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GENETIC AND BREEDING STUDIES IN A *CUCUMIS*
SATIVUS L. X *C.* *HARDWICKII* R. POPULATION

presented by

NEIL MADISON COWEN

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GENETIC AND BREEDING STUDIES IN A *CUCUMIS SATIVUS* L. X *C*. *HARDWICKII* R. POPULATION

BY

Neil Madison Cowen

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ABSTRACT

GENETIC AND BREEDING STUDIES IN A *CUCUMIS SATIVUS* L. X *C. HARDWICKII* R. POPULATION

BY

Neil M. Cowen

The P_1, P_2, F_1 and F_2 generations of a *Cucumis sativus* L. x *C. hardwickii* R. interspecific cross were evaluated for 11 traits: seedling bitterness; spine color; nodes to first pistillate flower; percent (%) gycoecious nodes for nodes 1-20; percent (%) nodes with laterals; fruit number; number of fruits on the main stem; number of fruits on the laterals; fruit diameter; fruit length; and fruit yield. Significant genetic variation was observed for all traits in the F_2. High heritabilities and high gains from selection were observed for all traits except fruits on the main stem. Non-additive types of gene action probably are involved in the expression of most traits. It is concluded that *C. hardwickii* may serve as a source of genes for increasing yields in *C. sativus*.

Guidance Committee:

This thesis is condensed into a format suited and intended for publication in Euphytica.

To my daughter Candace Marie

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INTRODUCTION

Fruit yield in pickling cucumber (Cucumis sativus L.) for mechanical harvest have typically been limited to 1-2 fruits per plant (Miller & Hughes, 1969). Developing seeds in the first fertilized fruit inhibit the development of subsequently fertilized flowers. This inhibition severely limits the number of harvestable fruits per plant. This inhibitory effect is presumed to be due to internal sink competition. The developing fruit acts as a powerful sink for translocated photosynthates, the strength of which precludes further fruit set and development due to the unavailability of metabolites (McCollum, 1934; Neihuis & Lower, 1980).

Several approaches have been proposed for increasing fruit set per plant: both by plant breeding techniques as well as by physiological means. Breeding of parthenocarpic or seedless pickling cucumbers has been proposed as one method of increasing fruit set per plant (Pike & Peterson, 1969; Baker et al., 1973; Deena, 1973). The absence of developing ovules in the fruit reduces the inhibitory effect on subsequent fruit set. Deena (1973) and others (Connor & Martin, 1970) further proposed that breeding for small mature fruit size and delayed fruit set would lead to higher per plant fruit numbers. The physiological approach proposed by a large number of researchers (Robinson et al., 1971; Quebedaux & Beyer, 1972); Cantliffe, 1974; Elassar et al., 1974) utilizes chemical growth regulators to induce parthenocarpic fruit set in pickling cucumber cultivars which are not genetically parthenocarpic.

Recently, Horst and Lower (1978) proposed using *Cucumis hardwickii* R. as a source of genes for increasing fruit yields per plant in pickling cucumber. *C. hardwickii* is an annual, monoecious, short day, unadapted species which hybridizes readily with *C. sativus*, producing fertile F_1's. The fruit set and branching characteristics exhibited by *C. hardwickii* are atypical of *C. sativus*. *C. hardwickii* ordinarily has more and larger laterals than *C. sativus* as well as being capable of sequentially setting large numbers of seeded fruit (Whitaker & Davis, 1962; Horst & Lower, 1977, 1978; Robinson & Kowalski, 1978; Neihuis & Lower, 1979, 1980).

The present study was undertaken to clarify the inheritance of, gene action involved in, and estimate heritabilities and gains from selection for a number of fruit and growth habit characteristics in a *C. sativus* x *C. hardwickii* population.

MATERIALS AND METHODS

The material used in this study was MSU 41, a gynoecious inbred line of *C. sativus* which was selected out of GY14, by Dr. Baker at MSU, and LJ 90430, an inbred line of *C. hardwickii*.

Greenhouse Procedure

The P_1, P_2, F_1, and F_2 generations of the cross MSU 41 x LJ 90430 were sown in peat pots filled with VSP mix on December 9, 1980. The germinating seedlings were transplanted into raised beds filled with VSP mix on December 26, 1980. Temperatures were maintained at $24^{\circ} \pm 3^{\circ}C$ during the day and $18^{\circ} \pm 3^{\circ}C$ at night. Standard cultural practices for fertility, disease and insect control were followed for the duration of the experiment.

The plants were trained on bamboo stakes to a height of 2 meters, and all laterals were allowed to develop to a length of 2 nodes.

Seedlings were planted in a randomized complete block design with 3 replications of the P_1, P_2, and F_1 generations, and 12 replications of the F_2 in each 21 blocks.

All female flowers were hand pollinated. Flowers reaching anthesis during the day the pistillate flowers were to be pollinated were used. This procedure was continued throughout the entire pistillate flowering period for all plants in the experiment.

Data were collected on all plants for 11 traits; seedling bitterness; spine color; nodes to first pistillate flower; percent (%) gynoecious nodes for nodes 1-20; percent (%) nodes with laterals; total fruit number; number of fruits on the main stem; number of fruits on the laterals; fruit diameter (cm.); fruit length (cm.); and fruit yield (gm.). Seedling bitterness was evaluated using the tasting method described by Andeweg and De Bruyn (1959). Spine color was evaluated on either developing or mature fruit, and characterized as either black or white spined. Gynoecious nodes were defined as nodes bearing female flowers. Fruit diameter and length measurments were made on randomly selected fruits.

Statistical Procedure

Missing values for all characters were estimated using Yate's pseudo approximations (Neter & Wasserman, 1974).

Tests of genotypic ratios and tests for linkage of spine color, bitterness, nodes to first pistillate flower, and percent gynoecious nodes for nodes 1-20 were performed using the Chi square test for goodness of fit (Steel & Torrie, 1980).

Values for σ_G^2 and σ_E^2, the genetic and error variances, respectively, were calculated by equating estimated mean squares, from the analysis of variance, with expected mean squares and solving for the appropriate component of variance.

Heritability was calculated using the formula: $H^2=\sigma_G^2/ (\sigma_E^2/r+\sigma_G^2)$ where σ_G^2 and σ_E^2 are the genetic and error variances, respectively, and r is the number of replications. This formula gives heritability in the broad sense and on an entry mean basis.

Gains from selection were predicted using the formula: $G_c= (cK\sigma_G^2)/ (\sigma_E^2/r+\sigma_G^2)^{1/2}$ with G_c being the genetic gain per cycle, c the parental control value, K is the selection differential in standard units, r equals the number of replications, and σ_G^2 and σ_E^2 are genetic and error variances, respectively.

Tests for number of effective factors were performed using the Castle-Wright formula (Wright, 1937). This value is expressed as $K=R^2/ 8\sigma_G^2$ with K equalling the number of effective factors, R equalling the range of the F_2 population, and σ_G^2 representing the genetic variance. In the original formula, R was defined as the range of the parents in a mating, but Lawrance and Frey (1976) argued that the range of the F_2 segregates was a more appropriate estimate of R when the parents did not represent the genotypic extremes for segregating loci. An effective factor does not necessarily represent a single locus, but rather may represent a cluster of genes or even an entire chromosome.

Tests of gene action were performed for characters measured, when possible. Mid-parent values were compared with F_2 means: significant differences of these values suggest non-additive gene action, whereas nonsignificant differences are suggestive of additive gene action (Mather & Jinks, 1971; Rosielle & Frey, 1977).

Potence ratios were calculated for nodes to first pistillate flower and percent gynoecious nodes for nodes 1-20, using the formula $h_3 = (\bar{X}_{F1} - \bar{X}_{MP}) / (\bar{X}_{HP} - \bar{X}_{MP})$ where h_3 is the potence ratio, X_{F1} equals the mean of the F_1 generation, $\bar{X}_{MP}$ equals the mid parent value $(\bar{X}_{HP} + \bar{X}_{LP}) / 2$, and $\bar{X}_{HP}$ and $\bar{X}_{LP}$ are the mean of the parents having higher and lower expression of the character, respectively (Mather & Jinks, 1971). Potence ratios explain the direction (positive or negative) and degree (partial or complete) of dominance demonstrated by the loci under consideration.

Transgressive segregates were defined as those plants exceeding the high parent value by one standard deviation, where such information was available. Transgressive segregates for yield were defined as those plants equalling or exceeding the mean of the F_1 population. This definition was adopted since data were unavailable on one of the parents, and Neihuis and Lower (1980) have shown heterosis for yield in crosses of closely related _C. sativus_ inbred lines and _C. hardwickii_ line LJ 90430. Transgressive segregates were not defined for traits where data were not available for one of the parents, and where heterosis has not previously been observed.

RESULTS AND DISCUSSION

Significant variation was observed for all traits. F tests for genotypic effects were significant at the 0.0005 level for all traits assayed.

Bitterness, derived from the *C. hardwickii* parent, segregated in the F_2 (Cochran, 1937; Barnham, 1953; Andeweg & DeBruyn, 1959), giving a good fit to a 3:1 ratio ($0.25 < P < 0.5$; Table 1). Selection against seedling bitterness should be exercised in any breeding program, since seedling bitterness is associated with bitterness in fruit tissue. Contrary to expectation (Cochran, 1937; Hutchins, 1940; Shanmugasundaram et al., 1971) spine color segregated in a 9:7 ratio of black spine to white spine, ($0.90 < P < 0.95$) (Table 1). This ratio is different from the 3:1 or 15:1 ratio's reported previously; where pleiotropic effects on mature fruit color and fruit netting were reported as well (Hutchins, 1940). The sole report where a pleiotropic effect on mature fruit color (orange mature fruit color associated with black spine color) was not reported a 3:1 ratio was also observed (Cochran, 1937). The black spine color derived from *C. hardwickii* can be explained by a 2 gene epistatic model, therefore these genes probably are distinct from those controlling spine color in *C. sativus*. Linkage was tested for, and they are unlinked to the gene controlling bitterness.

Female expression was measured as nodes to first pistillate flower, and percent gynoecious nodes for nodes 1-20. Both measures gave similar results: frequency distributions were trimodal in the F_2 (Figures 1 and 2); number of effective factor pairs was estimated at 2 (Table 5); and potence ratios were nearly identical (Table 4). For the Chi square test, homozygous and heterozygous classes were defined in terms of the parents and F_1 respectively. In the case of nodes to first pistillate flower, the ratio was adjusted for misclassification of heterozygotes (Figures 1 and Table 1). When the Chi square tests were performed, both measures approximated a 1:2:1 ratio ($0.1 < P < 0.25$ and $0.9 < P < 0.95$, respectively). These results are similar to those reported by Kubicki (1969) where he obtained a 1:2:1 ratio for nodes to first pistillate flower in the F_2 of a cross between a gynoecious inbred line and a monoecious inbred line of *C. sativus*. He explained his results on the basis of segregation of alleles at the Acr locus. Because both measures fit a 1:2:1 ratio, and have nearly identical potence ratios, it is postulated that they are controlled by the same locus. This follows intuitively as well, for the following reason. A plant having a low number of nodes to first pistillate flower will have a high percent gynoecious expression for nodes 1-20. The converse is also true. Further, plants having an intermediate number of nodes to first pistillate flower will have intermediate gynoecious expression.

Both measures of gynoecious expression had high heritabilities: 0.94 and 0.93 respectively (Table 1). The high gains from selection (Table 2) also reinforces the conclusion that gynoecious expression is simply inherited. Based on this evidence, one would assume that the trait would be responsive to selection. However, transgressive segregates appeared at low frequencies or not at all (Table 3) indicating that gains might be rapid at first, but would likely level off soon.

Based on the estimate of number of effective factors (Table 5) percent nodes with laterals is under the control of a relatively small number of factors. Tests for types of gene action showed highly significant differences between the mid parent value and F_2 mean, suggesting some type of non-additive gene action involved in the expression of the trait. Further, the F_1 mean is equal to or greater than the mean of the high parent (Figure 3), suggesting dominance and/or epistasis is involved. The presence of dominance or epistasis does not allow an accurate estimate of the number of effective factors (Wright, 1937). Percent nodes with laterals also had a high heritability estimate (0.92, Table 2), and high gains from selection (Table 6). Because of the involvement of either epistasis or dominance the heritability value overestimates narrow sense heritability, and actual gains from selection would be less than predicted gains. Transgressive segregates could not be defined for percent nodes with laterals because the mean of the high parent plus one standard deviation gave a value greater than 1.0, therefore it was impossible for any individuals to fall in this class.

According to the test for number of effective factors (Table 5), fruit number is also under the control of a small number of factors. Narrow sense heritability for fruit number in C. sativus, as reported by Smith (Smith, Lower & Moll, 1978) using a random mating population derived from 18 inbred lines from various breeding programs in the U.S., was 0.17. Estimates of narrow sense heritability for fruit number in a cross with C. hardwickii is given by Horton as 0.88 using parent offspring regression (Horton, 1980; Lower, 1980). Our estimate of heritability for fruit number is 0.96 (Table 2). Lower (1980) indicated that the variance for fruit number is primarily additive with some additive x additive epistasis. Therefore narrow sense heritability should not be considerably less than our estimate of heritability. Gains per cycle of selection for fruit number, using S_1 recurrent selection and a 20% selection intensity, have been estimated by Lower (1980), for a gynoecious synthetic population and a C. hardwickii introgressed exotic population. Estimates of 0.37 and 0.49 were calcualted for the respective populations. The estimate of gain per cycle with S_1 recurrent selection and a 20% selection intensity would be 6.85. At a 10% selection intensity, gain was estimated at 8.61 (Table 6).

Number of fruits on the main stem is apprently much more complex than any other character examined. The number of effective factors estimate was higher than that of any other trait (a value of 18), including fruit yield (Table 5). The test for type of gene action suggests the involvement of non-additive gene action. Number of fruit on the main stem had the lowest heritability of any trait examined; 0.67 (Table 2). Gains from selection were much lower than either fruit number or fruit on the laterals (Table 6). Because non-additive types of gene action are probably involved in the expression of this character, narrow sense heritability is overestimated by this heritability estimate, and actual gains from selection will be less than predicted. Further evidence for the involvement of non-additive gene action in the expression of this trait is the extremely large number of transgressive segregates (Table 7) which amounted to more than 50% of the population.

Number of fruit on the laterals had a low estimate of number of effective factors (Table 5). However, because of the abnormal distribution in the F_2, non-additive types of gene action are probably involved (Figure 6). Number of fruit on the laterals had a high heritability: 0.95 (Table 1). Gains from selection were also high (Table 6) and explained 82% of the gains in selection for fruit number.

Table 1. Chi square test for goodness of fit for several traits in the cross *Cucumis sativus* x *C. hardwickii*

		Frequency/Class[z]					
Trait	Gen.	P_1	F_1	P_2	Expected Ratio	χ^2	P
Bitterness	F_1			63	0:1		
	F_2	68		184	1:3	0.529	0.25 <P<0.5
Spine Color	F_1			63	0:1		
	F_2	108		140	7:9	0.004	0.9 <P<0.95
Nodes to 1st pistillate flower	F_1	18	45				
	F_2	90	105	57	1.56:1.44:1	3.15	0.1 <P<0.25
% gynoecious nodes, nodes 1-20	F_1		63				
	F_2	62	129	61	1:2:1	0.151	0.9 <P<0.95

[z] P_1, P_2, and F_1 are defined in terms of the respective generations or as indicated in the text.

Table 2. Broad sense heritabilities for various traits in the cross *cucumis sativus* x *C. hardwickii*

Trait	H^2
Nodes to first pistillate flower	0.94
% gynoecious nodes, nodes 1-20	0.93
% nodes with laterals	0.92
Fruit number	0.96
Fruits on the main stem	0.67
Fruits on the laterals	0.95
Fruit diameter	0.89
Fruit length	0.89
Fruit yield	0.94

[z] r = 12

Table 3. Test of gene action for several traits in the cross *Cucumis sativus* x *C. hardwickii*

Traits	P_1	P_2	MP	F_2	t value
Nodes to 1st pistillate flower	2.30	31.6	16.95	11.12	6.26**
% gynoecious nodes, nodes 1-20	93.02	0.08	46.55	38.3	2.50**
% nodes with laterals	0.07	0.85	0.46	0.63	5.04**
No. fruit on main stem	1.49	0.0	0.74	3.41	5.56**

**significant at the 0.01 level

^{z} all values x 100

Table 4. Potence ratios for 2 measures of gynoecious sex expression in the cross *cucumis sativus* x *C. hardwickii*

Measure	h_3	Description
Nodes to first pistillate flower	-0.528	Negative, incomplete dom.
% gynoecious nodes, nodes 1-20	-0.51	Negative, incomplete dom.

Table 5. Number of effective factor pairs by which parents in the cross *Cucumis sativus* x *C. hardwickii* for 11 traits

Trait	Number of effective factors (K)
Bitterness	1
Spine color	2
Nodes to 1st pistillate flower	2
% gynoecious nodes, nodes 1-20	2
% nodes with laterals	2
Fruit number	3
Fruit on the main stem	18
Fruit on the laterals	2
Fruit diameter	7
Fruit length	11
Fruit yield	6

Mean fruit diameter and mean fruit length showed normal distributions in the F_2 (Figures 7 and 8). Both had higher number of effective factors estimates than for most characters examined: 7 and 11 respectively (Table 5). Because of the normal distributions obtained in the F_2, additive gene action is suggested to be primarily responsible for their control. Fruit diameter and fruit length had lower heritability estimates than most characters assayed; values were 0.88 and 0.89 respectively (Table 2), and moderate gains from selection (Table 6).

Number of effective factor estimates for fruit yield is low: a value of 6. Based on the work of Neihuis and Lower (1980) there is significant heterosis for yield in crosses of C. sativus with LJ 90430. This suggests either dominance,and/or epistasis is involved in the expression of the character. The heritability and gains from selection estimates for yield are exceptionally high (Tables 1 and 2). Because of the presence of either epistasis or dominance gains from selection will be less than predicted (gains estimated @ 260% of C. sativus parent mean for S_1 selection; Tables 6 and 8).

With the exception of fruits on the main stem, high heritabilities and gains from selection were observed from all traits. As indicated, non-additive types of gene action were probably involved in the expression of the traits assayed, therefore actual gains from selection will likely be less than predicted gains. Further, the estimates of heritability overestimate narrow sense heritability.

Selection for high yielding, multiple fruited, multiple branching lines with the desired degree of female expression and mature fruit size is potentially possible in populations derived from the cross. No estimates of genotypic correlations have been made. This information would be of great value in the development of a selection scheme for this population, where it may be necessary to use indexed selection to optimize gains from selection for more than one trait. Because of the probable involvement of non-additive types of gene action and the occurance of heterosis for yield, one can capitalize on these potential increases primarily in a hybrid product. Therefore the use of some type of interpopulation improvement scheme could be justified.

Table 6. Gains per cycle from selection with a 10% selection differential for various traits in the cross *Cucumis sativus* x *C. hardwickii*

Trait	Mass[z]	Selection Scheme S_1	S_2
Nodes to 1st pistillate flower	7.0	14.61	18.08
% gynoecious nodes, nodes 1-20	22.48	44.97	55.75
% nodes w. laterals	0.21	0.43	0.53
Fruit number	4.3	8.61	10.64
Fruits on the main stem	0.73	1.45	1.88
Fruits on the laterals	3.56	7.11	8.8
Fruit diameter	0.32	0.63	0.79
Fruit length	0.95	1.9	2.37
Fruit yield	343.36	686.73	849.76

[z] one parent selected after pollination

Table 7. Transgressive segregates for various traits in the cross *Cucumis sativus* x *C. hardwickii*

Trait	Definition	Number	%
Nodes to first pistillate flower	<1.6	1	0.39
% gynoecious nodes, nodes 1-20	<97.0	0	0.00
Fruit on the main stem	>2.08	145	57.54
Fruit yield	>1530.4 gm.	4	1.6

Table 8. Generation means for several traits in the cross *Cucumis sativus* x *C. hardwickii*

Trait	Generation mean P_1	P_2	F_1	F_2
Nodes to first pistillate flower	2.30	31.6	9.22	11.12
% gynoecious nodes,[y] nodes 1-20	93.02	0.08	22.86	38.3
% nodes w. laterals	0.07	0.85	0.88	0.63
Fruit number	1.48	---[z]	17.56	6.58
Fruits on the main stem	1.48	0.0	4.53	3.41
Fruits on the laterals	0.0	---[z]	13.03	3.17
Fruit diameter (cm.)	5.56	---[z]	4.56	4.54
Fruit length (cm.)	11.09	---[z]	8.26	8.08
Fruit yield (gm.)	262.71	---[z]	153.40	587.71

[y] all values x 100

[z] means unavailable

Figure 1. Frequency distribution of nodes to first pistillate flower for the P_1, P_2, F_1, F_2 generations of the cross *Cucumis sativus* x *C. hardwickii*

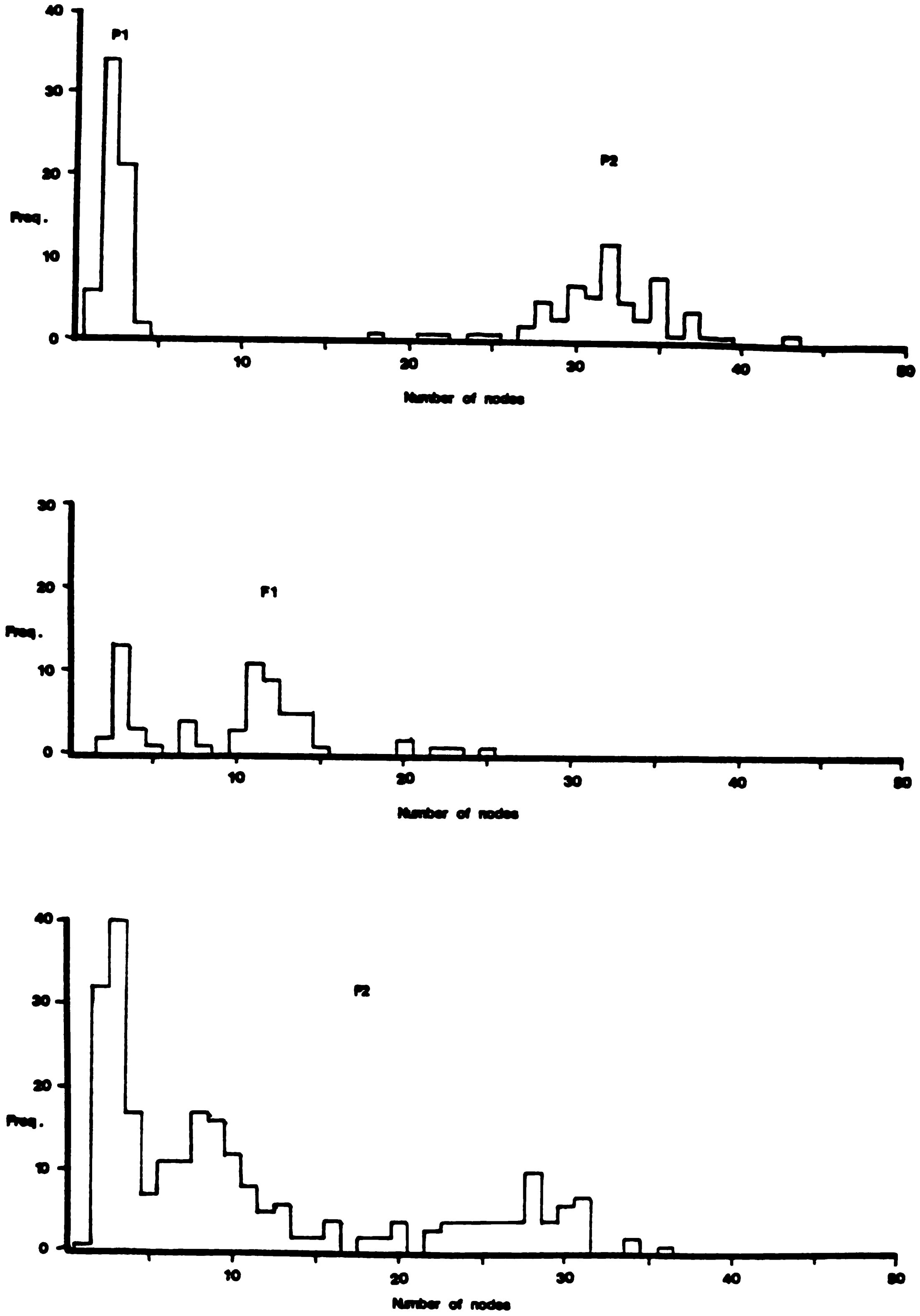

P1
P2
Freq.
40
30
20
10
0
10
20
30
40
50
Number of nodes
F1
Freq.
30
20
10
0
10
20
30
40
50
Number of nodes
F2
Freq.
40
30
20
10
0
10
20
30
40
50
Number of nodes

Figure 1.

Figure 2. Frequency distribution of percent gynoecious nodes for nodes 1-20 for the P_1, P_2, F_1, and F_2 generations of the cross *Cucumis sativus* x *C. hardwickii*

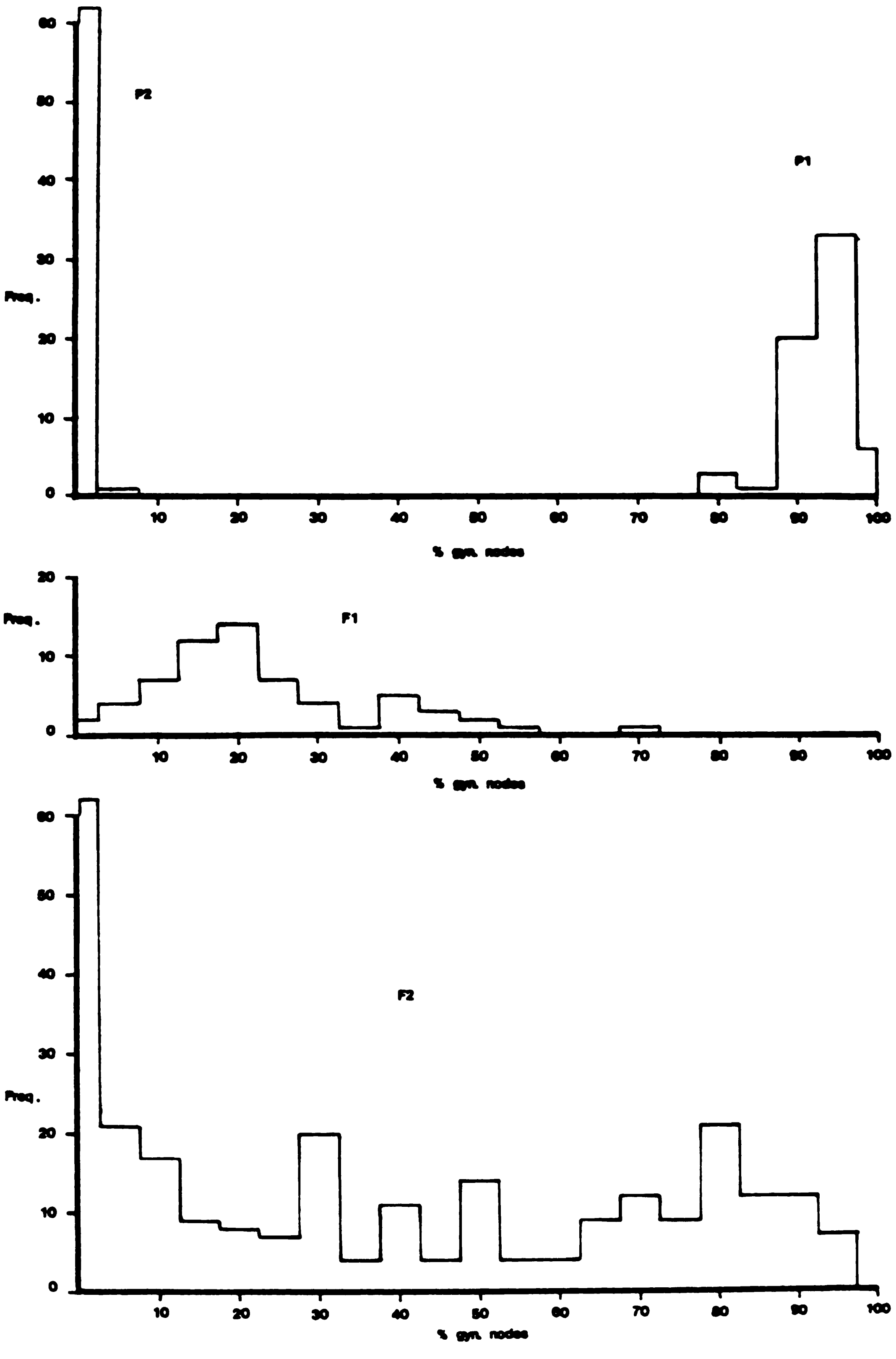

60
50
40
30
20
10
0
Freq.
P2
P1
10
20
30
40
50
60
70
80
90
100
% gyn. nodes
20
10
0
Freq.
F1
10
20
30
40
50
60
70
80
90
100
% gyn. nodes
60
50
40
30
20
10
0
Freq.
F2
10
20
30
40
50
60
70
80
90
100
% gyn. nodes

Figure 2.

Figure 3. Frequency distribution of percent (%) nodes with laterals for the P_1, P_2, F_1, and F_2 generations of the cross *Cucumis* *sativus* x *C*. *hardwickii*

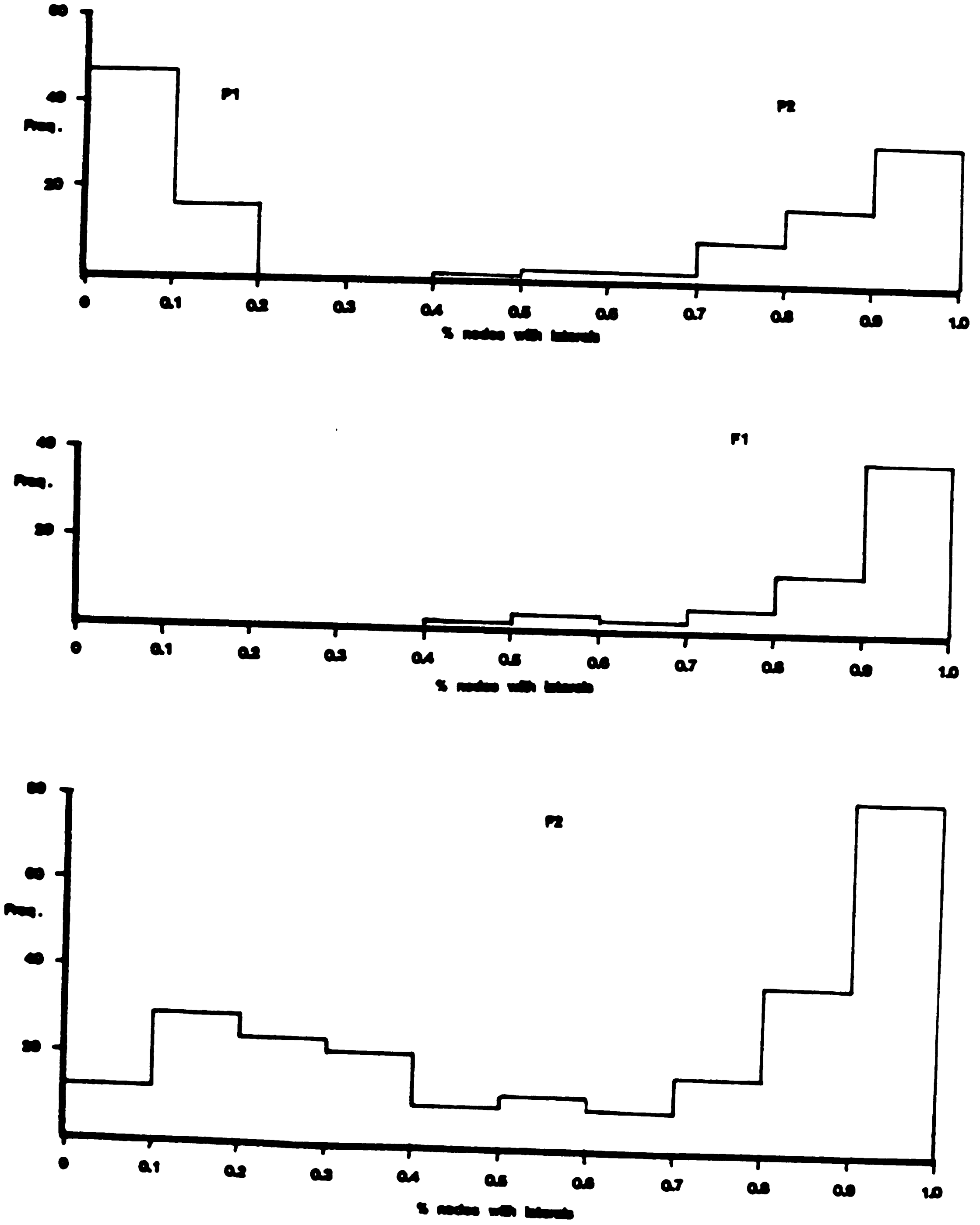

60
40
20
Freq.
P1
P2
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
% nodes with intervals
40
20
Freq.
F1
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
% nodes with intervals
80
60
40
20
Freq.
F2
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
% nodes with intervals

Figure 3.

Figure 4. Frequency distribution of fruit number for the P_1, F_1, and F_2 generations of the cross *Cucumis sativus* x *C. hardwickii*

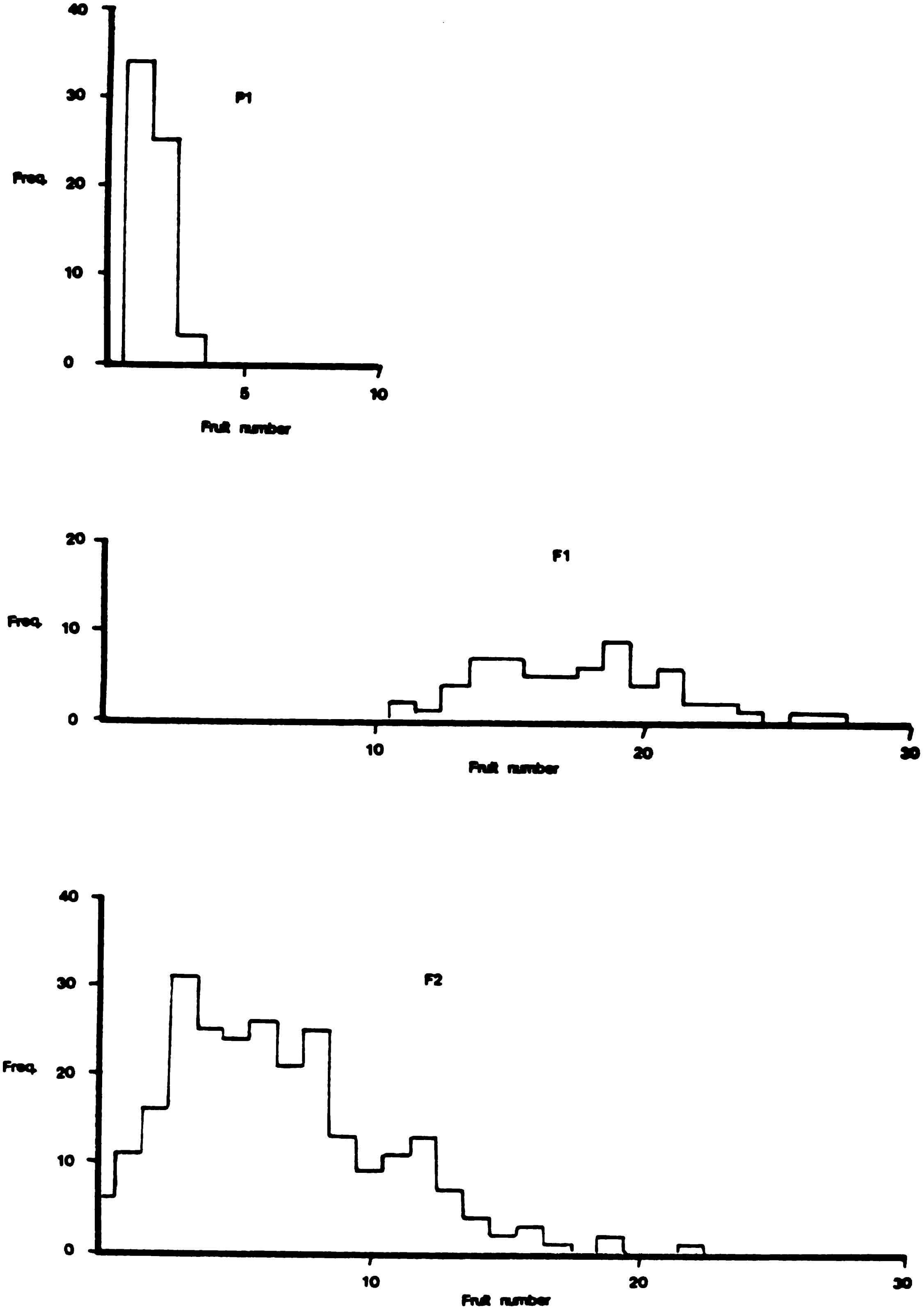

40
30
P1
Freq.
20
10
0
5
10
Fruit number
20
F1
Freq.
10
0
10
20
30
Fruit number
40
30
F2
Freq.
20
10
0
10
20
30
Fruit number

Figure 4.

Figure 5. Frequency distribution of fruits on the main stem for the P_1, P_2, F_1, and F_2 generations of the cross *Cucumis sativus* x *C. hardwickii*

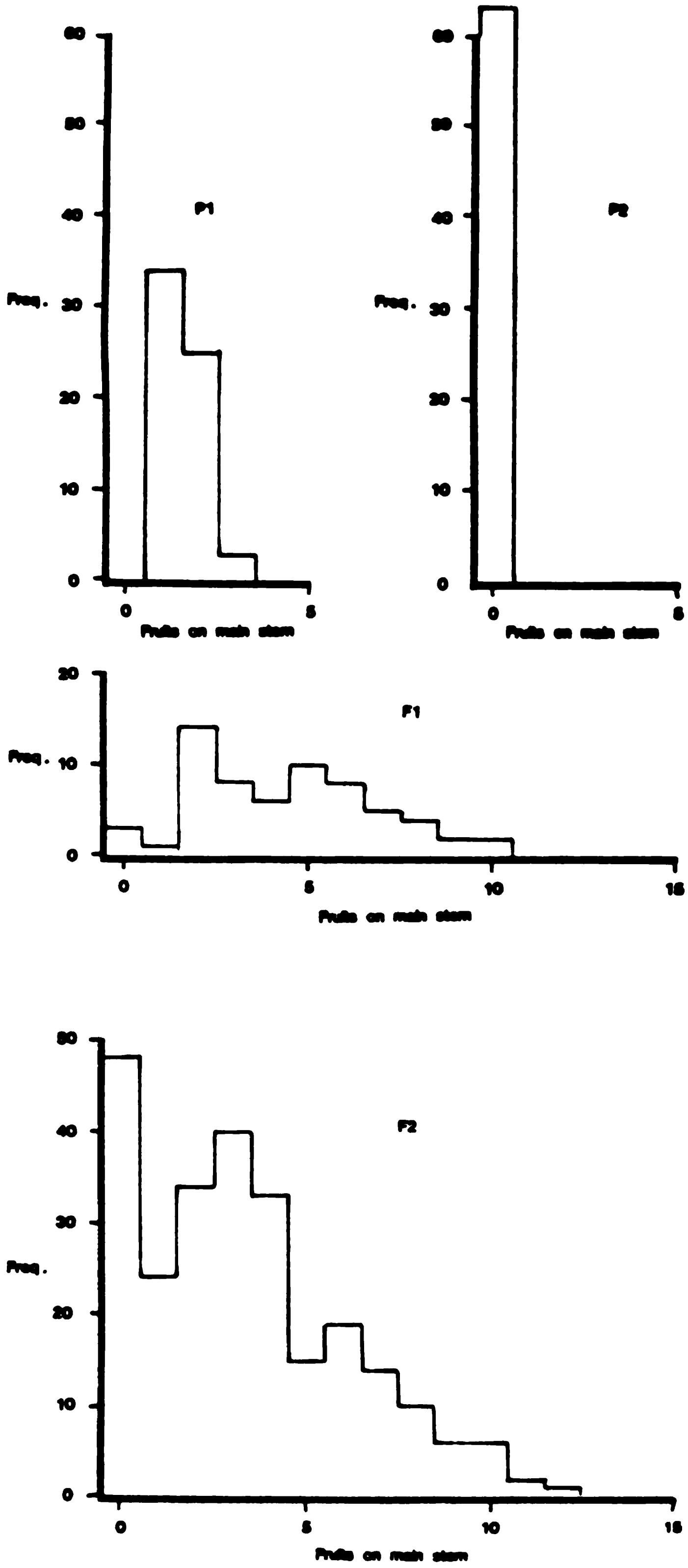

60
50
40
P1
Freq.
30
20
10
0
0
5
Fruits on main stem
60
50
40
P2
Freq.
30
20
10
0
0
5
Fruits on main stem
20
F1
Freq.
10
0
0
5
10
15
Fruits on main stem
50
40
F2
30
Freq.
20
10
0
0
5
10
15
Fruits on main stem

Figure 5.

Figure 6. Frequency distribution of fruits on the laterals for the P_1, F_1, and F_2 generations of the *Cucumis sativus* x *C. hardwickii*

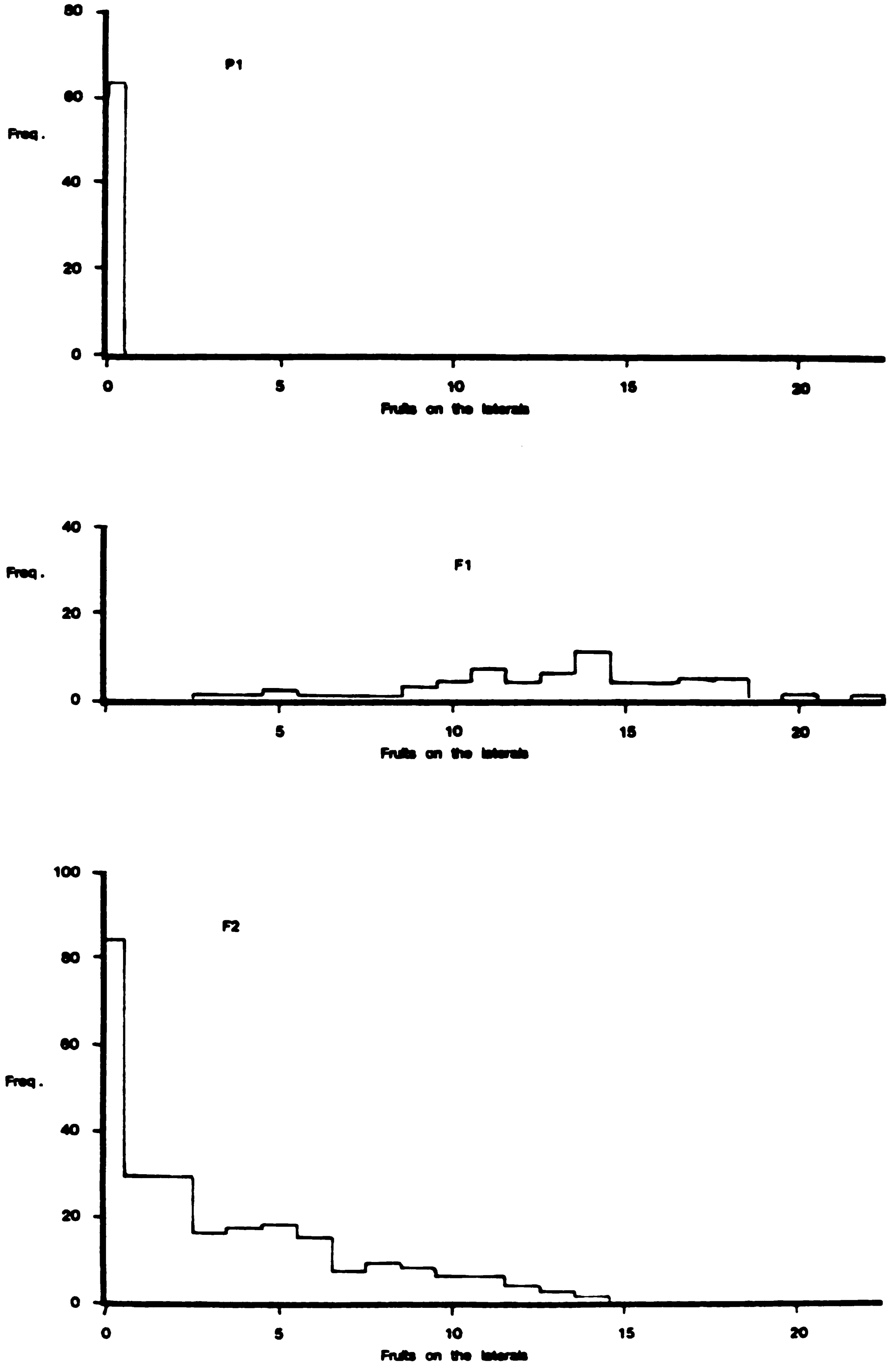
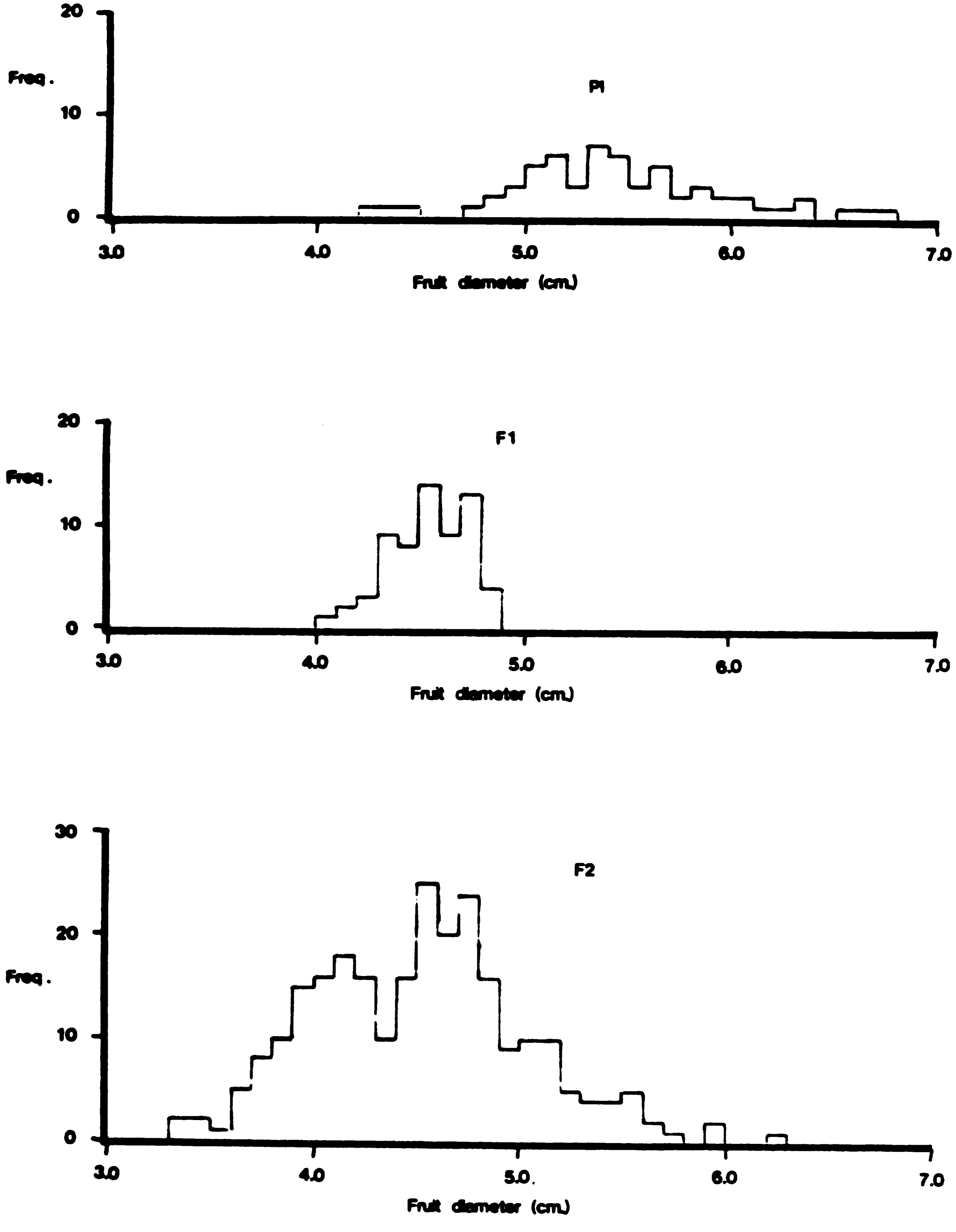

P1
Freq.
80
60
40
20
0
0
5
10
15
20
Fruits on the laterals
F1
Freq.
40
20
0
5
10
15
20
Fruits on the laterals
F2
Freq.
100
80
60
40
20
0
0
5
10
15
20
Fruits on the laterals

Figure 6.

Figure 7. Frequency distribution of mean fruit diameter in cm. for the P_1, F_1, and F_2 generations of the cross *Cucumis sativus* x *C. hardwickii*



P1
Freq.
20
10
0
3.0
4.0
5.0
6.0
7.0
Fruit diameter (cm.)
F1
Freq.
20
10
0
3.0
4.0
5.0
6.0
7.0
Fruit diameter (cm.)
F2
Freq.
30
20
10
0
3.0
4.0
5.0.
6.0
7.0
Fruit diameter (cm.)

Figure 7.

Figure 8. Frequency distribution of mean fruit length in (cm.) for the P_1, F_1, and F_2 generations of the cross *Cucumis sativus* x *C. hardwickii*

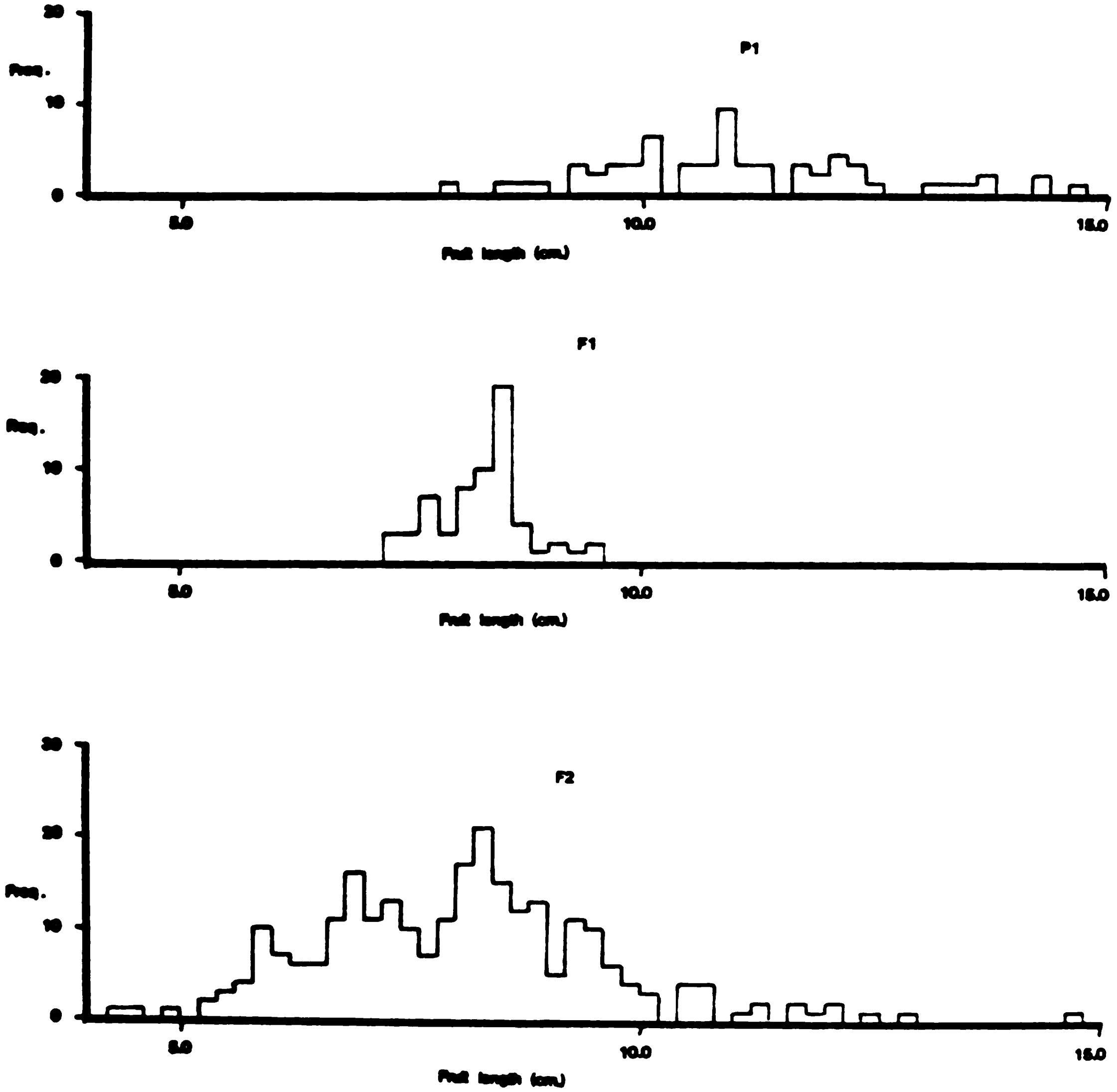

P1
20
Freq.
10
0
5.0
10.0
15.0
Fruit length (cm.)
F1
20
Freq.
10
0
5.0
10.0
15.0
Fruit length (cm.)
30
F2
20
Freq.
10
0
5.0
10.0
15.0
Fruit length (cm.)

Figure 8.

Figure 9. Frequency distribution of fruit yield in gm. for the P_1, F_1, and F_2 generations of the cross *Cucumis sativus* x *C. hardwickii*

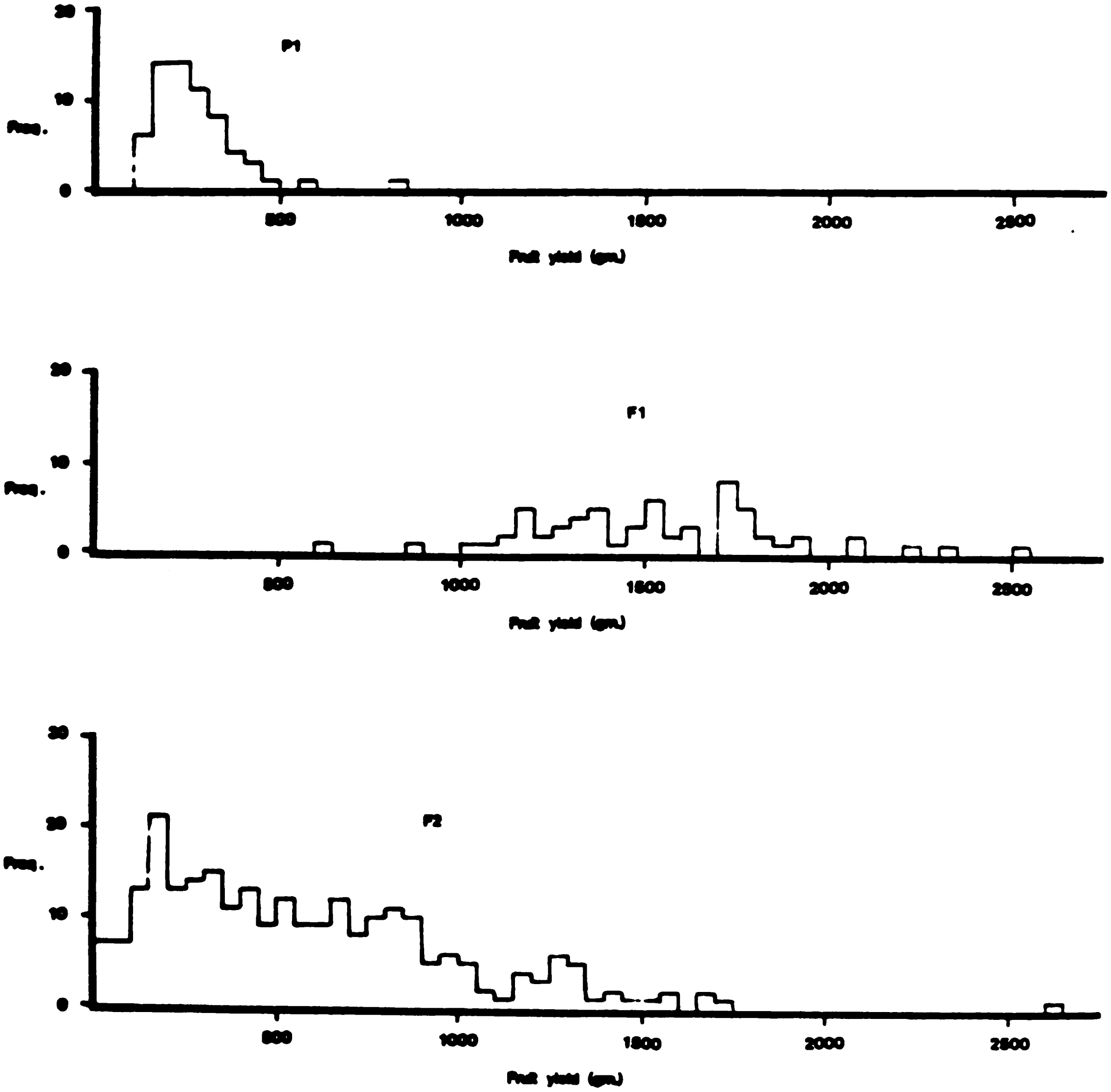

P1
20
10
0
Freq.
500
1000
1500
2000
2500
Fruit yield (gm.)
F1
20
10
0
Freq.
500
1000
1500
2000
2500
Fruit yield (gm.)
F2
30
20
10
0
Freq.
500
1000
1500
2000
2500
Fruit yield (gm.)

Figure 9.

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APPENDIX

APPENDIX

Analysis of variance

Table 9. Analysis of variance of nodes to first pistillate flower for the cross *Cucumis sativus* x *C. hardwickii*

Source	S.S.	d.f.	MS	F test	Prob
Block	1143.8005	20	57.190023	0.983	>0.5
Genotype	31977.23	20	1598.8615	27.479	<0.0005
Error	23041.15	396	58.1847		
Total	57172.18	436			

Table 10. Analysis of variance of percent gynoecious nodes. nodes 1-20 for the cross *Cucumis sativus* x *C. hardwickii*

Source	S.S.	d.f.	MS	F test	Prob
Block	17087.01	20	854.3503	1.302	0.1<P<0.5
Genotype	308638.91	20	15431.95	23.519	<0.0005
Error	259839.18	396	656.1343		
Total	585555.10	436			

Table 11. Analysis of variance of percent nodes with laterals for the cross *Cucumis sativus* x *C. hardwickii*

Source	S.S.	d.f.	MS	F test	Prob
Block	2.419996	20	0.12099979	1.782	<0.025
Genotype	28.157891	20	1.407895	20.736	<0.0005
Error	26.751588	394	0.0678974		
Total	57.329475	434			

Table 12. Analysis of variance of fruit number for the cross *Cucumis sativus* x *C. hardwickii*

Source	S.S	d.f.	MS	F test	Prob
Block	442.5535	20	22.127675	1.764	0.1<P<0.25
Genotype	9114.2467	17	536.1322	42.734	<0.0005
Error	4215.3989	336	12.5458		
Total	13772.20	373			

Table 13. Analysis of variance of number of fruits on the main stem for the cross *Cucumis sativus* x *C. hardwickii*

Source	S.S.	d.f.	MS	F test	Prob
Block	239.9169	20	11.995846	1.679	0.025<P<0.05
Genotype	460.3398	17	27.078812	3.79	<0.0005
Error	1971.5876	336	7.14397		
Total	2671.8434	373			

Table 14. Analysis of variance of number of fruit on the laterals for the cross *Cucumis sativus* x *C. hardwickii*

Source	S.S.	d.f.	MS	F test	Prob
Block	327.1032	20	16.355161	1.416	0.05<P<0.1
Genotype	6353.7468	17	373.7498	32.353	<0.0005
Error	3881.6015	336	11.5524		
Total	10562.45	373			

Table 15. Analysis of variance of fruit diameter for the cross *Cucumis sativus* x *C. hardwickii*

Source	S.S.	d.f.	MS	F test	Prob
Block	8.130383	20	0.40651915	1.776	0.01<P<0.025
Genotype	56.13291	17	3.301936	14.427	<0.0005
Error	75.983912	332	0.22887		
Total	140.2472	369			

Table 16. Analysis of variance of fruit length for the cross *Cucumis sativus* x *C. hardwickii*

Block	93.917248	20	4.695862	2.444	<0.001
Genotype	497.9096	17	29.2888	15.244	<0.0005
Error	637.8766	332	1.9213		
Total	1229.7035	369			

Table 17. Analysis of variance of fruit yield for the cross *Cucumis sativus* x *C. hardwickii*

Source	S.S.	d.f.	MS	F test	Prob
Block	6846028.	20	342301.4	2.696	<0.001
Genotype	60055287.	17	3532664.0	27.82	<0.0005
Error	42664054.	336	126976.4		
Total	109565369.	373			