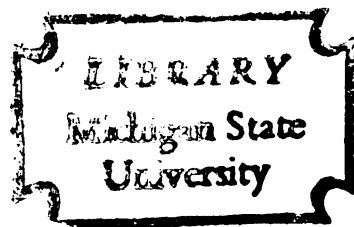




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HABIT IN GYNOCIOUS PICKLING CUCUMBER
(Cucumis sativus L.)
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INHERITANCE OF MULTI-PISTILLATE FLOWERING
HABIT IN GYNOECIOUS PICKLING CUCUMBER
(Cucumis sativus L.)

By

Anand Keshav Nandgaonkar

A THESIS

Submitted to
Michigan State University
in partial fulfillment of the requirements
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ABSTRACT

INHERITANCE OF MULTI-PISTILLATE FLOWERING HABIT IN GYNOECIOUS PICKLING CUCUMBER (Cucumis sativus L.)

By

Anand Keshav Nandgaonkar

Progenies of crosses between two multi-pistillate (MP) and two single-pistillate (SP) gynoecious pickling cucumber (Cucumis sativus L.) cultivars were used to determine the inheritance of MP expression. From the study it appears that MP is recessive to SP expression. Genetic analysis suggests that one or two major genes with several modifying factors affect this character. The gene symbol proposed for multi-pistillate expression is mp. The genetic information on MP expression should be helpful in cucumber breeding programs.

Guidance Committee:

This thesis is condensed into a format suited and intended for publication in the Journal of the American Society for Horticultural Science.

To the memory of my uncle

DADA

A. N. Kotibhaskar

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INTRODUCTION

The development of pickling cucumber (Cucumis sativus L.) cultivars for once-over mechanical harvest has received considerable efforts from plant breeders. Most of the cucumber acreage in Michigan is mechanically harvested; however, greater yields are desirable with once-over harvest.

The combination of highly female expression with concentrated fruit-set is a requirement for high yields in once-over harvest systems. Currently used pickling cucumber hybrids produce from one to two fruits per plant for once-over harvest (1,7,8,12). This low fruit-set is due partially to 'first-fruit' inhibition (2,3,9,10,17). This yield inhibition might be overcome by breeding varieties which simultaneously develop several fruits at the same node. This approach was first suggested by Tiedjens (16) and more recently by Cantliffe (2) and Uzcategui and Baker (17). Uzcategui and Baker reported a significantly greater number of fruits per plant with multi-pistillate (MP) flowers per node as against single-pistillate

(SP) flower per node (Figure 1). The greater number of flowers available for pollination possibly increased the number of fruits per plant by circumventing first-fruit inhibition. The development of pickling cucumber hybrids with multi-pistillate flowering might be suited better to once-over harvest than presently used hybrid cultivars with single-pistillate expression.

Multiple bisexual flowers per node has been observed by cucumber breeders in hermaphroditic lines, but single-pistillate is common in monoecious and gynoeceious lines. Gynoeceious and hermaphroditic lines were used to produce gynoeceious F_2 recombinants with multi-pistillate flowering (17).

The genetics of clustering flowers (multiple-hermaphroditic flowers per node) is conditioned by a single dominant gene closely linked with hermaphroditic expression (15), which is controlled by the m locus (4). The purpose of this study was to determine the genetics of single- and multiple-pistillate flowering in gynoeceious cucumber lines.

Figure 1.A.--Single-pistillate (SP) flower expression
in gynoeceious cucumber.

Figure 1.B.--Multi-pistillate (MP) flower expression
in gynoeceious cucumber.



Figure 1.A.



Figure 1.B.

MATERIALS AND METHODS

Parental material. The two MP gynoeceious lines, 604 G and 598 G described by Uzcategui and Baker (17) were crossed with the two SP gynoeceious lines, GY 14¹ and 551 F², to produce reciprocal F_1 , F_2 and BC_1 populations.

All crosses for experimentation were produced in the greenhouse by controlled pollination using standard methods.

Genetic analysis. In the spring of 1980, plants of P_1 , P_2 , F_1 , F_2 , and BC_1 populations from the four crosses were grown in the greenhouse on raised benches containing a commercial peat-based medium. Fourteen-day-old seedlings were transplanted on the greenhouse benches in a randomized complete block design with three replications. Five plants each per replicate of the P_1 , P_2 , F_1 and BC_1 generations, 20 plants per replicate of the F_2 generation and 10 plants

¹GY 14 released by Dr. W. C. Barnes, Clemson University, Clemson, S.C.

²551 F released by Dr. H. M. Munger, Cornell University, Ithaca, N.Y.

per replicate of the BC_1P_1 generation were grown. The plants were spaced 30 cm by 48 cm on the bench. The temperature was maintained at $27^{\circ} \pm 2^{\circ}$ C (day) and $21^{\circ} \pm 2^{\circ}$ C (night). The numbers of pistillate flowers per node were recorded for nodes 6 through 15 on the main stem as previously reported (17).

Evaluation of F_3 generation. Two to three shoot cuttings were made from randomly selected F_2 plants for all four crosses and were rooted in a mist chamber. All rooted cuttings were self-pollinated to produce F_3 seed.

In the late summer of 1980, seven F_3 populations from each of the 4 crosses and the parental populations were grown as previously described. The number of pistillate flowers per node on the main stem were recorded as mentioned above.

Statistical analysis. For all experiments, means and standard deviations were calculated from individual plant data. The reciprocal F_1 populations were not significantly different ($p=.05$), hence F_1 data were pooled. The method developed by Powers and Locke (11) was used to estimate the number of gene pairs differentiating the parents.

$$\bar{P}_1 (0.75) + \bar{P}_2 (0.25) = \bar{F}_2$$

Where $\bar{P}_1$ is the mean of dominant parent,

$\bar{P}_2$ is the mean of recessive parent, and
 $\bar{F}_2$ is the theoretical mean of F_2 population.

The chi-square tests were used to determine the goodness of fit of the observed data to the proposed genetic model (14).

RESULTS AND DISCUSSION

Parental material. The number of pistillate flowers per node were significantly higher for MP than SP lines (Table 1). Between experiments, the actual numbers of pistillate flowers per node varied more (2.6-6.3) for the MP lines, 604 G and 598 G, than for the SP lines, GY 14 and 551 F (0.9-1.1). Environmental conditions influence flowering of cucumber (4,6,13), and appear to play a more significant role in MP for the number of pistillate flowers per node than for SP expression.

Table 1. Characterization of parents for number of pistillate flowers per node (1979-1980).¹

Parental line no.	Pistillate flowers/node		
	Winter 79	Spring 80	Summer 80
604 G (MP)	5.2a	4.7a	2.6a
598 G (MP)	6.3a	5.7a	4.3a
GY 14 (SP)	1.1b	1.1b	1.0b
551 F (SP)	1.1b	1.1b	0.9b

¹Mean separation within columns by Duncan's multiple range test at 5% level.

Genetic analysis. MP and SP expression from the four crosses in this study suggested one or two major genes with several modifying factors affecting this character, SP being dominant to MP expression (Table 2). More than one pistillate flower per node in F_1 and BC_1P_2 populations as compared to the dominant parent probably is due to either heterosis (5), or modifying factors. Vigorous hybrid plants probably respond better to environmental conditions than the parental inbred lines (17). The skewness of the F_1, F_2

Table 2. Mean number of pistillate flowers per node in 2 MP x 2 SP crosses of gynoecious pickling cucumbers.

Generation	Total plants/ cross (No.)	Cross			
		604G x GY14	598G x GY14	604G x 551F	598G x 551F
		$\bar{X} \pm S.D.$	$\bar{X} \pm S.D.$	$\bar{X} \pm S.D.$	$\bar{X} \pm S.D.$
P_1 (MP)	15	4.7 ± 0.7	5.7 ± 0.7	4.7 ± 0.7	5.7 ± 0.7
P_2 (SP)	15	1.1 ± 0.2	1.1 ± 0.2	1.1 ± 0.2	1.1 ± 0.2
F_1	30	1.7 ± 0.3	1.9 ± 0.4	1.9 ± 0.2	1.9 ± 0.3
F_2	60	2.6 ± 1.2	2.3 ± 1.0	2.1 ± 0.7	2.6 ± 0.8
BC_1P_1	30	2.8 ± 1.1	3.4 ± 1.2	2.9 ± 1.2	3.7 ± 1.4
BC_1P_2	15	1.3 ± 0.3	1.6 ± 0.4	1.8 ± 1.2	1.5 ± 0.4

and BC_1P_2 populations (Figures 2-5) in all four crosses also supports the hypothesis of one or two major genes with several modifying factors with SP dominant to MP expression. Further evidence is based on the distribution of the BC_1P_1 populations.

The populations were analyzed using one-gene and two-gene models. For the one-gene model, classification of segregating populations, the class of 2.7-3.2 pistillate flowers per node was selected to divide SP and MP classes. This class approximated the arithmetic mean of the four parents used in this study. This separation of SP and MP classes is also suggested by the low number of individuals falling in this class for BC_1 to P_1 (MP recessive parent) populations for all four crosses.

Classification into two phenotypes, SP and MP, was followed by appropriate testing. The theoretical F_2 means were calculated for a one-factor-pair difference using the formula suggested by Powers and Locke (11). The calculated theoretical and observed means for the F_2 populations were not significantly different (Table 3).

Figure 2.--Frequency distributions for number of pistillate (♀) flowers per node of parents, F_1 , F_2 , BC_1P_1 and BC_1P_2 populations from gynodioecious MP by SP cucumber cross.

604 G X GY14

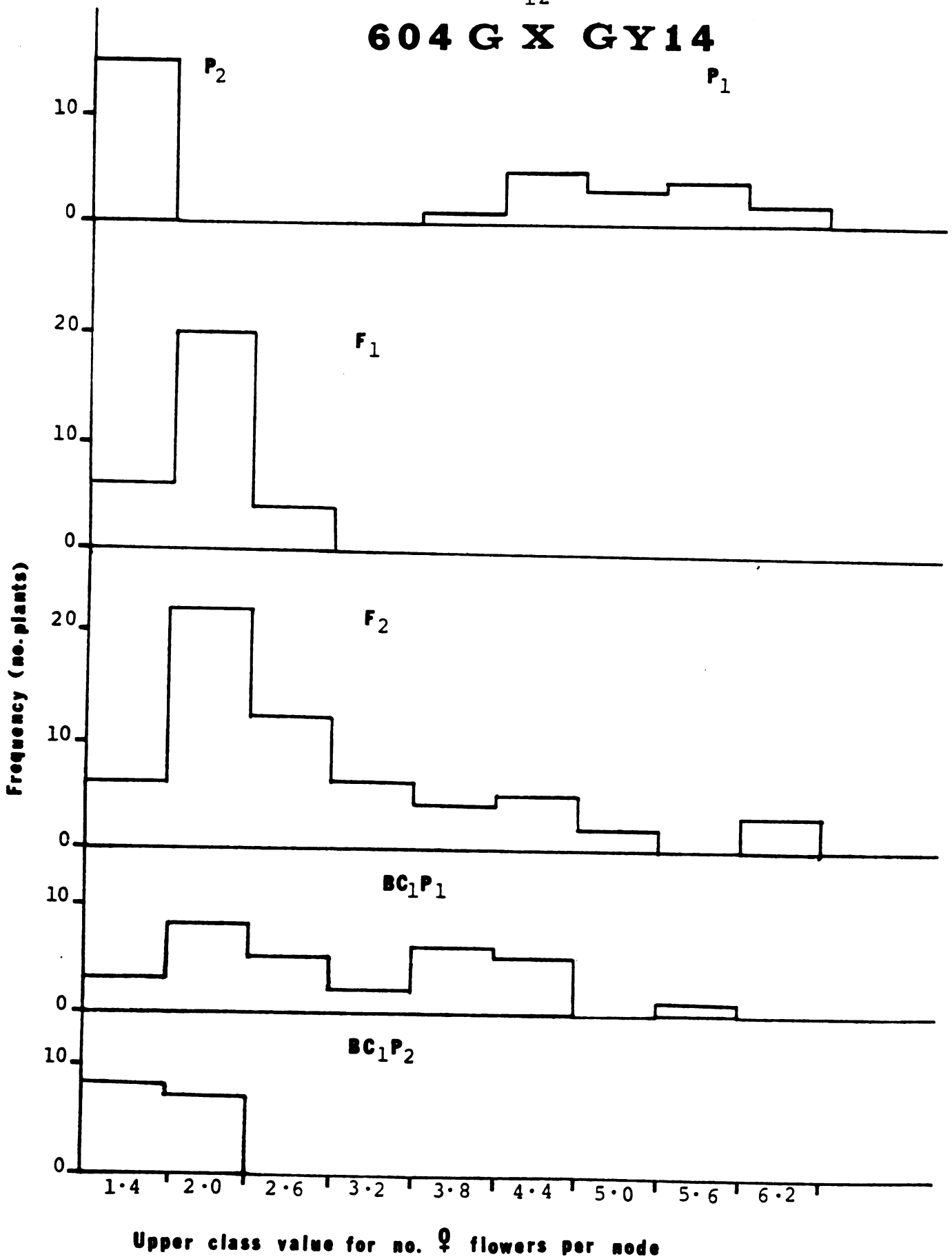


Figure 3.--Frequency distributions for number of pistillate (♀) flowers per node of parents, F_1 , F_2 , BC_1P_1 and BC_1P_2 populations from gynoeceious MP by SP cucumber cross.

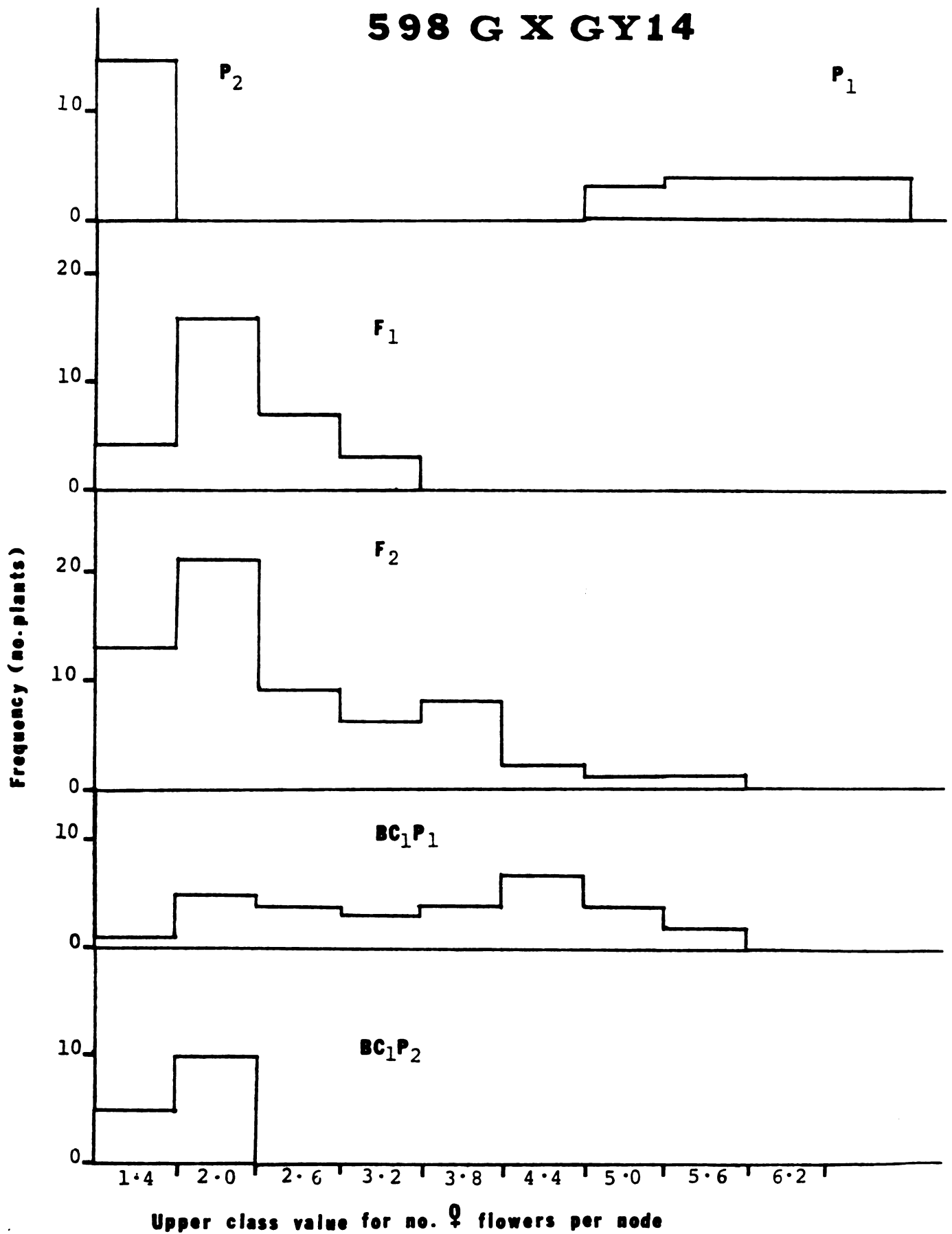
598 G X GY14

Figure 4.--Frequency distributions for number of
pistillate (♀) flowers per node of
parents, F_1 , F_2 , BC_1P_1 and BC_1P_2 populations
from gynoeceious MP by SP cucumber cross.

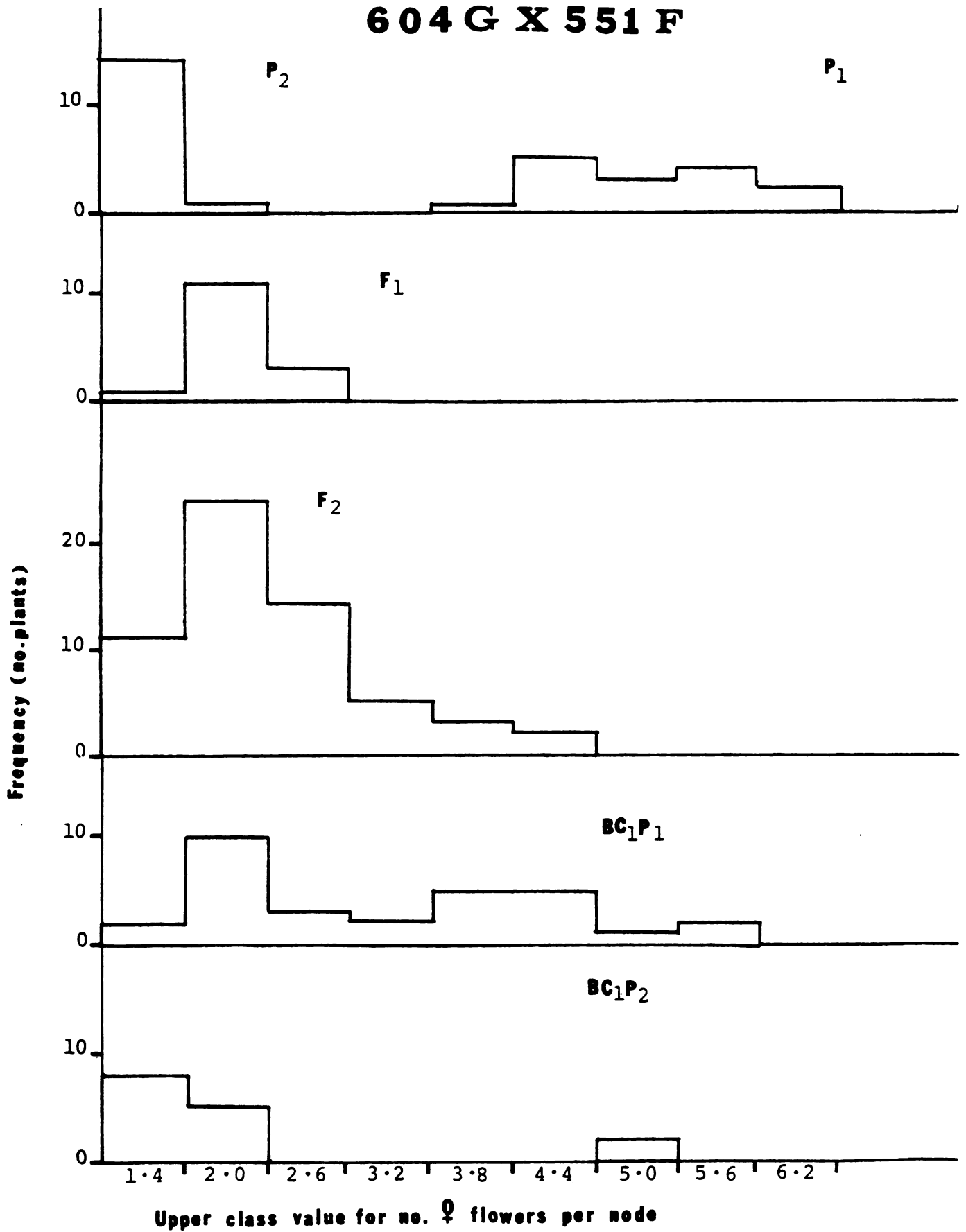
604 G X 551 F

Figure 5.--Frequency distributions for number of pistillate ($\frac{0}{4}$) flowers per node of parents, F_1 , F_2 , BC_1P_1 and BC_1P_2 populations from gynoeceious MP by SP cucumber cross.

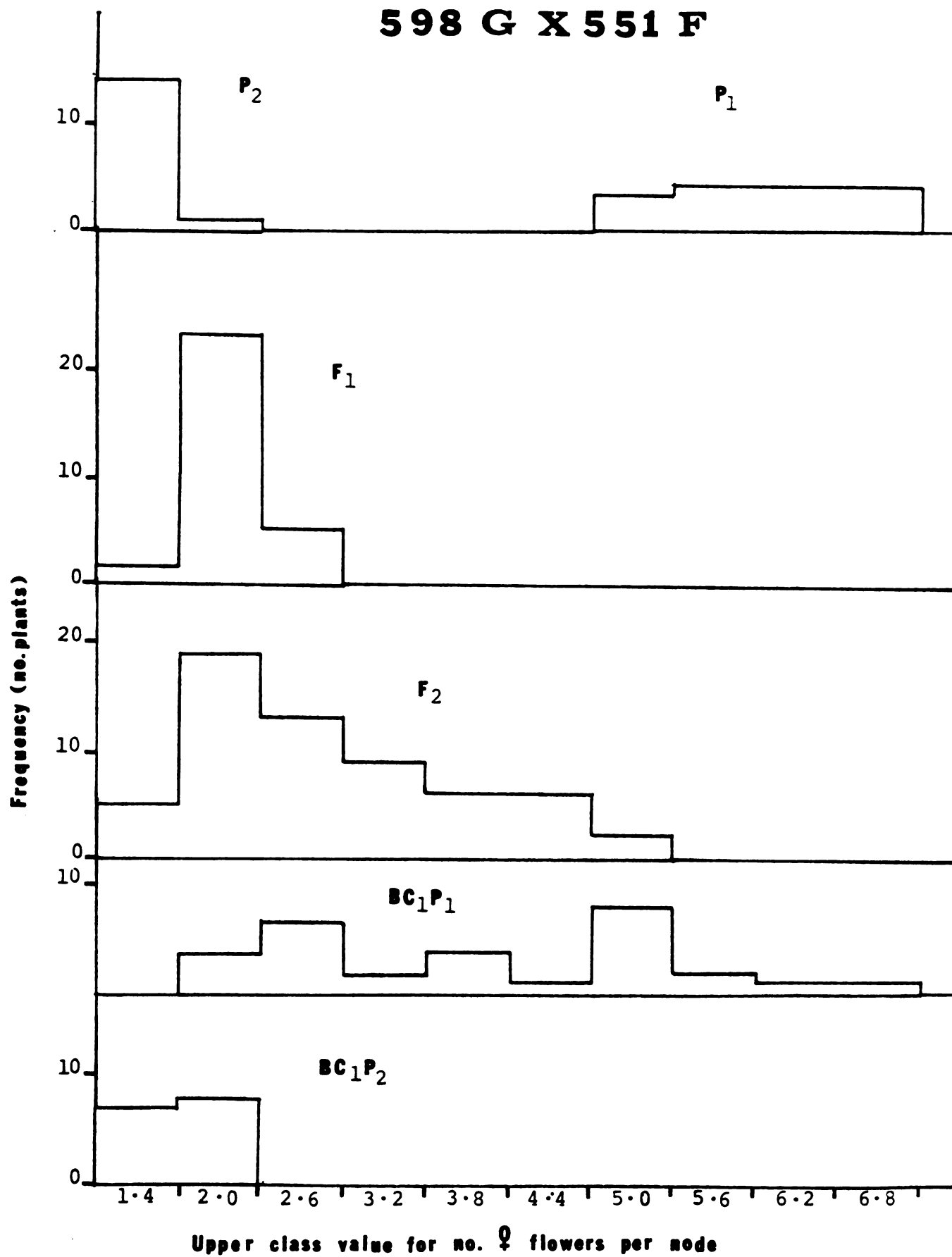
598 G X 551 F

Table 3. Calculated theoretical means and observed means for pistillate flowering habit in F_2 populations of pickling cucumbers derived from gynoeceious crosses of MP x SP lines based on one-factor-pair difference.

Cross/ F_2 population	Mean flower no./node		P value
	Theoretical	Observed	
604 G x GY 14	2.0	2.6	0.90>P>0.75
598 G x BY 14	2.3	2.3	P>0.99
604 G X 551 F	2.0	2.1	0.99>P>0.95
598 G x 551 F	2.3	2.6	0.90>P>0.75

Goodness of fit was determined for the segregating populations based on a single gene model with SP dominant to MP expression (Table 4). The expected F_2 ratio was 3SP:1MP and the expected BC_1P_1 ratio was 1SP:1MP. The P values obtained from the segregating populations ranged from 0.05 to 0.95, suggesting good fit to the proposed model.

The exception from the one-gene model was noted for the cross 604 G x 551 F. The F_2 population did not fit a 3:1 ratio (0.05>P) and BC_1P_2 segregated 2 MP plants when none were expected. These two exceptions suggest that there

Table 4. Segregation for single (SP) and multi-pistillate (MP) flower expression in four crosses of gynoeceious pickling cucumbers.

Population	Total plants (No.)	Class frequencies	Class	Expected ratio (SP:MP)	P value
		SP	MP		
<u>Cross I</u>					
604 G (MP)	15	0	15	All MP	-
GY 14 (SP)	15	15	0	All SP	-
F ₁	30	30	0	1:0	-
F ₂	60	44	16	3:1	0.90>P>0.75
BC ₁ P ₁	30	17	13	1:1	0.50>P>0.25
<u>Cross II</u>					
598 G (MP)	15	0	15	All MP	-
GY 14 (SP)	15	15	0	All SP	-
F ₁	30	30	0	1:0	-
F ₂	60	48	12	3:1	0.50>P>0.25
BC ₁ P ₁	30	17	13	1:1	0.50>P>0.25
BC ₁ P ₂	15	15	0	1:0	-
<u>Cross III</u>					
604 G (MP)	15	0	15	All MP	-
551 F (SP)	15	15	0	All SP	-
F ₁ ^{z/}	15	15	0	1:0	-
F ₂	60	52	8	3:1	0.05>P>0.025
BC ₁ P ₁	30	12	18	1:1	0.50>P>0.25
BC ₁ P ₂	15	13	2	1:0	-
<u>Cross IV</u>					
598 G (MP)	15	0	15	All MP	-
551 F (SP)	15	15	0	All SP	-
F ₁	30	30	0	1:0	-
F ₂	60	45	15	3:0	P>0.99
BC ₁ P ₁	30	13	17	1:1	0.50>P>0.25
BC ₁ P ₂	15	15	0	1:0	-

^{z/} Seed from reciprocal F₁ (551 F x 604 G) was obtained too late for inclusion, but later observation showed no differences in reciprocals.

may be two major genes with several modifying factors affecting this character. To test this theory, several factorial models were used. Only one model gave a good fit. This model is based on the assumption that 2 genes are involved, with one being completely dominant and another partially dominant. In this model an F_2 segregating ratio of 3:6:3:1:2:1 and a BC_1P_1 ratio of 1:2:1:1:2:1 were expected. The chi-square test for these ratios gave a good fit for the cross 604 G x 551 F ($0.75 > P > 0.50$).

Evaluation of F_3 generation. A total of 29 F_3 families from the four crosses were classified as either single pistillate, segregating or multi-pistillate (Table 5).

Table 5. Genetic analysis of 29 F_2 families resulting from four crosses of gynoecious cucumber for flowering habit in the F_3 generation.

Cross	No. Families	Class frequencies/class	
		SP/Segregating	Multi-pistillate
604 G x GY 14	7	6	1
598 G x GY 14	7	7	0
604 G x 551 F	7	6	1
598 G x 551 F	8	4	4

Table 6. Mean and range for flower number per node of F_3 families from 4 gynoeceious cucumber crosses.

Cross	Family no.	F_2	F_3	Pistillate flowers/ node (range)
		$\bar{X}$	$\bar{X}$	
604 G x GY 14	1	4.9	3.2	1.3 - 3.9
	2	1.7	1.9	1.3 - 2.7
	3	1.8	1.1	0.9 - 1.2
	4	2.1	1.2	1.0 - 2.3
	5	1.2	1.2	1.0 - 2.0
	6	1.8	1.6	1.0 - 2.9
	7	4.0	3.1	2.3 - 4.1
598 G x GY 14	1	1.3	1.3	1.0 - 1.9
	2	1.5	1.2	1.0 - 2.0
	3	2.4	1.9	1.2 - 2.6
	4	1.5	1.4	1.0 - 2.4
	5	2.0	2.0	1.6 - 2.7
	6	2.7	2.5	1.3 - 4.0
	7	1.9	2.3	1.0 - 4.2
604 G x 551 F	1	1.7	1.3	0.9 - 2.2
	2	1.9	1.4	0.9 - 2.7
	3	3.0	2.6	1.9 - 3.5
	4	1.7	1.6	1.0 - 2.6
	5	2.0	1.7	1.0 - 2.4
	6	2.7	2.3	1.7 - 3.9
	7	2.0	1.7	1.0 - 2.4
598 G x 551 F	1	4.8	3.7	2.9 - 4.2
	2	1.9	2.0	1.1 - 3.4
	3	2.7	2.2	1.2 - 4.7
	4	4.5	3.8	1.9 - 4.7
	5	3.3	2.8	1.5 - 4.2
	6	2.3	2.2	1.0 - 4.2
	7	1.8	1.3	1.0 - 1.7
	8	4.1	2.9	2.0 - 4.4

The data on individual plants in each family are presented in Table 6. The F_3 data support the F_2 data which suggest that multi-pistillate is recessive to the single-pistillate. Progenies of multi-pistillate F_2 plants produced multi-pistillate expression, while progenies from single-pistillate F_2 plants segregated. The segregation as observed in the F_3 generation also supports the theory that there may be one or two genes with several modifying factors affecting the pistillate flowering character in gynoeceious cucumber cultivars.

CONCLUSION

The multi-pistillate habit for gynoecious cucumber lines in this study appears to be recessive to single-pistillate. The genetic analysis suggests that one or two major genes with several modifying factors are affecting this character. The gene symbol proposed for multi-pistillate expression is mp. The genetic information of MP expression should be helpful in cucumber breeding programs. Earlier work (17) suggested that increased number of flowers per node subsequently increased fruit numbers per plant. Through the combination of backcrossing with progeny testing the MP character might be transferred to the parental lines of gynoecious pickling cucumbers. Subsequent development of hybrid cultivars with MP expression should result in high yields for once-over harvest.

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