1.55	2.10	30.20
	b	3.50	3.50	7.00	3.20	3.10	6.30	2.10	3.00	5.10	0.10	4.00	4.10	0.10	3.00	1.00	1.50	2.50	0.40	1.60	2.00	30.10
	a+b/2	3.50	3.50	7.00	3.15	3.15	6.30	2.05	3.00	5.05	0.15	4.00	4.15	0.10	3.00	1.00	1.50	2.50	0.48	1.62	2.10	30.20
5	a	3.60	3.40	7.00	3.05	3.25	6.30	2.15	3.05	5.20	0.40	3.40	3.80	0.20	3.00	0.75	1.75	2.50	0.55	1.55	2.10	30.10
	b	3.60	3.50	7.10	3.10	3.20	6.30	2.20	3.00	5.20	0.30	3.60	3.90	0.30	2.70	0.85	1.70	2.55	0.65	1.50	2.15	30.20
	a+b/2	3.60	3.45	7.05	3.15	3.25	6.40	2.17	3.03	5.20	0.25	3.60	3.85	0.10	3.00	0.80	1.73	2.53	0.60	1.53	2.13	30.26
	Total	33.35	33.65	70.00	31.35	31.65	63.00	21.40	30.30	51.70	2.60	37.80	39.80	1.65	29.75	9.30	16.25	25.55	5.55	15.05	20.60	301.85
	X	3.335	3.365	7.00	3.14	3.17	6.30	2.14	3.03	5.17	0.26	3.72	3.98	0.165	2.975	0.93	1.63	2.56	0.56	1.505	2.06	30.19
	SX	0.006	0.069	0.015	0.014	0.014	0.028	0.022	0.015	0.021	0.090	1.237	1.327	0.055	0.246	0.032	0.037	0.021	0.024	0.021	0.022	0.060
	R.L. %	11.02	11.12	22.14	10.39	10.49	20.88	7.08	10.03	17.11	0.861	12.32	13.18	2.201	9.854	3.08	5.40	8.48	1.85	4.97	6.82	100.67

Table (12) Characteristics of the chromosome complement of O. odorata.

Chromosome No.		Mean length and range of variation in microns			R.L. %	S : L	C.I.	Chromosome type
		Short arm	Long arm	Total				
I	$\bar{X}$	2.24±0.02	2.25±0.02	4.49± 0.01	23.96	1: 1.00	0.49	m
	range	2.00–3.56	2.15–4.56	4.30– 6.52				
II	$\bar{X}$	1.74±0.01	1.75±0.02	3.49± 0.01	18.62	1: 1.01	0.49	m
	range	1.53–3.25	1.35–3.25	3.20– 4.56				
III	$\bar{X}$	1.54±0.01	1.57±0.02	3.11± 0.03	16.60	1: 1.01	0.49	m
	range	1.32–3.25	1.15–3.25	2.50– 4.50				
IV	$\bar{X}$	1.12±0.03	1.43±0.03	2.55± 0.02	13.61	1: 1.27	0.44	sm
	range	1.05–2.68	1.32–3.20	2.32– 4.50				
V	$\bar{X}$	0.14±0.05	2.01±0.03	2.15± 0.03	10.73	1:13.86	0.07	t
	range	0.01–1.50	2.00–3.05	1.90– 3.20				
VI	$\bar{X}$	0.18±0.01	1.52±0.03	1.70± 0.03	9.17	1: 9.30	0.10	t
	range	0.08–2.15	1.32–3.20	1.50– 3.20				
VII	$\bar{X}$	0.14±0.05	1.37±0.03	1.51± 0.03	7.31	1: 9.45	0.10	t
	range	0.04–1.20	1.20–2.56	1.10– 3.20				
Total	$\bar{X}$			19.00± 0.08				
	range			16.82–29.68				

R.L. = Relative length of chromosome.

C.I. = Centromeric index.

sm = sub-metacentric.

S.L. Short to long arm ratio.

m = metacentric.

t = acrocentric.

Table 13 Length in microns of short arm, long arm and total of the homologus chromosome (a and b) of chromosome complement (I- VII) O. odorata and their average as measurement in mitotic metaphase plates(x. 2083). Relative length (R.C.) is calculated as percent of total length of the haploid complement tH.C.L.). Secondary constriction (S.C.) located in the short arm of chromosome V located.

Cell No.	Chromo.	I			II			III			IV			V			VI			VII			Total
		Short	Long	Total	Short	Long	Total	Short	Long	Total	Short	Long	Total	Short	Long	Total	Short	Long	Total	Short	Long	Total	
1	a a	2.25	2.25	4.50	1.70	1.80	3.50	1.50	1.50	3.00	1.00	1.500	2.50	0.20	1.80	2.00	0.01	1.60	1.70	0.10	1.20	1.20	18.50
	b	2.25	2.25	4.50	1.80	1.70	3.50	1.50	1.50	3.00	1.00	1.50	2.50	0.15	1.85	2.00	0.20	1.60	1.80	0.20	1.10	1.30	18.60
	a+b/2	2.25	2.25	4.50	1.75	1.75	3.50	1.50	1.50	3.00	1.00	1.50	2.50	0.18	1.82	2.00	0.15	1.60	1.75	0.15	1.15	1.30	18.55
2	a	2.20	2.30	4.50	1.75	1.75	3.50	1.60	1.60	3.20	1.20	1.30	2.50	0.10	2.00	2.10	0.20	1.40	1.60	0.10	1.40	1.50	18.90
	b	2.25	2.30	4.55	1.70	1.70	3.40	1.55	1.55	3.10	1.10	1.40	2.50	0.20	2.00	2.20	0.30	1.50	1.80	0.15	1.45	1.60	19.15
	a+b/2	2.23	2.30	4.53	1.70	1.75	3.45	1.57	1.58	3.15	1.15	1.35	2.50	0.15	2.00	2.15	0.25	1.45	1.79	0.13	1.42	1.55	19.03
3	a	2.10	2.40	4.50	1.80	1.80	3.60	1.60	1.70	3.30	1.20	1.40	2.60	0.05	2.00	2.05	0.10	1.40	1.50	0.20	1.16	1.36	18.85
	b	2.10	2.30	4.50	1.70	1.70	3.40	1.55	1.65	3.20	13.0	1.40	2.70	0.05	2.00	2.05	0.15	1.65	1.80	0.10	1.10	1.20	18.85
	a+b/2	2.15	2.35	4.50	1.75	1.75	3.50	1.50	1.75	3.25	1.25	1.40	2.65	0.05	2.00	2.05	0.13	1.52	1.65	0.15	1.10	1.25	18.85
4	a	2.20	2.30	4.50	1.80	1.70	3.50	1.60	1.60	3.20	1.20	1.30	2.50	1.50	1.85	2.00	0.25	1.50	1.75	0.20	1.20	1.40	18.95
	b	2.25	2.30	4.55	1.80	1.70	3.50	1.55	1.55	3.10	1.10	1.40	2.50	0.25	1.75	2.00	0.15	1.70	1.85	0.10	1.20	1.30	18.80
	a+b/2	2.23	2.30	4.53	1.80	1.70	3.50	1.57	1.58	3.15	1.15	1.35	2.50	0.20	1.80	2.00	0.20	1.60	1.80	0.15	1.20	1.35	18.83
5	a	2.10	2.30	4.40	1.60	1.90	3.50	1.50	1.50	3.00	1.05	1.50	2.55	0.20	1.60	1.80	0.20	1.40	1.60	0.20	1.15	1.35	18.20
	b	2.25	2.15	4.40	1.70	1.80	3.50	1.50	1.50	3.00	1.00	1.60	2.60	0.10	1.80	1.90	0.20	1.55	1.75	0.10	1.30	1.40	18.55
	a+b/2	2.17	2.23	4.40	1.65	1.85	3.50	1.50	1.50	3.00	1.03	1.55	2.58	0.15	1.70	1.85	0.20	1.55	1.70	0.15	1.22	1.37	18.40
	Total	22.05	22.85	44.90	17.35	17.55	34.90	15.45	15.65	31.10	11.15	14.30	25.45	1.45	18.65	20.10	1.85	15.30	17.15	1.45	12.26	13.65	18.35
	X	2.204	2.285	4.49	1.74	1.76	3.49	1.55	1.57	3.11	1.12	1.43	2.55	0.145	1.87	2.01	0.185	1.53	1.72	0.145	1.23	1.37	18.74
	Sx	0.732	0.758	1.489	0.012	0.021	0.015	0.015	0.023	0.035	0.033	0.030	0.021	0.055	0.600	0.655	0.004	0.259	0.263	0.055	0.409	0.036	0.086
	R.L. %	11.76	12.19	23.96	9.29	9.39	18.62	8.27	8.38	16.60	5.98	7.63	13.61	0.750	9.98	10.73	1.01	8.17	9.18	0.774	6.561	7.333	100.00

Table (14) The principal features of the haploid complement in the different species of oenothera.

Species	Chromosomes														Total L.
	I		II		III		IV		V		VI		VII		
	L.	Type	L.	Type	L.	Type	L.	Type	L.	Type	L.	Type	L.	Type	
O. nissensis	5.84	m	5.54	m	5.24	m	4.89	t	4.09	t	2.55	st	0.95	st	29.10
O. biennis	7.06	m	6.25	m	3.92*	t	2.61	t	2.34	t	2.02	st	1.25	st	25.45
O. coronifera	7.00	m	6.31	m	5.17	sm	3.98	t	3.14	t	2.56	st	2.06	st	30.22
O. odorata	4.49	m	3.49	m	3.11	m	2.55	sm	2.15	t	1.70	t	1.51	t	19.00

L. Length in micron.

m,sm,st and t represent metacentric, submetacentric, subacrocentric and acrocentric chromosome respectively.

* With satellite.

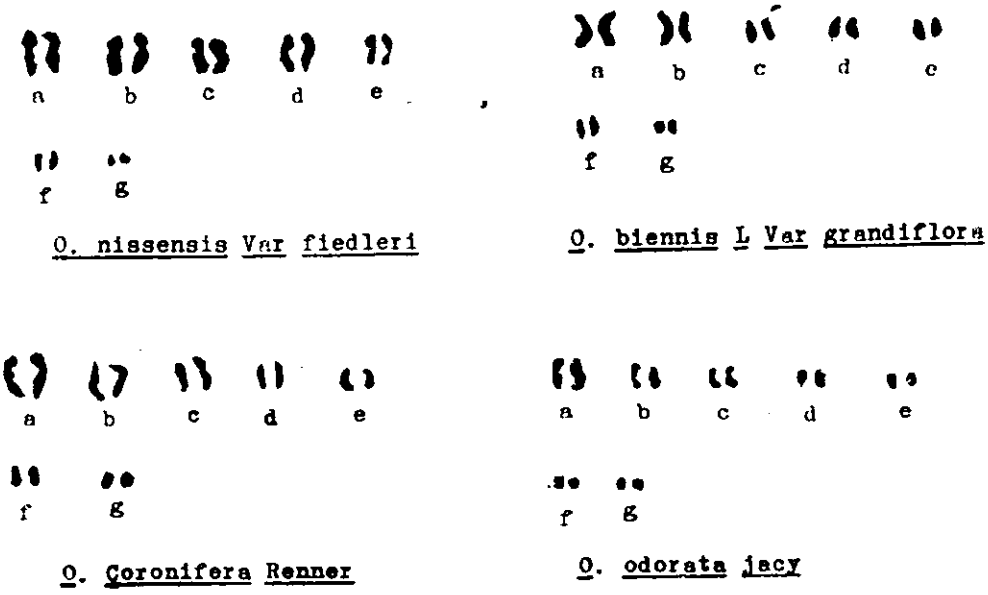

Fig. (25) Karyotype analysis in oenothera spp.

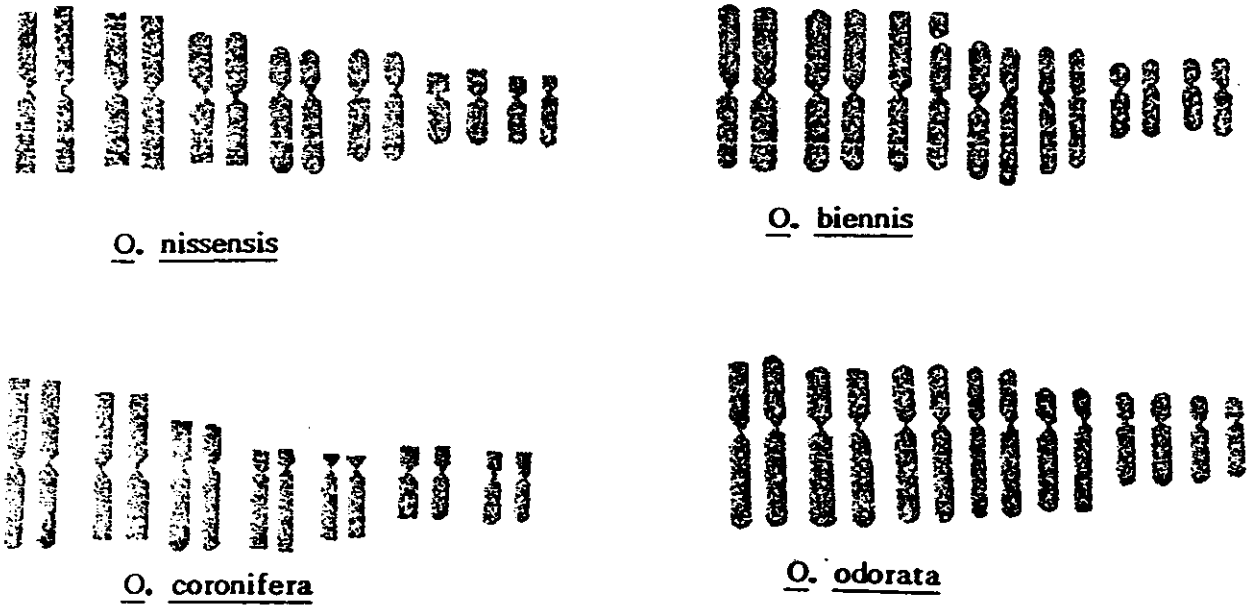

Fig. (26): Four idiogram of mitotic karyotype of O. niessenis; O. biennis, O. coronifera and O. odorata.

B- Interspecific hybrids :

1- O. nissensis x O. biennis :

Examination of the F_1 PMCs of the cross O. nissensis x O. biennis, table (15) indicated that the percentage of total abnormalities (4.27 %) exceeded each of the two parents. The kind of abnormalities in PMCs that take place in higher percentage than both parents were lagging (Fig.27) and bridge (Fig.28). The percentage of chromosomal and chromatid bridges detected in the hybrids between the two species was higher (1.71 %) than the two parents. This might be due to the presence of heterozygous inversions between homologous chromosomes. The higher percentage of lagging in F_1 (2.56 %) than the two parents might be attributed to dessimilarities of chromosomes in both species .

2- O. nissensis x O. coronifera :

Values of the two kinds of abnormalities in subsequent PMC's division were higher increased than those of the two parents (Fig.27) indicating the presence of heterozygous inversion between homologous chromosomes and the dessimilarities between chromosomes of the two species.

3- O. nissensis x O. odorata :

One cell from 80 PMCs exhibited bridge chromosomes in this cross, with (1.25 %) (Fig.28), while this bridge was

not observed in both parents for lagging chromosomes. The F_1 exceeded both parent.

4. O. biennis x O. coronifera :

The total percentage of abnormalities in F_1 was (3.00 %) with mean value (1.301). Fig. (2$). This value was higher than values in both parents (1,11 and 1.82 %, respectively).

5. O. biennis x O. odorata :

The number of cells with bridges was 3 cells with (1.52 %) from the total PMCs examined. This value in F_1 exceeded those of both parents. Also, the lagging chromosomes in F_1 PMCs were more than those in parents Fig. (2$).

6. O. coronifera x O. odorata :

The total abnormalities was (3.02 %) with mean value (1.51 %) for bridge and lagging chromosomes (Figs. 27 & 28), which higher than that of each of the two parents.

Generally, the total percentage of abnormalities (bridges and lagging) in the interspecific cross of oenothera was higher than the total percentage of these abnormalities in the parental species. This may be due to the degree of homology between the parental chromosomes.

III- Chromosome configuration for parents and hybrids:

1- Hybrid between O. nissensis (2n= 14) and O. coronifera (2n = 14) :

The frequency of each type of chromosome configurations and percentage of each type were calculated in metaphase I, table (16). Sixty three of the cells belonging to O. nissensis were examined. The most common types of configurations at metaphase I in this species were 6 ⊙ + 4 prs (31.80 %) and 10 ⊙ + 2 prs (26.57 %). For the other parent O. coronifera, 40 PMCs were examined. The most common types of configuration were 4 ⊙ + 4 ⊙ + 3 prs (27.50 %), 4 ⊙ + 5 prs (22.50 %) and 10 ⊙ + 2 prs (17.50 %).

In the hybrid O. nissensis x O. coronifera twenty five cells at metaphase I were examined. The most common types of configuration were 6 prs (Fig. 32) + 1 pair free (48.00 %), 5 prs (linear) + 2 prs free (32.00 %) and 7 prs (star) (20 %).

2- Hybrid O. niessensis x O. odorata: Table 17 :

The most frequent configuration for the parent species O. odorata were 10 ⊙ + 2 prs (28.05 %), 6 ⊙ + 4 prs (24.39 %) and 4 ⊙+ 5 prs (18.29 %). In the hybrid O. niessensis x O. odorata, thirty eight cells were examined. The most

common types of configuration were 7 prs (26.32 %), 6 prs (Zigzag) + 1 pair free (18.42 %) and 7 prs (star)(15.79%).

3- Hybrid O. niessensis x O. biennis: (Fig. 31) :

The most frequent configuration in the species O. biennis were prs (38.79 %), 4 ⊙ + 4 ⊙ + 3 prs (17.34 %) and 8 ⊙ + 3 prs (15.52 %).

In the hybrid O. niessensis x O. biennis, twenty three cells were examined, 5 prs (star) + 2 prs free were the most frequent configurations followed by 7 prs (30.44 %), Table (18)

4- Hybrid O. biennis x O. coronifera: (Fig. 36) :

From fourty cells examined in O. coronifera, 4 ⊙ + 4 ⊙ + 3 prs showed (27.50 %) and 4 ⊙ + 5 prs showed (22.50 %) in metaphase I.

In the hybrid.O. biennis x O. coronifera the examination of 21 in metaphase I, showed 5 prs (Zigzag) + 1 pair free (33.33 %). The next configuration was 12 ⊙ + 1 pair (28.57 %), Table (19)

5- Hybrid O. biennis x O. odorata: Table (20) :

In the parent O. odorata, 10 ⊙ + 2 prs (28.05 %) and 6 ⊙ + 4 prs (24.39 %) were high frequent configuration. While in the hybrid O. biennis x O. orodrata, the six linear chromosome + 4 prs free were high frequent (Fig. 35).

6- Hybrid O. coronifera x O. odorata: Table (21) :

In the parent O. coronifera, 40 cells were examined and the high frequent configuration were 4 ⊙ + 4 ⊙ + 3 prs (27.50 %) and 4 ⊙ + 5 prs (22.50 %). In the hybrid O. coronifera x O. odorata, the 12 cells (50 %) had 7 prs zigzag and 7 cells (29.17 %) had a 14 chromosome as a open ring. Generally, the total number of different types of chromosome configuration at metaphase I were 3 in the first hybrid, 7 in the second, 3 in the third, 5 in the fourth, 5 in the fifth, and 4 in the sixth one. The most frequent configurations were 6 prs (shape 8) + 1 pair freee in the first hybrid, 7 prs in the second; 5 pairs (star) + 2 prs free in the third, 5 prs (Zigzag) + 1 pair free in the fourth, 6 (linear) + 4 prs free in the fifth and 7 prs (Zigzag) in the sixth one (Fig. 37).

Similar results were found by Jean and Linden (1979) In the hybrids O. niessensis x O. odorata coronifera x O. odorata. The most frequent

Table (16): Chromosome configuration at Metaphase I in F_1 in hybird of O. nissensis x O. coronifera and its parents .

The hybrids or parents	Type of chromosome configuration	Number of cells observed	Percentage
O. nissensis	7 prs	7	3.18
	6 ⊙ + 4 prs	20	31.80
	8 ⊙ + 3 prs	11	17.46
	10 ⊙ + 2 prs	18	26.57
	4 ⊙ + 5 prs	10	15.90
	4 ⊙ + 4 ⊙ + 4 ⊙ + 1 prs	2	3.18
Total		63	100.00
O. nissensis x O. coronifera	5 prs (linear)+ 2 prs free	8	32.00
	7 prs (star)	5	20.00
	6 prs (shap 8) + 1 prs free	12	48.00
Total		25	100.00
O. coronifera	7 prs	3	7.50
	6 ⊙ + 4 prs	5	12.50
	8 ⊙ + 3 prs	2	5.00
	10 ⊙ + 2 prs	7	17.50
	4 ⊙ + 5 prs	9	22.50
	4 ⊙ + 4 ⊙ + 3 prs	11	27.50
	4 ⊙ + 4 ⊙ + 4 ⊙ + 1 prs	3	7.50
Total		40	100.00

Table (17): Chromosome configuration at metaphase I in F_1 hybrids of O. nissensis x O. odorata and its parents .

The hybrids or parents	Type of chromosome configuration	Number of cells observed	Percentage
O. nissensis	7 prs	2	3.18
	6 ⊙ + 4 prs	20	31.80
	8 ⊙ + 3 prs	11	17.46
	10 ⊙ + 2 prs	18	28.57
	4 ⊙ + 5 prs	10	15.90
	4 ⊙ + 4 ⊙ + 4 ⊙ + 1 prs	2	3.18
Total		63	100.00
O. nissensis x O. odorata	4 prs (zigzag) + 3 prs free	4	10.52
	5 prs (star) + 1 prs free	3	77.89
	7 prs (star)	6	15.79
	7 prs	10	26.32
	6 prs (zigzag) + 1 prs free	7	18.42
	5 prs (zigzag) + 2 prs free	5	13.16
Total		38	100.00
O. odorata	7 prs	12	14.63
	5 ⊙ + 4 prs	20	24.39
	8 ⊙ + 3 prs	9	10.98
	10 ⊙ + 2 prs	23	28.05
	4 ⊙ + 5 prs	15	18.29
	4 ⊙ + 4 ⊙ + 4 ⊙ + 1 prs	3	3.66
Total		82	100.00

Table (18): Chromosome configuration at Metaphase I in F_1 hybrids of O. nissensis x O. biennis and its parents.

The hybrids or parents	Type of chromosome configuration	Number of cells observed	Percentage
O. nissensis	7 prs*	2	3.18
	6 ⊙** + 4 prs	20	31.80
	8 ⊙ + 3 prs	11	17.46
	10 ⊙ + 2 prs	18	26.57
	4 ⊙ + 5 prs	10	15.90
	4 ⊙ + 4 ⊙ + 4 ⊙ + 1 prs	2	3.18
Total		63	100.00
O. nissensis x O. biennis	5 prs (stare) + 2 prs free	13	56.52
	7 prs	7	30.44
	6 prs (zigzag) + 1 prs free	3	13.04
Total		23	100.00
O. biennis	7 prs	45	38.79
	6 ⊙ + 4 prs	12	10.35
	8 ⊙ + 3 prs	18	15.52
	10 ⊙ + 2 prs	3	1.49
	4 ⊙ + 5 prs	10	8.62
	4 ⊙ + 4 ⊙ + 3 prs	20	17.34
	4 ⊙ + 4 ⊙ + 4 ⊙ + 1 prs	8	6.90
Total		116	100.00

* Prs.= Pairs.

** ⊙ = Circul.

Table (19): Chromosome configuration at Metaphase I in F_1 hybrid of O. biennis x O. coronifera and its parents.

The hybrids or parents	Type of chromosome configuration	Number of cells observed	Percentage
O. biennis	7 prs	45	38.79
	6 ⊙ + 4 prs	12	10.35
	8 ⊙ + 3 prs	18	15.52
	10 ⊙ + 2 prs	3	1.49
	4 ⊙ + 5 prs	10	8.62
	4 ⊙ + 4 ⊙ + 3 prs	20	17.34
	4 ⊙ + 4 ⊙ + 4 ⊙ + 1 prs	8	6.90
Total		116	100.00
O. biennis x O. coronifera	5 prs (linear) + 2 prs free	2	9.52
	5 prs (zigzag) + 1 prs free	7	33.33
	6 ⊙ + 6 ⊙ + 1 prs free	3	14.29
	4 prs (zigzag) + 3 prs (linear)	3	14.29
	12 ⊙ + 1 prs	6	28.57
Total		21	100.00
O. coronifera	7 prs	3	7.50
	6 ⊙ + 4 prs	5	12.50
	8 ⊙ + 3 prs	2	5.00
	10 ⊙ + 2 prs	7	17.50
	4 ⊙ + 5 prs	9	22.50
	4 ⊙ + 4 ⊙ + 3 prs	11	27.50
	4 ⊙ + 4 ⊙ + 4 ⊙ + 1 prs	3	7.50
Total		40	

Table (20): Chromosome configuration at metaphase I in F_1 hybrid of O. biennis x O. odorata and its parents.

The hybrids or parents	Type of chromosomes configuration	Number of cells observed	Percentage
O. biennis	7 prs	45	38.79
	6 ⊙ + 4 prs	12	10.35
	8 ⊙ + 3 prs	18	15.52
	10 ⊙ + 2 prs	3	1.49
	4 ⊙ + 5 prs	10	8.62
	4 ⊙ + 4 ⊙ + 4 ⊙ + 1 prs	8	6.90
Total		116	100.00
O. biennis x O. odorata	10 ⊙ + 2 prs free	5	26.32
	14 ⊙	4	21.05
	6 (linear) + 4 prs free	7	36.84
	2 prs (group) + 2 prs group + 3 prs	2	10.53
	2 prs (group) + 5 prs free	1	5.26
Total		19	100.00
O. odorata	7 prs	12	14.63
	6 ⊙ + 4 prs	20	24.39
	8 ⊙ + 3 prs	9	10.98
	10 ⊙ + 2 prs	23	28.05
	4 ⊙ + 5 prs	15	18.29
	4 ⊙ + 4 ⊙ + 4 ⊙ + 1 prs	3	3.66
Total		82	100.00

Table (21): Chromosome configuration at metaphase I in hybrids of O. coronifera x O. odorata and its parents .

The hybrids or parents	Type of chromosome configuration	Number of cells observed	Per-centage
O. coronifera	7 prs	2	7.50
	6 ⊙ + 4 prs	5	12.50
	8 ⊙ + 3 prs	2	5.00
	10 ⊙ + 2 prs	7	17.50
	4 ⊙ + 5 prs	9	22.50
	4 ⊙ + 4 ⊙ + 3 prs	11	27.50
	4 ⊙ + 4 ⊙ + 4 ⊙ + 1 prs	3	7.50
Total		40	100.00
O. coronifera x O. odorata	12 ⊙ + 1 prs	3	12.50
	7 ⊙ + 7 ⊙	2	8.33
	4 chromosome opend ring	7	29.17
	7 prs (zigzag)	12	50.00
		24	100.00
O. odorata	7 prs	12	14.63
	6 ⊙ + 4 prs	20	24.39
	8 ⊙ + 3 prs.	9	10.98
	10 ⊙ + 2 prs	23	28.05
	4 ⊙ + 5 prs	15	16.29
	4 ⊙ + 4 ⊙ + 4 ⊙ + 1 prs	3	3.66
Total		82	100.00

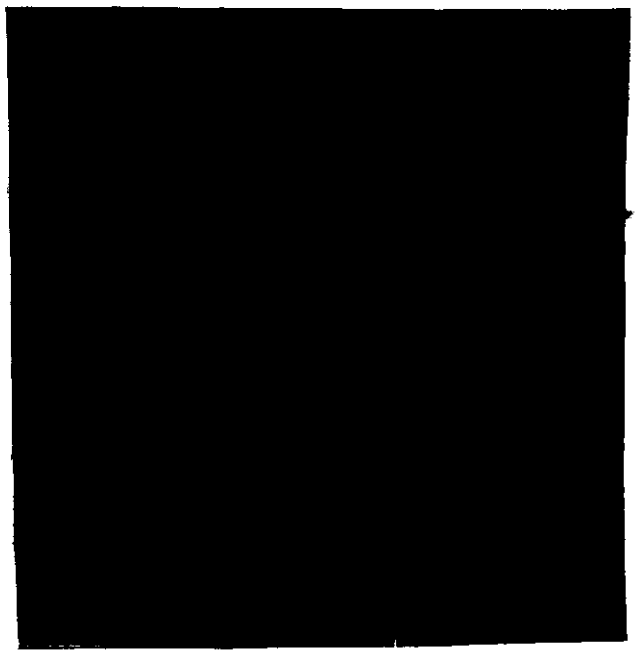

Fig. (29): Photomicrographs showing abnormalities in diakinesis stage in O. nissensis parent :

1- Two circles 7 chromosomes in each circle.
2- 7 biavalens.
3- Circle from 8 chromosomes, 3 prs.
4- 3 circles in each 4 chromosomes and one prs.
5- Circle from four chromosomes and two prs.
6- Circle from four chromosomes and 5 prs.
7- Circle from sex chromosomes and two prs/

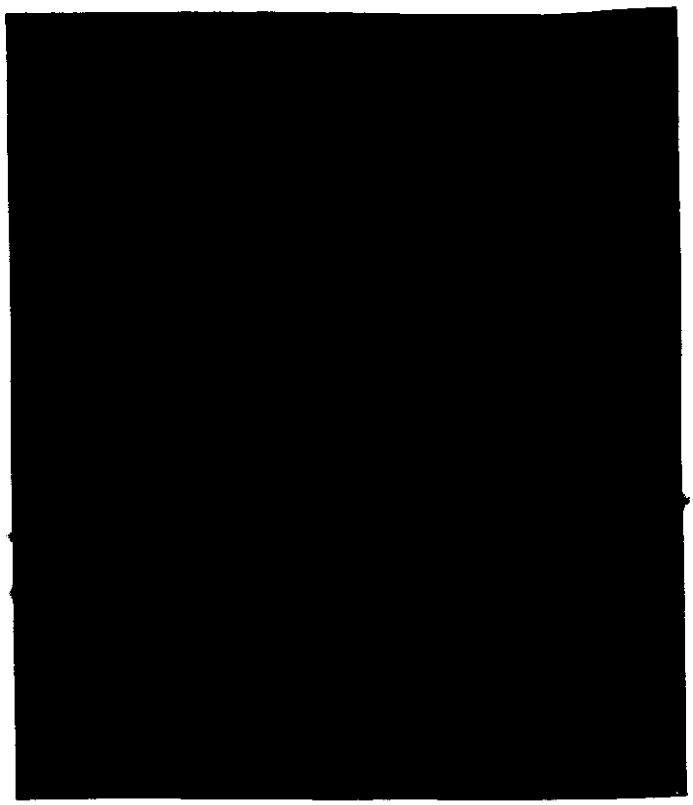

Fig. (30): Photomicrographs showing abnormalities in diakinesis stage in O. biennis:

1- O 6, 4 prs.
2- 7 prs.
3- O 8, 3 prs.
4- O 10, 2 prs,
5- O 4, 5 prs.
6- O 4, O 4, O 4 and one prs.
7- O 4, O 4, O 3 prs.
8- O 4, O 4, 3 prs.

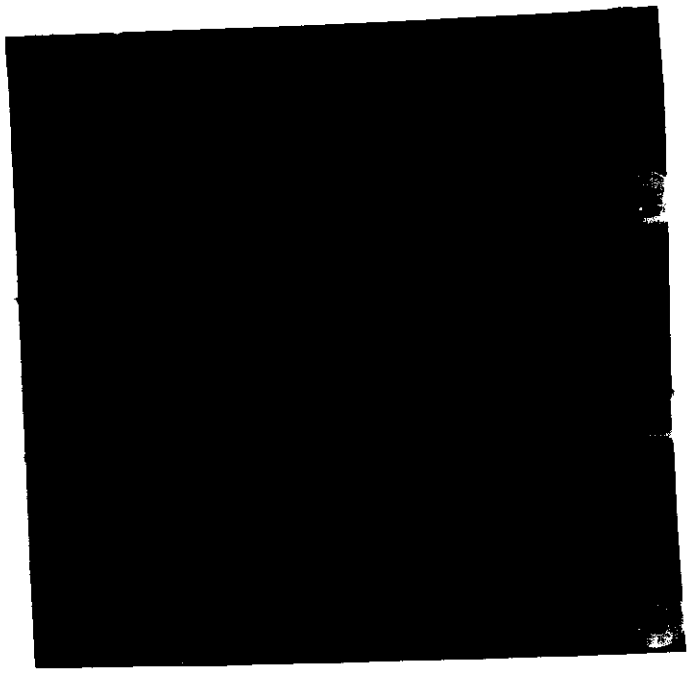

Fig. (31): Photomicrographs showing abnormalities in diakinesis stage in O. coronifera.

1- O 6, 4 prs,
2- 7 prs,
3- O 8, 3 prs,
4- O 6, 4 prs,
5- O 10, 2 prs
6- O 4, O 4, 3 prs,
7- O 4, O 4, 3 prs,
8- O 4, O 4, O 4, 2 prs
9- O 10, 2 prs.

Fig. (32): Photomicrographs showing abnormalities in diakinesis stage in O. odorata :

1- O 4, O 4, O 6.
2- 7 prs.
3- O 8, 3 prs.
4- O 10, 2 prs.
5- O 4, 2 prs.
4- O 8, 3 prs.
7- O 6, 4 prs.
8- O 8, 3 prs.

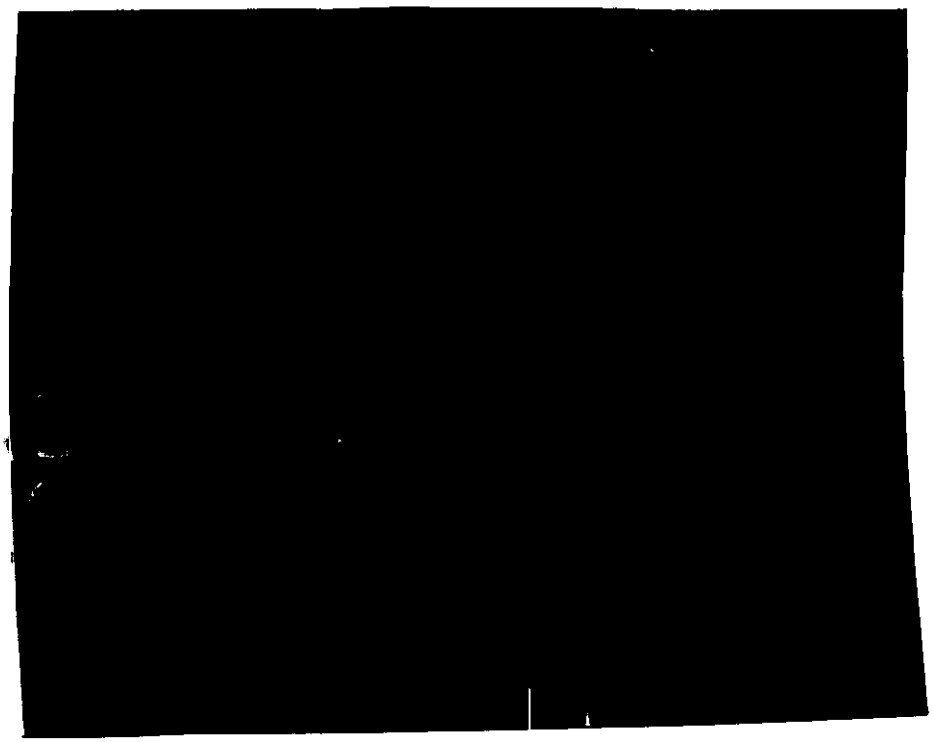

Fig. (34): Photomicrographs showing abnormailities in diakinesis stage in hybrid O. nissensis x O. coronifera.

1, 2, 5: 7 prs (stare).

3: 5 prs (liner), 2 prs free.

4: 6 prs line 8, 1 prs.

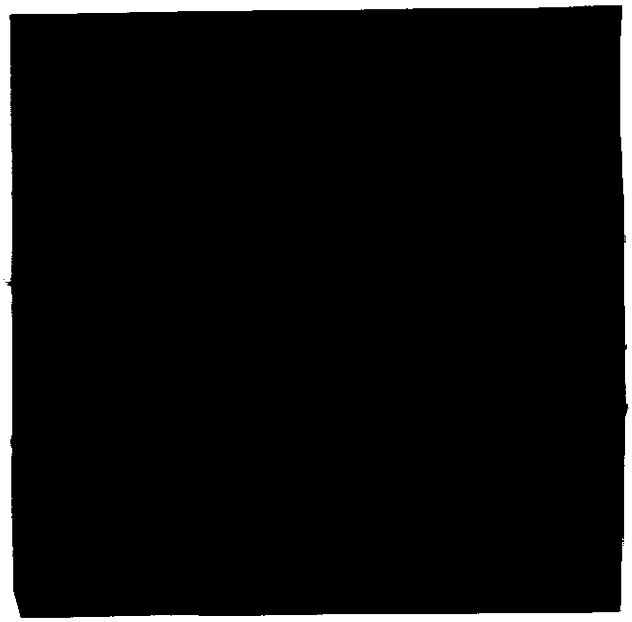

Fig. (35): Photomicrographs showing abnormalities in diakinesis stage in hybrid O. nissensis x O. odorata.
1, 2, 9: 7 prs (stare)
3: 4 prs (Zigzage), 3 prs free
4, 6: 7 prs (cricle) .
5: 5 prs (Zigzage), 2 prs free.
7, 8: 4 prs (stare), 3 prs free.

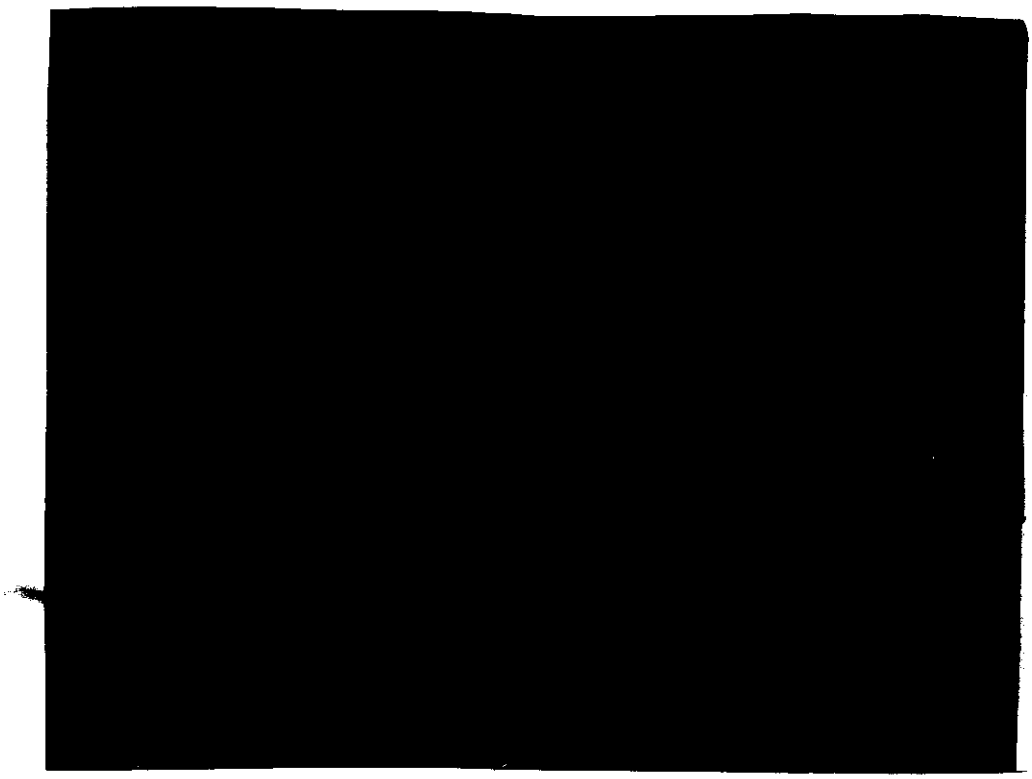

Fig. (3.6): Photomicrographs showing abnormalities in diakinesis in hybrid (O. biennis x O. coronifora.
1: 5 prs (Zigzage); 2 prs free.
2: 5 prs (liner), 2, prs free.
3: 4 prs (Zigzage), 3 prs (liner).
4: 5 prs (ring), 2 prs free.

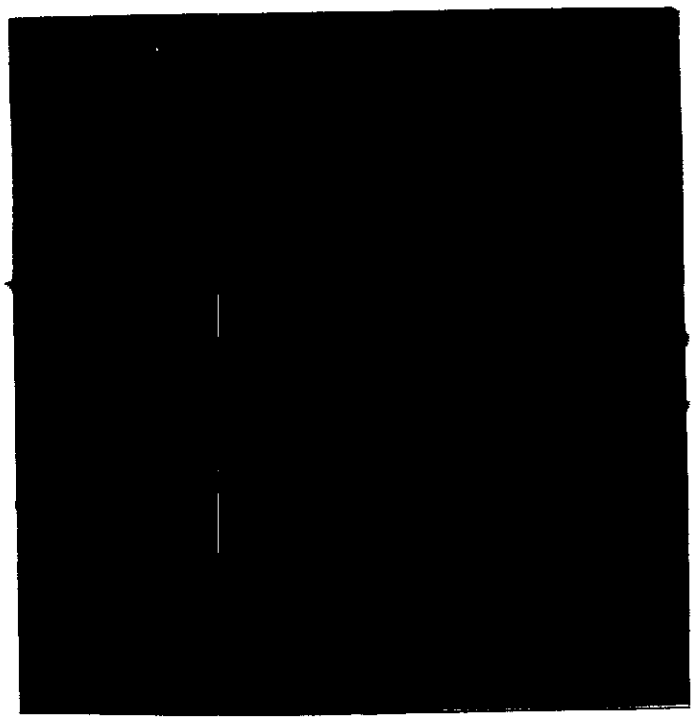

Fig. (38): Photomicrographs showing abnormailities in diakinesis stage in O. coronifera x O. odorata :

1, 5, 6, 7 : 6 prs (ring), 1 prs free.

2, 3 : 7 prs (ring),

8, 9 : 7 prs (Zigzage).

configuration were 7 prs. These results are in agreement with those found by Steiner and Stubbe (1986).

Steiner and Stubbe (1984) stated that when chromosome pairing at meiosis is studied in stable species, it gives informations about the potentialities for genetic recombinations possessed by species. The nature of chromosome pairing in interspecific hybrids may provide information concerning the role, if any chromosomal changes have played in the origin of the species concerned.

In all PMCs of the interspecific hybrids, bivalents were observed, however, with different frequencies depending on the degree of homology between the parental chromosomes.

c- Pollen stainability :

The fertilit y of interspecific hybrids is an important indicator of biosystematic relationships, since it may measure the ability of the parental species to exchange genes.

Pollen viability was estimated in each of the four species under investigation, showing that there was about 22.38 % unviable pollen grains in the species O. nissensis (Table 22). However, the percentage of unviable pollen grains were 8.31 % and 5.40 %, in the species O. coronifera and O. odorata , respectively.

The pollen viability was also estimated in the six F_1 crosses and the six reciprocal crosses. In the F_1 cross O. nissensix x O. biennis, the univable pollen grains were decreased compared with O. nissensis. However, the usage of O. nissensis as a female parent increased the percentagge of unviable pollen grains more than in the previous cross (21.28 %). In this instance, Skiebe (1972) indicated that the higher fertility resulting from the influenced repeated selfing or cross pollinations of plants are produced by mitotic or meiotic polyploidization. In F_1 of the cross O.nissensis x O. coronifera, the percentage of univiable pollen grains (6.66 %) not exceeded parents. While, in the reciprocal cross this value (11.72 %) exceeded the parent O. coronifera (8.31 %), and this might be due to the usage of O. coronifera as a female parent. In the cross O. nissensis x O. odorata, the percentage of unviable pollen grains was (8.18 %), while the usage of O. odorata as a female parent, this percentage was high (11.97 %). Table (2)

The hybrid O. biennis x O. coronifera have the percentage of unviable pollen grains 14.42 % which exceeded that percentage in both parents. But when O. coronifera was used as a female, this percentage was decreased 6.65 %.

In F_1 of the cross O. biennis x O. odorata, the percentage of unviable pollen grains was 13.37 % exceeding both parents while in the reciprocal cross, this ratio become higher than that of the parent O. odorata only. Fig.(39,40)

Finally in F_1 of the cross O. coronifera x O. odorata, the percentage of unviable pollen grains was relatively higher (10.60 %) than in the both parents (9.99 and 5.40 %). In the reciprocal cross O. odorata x O. coronifera, the percentage of unviable pollen grains was (8.52%) reaching the limit of the parent O. coronifera (8.31 %), showing the same trend as in the species O. odorata. Confirming these results, Yamaguchi (1981) found that the polyploides in oenothera were fertile when used as male rather than female parents.

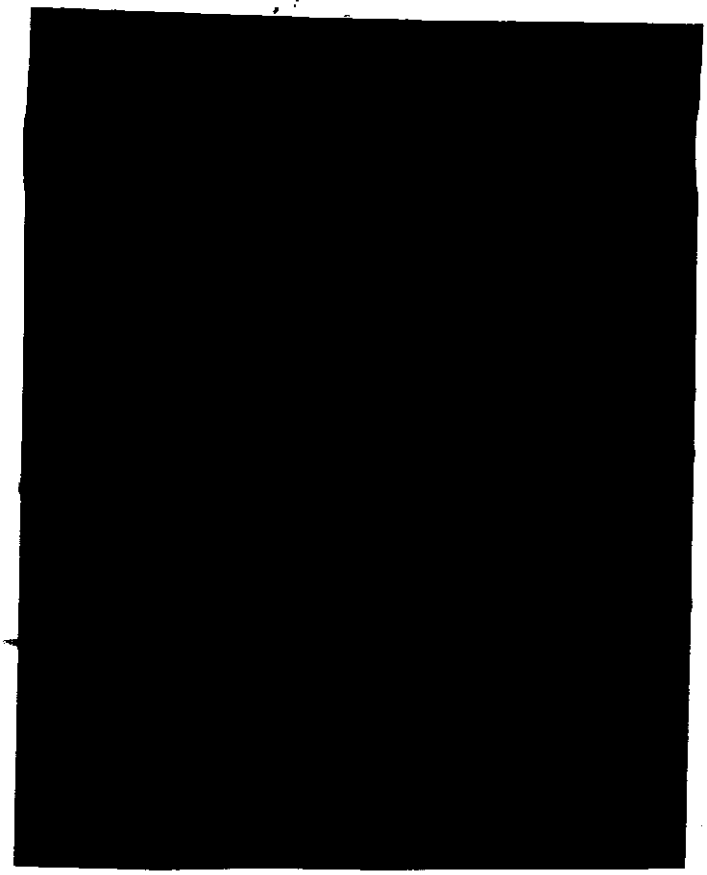

Fig. (39):

1: **Viability of pollen grean of** O. nissensis

2: Viability of pollen grean of O. biennis

3: Viability of pollen grean of O. coronifera

4: Viability of pollen grean of O. odorata

5: ♂ O. nissensis x O. biennis ♀

6: ♂ O. biennis x O. nissenesis ♀

7: ♂ O. nissensis x O. coronifera ♀

8: ♂ O. coronifera x O. nissensis ♀

Fig. (40): Viability of pollen grean of hybrids :

1: Pollen grean of ♂ O. nissensis x O. odorata ♀
2: Pollen grean of ♂ O. odorata x O. nissensis ♀
3: Pollen grean of ♂ O. biennis x O. coronifera ♀
4: Pollen grean of ♂ O. coronifera x O. biennis ♀
5: Pollen grean of ♂ O. biennis x O. odorata ♀
6: Pollen grean of ♂ O. odorata x O. biennis ♀
7: Pollen grean of ♂ O. coronifera x O. odorata ♀
8: Pollen grean of ♂ O. odorata x O. coronifera ♀