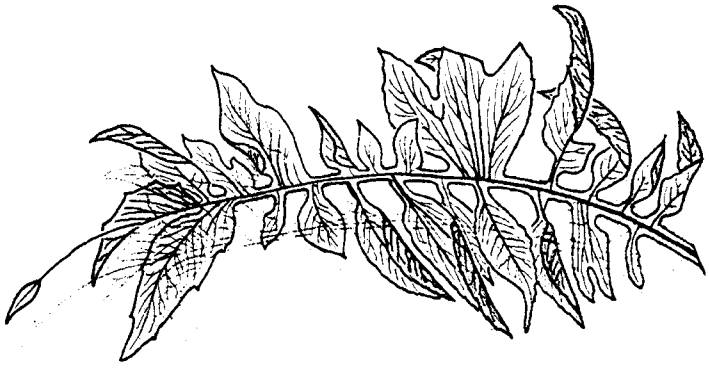
REPORT

of the

TOMATO GENETICS COOPERATIVE



NUMBER 13 FEBRUARY 1963

DEPARTMENT OF VEGETABLE CROPS
UNIVERSITY OF CALIFORNIA
DAVIS, CALIFORNIA

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TOMATO GENETICS COOPERATIVE

Number 13 February, 1963

Department of Vegetable Crops
University of California
Davis, California

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Cover design was traced from a leaf typical of the fifth node of the wiry-4 ($\underline{w}_4$) mutant.

Minutes of the Corvallis Meeting

August 27, 1962

A short business meeting of the membership was held at 4 PM in room 325 Cordley Hall, Oregon State University. The meeting was attended by 27 members and friends, including two members of the Coordinating Committee. The following announcements were made on behalf of the Coordinating Committee. Membership stands at 256 and the treasury at $227.41, the former showing an increase, the latter, a decrease in comparison with figures of the preceding year. TGC 13 will include a linkage summary and a revised stock list that will cover items not included in the latest gene list. Research notes and other regular items will appear in TGC 13.

The meeting featured a talk by Dr. Edwin James on the purposes and functions of the National Seed Storage Laboratory. Dr. James emphasized aspects of the facility that pertained to the preservation of genetic stocks, and he outlined the procedures for depositing seeds of such lines in the storage. This very helpful presentation provided the necessary incentive for the TGC to arrange storage of tomato genetic stocks.

C. M. Rick

Secretary pro tem.

LINKAGE SUMMARY

The following reports have been received from linkage cooperators:

Chromosome 1 -- R. K. Soost. He is at present testing inv, ms_6, au, y, and pr. He finds br too difficult to score under California conditions. His tests show no linkage of gs with the genes of this group.

Chromosome 2 -- L. Butler. "I am concentrating on five-point backcrosses to clarify the linear order of the 20 genes in chromosome 2. The gene bip has been crossed with marker stocks and the F_1's are being grown."

-- C. D. Clayberg reports nothing new with the ms genes.

Chromosome 3 -- G. W. Bohn. He has seed for the F_2 progenies from crosses ms_9 r X r wf, ms_9 r X pau, and ms_9 r X sy. He will be glad to furnish seed to anyone wishing to study the linkages or obtain multiple marker stocks.

Chromosome 4 -- G. S. Khush. "From the combinations which I have scored up till now, the gene order appears to be: clau, ful, ra, ven, e, di. Induced deficiencies reveal that clau and ful are located on the short arm of 4."

Chromosome 5 -- H. W. Young. "We have obtained some true-breeding Bp stocks. I believe we have all the three-point combinations of the genes gg, wt, n, tf, Bp, and mc. Additional crosses with Fw and sd are now in process. We are now recovering Fw more readily. With early obstacles overcome, our chief problem is one of producing sufficient progeny from the cross to obtain careful linkage data. Field plantings have been generally unreliable because several of the mutants are masked. Greenhouse production in pots has been much more satisfactory."

Chromosome 6 -- J. C. Gilbert. "We have new plantings now but considerable more work remains to be done. Tomatoes with multiple disease resistance seem to be much easier to grow here than most of the genetic stocks. We will try to do better next year."

Chromosome 7 -- R. G. Creech. "Have just begun linkage studies with gs. From E. A. Kerr I obtained 6 stocks containing gs and the following marker genes: lg_5, c, j_1, gf, mc, wf, y, bi, l, sp, a, d, e, bp. I would like to obtain seeds of all mutants which are known or suspected to be on chromosome 7."

Chromosome 8 -- C. M. Rick. An up-to-date summary of the nine genes and the position of the spindle fibre attachment is contained in a note in this issue.

Chromosome 9 -- R. W. Robinson and W. Mishanec. "Fifty additional mutants were tested for linkage with ah since the last linkage summary, but only one showed evidence of being on chromosome 9. No double recessives were found among the 843 F_2 plants grown by Rick, who discovered the linkage, or by us. Since it was previously known that ah is very closely linked with wd, and that nv is extremely close to Tm_2, all the genes known to be on chromosome 9 are closely linked together."

Chromosome 10 -- E. A. Kerr. The summer's data are now being worked and should be ready for inclusion in this TGC news letter. Xa_2 on the map = Persson's "A".

Chromosome 11 -- A. B. Burdick. No report.

Chromosome 12 -- Not assigned.

Group rv, sf -- W. Williams. No report.

La, na -- Not assigned.

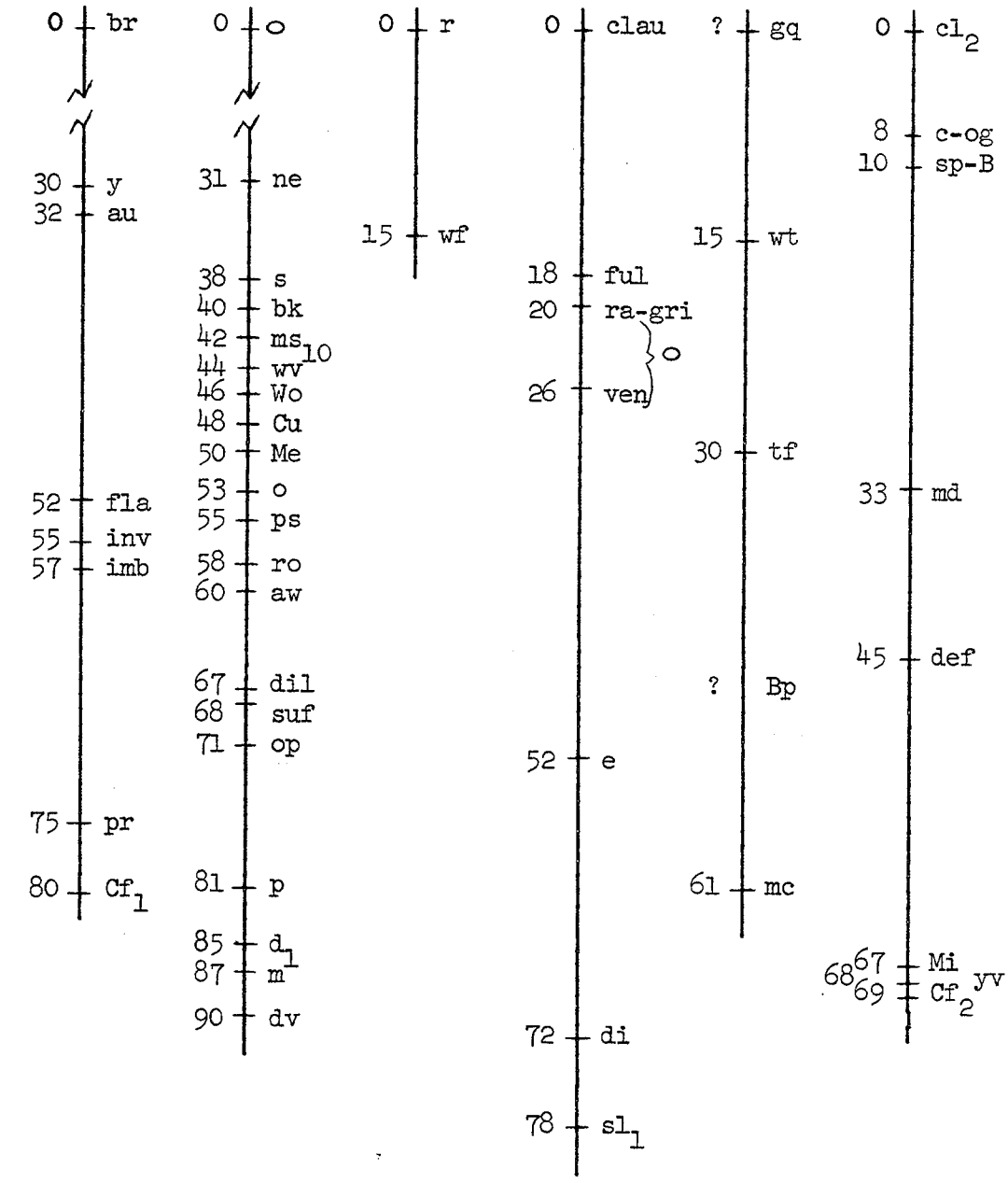
The screening of the genes and the assigning of them to their linkage group has been proceeding faster than the cooperators have been able to place them in their proper linear order, but as more multiple markers with seedling traits become available this problem should be overcome. The maps on the following page have been prepared as working interum maps with the relative positions shown. Since in most cases the linkage values given are ± 8%, some genes may later change positions with nearby genes.

L. Butler,

Chairman, Linkage Committee

Revised linkage maps

Chromosomes

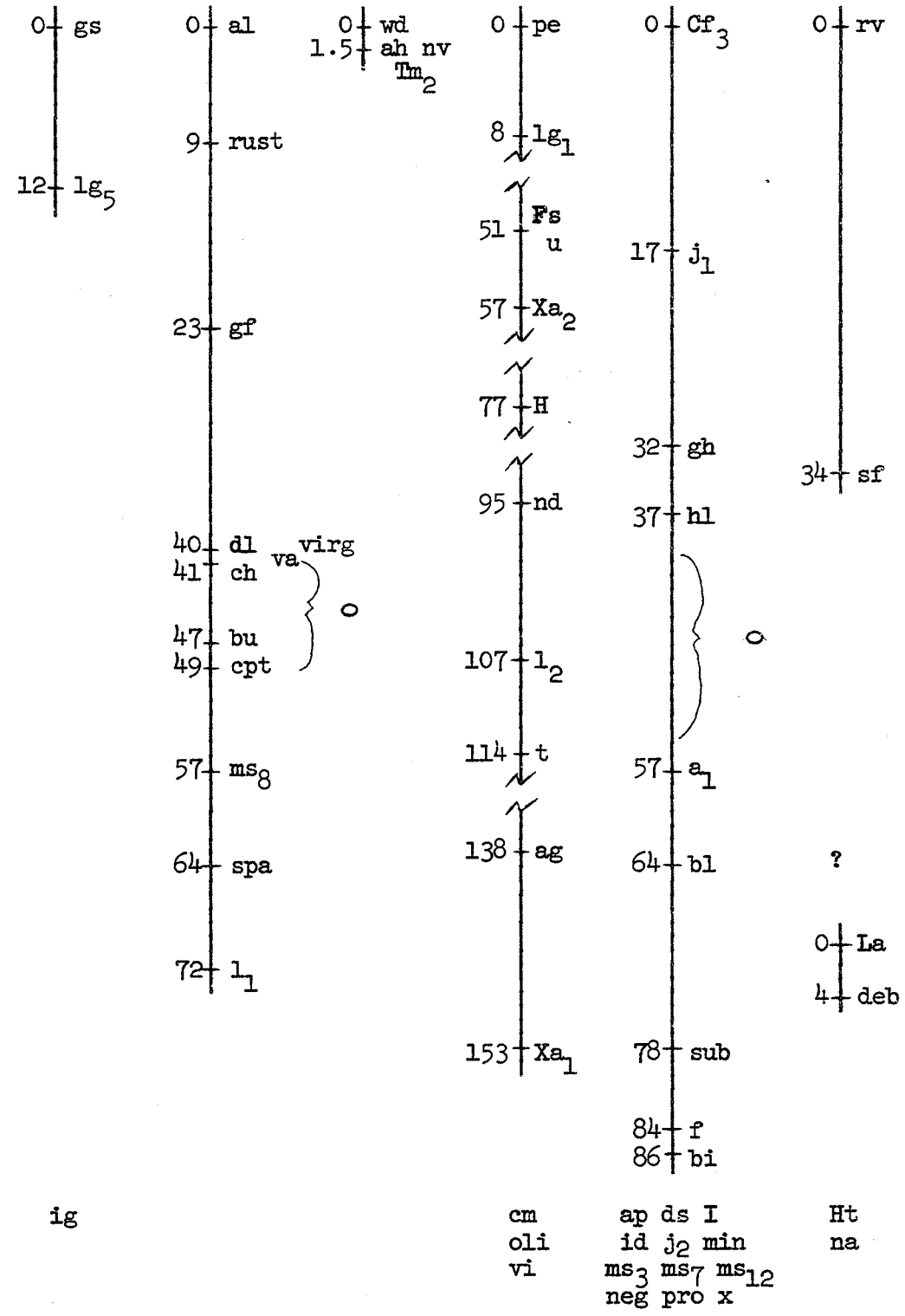


* cb Jau in ms6 per sit | bip Lx ms2 ms15 prun v2 | ms9 pau Od sy | afl ht intro ls si Ve vg w1 w4 | Fw inf n sd | mu ri yg2 yg3

o - approximate position of centromere
*Genes located by two-point or trisomic test only

Revised linkage maps (continued)

Chromosomes



o - approximate position of centromere
*Genes located by two-point or trisomic test only

PART I

RESEARCH NOTES

Andersen, W. R. Cytoplasmic sterility in hybrids of Lycopersicon esculentum and Solanum pennellii.

Cytoplasmically influenced male-sterility has appeared in the F_2 and BC generations from the cross L. esculentum and S. pennellii. The F_1 appears normal with moderate fertility.

Male sterility can be detected in segregating generations by per cent pollen abortion as judged by aceto-carmine smears. A complex of anther modifications associated with the pollen abortion also appears. This consists of (1) reduction in size of individual anthers, (2) a shift in color from bright yellow to pale green, (3) a peculiar lengthening of the filament, and (4) a marked tendency for the anther column to fall apart. In rare cases the anther whorl appears developmentally shifted toward a corolla-like structure.

As part of a study to determine certain properties of this cytoplasmic-genetic effect, the ensuing experimental scheme was followed:

1. L. esculentum, var. VF 11 X S. pennellii, accession: Atico, Peru, was backcrossed successively to S. pennellii, always with the latter as male parent.

2. Populations of the above lineages were compared in a completely random design and originally consisted of the following census: (a) ten S. pennellii plants cloned from the original pollen parent, (b) ten F_1 plants from the original cross, (c) 65 BC^1 plants, and (d) 240 BC^2 plants. (The BC^2 population was composed by taking a sample of approximately five hybrid seeds from each BC^1 seed parent.)

3. In order to determine any effect on female fertility, samples of 40 BC^2 plants and 27 BC^1 plants were pollinated in the greenhouse with pollen from S. pennellii. Ten flowers per plant were treated and number of fruit set per plant was counted four weeks later.

4. A simple index for the anther alteration was obtained by measuring the length of the anther column in millimeters.

5. Per cent pollen abortion was determined by aceto-carmine smears assuming that only viable pollen will stain.

Table 1. Summary of data on anther length, pollen abortion, and fruit set.

Generation	No. plants	Anther length		t Value	Average pollen abortion	Flowers with 100% aborted pollen	Fruit set[a]
		Mean	Variance				
		mm	mm^2		%	%	%
S. pennellii	10	7.14	0.81				
F_1	10	7.28	0.73		52.2	22.2	35
BC^1	36	5.78	1.49	6.45	78.5[c]	36.1	34[c]
BC^2	90[b]	4.59	1.11		90.1[d]	65.1	34[d]

[a] Based on number of fruits set per pollination (10 flowers pollinated per plant).
[b] Measurements based on 3 plants from each of 30 BC^2 families (BC^1 x *S. pennellii*).
[c] Based on 27 BC^1_2 plants.
[d] Based on 40 BC^2 plants.

The means of the backcross generations show a persistent shift away from the means of F_1 and recurrent parent. The t value for anther length in Table 1 indicates a highly significant difference between the means of BC^1 and BC^2.

The trend toward greater pollen abortion is also shown, and this trend is associated with an increase in flowers with 100% sterile pollen.

The following conclusions can be drawn from this study.

1. As the proportion of *S. pennellii* genome is increased in the hybrid generations, the means for anther length shift unidirectionally away from the F_1 recurrent *S. pennellii* parent.

2. Evidence is indicated for increasing upset in pollen developmental processes from F_1 through BC^2.

3. No effect on female fertility is evidenced under the conditions of the experiment.

4. The observed shift in the means away from the values of the recurrent parent is in direct contrast to expectations prescribed by classic genetic theory. Basically the progeny of each succeeding backcross should increasingly resemble the recurrent parent in all characters. Since *L. esculentum* was used as the original female parent and *S. pennellii* was used as the recurrent male parent in all crosses, it is proposed that certain cytoplasmic entities possessed by *esculentum* were passed through the maternal cytoplasm each generation. The genome possessed by this particular form of *S. pennellii* is sensitive to these cytoplasmic entities. This cytoplasmic-genetic interaction is manifest by the peculiar behavior of the characters under study.

Butler, L. The cross-over values for chromosome 2.

Backcross data have eliminated some of the inconsistencies which appeared in some of the cross-over values given in TGC 12, but more 3- and 4-point data are needed before the order of some of the genes will be permanently fixed. The latest values are:

	m	d	p	op	suf	dil	aw	ps	o	ro	Me	Cu	wv	bk	Wo	ms_{10}	s
dv	6	5					19	15	22	20		23		36	28	15	35
m		2	6				15		28	6	25	25		20	26	35	20
d			4	12	14	15	18	13	16	23	24	25	25	25	31	30	31
p				10	7	15	15	10	15		15			27	27	15	29
op											14				17		24
suf							8		11	6	14	17		33	24	32	29
dil							11		7	7	11			16	8		12
aw										15	10	8	18	30	11	34	35
ps											14	13	17	22	14	15	28
o											22		9	18	22		24
ro											25	20	14				
Me													6		4	6	11
Cu														10	3	12	11
wv															8		
bk																	9
Wo																2	8
ms_{10}																	19

Butler, L. The linkage of divergens di, with e, sl_1, and w_1

I reported in TGC 12 that di and e were linked, and that di and sl_1 also appeared to be linked. This summer the linkage of these three genes has been confirmed, and the tests have also included wiry w_1. The data below show that these four genes are all located in the linkage group associated with chromosome 4.

									Cross-over
di e	R	745	+ +	382	+ e	318	di +	9 di e	16.0 ± 2.5
di e	C	1040	+ +	159	+ e	162	di +	263 di e	21.7 ± 1.2
di sl_1	R	614	+ +	226	+ sl_1	307	di +	0 di sl_1	6.0 ± 2.8
di w_1	R	318	+ +	134	+ w_1	108	di +	2 di w_1	14.4 ± 4.1
e sl_1	R	520	+ +	180	+ sl_1	264	e +	12 e sl_1	23.7 ± 2.8
e w_1	R	514	+ +	154	+ w_1	239	e +	30 e w_1	37.8 ± 2.7

The map for these genes would be:

e 20 di 6 sl_1 12? w_1

Chmielewski, T. M. A factor from L. minutum affecting the beta-carotene content.

The fruit color in the BC_1 generation (L. esculentum x L. minutum) x L. esculentum shows continuous gradations from yellow similar to rr through orange to red. L. minutum has whitish-green fruits (TGC 12:21-22); the L. esculentum parent was the red variety Stonor's Exhibition. The chromatographic analysis proved that some of the orange fruited plants of the BC_1 contained much higher concentration of beta-carotene than the normal tomatoes. A plant designated L.35-1 revealed the highest level: 3.16 mg of beta-carotene per 100 g fresh weight. (Genet. Pol. 3(2):155-159, 1962).

After selfing, the plant L.35-1 gave progeny segregating into red-fruited and orange-fruited individuals, the segregating ratio was close to 1 red : 3 orange. The intensity of the orange color varied from tangerine to orange-red. Eight orange-fruited plants were backcrossed with Stonor's Exhibition; the results are given below.

			BC_2		
	orange	x red	orange	red	?
1.	L.57-2	L.28	22	22	3
2.	L.57-7	"	48	--	-
3.	L.57-13	"	47	39	-
4.	L.57-18	"	28	22	4
5.	L.57-19	"	38	26	4
6.	L.57-20	"	50	--	-
7.	L.57-22	"	30	22	3
8.	L.57-28	"	41	43	-

It appears that the two plants, viz.L.57-7 and L.57-20, were homozygous for a dominant factor which determines orange fruit color. The six remaining plants were heterozygous for this factor and they segregated into 1 red : 1 orange when crossed with red-fruited tomato. There were, however, a few plants intermediate between the two types of color.

Chemical analysis indicated again that the orange-fruited plants of BC_2 contained a higher quantity of beta-carotene than normal tomato strains. The amount of beta-carotene varied from 1.56 to 3.38 mg per 100 g fresh weight according to the plant.

The factor derived from L. minutum resembles the gene B in its expression and mode of inheritance. Tests for allelism with B will be carried out in the near future.

Clayberg, C. D. Large circle synthesis - a progress report.

In 1958 I initiated a project to synthesize a true-breeding tomato strain of 12II that would give ⊙24 when crossed to any variety having the normal chromosome arrangement. Of the two techniques developed for attaining this goal, successive irradiations and crossing-over in differential segments, I have adopted the former. The latter requires that a good selection of already induced translocation stocks be available in which the chromosomes involved have been identified and the general locations of the breaks are known. The successive-irradiations technique in its simplest form consists of treatment cycles of three generations each: (1) fertilization of a homozygote with its own irradiated pollen; (2) locating and selfing new ⊙4 plants and test-crossing them to identify desired arrangements; and (3) testcrossing of homozygotes in the selfed progeny to distinguish the desired new translocation strain from the old one. I have modified this procedure by intercrossing different ⊙4 plants in step (2). This permits the addition of two new reciprocal translocations per irradiation treatment instead of one. Also, it reduces the number of generations required to add two reciprocal translocations from six to four. The first treatment cycle resulted in a true-breeding line which will give 2 ⊙4 when crossed to a normal tomato variety. The materials used to initiate the first cycle were two different ⊙4 stocks of Barton's (1954). The project is presently in its second cycle, whose testcrosses indicate that the product will be a strain giving ⊙8 + ⊙4.

Gilbert, J. C., and J. C. Acosta. Persistence of green gel around seed of ripening fruits and its apparent linkage with the sp locus on chromosome 6.

Genetic differences among tomato lines in the persistence of green color in the gel around seeds of ripening fruits was found not to be influenced in its expression by either nitrogen or calcium in field applications in Hawaii. This character is usually well expressed in Hawaii and has shown a high degree of dominance in crosses involving two green gel parents (STEP 305 and the bacterial wilt resistance line, HES 6244) with the variety Maui which does not show a persistence of this green color in the gel.

Although the green color in the gel of HES 6244 is a little darker than that in STEP 305, crosses between either of these two unrelated lines and the Maui variety showed very similar results. Forty F_1 plants and 40 BC plants to a green gel parent all showed green gel, whereas 96 plants from the backcross to Maui showed a range of gel color from yellow (Maui type) thru intermediate colors to green (as in STEP 305 and HES 6244). Some 10 ripe fruits were sampled from each plant.

Maui is a determinate variety, whereas the STEP 305 is indeterminate. In the F_2 of this cross, 24 out of 360 plants were quite free of green in the gel around seeds of newly ripened fruit. Of these, 17 were determinate (spsp), and only 7 were indeterminate plants.

In the Maui x 6244 cross, an F_2 group of 297 plants showed 18 free of green gel in newly ripened fruits. Of these, 16 were of the parental type

(determinate and yellow gel), whereas two were of the recombinant types (indeterminate and yellow gel). As the indeterminate plant habit is dominant, this is a highly significant deviation from the expected ratio, and it suggests that one and possibly both genes conditioning the color of the gel are linked to the sp locus in chromosome 6.

The F_2 ratios 297/18 and 360/24 fit a two-gene segregation for gel color in the crosses of Maui x STEP 305 and Maui x HES 6244.

Hardon, J. J. Fruit and seed set on exised stems.

Testing for self-compatibility versus self-incompatibility in F_2 and backcross hybrids of L. esculentum x S. pennellii was highly facilitated by a method using detached stems suggested by successful application in grasses (Keller, Agron. J. 35: 617-623, 1943) and legumes (Battle, Agron. J. 41:141-143, 1949) and presently used widely in potato programs (Meinert, personal communication). This method aided in overcoming the extremely low fruit and seed set of the hybrids under field conditions during the summer in Davis.

Flowering branches 10 to 15 inches long with at least one open flower and none past the flowering stage were cut from the plants and put immediately in water. The leaf area was reduced to approximately one-third. Pruning the top seemed to improve the fruit set. The flowering branches were transferred into the greenhouse and put in small (1 pint) milk bottles with normal tap water. No nutrients were added. Pollinations were usually made the following day and repeated four days later. Changing the water every four days by flushing the bottles with a water hose in general limited development of bacteria and algae sufficiently. No exact data were collected on relative fruit and seed set compared with plants in the field. Pollination of one branch of about six flowers usually was sufficient to establish the compatibility of the plant. Ripe fruit of roughly half normal size were obtained without difficulty. The seeds had good viability. In addition to species hybrids, male sterile tomato plants (ms_{33}) also gave satisfactory results.

This method may be useful where large numbers of plants have to be crossed as female parents and space is prohibitive for growing them in the greenhouse. Between 80 and 100 plants can be tested on one square meter of bench space.

Khush, G. S. Identification key for pachytene chromosomes of L. esculentum.

The tomato chromosomes can be divided into groups satisfactorily on the basis of their pachytene morphology. Additional morphological features permit subdivision of members within a single group. The following key has been found useful for the identification of each chromosome by beginners in tomato pachytene cytology.

CHROMOSOMES WITH NUCLEOLUS

Chromosome 2

CHROMOSOMES WITHOUT NUCLEOLUS

I. Chromosomes with median centromeres (No's. 5, 11, and 12).

- (a) A small achromatic region in the middle of chromatic region of long arm. Ch. 11
- (b) Achromatic and chromatic regions of both arms equal in size. Ch. 12
- (c) Achromatic region of short arm about double the length of chromatic region of the same arm. Ch. 5

II. Chromosomes with sub median centromeres (No's. 1, 3, 4, and 6-10).

A. Chromatic region of short arm consisting of one conspicuous cluster of chromomeres compressed together (No's. 3, 4, and 6).

- (a) Chromatic region of long arm consisting of two distinct clusters of chromomeres. Ch. 6
- (b) A big knob present in the achromatic region of long arm at a distance of 5 μ from end of chromatic region. Ch. 4
- (c) Conspicuous knob replaced by three small lightly staining chromomeres. Ch. 3

B. Chromatic region of short arm consisting of more than one cluster of chromomeres (No's. 1, 7-10).

- (a) Achromatic region of long arm, 6 times the length of chromatic region of the same arm. Ch. 1
- (b) Achromatic and chromatic regions of the long arm equal in length. Ch. 10
- (c) Chromatic region of long arm consisting of discreet chromomeres of about equal size. Ch. 9
- (d) One small chromomere present at the end of chromatic region of short arm. Ch. 8
- (e) Two small chromomeres present at the end of chromatic region of short arm. Ch. 7

Lesley, J. W. Probable interaction of jointless-1 (j_1) with blue-green (be) and singed (sn).

Rick and Sawant (Proc. A.S.H.S. 66:254-360, 1955) found evidence of interaction of j_1 with mc and particularly with sp, which suppressed leafiness. A similar relation was found in a cross of j_1 be and an sn d_1 woolly (Porte) plant. In two F_2 families consisting of 139 plants, two were jointless and leafless and two others bore both jointed-leafless and jointless-leafless inflorescences. As neither Wo nor d_1 is believed to interact with j_1, be and sn are suspect. None of the additional plants were singed. In another cross involving j_1, sn, be, and sp, 31 of the 78 backcross plants were essentially jointless-leafless but with an occasional leaf. In five BC selfed families, 20% of the j_1 plants had an occasional leafless inflorescence. Two of these families evidently were sp^+sp^+. Of the 11 variant BC selfed plants, 7 carried the dominant alleles $be^+sn^+sp^+$, but the most extreme variant was non-singed sp be (Table 1). A jointless-leafless, jointless-leafy BC plant outcrossed to j_1 gave 8 normal jointless plants, suggesting that the aberrant plant was j_1. A third cross between be j_1^+ and tf wf mc j_1 gave in F_2 a blue-green jointed-leafy plant. Two blue-green F_3 were mixed jointed-leafy and jointless-leafy. Four F_4 families from F_3 blue-green jointed-leafy, jointless-leafy gave 45 plants of the parental type but without abscission

(Table 1). These F_4 families were remarkably unfruitful. The jointed, non-abscission condition was observed by Rick and Sawant (loc. cit.) in mc plants. Unfortunately these blue-green plants were not scored for mc. Probably all the F_3 and F_4 plants in this third cross were $j_1 j_1$. Blue-green like self-pruning has a growth-inhibiting effect. It contains a small inversion but is usually quite fertile either homozygous or heterozygous. A backcross of be c a j_1 x be c a j_1 apparently contained only normal j_1^+ and j_1 plants, but this evidence is not conclusive. It seems that these changes in the jointless-1 phenotype are caused by interaction of either sn or be or the combination of them with j_1. The data also support the conclusion of Rick and Sawant (loc. cit.) that the jointless-1 phenotype is extremely variable and that j_1 interacts with macrocalyx.

Table

Parentage	Generation	j_1^+	j_1	Jointless leafy and jointed leafy	Jointless leafless	Jointless leafless and jointed leafless	Jointless leafless and jointless leafy
j_1 be Wo d_1 sn	F_2	58	17		1		
	F_2	45	15		1	2	
j_1 be c j_1^+/j_1 sp^+/sp sn	BC	3					1
	BC	3	5				
	BC	1					1
	BC	21	14				29
	BC selfed	10	3				3
	BC selfed	0	5				1
	BC selfed	0	24				5
	BC selfed	23	7				2
	BC selfed	28	4				0
jointless leafless and jointless leafy j_1	BC	0	8				
be tf wf mc j_1	F_3			2			
	F_4			16			
	F_4			7			
	F_4			15			
	F_4			7			

Martin, F. W. Competition of pollen containing different S alleles in L. esculentum-L. hirsutum crosses.

Although the cross of L. esculentum x L. hirsutum form hirsutum may be readily accomplished, the production of the F_2 generation by self-pollination is rendered impossible by self-incompatibility of the F_1 hybrids. Furthermore, tests of crossability among such hybrids frequently are entirely unsuccessful. As the F_2 generation is frequently desired for recombination studies, an attempt was made to discover the barrier to crossing of F_1's and to circumvent the barrier if possible. The fact that inspections of styles after crosses among F_1's revealed stoppage of pollen-tube growth suggested that the same S allele was present in all plants.

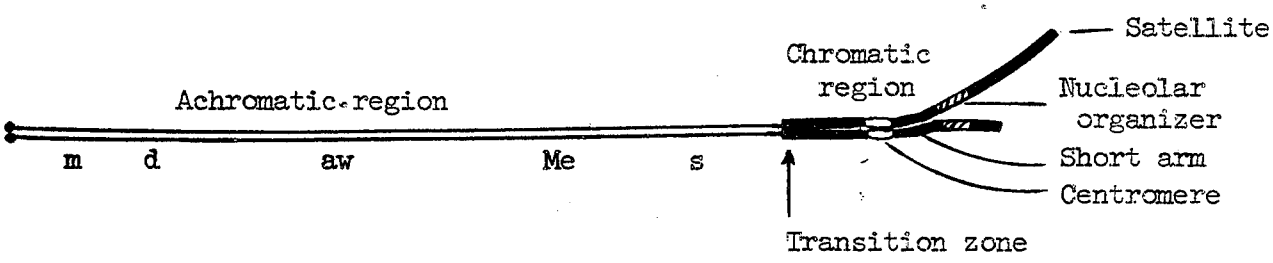
To test this contention, 3 plants of L. hirsutum f. hirsutum (Blood and Tremmeling Collection, Cajamarca, Peru, USDA PI. 127827) with genotypes of S_1S_2, S_1S_3, and S_2S_3 were crossed to the L. esculentum variety Tiny Tim. Twenty hybrids of each cross were grown and tested for self-incompatibility and crossability within the family. All plants were self-incompatible. Each family was screened for mating types by pollinating all individuals with pollen from at least two different sibs.

In two families, the progeny from males S_1S_2 and S_2S_3, a single mating type was found. This mating type was identical in both families and was apparently S_2S_f. In the third family, progeny of male S_1S_3, two mating types were found, one of 17 and one of three plants. These two types were reciprocally compatible with the mating type of the first two families, suggesting that one was of the genotype S_1S_f and the other was S_3S_f. The progeny of these matings segregated for parental characteristics and were apparently F_2's.

In another experiment each of the three parent f. hirsutum plants were crossed to 10 freshly-opened flowers of a compatible single-plant clone of another accession of L. hirsutum from the same locality (Rick's LA253, Ochoa 6). After 12 hours the styles were removed, fixed, and later inspected for pollen-tube growth. Because of differences of lengths of individual tubes in the styles, it was impossible to accurately compute mean lengths per style. Nevertheless, the longest tubes from the plant S_1S_3 were significantly ($F = 3.75$) shorter than the longest from the other two parent plants (mean lengths of longest pollen tubes equalled 7.6 mm., 8.7 mm., and 9.0 mm., respectively).

The data constitute evidence for differences in growth rates of pollen tubes determined by S alleles. Such differences could account for the two families of only one mating group and the 17:3 ratio of the two mating groups of the third family. The data also suggest a method for the production of F_2 generations. To be certain of cross-compatible F_1 hybrids, it is necessary to grow three hybrid families using three different, cross-compatible parents.

Moens, P. B. Linkage of chromosome #2 markers with the satellites (submitted by L. Butler).



From Barton's (1951) and Snoad's (1962) work it appears that there is no crossing-over in the chromatic region of #2 chromosome. Therefore, the linkage of a gene with the satellite estimates the genetic distance from the gene to the transition zone.

The following crosses were made:

$$\frac{d\ \ Me\ \ long}{+\ \ +\ short} \times \frac{d\ \ +\ \ short}{d\ \ +\ \ short}, \quad 433 \text{ plants}$$

$$\frac{m\ \ aw\ \ short}{+\ \ +\ \ long} \times \frac{m\ \ aw\ \ short}{m\ \ aw\ \ short}, \quad 361 \text{ plants}$$

791 plants were grown to maturity, scored in the field for genetic markers, and scored for satellite length in the laboratory.

Markers	Total backcross plants	Number of recombinants	C.O. %
Me-satellite	433	181	41.80 ± 2.37
d-satellite	433	216	49.88 ± 2.42
aw-satellite	361	168	46.54 ± 2.63
m-satellite	361	171	47.36 ± 2.63

Taking the distance Me - s at 10%, a value of 32% would be indicated here for the distance from s to the transition zone which, is not far from the 38% reported by Snoad (from translocation data).

From observations at early diplotene it appears that at the transition zone there is a high incidence of chiasmata. Some 43% of 400 cells in early diplotene were found to have a chiasma in the transition zone. This would correspond to 22% crossing-over, somewhat less than the observed 32%. However, the appearance of localized chiasmata at the transition zone indicates that s is physically closer to the transition zone than would appear from the genetic data.

Moens, P. B. The cytologic and genetic behaviour of a partial isochromosome #2. (submitted by L. Butler).

Plant #316 was found to have 13 bodies at diplotene but the plant did not behave like a trisome. Growth, flowering and fruit set were normal. The plant was derived from

San Marzano trisome (from Dr. C. M. Rick) having 3 long satellites x T 2104 (L. Butler) recessive for dv aw op bk s having 2 short satellites

Plant #316 was found to have:

1 normal chromosome #2 with a short satellite
1 normal chromosome #2 with a long satellite
1 abnormal chromosome of the configuration
long satellite - nucleolar organizer - short arm - centromere - ? - short arm - nucleolar organizer - long satellite.

Most frequently the homologous arms of the partial isochromosome lie together. There appear to be two closely linked centromeres which function as one centromere. The partial isochromosome, therefore, behaves much like a normal isochromosome and is inherited as such.

So far 81 plants of an F_2 of 90 plants have been examined for the presence of the extra chromosomes. It was found that 30 plants carried the partial isochromosome while three plants had different configurations.

Plant 15 probably has two half partial isochromosomes and has regularly 15 bodies at diplotene.

Plant 72 has two partial isochromosomes giving the plant a total of six short arms and six satellites.

Plant 89 has a partial isochromosome plus half of one.

Since only one plant carries two partial isochromosomes, it is likely that only one of the parents transmits the extra chromosome. A considerable loss of extra chromosomes is apparent at the second telophase of P.M.C. About 40% of the cells have two bodies lagging (based on 300 cells). Percentage lagging at first anaphase provides no measure of loss. It was observed that the lagging extra chromosome will remain present and divides independently at the second meiotic division.

The following cyto-genetic correlations were obtained:

1. F_2 plants not having an extra chromosome.

Satellites	+ +	+ s	aw +	aw s
long long	11	1	1	2
long short	12	2	3	3
short short		2	1	6

2. F_2 plants having an extra chromosome.

Satellites	+ +	+ s	aw +	aw s
long long	6		1	
long short	12	1		1
short short	2	1		1

The distance aw - s is 20%, somewhat below normal. The correlation between s and the satellite length was calculated by the maximum likelihood method, using six classes (courtesy Mr. R. Corbeil) and was found to give a linkage of 20.32 ± 3.19. This is considerably less than the 32% predicted in another paper here (Linkage of Chromosome #2 Markers with the Satellites). However, low quantities of buds from the greenhouse-grown plants in the winter have, in several cases, necessitated the scoring at less favourable stages and the data may still have some errors in them.

Retig, N., and N. Kedar. Dwarf indeterminate and determinate lines adapted to subtropical climates.

In order to decrease production costs many attempts have been made in Israel to grow tomatoes without use of supporting trellises. These efforts have been unsuccessful, the main obstacles being sunscald and inferior fruit quality in varieties of conventional types. Therefore an attempt has been made to produce lines with 1) very short internodes and 2) indeterminate or determinate growing habit. Crosses between the indeterminate Moneymaker (internodes av. 4.3 cm) and the low determinate Acc. 334 (internodes 1.0 cm, obtained originally from Urbana, Illinois) gave an F_1 with internode length of 2 cm. The F_2 selection was made for low and compact plants with fruits protected by ample foliage. In 1962, lines (F_5) of two distinct types had been developed: 1) Bushy, indeterminate dwarfs about 30-40 cm high--fruits very well protected against sunscald. Yields in 1962 were 2-4 pounds per plant. 2) Bushy, determinate dwarfs with rather good protection against sunscald. Yields about 5-6 pounds per plant. In both types Fusarium-resistant lines with medium-sized globular fruits and lines with flattened fasciated fruits are being tested. Optimum planting rates appear to be between 12,000 to 20,000 plants per acre.

The new bushy plant type appears most promising for processing varieties. Short internode lines with fruit characters from Kcl46, Webb Special, Tamar, and Roma are being developed.

The genetics and physiology of the "short internode" character and its effect upon microclimate and fruit quality is under investigation. Present data indicate that more than one gene is involved. Its expression appears to depend on light intensity, as plants grown under greenhouse conditions show highly lengthened internodes.

Rick, C. M. Abnormal segregations on chromosome 4.

The phenomenon reported here was first encountered in segregations of $\underline{w}_4$. The F_2's of most combinations between $\underline{w}_4$ and diverse genetic stocks provide good fits for a Mendelian recessive (TGC 11:18), but in tests with several of Stubbe's mutants in var. Condine Red, $\underline{w}_4$ segregates in great excess (359+ : 1226 (77.3%) $\underline{w}_4$; 1102+ : 4379 (81.1%) $\underline{w}_4$; 259+ : 1016 (79.7%) $\underline{w}_4$ in three different series). In all cases the F_1's had normal phenotype. F_3 tests of + segregants showed that all of the latter were heterozygous, and 96% segregated in the same abnormal fashion. These data discount dominance reversal and zygotic elimination as explanations of the disturbance. If gamete elimination is involved, it must affect both sexes. If both sexes are affected equally, the ratio of functioning gametes must be in the neighborhood of 1+ : 9$\underline{w}_4$; if elimination of + gametes in one sex is complete, the gamete ratio in the other must be approximately 2+ : 8$\underline{w}_4$.

In subsequent studies it was found that segregations of other genes were similarly distorted with the following F_2 frequencies: $\underline{w}_1$ (69.8%), afl (51.1%), e (10%), ful (0.56%), di (12.3%), the last three entering the crosses on a CoR chromosome. Since four of these genes are known to be on chromosome 4, $\underline{w}_4$ and afl are definitely implicated. A cross between $\underline{w}_1$ and $\underline{w}_4$ yields only +, proving that they are not allelic, but the possibility remains that they might be neighboring duplications. The F_2 of this cross has not yet been grown. The different levels of distortion observed with

each of these genes renders unlikely any such explanation as paramutation or other mutational phenomena, but strongly suggest that map distance from some sort of gamete eliminator governs the degree of disturbance. Assuming equal gamete elimination for both sexes, the map distance from a gamete killer with 100% penetrance would be 9-12 for $\underline{w_4}$, 16 for $\underline{w_1}$, 29 for afl, 7 for ful, 32 for e, and 35 for di. These spatial relations for ful, e, and di are in the right order and roughly approximate known map distances.

The elimination has occurred only in hybrids with CoR derivatives as one of the parents and a limited number of lines as the other, including sources of $\underline{w_4}$, $\underline{w_1}$, nv, and a rv-sf stock. Although the lineage of chromosome 4 is not clear in all of these stocks, both sf and $\underline{w_4}$ are spontaneous mutants in var. Pearson, and it is possible that chromosome 4 in all other stocks trace to Pearson or some ancestral stock. The distortion can occur in the absence of a wiry gene. Cytoplasm is not implicated because the effect is transmitted through reciprocal crosses. The factor from Condine Red is transmitted like a single gene as ascertained from the 1 normal : 1 distorted F_3 segregation observed in the cross CoR/+ x $\underline{w_4}$. It is thus established that two gene-like elements are necessary for this abnormal behavior: one from Condine Red and the other from Pearson and possibly other sources.

CoR/Psn hybrids show considerable abortion of pollen and ovules, although it is still not clear whether abortion is always associated with disturbed segregation. Chromosome 4 appears entirely normal in pachytene according to examinations by Dr. G. S. Khush. Pairing at diakinesis and metaphase appears normal for the entire complement, and telophase counts of many cells have not deviated from 12-12. Cytological evidence therefore gives no indication of a meiotic drive phenomenon. Although no explanation has yet been found that is entirely compatible with all observations, the best fit is provided by a gamete killer of complementary determination and incomplete expression. Map distance from the locus of this activity would determine the intensity of action. Further tests are now in progress to test this hypothesis.

Rick, C. M. Inheritance and linkage relations of Jaundiced (Jau). A single partly chlorophyll-deficient seedling was found in a trisomic F_2 segregating for triplo-9, ug, Nr, and tr. None of these genes has conditioned yellowing of the foliage under our conditions, and no similar character has been known in any of the source lines for these genes and the triplo-9 stock. The phenotype, which is rather consistent in seedling stages, is a yellowish-green off-color that affects all vegetative parts. The growth rate is slower so that the Jau segregants form a second tier of the F_2 at 1/2-3/4 the normal height. The color difference can often be detected in the field in spring, but not in the main season. Growth is also retarded in the field, but plants are reasonably fruitful. The name was selected to describe both the phenotype and the sickening nature of segregation.

The dominant nature of Jau is clearly revealed by many F_1's between plants of its phenotype and many different genetic testers. The total segregation in 25 small F_1 families was 199+ : 134 Jau, the difference from 1:1 being highly significant. Jau does not breed true, as revealed from the segregation in every F_3 family descending from 76 Jau plants of the preceding generation. The total segregation for 13 F_2 families is 1629+ : 2561 (61.12%) Jau, with a highly significant heterogeneity

(49.19; 13 d.f.). Segregation ratios have always fluctuated to a notable extent. In most respects genetic behavior of Jau closely parallels that of La, and I am inclined to interpret both as monogenic dominants that are homozygous lethal and that also tend to be weaker and sometimes lethal in heterozygotes. A digenic explanation, though not ruled out, is considered less likely.

Linkage tests have been made between Jau and other markers, independence having been noted with the following genes: au, y, d_1, Wo^m, e, a_1, c, tf, dl, ah, H, La, rv, w_4, and various others of the Stubbe I and III series. Significant dissociation with imb, inv, and pr is noted in the accompanying table. While the deviation is highly significant in certain tests, the ratios within the Jau^+ fractions are not modified as expected by linkage. Any ideas to explain such anomalous segregation would be welcome. The independence between Jau and other markers and the dissociation trend that it displays with these three markers seem to implicate Jau with chromosome 1. Maybe future tests will clarify this situation.

Combination	+ +	Jau-+	+ t	Jau-t	Adj. cont. χ^2
Jau-imb	77	121	27	19	5.20
	73	90	23	26	N.S.
inv	103	159	30	16	9.67
	89	170	24	9	16.05
	113	193	56	2	67.32
pr	216	136	61	20	4.96

Rick, C. M. Linkage relations of bl, cl_2, ht, and nv.

Until 1962 the two genes bl and cl_2 persistently resisted trisomic identifications of their respective linkage groups. Since the former had been tested with negative results against all trisomics except triplo-11 and the latter with all save triplo-6, appropriate crosses were made between these mutants and multiple markers for the respective untested chromosomes. Both proved to be good leads, as the following data substantiate. During the past year a test was also made between cl_2 and triplo-6 with results that confirmed this linkage.

The F_2 segregations are summarized in the following table. In spite of the limitations of F_2 analysis and the small size of families, the results are fairly consistent with previously extablished map distances and give reasonably good approximation of the loci. The usefulness of the first family is somewhat limited by the fact that it was partly rogued by mistake to a_1 and c before planting to the field. The linkage value is estimated from the fraction of the family that was completely rogued to the markers. The proportion of bl is excessively high in the last family for unknown reasons, yet it yields linkage values that are consistent with the first family and with older maps of chromosome 11.

The locus of bl is clearly on the long arm of chromosome 11. The recombination values would spot it about 15 units to the right of a_1. This position is, furthermore, the only one compatible with the fact that the single crossover between bl and a_1 in the third family was also homozygous

j_1-hl-a_1-bl. Information about the locus of cl_2 is less critical; a comparison of map distances would place it to the left of, but close to, c.

Earlier experiences with ht-e in seedling F_2's suggested a linkage between them, but ht is so epistatic to e in these early stages that classification was not dependable. The family reported here was field grown, and the data are considered trustworthy because the interactions were clear, other genes segregated normally in the family, and e gave normal ratios in other contemporary families. Classification in the nv-ah segregations was excellent.

Seeds of the mutants and respective linkage segregations have been sent to linkage cooperators.

Pedigree	Combination	+ +	+ t	m +	m t	χ^2	C.O.
F_2 bl-d_2 x a_1-c (partly rogued to a_1 and c)	bl-a_1	105	194	46	4	54.19	16.0
	cl_2-c	95	195	58	1	82.91	8.5
F_2 cl_2 x c-md-yv	cl_2-c	129	45	57	0	16.70	0
	cl_2-md	129	45	54	3	8.86	26.0
	cl_2-yv	133	41	45	12	0.03	48.0
F_2 bl x a_1-hl-j_1	bl-a_1	97	29	77	1	16.45	14.5
	bl-hl	104	22	72	6	3.10	36.0
	bl-j_1	103	23	66	12	0.04	47.0
F_2 ht-e	ht-e (rogued to ht)			45	0	13.69	0
F_2 nv-ah	nv-ah	44	31	15	0	7.72	0
	nv-ah	918	480	343	0		

Rick, C. M. New linkage testers. Considerable effort is ordinarily wasted between the screening cross that associates a new mutant with its chromosome and the multiple point cross that approximates its locus. I have been synthesizing new tester stocks with the idea that they might be used to accomplish both objectives in a single cross. Two strategically placed markers--ideally one in the middle of each arm of an isobrachial chromosome--with a sensitivity of 40 units on either side should suffice for the tomato map lengths as we now know them. Other requirements are that the markers be well-defined seedling characters, yet reasonable performers in the field; that epistatic effects are not overwhelming; and that the combination of genes does not weaken the stock excessively. Taking account of these limitations, I have concluded that four markers--two pairs marking two chromosomes--should be the maximum per stock. Six tester stocks with a total of 24 markers would thus be needed for the tomato complement. At the rate that good mutants are being accumulated and located on the maps, such a set of testers does not seem an unreasonable goal. The following list marks our progress to date:

Stock number	Markers	Chromosomes
LA780	c-yv ag-H	6, 10
LA782	sy sf	3, ?
LA783	au Wo^m-d tf	1, 2, 5
LA783	ful-e a_1-hl	4, 11
LA785	$dl-l_1$ ah La	8, 9, ?

These stocks have been used in tests with several new mutants and segregations have worked out reasonably well. With the acquisition of new material I am confident that they will be improved. Seeds in very limited quantity are available to anyone interested in trying them.

Rick, C. M. Search for S locus.

Martin (Genetics 46:1443-1454, 1961) found that the self-incompatibility of L. chilense behaved in backcross transfers to L. esculentum as if determined by two or more dominant genes, of which one showed linkage relations to genes of chromosome 2. This report deals with an attempt to determine whether or not the gene on chromosome 2 is indeed the S locus itself. By crossing one of Martin's SI BC derivatives which carried Wo d_1 with F_1 (L. esc. x L. chil.) of the opposite mating type, it was possible to derive a plant (61L445-11) which proved by progeny test to be S_1/S_2; Wo d/+ +. By itself, the ease with which this plant was secured suggests independence between S and the other markers. Progenies of the test cross of this plant as male parent with L. esc. d/d permit segregation of the S alleles and markers of chromosome 2 in order to detect random or non-random assortment. A male-sterile female parent was used because the disappointing seed yields (in this instance, a mean of 12.7 seeds, 4.3 seedlings per fruit) require large-scale hybridization. The total segregation of marker genes in two sowings was 87 + +, 12 + d, 28 Wo +, 261 Wo d, with a recombination value of 10.3%. Such departures from normal segregation ratios and linkage values are commonplace in chilense hybrids and do not reflect mistakes in pedigrees or progeny classification.

Since it was not possible to make mating tests with all progenies, a sample of 121 plants was taken at random with respect to vigor and all other characters except that approximately equal numbers of Wo and + were taken for the sake of efficiency of the linkage test. Of the 111 plants that survived to flowering and permitted satisfactory mating tests with the S_1 and S_2 testers (F_1 L. esc. x L. chil.), 51 (45%) were compatible with both and were therefore non-discriminatory for purposes of the Wo-d linkage test. According to Martin's hypothesis, these failed to receive dominant genes from both loci that are essential to the determination of SI; the approximate 1:1 ratio supports the two-gene hypothesis.

The two plantings were made in different seasons, and a necrotic character, which might have been identical with the one described by Martin, was strongly manifested in one, but rather weakly in the other. Segregation in the various combination pairs is summarized in the following 2 x 2 tables:

Mat. type	+	Wo
1 & 2	43	17
Indet.	13	38
χ^2	21.71	

	+	d
1 & 2	48	12
Indet.	14	37
χ^2	28.79	

	+	Nec.
1	3	14
2	13	0
χ^2	16.90	

	+	Wo
1	20	11
2	23	6
χ^2	0.97	

	+	d
1	26	5
2	22	7
χ^2	0.20	

	+	Nec.
+	15	13
d	11	4
χ^2	0.86	

	+	Nec.
+	16	10
Wo	11	7
χ^2	0.08	

From the above information it is clear that the segregation for S alleles and necroses was independent of the chromosome 2 markers, whereas the necrotic character was strongly linked with S_1. A highly significant association was also noted between the presence or absence of a mating type reaction on one hand, and the segregation of Wo and d on the other. Such relationships would be expected had the parent been heterozygous for the incompatibility locus (SI), the dominant SI gene having been located on one homologue, Wo and d on the other. The data are ambiguous as to the location of this gene: recombination values being 19.8 for Wo-d, 27.0 for SI-Wo, 23.4 for SI-d, and the proportion of SI-Wo-d and + + + recombinants being excessively high (15.3%) for a position of the SI locus between Wo and d as ascertained by Martin. Whatever these inconsistencies, it is clear that the S locus is not on chromosome 2 and that the necrotic character in this segregation was not the same one treated by Martin.

Rick, C. M., W. H. Dempsey, and G. S. Khush. Trisomic studies. Cytological investigations during the year require a revision of the tomato linkage groups. Routine examination of pachytenes revealed that the extra chromosomes of two of the trisomics had been wrongly identified. The correction amounts to interchanging the numbering of triplo-5 and 7. The gs-lg_5 group should now be identified with chromosome 7 and the wt-tf-mc group corresponds to chromosome 5.

Since previous studies revealed that triplo-11 had also been misidentified, efforts were made to find the true primary trisomic for chromosome 11. The problem was tackled by systematically testing each off-type trisomic in the collection for the segregation of a_1 which is known from deficiency studies to reside on 11. One of the trisomics derived from a Red Cherry triploid consistently gave trisomic ratios for a_1 (see data given below). Pachytene figures for this type show clearly that chromosome 11 is the extra one. The morphological modifications in triplo-11 follow a general tendency toward diminutiveness. Leaves are particularly reduced in size and number of segments. Stems are thin and the plant appears to be considerably more branched and compact than the corresponding 2N Red Cherry. The large trichomes are sparse on stems, and styles very long in triplo-11. Some of the trisomic plants of this line show a strong tendency toward

parthenocarpy; but seed yields are generally disappointing. Fruit shape, as nearly as can be judged in a cherry tomato, is somewhat elongate.

The only other item requiring explanation is the new gene Lx (Lax), identified by trisomic segregation and linkage test with chromosome 2. This character is an elongate, acute-segmented, pendant leaf derived from the variety Laketa. In 13 F_2 families tested, it segregated as a dominant, although a dosage effect was evident. The total segregation was 171+ : 631Lx without a significant indication of heterogeneity (χ^2 = 21.390, 13 d.f.). The trisomic segregation for chromosome 2, summarized below, with its excess of + reveals a strong deviation from the normal inheritance of Lx. This relationship with chromosome 2 is confirmed by a linkage test with d_1 (5 ++ : 15 +d : 84 Lx+ : 18 Lx d). The deviation from random association is highly significant (χ^2 = 23.07) and the linkage distance between d_1 and Lx is estimated at about 20 units.

In all families summarized below, other genes were segregating in normal ratios, and in other trisomic F_2 families, a_1, cl_2, ls, and Lx segregated normally.

Summary of trisomic segregations
1962

Family	Chromosome	Phenotype	2N	2N+1	Total
62L885 & 886	2	Lx^+	51	3	54
		Lx	32	14	44
62L877 & 878	4	ls^+	71	23	94
		ls	10	0	10
62L1918 & 1919	4	ls^+	131	20	151
		ls	8	0	8
62L909	6	cl_2^+	71	2	73
		cl_2	8	0	8
62L1130 & 779	11	a_1^+	seedling only		162
		a_1			15
62L1125	11	a_1^+	36	7	43
		a_1	3	0	3

Rick, C. M., and G. S. Khush.
Linkage analysis of chromosome 8.

Our attention to this group in the past three years has been concentrated on the dl-bu-l_1 region. Perhaps the most important development has been the delimitation of dl to the short arm and l_1 to the long arm of chromosome 8. Following the method we used for chromosome 11 (Genetics 46:1398, 1961), normal pollen was irradiated and applied to stigmas of ms_2-dl-bu-l_1. Among the progeny appeared various mutants, including one unmistakeable dl and another that was l_1. The former was deficient for most of the achromatic region of the short arm of 8, while the latter was a translocation monosomic, deficient for the long arm of 8 and the short arm of 9. Since the interchange breaks were most likely in centromeres, it follows that bu is

probably on the short arm somewhere in the chromatic region. It is interesting to note that Notani (TGC 12:34) also concluded that the centromere was situated between bu and l_1 from his analysis of trisomic segregations.

Linkage data that have not been presented previously are summarized in the following table. The positions of al and gf have not been changed since the last summary in TGC 10 because no new analyses have been made. Eight separate estimates of the dl-l_1 distance have been made from the sums of distances between intervening loci, ranging from 26 to 38 with a mean near 32. The most recent tests for ch, which we feel are more reliable than the ones previously reported, shift the locus from 65 to 41. That it must lie to the left of bu is revealed by the facts that all ch-bu crossovers have also been l_1 and that dl-ch crossovers are rare. The positions of cpt at 49 and spa at 64 are better established than the ones reported from the first tests. No indications were found of linkage between either dl or bu and yg_4. It follows that if yg_4 lies on chromosome 8 it must be distal to al, thereby putting it "way out". We also have a limited amount of BC data that do not confirm a linkage between ms_{17} and l_1.

The map presented in the linkage summary on page 6 provides the best approximation to these findings.

Pedigree	Combination	+ +	+ t	m +	m t	C.O.
F_2 ch x dl bu 1	ch-dl	174	78	70	1	12.5
	ch-bu	178	69	75	1	13.0
	ch-l_1	178	69	69	7	32.0
	dl-bu	235	9	18	61	8.5
	dl-l_1	214	30	33	46	23.0
	bu-l_1	225	28	22	48	17.5
F_2 ch x dl bu 1 (Rogued to dl)	dl-ch		133		0	0
	dl-bu		9		124	6.0
	dl-l_1		73		59	33.0
F_2 ch x dl bu 1	ch-dl	89	48	33	0	0
	ch-bu	88	49	33	0	0
	ch-l_1	85	52	31	2	21.5
	dl-bu	116	6	5	43	6.5
	dl-l_1	99	23	17	31	24.5
	bu-l_1	98	18	23	31	25.0
F_2 va^{virg} x dl bu 1 (Rogued to va)	va^{virg}-dl	Disc.		270	0	0
	-bu	746	va^+	268	2	3.0
	-l_1			249	21	29.0
F_2 yg_4 x dl bu (Rogued to yg_4)	yg_4-dl	Disc.		36	11	
		573	yg_4^+	37	10	

F_3 cpt x dl bu l_1 prog of cpt only
Chromosome exchanges: cpt-1 15/64 = 23.4%
cpt-dl 5/64 = 7.8%
cpt-bu /64 = 1.6?%

F_3 ch x dl bu l_1 prog of ch only
Chromosome exchanges: ch-l_1 8/30 = 26.7%
ch-dl = 0
ch-bu 2/30 (both ch bu 1) = 6.7%

Stettler, R. F. Further results on the dosage effect of the lanceolate gene.

As previously reported (TGC Report No. 12, 1962), the first indications of dosage effect of lanceolate (La) were observed among a small progeny resulting from a cross LaLa++ x ++++. Since this phenomenon seemed of promise for a better understanding of the morphogenetic effects of lanceolate, a more thorough investigation was initiated. In the course of this study the following tetraploid genotypes were recovered:

Parents	Segregation of progenies ++++	La+++	LaLa++	LaLaLa+	LaLaLaLa	Total	Chi square*
LaLa++ x ++++	6	21	5			32	(0.091)
LaLa++ selfed	1	5	14	7	(3)	30	
La+++ selfed	33	59	34		(1)	126	0.524
++++ selfed	49					49	

*On the basis of chromosome segregation

The classification of ++++, La+++, LaLa++, and LaLaLa+ genotypes was consistent in several families. Greater difficulties were met in recognizing the LaLaLaLa segregants. The four individuals classified as such showed morphological variation ranging from "reduced" to "modified." One of the "modified" seedlings developed a plumule which, however, did not elongate into a shoot. Dissection of all those seeds that did not germinate revealed many more "reduced" embryos far in excess of expected numbers for LaLaLaLa. Similar findings have been reported by L. Monaco in TGC 11, 1961. Progeny tests of LaLa++ types were hampered by low fertility, and none of the numerous crosses with LaLaLa+ plants succeeded.

In addition to the various tetraploid types, two triploid plants were recovered, one of which was classified as La++, the other as LaLa+. Attempts to verify these genotypes were not conclusive.

Among the many morphological characters studied, the following ones were found to exhibit significant dosage effects:

Organ		Character	Trend with increasing La-dosage
shoot system		apical dominance	decrease
leaf:	terminal leaflet	length/width ratio	increase
	terminal leaflet	number & size of marginal lobes	decrease
	lateral leaflets	number, size	decrease
inflorescence:	flower	number per inflorescence	decrease
	flower	fertility	decrease
	anthers	degree of tube formation	decrease
	sepal	length	decrease

An anatomical investigation has been initiated to determine the time and place of divergence in histogenetic events responsible for the ultimate difference in morphology.

Thompson, A. E. Frequency of multiple cotyledons in selected and unselected populations.

A rather high frequency of plants with three and four cotyledons was observed in a seedling population. Self-pollinated seed was obtained from six plants with three cotyledons and from three plants with four cotyledons. Seedling populations were grown and classified. The following data indicate that selection was totally ineffective in increasing the frequency of multiple cotyledons.

	Number of plants (Cotyledon number)			Percent with multiple cotyledons
	2	3	4	
Unselected population	719	9	3	1.53
3-Cotyl. selections	3230	18	1	0.58
4-Cotyl. selections	1024	2	1	0.29

Thompson, A. E. Inheritance of albescent (alb), a new unstable chlorophyll mutant.

The new unstable chlorophyll mutant reported in the 1962 TGC Report (12:46) has been given the name albescent (alb). This should not be confused with an allele of ghost (gh) that was provisionally designated as albescent until tests definitely established its allelic relationship with ghost (TGC 6:31-32, TGC 7:15-16).

Data for crosses between albescent and normal clearly indicate the recessive nature of the character.

	+	alb	Chi-square
F_1	All	0	----
F_2	147	56	0.72
Testcross	293	290	0.02

Crosses were made between albescent and ghost to test for possible allelism, since they superficially resemble each other. The following data clearly indicate that alb and gh are not allelic and are also independent.

Type of cross	+/+	alb/+	+/gh	alb/gh	Chi-square[a]
alb x gh F_1	48	0	0	0	----
gh x alb F_1	76	0	0	0	----
alb x gh F_2	1005	310	291	76	1.33
gh x alb F_2	821	267	268	76	0.86
gh x alb F_1	49	55	0	0	0.35

[a]Contingency Chi-square for F_2's.

A deficiency of gh was observed in the alb x gh F_2, but a good fit to the 9:3:3:1 ratio was obtained in the reciprocal cross.

Plants classified as the double recessive alb alb gh gh were similar to ghost in the seedling stage, but reduced in size and vigor. The cotyledons in contrast to ghost were chlorotic and served as the principal differentiating characteristic. Cotyledons of ghost may show slight chlorotic symptoms, and these cotyledons usually increase in size, and apparently give support to the plant through photosynthesis. The cotyledons of the double recessives in some instances tend to increase in chlorophyll content and appear nearly normal, but not to the extent usually observed in ghost. None of the plants of the double recessive have been observed to reach maturity, and most die at a relatively early stage.

Thompson, A. E., M. L. Tomes, J. P. McCollum, and E. V. Wann. Pigment analysis of crimson. Butler recently reported a new fruit color and named it crimson (TGC 12:17-18). Three Illinois accessions of this material were obtained from W. Shumovich in March, 1960, and two more directly from Butler in October, 1960. The line obtained by Purdue was received from T. O. Graham during the spring of 1962 under the proposed designation, "High Crimson." A cooperative effort is now being made between Illinois and Purdue to characterize the pigment constituents and provide a basis for genetic analysis and selection procedures for the development of commercially adapted varieties containing this character.

Data in Table 1 are typical of those obtained in other analyses. Pigments were extracted with hexane using McCollum's method. The main effect of the crimson character is to lower the quantity of carotene produced in the fruits with little change in the total carotenoids. The reduction occurs in both locular and wall tissue, but is visually more apparent in the locular region.

The data from Purdue in Table 2 closely support those presented in Table 1 with regard to lycopene and beta-carotene. Even though pigment quantities were somewhat higher in September than in August, the ratios were almost identical at both dates. The polyene content of crimson appears to be somewhat higher than that of the normal variety.

Accurate visual classification of crimson has been difficult to make. Preliminary information (Table 3) indicates that crimson in combination with high pigment alters the red/yellow color ratio in a manner similar to that expected in normal crimson, but possibly to a greater degree. If the data in Table 3 are found to be reliable, it opens up the possibility of studying the inheritance of crimson on a homozygous hp background. Research in this area is now in progress. In view of the possibility of high pigment-crimson combinations, it is thought desirable to designate Graham's line simply as "Crimson" rather than "High Crimson."

Table 1. Carotenoid pigments and color of fruits of three varietal types grown in the Vegetable Crops Greenhouse, Urbana, Illinois, harvested at incipient coloring in February and March, 1962, and ripened for 14 days at 68°F.

Variety	Type of sample	Number of samples	Total no. of fruits	Carotenoid pigments (µg/g) Total	Carotene	T/C ratio	Hunter a/b
Crimson[a]	Whole fruit	17	138	63.8	2.0	32.6	1.97
	Locule	11	111	61.8	5.0	12.2	1.62
	Wall	11	111	64.6	1.5	42.8	2.17
Campbell 146	Whole fruit	6	46	65.7	4.2	15.6	2.10
	Locule	6	46	61.9	11.0	5.6	1.53
	Wall	6	46	65.5	2.7	24.3	2.18
Y-13 (hphp)	Whole fruit	4	27	94.4	7.3	12.9	2.15
	Locule	3	20	63.0	10.4	6.1	1.48
	Wall	3	20	97.3	7.0	13.9	2.31

[a]Combined means of three different lines.

Table 2. The means and standard deviations of carotene pigment and polyene content (micrograms/gram fresh weight) in mature fruits of the tomato varieties Campbell 146 and Crimson at two different times during the season. Purdue O'Neal Farm - 1962.

	Campbell 146		Crimson	
	August 15	September 6	August 15	September 6
Number of samples	6	11	6	10
Phytoene	9.26 ± 2.27	11.26 ± 2.46	11.81 ± 2.57	15.08 ± 2.61
Phytofluene	3.15 ± 0.33	4.80 ± 1.23	3.63 ± 1.01	5.78 ± 0.99
Beta-carotene	4.72 ± 0.98	5.08 ± 0.65	2.25 ± 0.24	3.02 ± 0.37
Gamma-carotene	0.94 ± 0.24	0.94 ± 0.22	0.61 ± 0.15	1.02 ± 0.18
Lycopene	59.00 ± 9.79	64.70 ± 11.92	60.00 ± 7.87	80.24 ± 10.34
Lycopene/beta-carotene ratio	12.5	12.7	26.7	26.6

Table 3. Carotenoid pigments of field ripe fruits harvested in September, 1962, at Urbana, Illinois.

Variety	(Micrograms/gram) Total	Carotene	T/C ratio
Campbell 146	98	2.8	35
Crimson	75	1.4	54
High pigment	155	7.6	21
High pigment-crimson	153	2.4	64

Walkof, C. A dominant to recessive color mutation.

A sectorial chimera, which affected an entire tomato fruit, occurred at Morden in a group of F_1 plants of the Blazer hybrid that were included in a variety trial. Blazer was developed by the Ferry-Morse Seed Company from the three-way cross, Orange King x (Bounty outcrossed probably to Redskin). The chimera was a colorful example of the mutation of a dominant character to the recessive. The affected fruit was sharply sectored through the polar axis, with one half being the dominant red color and the other half recessive tangerine. The time of mutation evidently occurred in the early bi-cellular developmental phase of the floral meristem. The seed from each colored half sector was grown separately to produce F_2 plants. Those from the red sector segregated in a monofactorial manner: 2 red-fruited to 1 tangerine-fruited, just like the plants from the usual red fruits of Blazer. However, the plants originating with the tangerine sector had only tangerine-colored fruits. Staminal cone color (yellow vs orange-colored) segregated in a similar manner. One F_3 line from the red sector segregated for foliage color (normal vs xanthophyllic) in 3:1 proportions. Three F_3 lines from the tangerine sector produced all xanthophyllic plants, and five lines gave normal to xanthophyllic in 2:1 proportions.

Walkof, C. A unique, sectored, skin color chimera.

A sectorial chimera which affected only the epidermal layer of a fruit from the Morden 2-60 tomato occurred in a unique manner. The sectors were orange-colored and not prominent. Seed taken from locules adjacent to the sectors produced plants of which 25 per cent had one fruit each with a bright orange sector. In contrast, the seed from locules not adjacent to the sectors produced plants, also in a 25 per cent proportion, but the color of the sectors was a dull or diluted orange shade much like that of the original sectored fruit. Only in one instance were two sectored fruits found on one plant. The proportions of plants with sectored fruit indicated a single gene control of the chimera. The specific location of sectored fruit on an affected plant was not established.

Walkof, C., and R. B. Hyde. Acid inheritance under monogenic control.

Analyses were made of the titratable acidity from the fruits of six generations from the cross Morden W024MD x Early Lethbridge which were grown in three tests. Results indicated simple inheritance for this component of the tomato. Comparisons of the means of the generations suggested incomplete dominance for the high acid values. The F_2 data produced a bimodal curve typical of the 3:1 Mendelian ratio. The parents of the cross vary widely in the total acid content of the fruit. A low acid analysis of 0.17 per cent is typical of the W024MD tomato, and a high acid analysis of 0.56 per cent for Early Lethbridge. A total acid content of 0.45 per cent and over is imperative in tomatoes grown for processing purposes.

Young, P. A. Characters without named genes.

Limited by the generic possibilities of Lycopersicon, tomato characters vary almost infinitely. Already, 370 tomato genes have been named (TGC 12:3-14). Many characters without named genes were listed in TAES Bul. 698. The following characters add to those in Bul. 698. Characters without literature

citations were studied at the Tomato Laboratory at Jacksonville.

Abortive seeds: Hotset in hot weather (TAES L-386); L. esculentum x L. peruvianum.

Anthracnose resistance: Phytopath. 42:113; Plant Dis. Rptr. 37:317 and 43:519.

Apple-green fruit color; Ontario variety.

Bacterial spot and canker resistances: Phytopath. 44:409.

Bacterial wilt resistance; recessive; Phytopath. 42:628.

Blue-green leaflets; recessive; G2117B in greenhouse and field; TGC 8:24.

Bracts and pseudostipules: Jour. Heredity 34:199.

Canescent stems; partly dominant in L. peruvianum. Jour. Heredity 34:199.

Catfacing (physiological); varieties differ in susceptibility; n-allele may prevent it; symptom is very irregular blossom end of fruit. Tex. Agr. Exp. Sta. Bul. 698, p. 49.

Chlorophylls, carotenes and lycopenes: Proc. ASHS 78:464; TGC 6:28 and 11:8.

Cold setting ability: Early Lethbridge, Early Alberta, Cold Set, Swift, Earlinorth, Viceroy; 45°.

Core pulls out of ripe fruit when picked; Guam; TGC 9:39; occurs in both j and J-allele tomatoes; major problem with J-allele greenhouse tomatoes; calyx often is left on greenhouse tomatoes picked ripe to avoid pulling out top cores, and for advertising.

Additional explanation of last paragraph: It is customary in Ohio to leave the calyx and stem below the abscission layer of the fruits when they are picked ripe; this custom probably started to avoid pulling the cores out of part of the fruits (as I sometimes do here). However, it was found that the fresh green calyx on the fruits made a nice advertising marker showing that they are very fresh greenhouse tomatoes. OHIO WR7 (J-allele) variety is very popular in Ohio. It is a selection from the famous OHIO WR3 that was reselected for freedom from fruit pox that is an inherited abnormality, at least part of the time. It is much more apt to appear in hot weather than in cool weather.

Concentric and cuticle cracking (rain checks) of fruits; TAES Circ. 113.

Cracking: physiological puffing may prevent severe cracking.

Curly top virus resistance; Owyhee variety: Idaho AES Bul. 298.

Dark green leaflets; much darker in Pearson than in Rutgers varieties.

Dark green meridian lines in peel of large green fruits; Earliana var. Tex. AES Bul. 698, Fig. 12, A,B. (This character appeared in many Earliana descendents).

Droopy leaflets with slender tips; not wt-allele; TAES Bul. 698; G738 selection.

Droopy flowers shed rain and set fruits in wet weather; Nagcarlang purple tomato and G2188.

Didymella lycopersici resistance: Plant Dis. Rptr. 43:59.

Epinastic rachis of W1083; downward curled leaflets.

Extremely dwarfed plants: Tiny Tim and Hardin's Miniature; polygenic with d, et al.

Early dying of lower leaves in very early varieties; poor leaf retention.

Firm vs. soft ripe fruits: Oxheart and Sioux are soft; CP1951 is firm; TGC 10:6.

Fruit pox makes corky lenticel-like spots in fruit peel; associated with light colored dots and short lines in unbroken peel. Phytopath. 30:343-345. Tex. AES Bul. 698, Fig. 10d.

Fruit size: polygenic and associated with f, lc and O-alleles.

Grooves over locule walls: San Marzano type; Genetics 33:405.

Heat sterility resistance: Hotset, Cold Set, Early Alberta, Early Lethbridge; TAES L-386.

Light green stripes in green peel; marker for Pinkdeal tomato; TAES L-566.

Large or small top fruits; small on Gulf State Market; large on Pinkdeal and Rutgers.

Mottled ripe fruits: G1245 and G1236; also over-ripeness.

Netted chlorophyll; radiation mutation; TGC 6:19; Genetics 41:791.

Odor of stems: L. esculentum is different from L. peruvianum; TGC 7:12.

One and 3-cotyledon seedlings; about 0.0001%; TGC 2:7.

Open stylar scars; rot hazard: Fortney, Mich. Univ. Microfilms #58-1775.

Persistent flowers and calyx; S1112; Bot. Gaz. 114:449.

Pink gold fruits: G509, G1219; G1391, L. peruvianum crosses; TGC 2:13 and 6:28.

Phoma rot resistance: Plant Dis. Rptr. 43:61.

Powdery mildew resistance: TGC 5:14.

Pruny plants; too-early branching; polygenic with bu, br and modifiers.

Prominent top cores in Pearson, Homestead, Pinkdeal, etc.; usually large cores in large fruits.

Pointed blossom-ends: Oxheart, Laketa, San Marzano; Pearson in E. Texas; TGC 4:18, 19.

Purple-red and pink (fuchsia) fruit flesh: Modifier of R-allele in Gulf State Market very ripe fruits.

Racemose flowers: S1112; Bot. Gaz. 114:449.

Rooty stems: G1393; TGC 2:12.

Seedling vigor: vigorous in Rutgers and Pearson, etc.; weak in some varieties.

Smooth leaflets: Golden Sphere marker character.

Tobacco etch resistance: Plant Dis. Rptr. 43:64.

Topless plants 4 to 12 inches tall; percentage too high in S1548; young plants lack top buds as a genetic defect; extremely determinate with only bottom leaves; no progeny.

Undesirable fruit flavor: Jour. Elisha Mitchell Sci. Soc. 69:84.

Vitamin C: superior concentrations in High-C and Doublerich varieties.

Variegated white leaflets: TGC 7:10.

Viscosity of tomato juice: inherited varietal differences; TGC 5:14.

Withered tops: TGC 4:18.

Yellow bottoms on green fruits: STEP348; whitish on Gulf State Market; light green on Rutgers.

Yellow-green leaves on Golden Colossus tomato; Jour. Hered. 43:25.

Yielding ability: polygenes and physiology. Iowa Agr. Exp. Sta. Bul. 397:324.

Young, P. A. Smudged fruits. The ripe fruits of Lycopersicon peruvianum (L.) Mill. are green with purple to black smudge or broad stripes on sunny sides. This smudge character was studied in crosses with L. esculentum Mill. with the A_1-allele to determine the inheritance of smudge. The A_1-allele causes purpling of the bases of the stems below the leaves of plants 1 to 12 inches tall and also some purpling of the epidermis of the tops of plants in dry weather. Most of the stems are green (Tex. Agr. Exp. Sta. Bul. 698). Plants with the smudge character showed purple to black smudge in the peel of the sunny sides of few to many fruits per plant, especially when the plants were exposed to temperatures of 35 to 50°F. The smudge fruits nearly always occurred on plants with very purple stems that often also showed interveinal purpling of the leaflets. Certain plants were indefinitely classified for purple or green stems. Smudge was described in TGC 2:12, 1952 and TGC 4:18, 1954.

The peel was green under the calyx of smudge fruits, so light appears necessary for development of the purple or black color. Cool fall weather or soil deficient in nitrogen and phosphorus apparently increased the development of the purple or black color.

G1219 F_2 tomato with many smudge fruits was a selection of W. S. Porte's No. 48B380 with the geneology: Stokesdale X (Rutgers X Pan America) X ((Michigan State Forcing X L. peruvianum) X San Marzano from V. M. Watts. In 1962, G1219 selection segregated with 30 plants having smudge and purple stems vs. 15 plants with normal fruits and green stems. This 2:1 segregation of 45 plants indicates that smudge is a dominant character.

G1367 came from G1219B F_3 with smudge and purple stems X stokesdale in 1949. G1367E F_4 with prominent smudge was crossed with Homestead in 1959 and gave G2157, G2158, G2165 and G2171. Unfortunately, the F_1, F_2, and many of the F_3 plants were tested in rich damp soil and the large shady plants did not facilitate expression of mild and moderate smudge and purple stems; so accurate segregation ratios were not secured.

The tomato plants for Table 1 were raised in deep sandy soil that was deficient in nitrogen, phosphorus and water; so the plants were small and exposed their fruits and stems to hot sunshine. These plants were tagged, examined three times and labeled for smudge and stem color. Due to variable prominence, smudge was classified as: 0 for no smudge (normal green unripe fruits), 1 for mild but definite smudge with many purple dots in the peel, 2 for moderate smudge, and 3 for prominent dark smudge in 1/4 or more of the surface of the fruit. The 87 plants from G2157B, G2157C and G2158K were all

homozygous for smudge with purple stems. The F_3 and F_4 plants were calculated separately without changing the conclusions.

Chi-square analysis of the data in Table 1 showed that in only 5% of similar cases would so great a deviation from a 3:1 ratio occur by chance in the heterozygous selections. Thus, this is not a simple Mendelian segregation but a 2 1/3:1 ratio.

Smudge is a dominant character with prominent expression only when the fruits are exposed to much sunshine. Smudge appears to be pleiotropic or due to more than one gene, and the present evidence hardly justifies naming one gene for it. Smudge and purple stem showed difficulty in penetrance and expressivity associated with growing conditions. Possibly the genotypes differ although they are supposed to be the same. Smudge presumably came from Lycopersicon peruvianum.

Table 1. Segregation for smudge vs. normal fruit colors in G2157 and G2158 tomatoes. August 20, 1962.

	Degrees of smudge on fruits, July 4, 1962					May 8, 1962		
Selection	0 (green)	1	2	3	Total smudge	Purple stems	Green stems	Total plants
	(Number of plants)					(Number of plants)		
G2157D F_3	25	1	5	36	42	43	24	67
G2157E F_3	22	6	19	22	47	48	21	69
G2157F F_3	10	8	17	36	61	59	12	71
G2158E F_4	13	3	18	16	37	32	18	50
G2158F F_4	2	4	4	4	12	5	9	14
G2158H F_4	20	3	15	18	36	37	19	56
G2158J F_4	16	11	10	10	31	32	15	47
G2158L F_4	6	1	6	1	8	7	7	14
Totals	114	37	94	143	274	263	125	388
Percentages	30%				70%	68%	32%	

The following Research Notes were received too late to be placed in proper alphabetical order.

Foskett, R. L., and M. N. K. El Sayed.
Masking of the sp gene in Dwarf Champion.

Dwarf Champion variety contains the dwarf (d_1) and jointless (j_1) genes and has the typically indeterminate number of three leaves between inflorescences. It was found, however, that Dwarf Champion is genetically determinate. Furthermore, while the average number of leaves between inflorescences was slightly greater among plants containing sp^+, in all populations studied the modal number of leaves on jointless plants was three, regardless of the presence of sp. The data presented below represents one part of this study. The results are similar to those obtained from several hundred plants of F_3 progenies.

Parents	Number of plants	Number of leaves between 1st and 2nd inflor.
Dwarf Champion, j_1	4	3.00
Rutgers, sp^+, j_1^+	4	3.00
Fireball, sp, j_1^+	4	1.00
F_1 Progenies		
Dwarf Champion x Rutgers	2	3.00
Rutgers x Dwarf Champion	4	3.00
Dwarf Champion x Fireball	4	1.50
Fireball x Dwarf Champion	4	1.25
F_2 Progeny		
Fireball x Dwarf Champion		
jointed segregates	10	1.30
jointless segregates	6	2.50

Foskett, R. L., and H. Inayatullah.
The use of seed weight and Chlorox for detection of polyembryonic seeds.

In one experiment, Beefsteak seed was separated into two groups by means of an air column seed separator. The heaviest one-third (by volume) was compared with a randomly selected sample from the original seed lot for number of twin seedlings. The heavy seed produced 18 twins from 1,000 seeds, while the unseparated seed produced 7 twins from 1,000 seeds. In another experiment, seed of several varieties was separated into three weight classes, with the following results. The heaviest seed class was approximately 24 percent of the entire seed lot.

Average weight per seed	No. seeds	% germination	No. twins
2.02 mg.	6,000	75.9	1
2.66	6,000	90.9	4
2.98	6,000	94.7	12

It was also found that soaking seed in Chlorox for five minutes clarified the seed coat tissue so that twin frequency was higher. The twin embryos could not be seen, but embryo outlines in single embryo seeds were more clearly discernible. Those seeds in which the embryo outline

was not clear were suspected of containing twins. The use of heavy seeds and Chlorox together increased the incidence of twins.

Treatment	Seed lot	Visual selection	No. seeds	Percent germination	Twin frequency
Chlorox	heavy		500		1:56
		embryo not visible	87	92	1:17
		embryo visible	413	95	1:103
	random		500		1:125
		embryo not visible	42	83	0
		embryo visible	458	95	1:114
None	heavy		500	97	1:56
	random		500	94	1:167

Györffy, B., and J. Mako. Pollen abortion in autotriploid and sesquidiploid tomatoes.

The great viability of wild or primitive genotypes of tomato in comparison to the highly selected cultigens was recently reported by Rick and Notani (1961). In this connection it is of interest to tally the degree of pollen abortion in different triploid and sesquidiploid hybrids. The cotton-blue staining tests gave the following percentages of abortive pollen:

Autotriploids

L. peruvianum, L-21	54
L. esculentum, var. piriforme, P-11	60.2
piriforme, P-2	72.1
var. cerasiforme, C-6	83.5
cerasiforme, C-6	93.5
convar. esculentum	85-95 (see Rick and Butler, 1956).

Sesquidiploids

L. pimpinellifolium - L. peruvianum	68.1
L. esculentum, San Marzano - L. peruvianum	67.4
Bounty - L. glandulosum	73.9
Bounty - L. hirsutum var. glabratum	83.8
San Marzano - L. hirsutum var. glabratum	80.0
Mikado - L. peruvianum	83.4

The data indicate a gradual increase in the pollen abortion of the triploids in the order : wild species, primitive species, and intensively selected cultivars. The same tendency was revealed also among the sesquidiploid inter-subgeneric hybrids.

Györffy, B., and J. Mako. Two aneuploid progenies from a sesquidiploid tomato hybrid after uncontrolled pollinations.

Highly sterile hybrid plants between 4x L. pimpinellifolium and 2x L. peruvianum were transplanted in 1958 to nursery flats and left to uncontrolled natural pollination. In the 1959 season another series was grown in the field which was secured by vegetative

propagation of the original plants. These were not isolated spatially, and close by there were different cultivated tomato varieties and different wild species, respectively. The resulting seed set was very poor, an average of one seed per fruit. The first-generation progeny of sesquidiploids were grown in two seasons (1959 and 1960), again in the same nursery flat, and many of the mature plants had a seed set after open pollination. The combined data of the distribution of chromosome numbers in both first- and second-generation aneuploid progenies are presented in the table.

Aneuploid generation	Chromosome numbers																
	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
First	1	-	1	-	4	3	5	30	46	47	26	-	-	-	-	-	-
Second	2	7	8	20	29	25	26	7	4	-	-	-	-	-	1	-	1

The wide distribution of the chromosome numbers in the two aneuploid generations represents nearly the complete range of chromosome numbers between diploid and triploid. The high transmission of extra chromosomes is clearly encountered in both generations, 2n=32 and 33 being the most frequently represented classes in the first aneuploid progeny, and 2n=28 in the natural offspring of these first-generation aneuploid plants. The tendency to decrease the transmission of the extra chromosomes is also obvious in the second aneuploid generation. The morphological characteristics revealed a very striking diversity. Since the original sesquidiploids are very unfruitful, it is assumed that most of the aneuploids were likely the result of bee-pollination with pollen from other aneuploid individuals and other tomato accessions growing in the same plantings. The unexpected composition of the two generation progenies of the sesquidiploid L. pimpinellifolium - L. peruvianum provides further evidence of the greater tolerance of aneuploidy by primitive and wild tomato genotypes than by the intensively selected horticultural varieties reported by Soost (1958) and Rick and Notani (1961).

Lapushner, Dwora, F. E. Nitzany, and S. Cohen. Linkage of Tm_2 and nv with a lethal factor. (Submitted by R. Frankel).

Seeds obtained from P. G. Smith (designated 59 MVN 13-1 ⊠) supposedly free of virescence linkage with Tm_2 yielded a ratio of approximately 2 resistant to 1 susceptible plant (12:5) when inoculated with a local wild strain of TMV.

Eleven of the resistant plants showed local lesions after inoculation, and one plant (205-15) was free of local lesions upon repeated inoculation. None of the resistant plants was virescent.

The following progenies, approximating a 1:2 ratio, were obtained upon selfing the resistant plants:

		Progeny	
		No. of plants susceptible to TMV	No. of plants resistant to TMV
Parent plants showing local lesions:	205-1 ⊠	6	7
	205-2 ⊠	15	38
	205-7 ⊠	5	3
	205-10 ⊠	12	21

		Progeny	
		No. of plants susceptible to TMV	No. of plants resistant to TMV
Parent plants showing local lesions:	205-12 ⊠	17	22
	205-14 ⊠	31	57
	205-17 ⊠	20	33
Parent plant free of local lesions	205-15 ⊠	85	183

Pollination of 3 breeding lines with the pollen of the resistant plant 205-15 yielded a 1:1 ratio of susceptibility to resistance.

This information affirms Smith's note in TGC 12 that the presumed broken linkage is instead an added lethal factor, and that all above plants were heterozygous for $\underline{Tm}_2$.

A germination test using all seeds resulting from selfing a resistant plant (205-15) showed a normal rate of germination (90% +). It appears therefore that any lethal factor did influence either seed development before pericarp production or seedling mortality after germination. The latter possibility is being checked.

Menzel, M. Y. Preferential pairing in a Lycopersicon esculentum - Solanum lycopersicoides allotetraploid.

Rick (1951, P.N.A.S. 37: 741-744) reported a high frequency of bivalents at metaphase I in allotetraploids obtained by colchicine treatment of L. esculentum-S. lycopersicoides F_1 hybrids. Since two F_1's (4-47 and 4-54) showed virtually complete synapsis at pachytene and no visible differences between pairs of homeologues except a difference in the length of one proximal heterochromatic region in each of four pairs (Nos. 2, 4, 9, and 10) (Menzel, 1962, Amer. Jour. Bot. 49:605-615), it seemed worthwhile to re-examine the first meiotic division in an allotetraploid in order to shed light on the nature of the preferential pairing. Fixed buds of an allotetraploid clone (4-48), derived from a third F_1 individual, were kindly supplied by Dr. Rick, and pollen mother cells (PMC's) at pachytene, diakinesis, and metaphase were studied. Analysis of data from diakinesis is not yet complete.

Clone 4-48 has 49 chromosomes ($4x + 1$). The extra chromosome is a tomato chromosome belonging to one of the smaller, non-nucleolar, sets of unequal homeologues, and has been tentatively identified as chromosome 10. Pairing configurations are symbolized below by Roman numerals.

At pachytene, all of the chromosomes were synapsed in most cells except for an occasional I or a partially unsynapsed III attributed to the presence of the extra chromosome. Occasionally all 24 paired proximal regions could be traced in a single nucleus, but it was not possible to follow more than a small proportion of the 47 distal regions. Hence pachytene pairing was recorded only for proximal regions.

Ignoring the extra chromosome for the moment, if synapsis were at random, 2/3 of the 12 sets of 4 homeologues would give only equal pairs and 1/3 would give equal and unequal pairs in a ratio of 1:2. The expected frequency of unequal proximal regions would therefore be $1/3 \times 2/3 = .222$.

Scoring of 799 proximal regions from 60 pachytene nuclei gave the following results:

	proximal regions		
	equal	unequal	$X^2 = 186.39$, 1 d.f.,
observed	782	17	
			$p = \ll 0.01$
expected	621.62	177.38	

Synapsis is evidently highly preferential in the proximal regions, at least for those sets of four which differ in length.

In order to determine whether this conclusion is also justified in regard to the achromatic regions and the equal chromatic regions which cannot be scored directly for preferential pairing at pachytene, expected versus observed frequencies of quadrivalents were compared. Expected frequencies of quadrivalents and other configurations were derived from the following assumptions: (a) Synapsis is complete and is initiated by two's at one position (two parallel points of synapsis) in each set of four homologous arms; (b) Each position of initiation involves two pairs of homologous arms at random. (The same results would ensue if both positions of initiation occurred in the same arm but were located some distance apart. If synapsis were initiated at only one position, no quadrivalents would form regardless of whether synapsis were random or preferential. More than two positions of initiation would increase the expected frequency of multivalents.)

On these assumptions, for any given set of four chromosomes, both positions of initiation would involve the same pairs of chromosomes and give 2 II's in 1/3 of the cases, and would involve different pairs of chromosomes and give a IV in 2/3 of the cases. Each set of four should therefore contribute a mean of .66 IV per PMC and 11 groups should contribute a mean of 7.26 IV per PMC. A similar analysis of a group of 5 chromosomes leads to expected values of .20 I, .40 II, .26 III, .13 IV, .53 V per cell. The mean expected pachytene pairing for all 49 chromosomes of 4-48 is therefore .20 I, 7.66 II, .26 III, 7.39 IV, .53 V.

In 60 pachytene nuclei, 9 I's (.15/PMC), 4 III's (.07/PMC), 14 IV's (.23/PMC) and no V's were observed, suggesting that one or both of the assumptions concerning synapsis was incorrect. But since only IV's having exchanges of partners in the proximal regions could be scored, and since only a fraction of the distal regions could be traced in most nuclei, it was impossible to be sure that the unscored regions did not conceal a much higher frequency of IV's than the scored regions.

Frequencies of different configurations can be scored accurately at metaphase I. Expected metaphase frequencies of I's, II's, III's, IV's and V's were calculated, making the same assumptions as before concerning synapsis plus the additional assumption (c) that chiasmata are distributed at random among previously synapsed arms. Expected frequencies with which given pachytene configurations would retain 4, 3, 2, 1, or 0 chiasmata at metaphase I are given by the expansion of the binomial $(p + q)^4$, where p = the frequency with which a given pair of arms remains connected by one or more chiasma until metaphase (= "metaphase chiasma frequency per pair of homologous arms"), and q = 1-p. The following table compares observed frequencies in 42 metaphase I cells of 4-48 with expected frequencies for different values of p:

	Mean number per PMC of				
	I	II	III	IV	V
observed	.55	22.12	.74	.50	.00
expected (p = .84, observed freq. in 4-48)	1.92	8.28	.86	6.65	.26
(p = .745, mean of the two parents)	4.20	8.77	1.39	5.56	.16
(p = .55, frequency in the F_1)	11.37	9.54	2.09	3.00	.05

The data show that II's are much more frequent and IV's much less frequent than expected and hence indicate that at least one of the three assumptions is incorrect. Morphology of metaphase I bivalents suggests that assumption (b) is incorrect and that synapsis is not at random; random synapsis would lead to some unequal II's at metaphase I, regardless of how synapsis is initiated or how chiasmata are distributed. Unequal II's, so conspicuous in the F_1, were completely absent in the allotetraploid, although 14 of the 21 IV's recorded were composed of chromosomes of two different sizes. It therefore seems justifiable to conclude that synapsis is highly preferential in all regions in the allotetraploid.

The observed metaphase chiasma frequency per pair of homologous arms in the allotetraploid (.84) considerably exceeds those of the F_1 (.55), the tomato parent (.61), and the mean of the two parents (.61 $+$ .88/2 = .745) and approaches that of the solanum parent (.88). Apparently chiasma frequency is under partially dominant genetic control by factors from S. lycopersicoides.

Rick, C. M., and J. E. Boynton. Continued linkage tests with mutants of Stubbe's groups I & III.

Linkage tests have been continued with the same procedures reported in previous TGC Reports. Seven new linkages are reported, for which results of all completed tests are given in the following tables. Linkages are indicated by L, suggested but non-significant indications of linkage by S, and no significant departures from random recombination by X. Data for the last two categories are not presented, but records are kept for anyone who might need them.

The hookup between pr and y reported in TGC 12:43 for fla has been confirmed by similar relations for imb and inv. It therefore appears certain that all of these genes are on chromosome 1 with the following order: (au-y) - fla - Jau? - inv - imb - pr. Linkage data for the Jau combinations are given in the separate note on this mutant.

The relationship between prun and chromosome 2 was established by crosses with o. The elongate fruit of this mutant strongly suggested the phenotype of o. The test was carried to F_2 because both genes act in a partially dominant fashion. The combined segregation from several families was: 60 with elongate fruit, 49 intermediate, and 2 nearly normal rounds. These results suggest that prun and o are located close to each other with 1-2 units of crossingover between them.

The previously reported evidence for the presence of sub on chromosome 11 (TGC 10:13, 11:22) was contradictory, but our new results from the cross

sub x a_1 - hl indicate that sub must be on 11. The new data suggest the order hl - a_1 - sub, which is confirmed by the fact that four homozygous hl - a_1 - sub recombinants were recovered from the F_2.

Results with si are contradictory in respect to its relations with cm and w_4. Abnormal monogenic segregations appear in both combinations. In view of the excellent classification in si-w_4 families, si must be on chromosome 4. The possibility that cm also exists there must be kept in mind, but trisomic segregations for cm are normal for 4 but markedly affected for 10.

Seeds of the mutants and respective linkage F_2's have been sent to linkage cooperators.

Linkages with Dr. Stubbe's mutants detected in 1962

Tester	Chromosome	Stubbe I						Stubbe III
		imb	inf	inv	per	prun	sub	si
a_1	11	X	X	X	X	X	L	X
ah	9	X	X	X	X	X	X	X
au	1	L	X	L	S	X		X
c	6	X	X	X	X	X	X	X
dau (ff)	4	X	X	X	X			
cm	10							L
d_1	2	X	S	X	X	S	X	X
dl	8	X	X	X	X	X	X	X
e	4	X	X	X	X	X	X	X
H	10	X	X	X	X	X	X	S
hl	11						L	
Jau	1	S	X	L	L	S		X
l_1	8	X	S	X		S		X
La	?	X	X	X	X		X	
mc	5	X	L	X	X		X	X
pr	1	L	S	L	S		X	X
r	3	X	X	X		X		
rv	?			X	X		X	
sf	?	X	X	X			X	
sy	3	X						
t	10	X	X	X			X	X
tf	5	X	X	X	X	X	X	X
u	10	X	X	X	X	X	X	X
w_4	4	S		X	X	X		L
wf	3	X	X	X	X		X	X
Wo^m	2	X	X	X	X			
y	1	L	X	X	L	X	X	
yv	6		X		X	X	X	X

Segregational data for linkages with Dr. Stubbe's mutants

Combination	++	+ t	m +	m t	Adj. cont. chi-square	Co.
imb-au	135	64	83	7	18.59	27.0
	374	85	115	17	1.90	44.0
	164	56	60	6	7.07	33.0
-pr	153	49	74	2	15.82	19.5
-y (rogued to imb)			185	27	6.44	40.5
inf-mc (partly rogued to inf)	29	17	23	0	9.40	0
inv-au	303	98	104	12	9.84	36.0
	170	58	36	10	0.12	
	282	100	77	11	6.68	37.0
-pr	115	42	56	2	12.74	21.0
	375	171	156	7	47.32	21.0
per-au	152	47	42	5	3.10	36.5
-y (rogued to per)			24	1	4.81	20.0
sub-a_1	288	127	110	6	29.79	23.0
-hl	296	119	103	13	12.33	34.0
si-cm	210	112	105	14	21.45	20.5
	381	168	250	20	53.75	27.32
-w_4	73	50	25	3	8.08	27.0
	327	213	88	0	45.83	0

Shapiro, N., and A. B. Burdick. Biochemical approaches to radiation damage in pollen.

We have assayed for amino acids and sugars using pollen from line 206 of L. pimpinellifolium. Through qualitative and quantitative analyses, we hope to relate our results with the effects of X-rays and hydration.

Several assay methods have been tried, and observations have been made on the ninhydrin-positive substances and sugar content of ungerminated and germinated pollen. The best method is as follows:

1. We grind 3 mg of pollen in sterile sand and make three 1 ml 80% ETOH extractions each followed by centrifugation and separation of the supernatant. This 3 ml of supernatant is then evaporated to 1 ml by heating slowly and blowing cool air across the surface. Various concentrations (lambda) of this 1 ml evaporate were spotted on chromatograms.

2. Pollen was germinated in 3 ml of a solution of 25% sucrose with 60 ppm of boron, and the sugar solution and pollen tubes were analyzed separately. We separated the grains and tubes from the solution by centrifugation. Grains and tubes were extracted with ETOH and analyzed as above. Sugar solutions were spotted directly on chromatograms.

3. The chromatograms were run 20-40 hours using a butanol-acetic acid-water (5-1-4) solvent, air dried and sprayed with ninhydrin or p-anisidine-HCl (for sugar analysis).

Ungerminated pollen extracts yielded five ninhydrin-positive substances and one sugar. Two of the ninhydrin-positive spots were identified as the amino acids asparagine and proline. Sucrose was identified as the single sugar.

During one of our experiments, ungerminated pollen of line 206 was compared with line 018 of L. esculentum. The latter line yielded three sugars and eight ninhydrin-positive spots.

After two hours of germination (line 206), asparagine and proline were absent. After seven hours, all ninhydrin-positive substances disappeared. At both two and seven hours of germination, three of the four sugars present on chromatograms were identified as sucrose, glucose and fructose.

The ninhydrin-positive determinations were possible only with the ETOH extracts. Recent work using the Yemm-Cocking method for determining amino nitrogen showed strong nitrogen activity in the sugar extracts and less in the alcohol extracts. This does not prove that the sugar-nitrogen activity comes solely from amino acids. It does, however, make less precise the appraisal of the total number of amino acids present.

Shapiro, N., and A. B. Burdick.
Frequency in seedling leaves of mottled sectors induced by irradiation of seed.

The results reported in this note were recorded in the course of an experiment on dry sensitivity and partial hydration protection (reported in TGC 13). The interpretations to follow may suffer in two ways because: 1) only two doses were compared and 2) dry seed at one dose was compared with hydrated seed at another dose. However, the results are compatible with those of Stein and Steffensen (Zeitschrift fur Vererbungslehre 90, 483-502, 1959), who showed that, following seed irradiation, the amount of genetic damage per unit dose (average number of yellow-green sectors per leaf) in somatic tissue of the corn plant was correlated with the position of the leaf on the plant. The average number of sectors per leaf in lower leaves increased with dose while the number in higher leaves did not.

By studying the distribution of plant color sectors on successively formed leaves one can reconstruct the developmental events within the apical meristem. We predict, from what is known of leaf histogenesis in monocots and perhaps dicots, that the earlier in ontogeny a mutation occurs the larger the sector will be. In the case of tomato, this could be expressed as sectors on several leaflets per leaf.

The conditions and results of our experiments were as follows:

1. Irradiation was given to md/+ seed. Seed was irradiated either as dry seed or after soaking in distilled water for 30 minutes at 0°C.
2. Totals of 4137 and 4195 seedlings were counted for the non-irradiated dry and the non-irradiated dry-wet series, respectively. No mottled mutations were noted.

3. Seed irradiated dry at 7500r yielded a ratio of mottled sectored seedlings to total seedlings of 81/10,442 ($7x10^{-3}$). Seed irradiated wet at 30,000r yielded 137 mottled sectored seedlings out of 10,800 ($12x10^{-3}$). The mottled mutation rates per r were $9.3x10^{-7}$ for the irradiated dry-wet treatment.

4. In few cases, sectors occurred bilaterally. This could imply a common origin of damage occurring quite early in the ontogeny of a leaf. Cell divisions of primordial cells carrying the same mutant and subsequent isolation of these cells on either side of the bilateral axis could explain these results.

5. The evidence in the table shows that leaves 1-3 increase in the number of sectored leaflets with an increase in dose; leaves 4-6 do not. There is a decrease in the frequency of sectored leaflets in leaves 4-6 with an increase in dose; while at the same time the total number of seedlings showing sectors is higher at the higher dose. These results may be explained if we assume that the cells were in meristematic condition when irradiated, and that those giving rise to early leaves had to go through fewer cell divisions than cells forming later leaves.

TABLE. Average number of leaflets per leaf (ratio)[1] with mutant sectors of mottled (md) after seed irradiation of md/+ heterozygotes.

Treatment[3]	Leaf number[2] 1	2	3	4	5	6
D(7500r)	1.00($^{2}/_{2}$)	1.20($^{12}/_{10}$)	1.47($^{25}/_{17}$)	1.79($^{50}/_{28}$)	1.80($^{27}/_{15}$)	2.12($^{17}/_{8}$)
D-W (30,000r)	1.64($^{18}/_{11}$)	1.67($^{15}/_{9}$)	1.85($^{37}/_{20}$)	1.74($^{75}/_{43}$)	1.67($^{50}/_{30}$)	1.94($^{35}/_{18}$)

[1]The total number of leaflets with a sector divided by the total number of sectored leaves. The primary leaf and secondary leaflets are considered as leaflets.

[2]Leaf numbering starts with the first true leaf.

[3]D = Dried over $CaCl_2$ for one day at 0°C followed by 7500r (25°C).
D-W = Dried over $CaCl_2$ for one day, then 1/2 hour soaked in distilled water at 0°C followed by 30,000r at 25°C.

Shapiro, N., and A. B. Burdick.

The effect of partial hydration on genetic response using X-irradiated tomato seed.

Problems of somatic-genetic and dry sensitive-partial hydration protection responses to mutagenic doses of irradiation have been studied.

Early evidence, using irradiated dry seed and seed irradiated after partial hydration, suggested a similar pattern of somatic and genetic response. That is, somatic (ability to germinate and produce surviving R_1 seedlings) and genetic (R_1 pollen abortion and R_2 mutations) responses showed a high sensitivity in dry and a high resistance in partially hydrated seed. These results suggested the use of multiple recessive heterozygotes and the hydration protection response in an "uncovering" experiment for mutations at specific loci.

The following irradiation induced mutations (netted (nd), mottled (md), yellow-green 3 (yg_3) and yellow green 6 (yg_6), and the spontaneous mutation (potato leaf (c)) were combined as follows:

1) c md/yg_3 nd, 2) md c/yg_3 yg_6, 3) c yg_3/md yg_6, 4) nd yg_3/md yg_6. Three thousand crosses yielded 36,000 F_1 seed.

Dry seed was irradiated with 7500r; wet seed 30,000r. The two doses gave similar somatic responses. Mutants yg_3 and yg_6 were not separable in seedling classification of "uncovered" mutant leaf sectors. The two mutants were, therefore, classified as yg.

The evidence presented in the table indicate the following:

1) Although mutation rates per treatment increase with a four fold increase in dose, the mutation rates per r are lower using a higher dose under D-W conditions. The mean induced mutation rates per r for md, yg_3 and yg_6 are, at D(7500), 1.1×10^{-6} for md and 4.1×10^{-7} for the two yg genes, and at D-W(30,000), 4.4×10^{-7} for md and 2.5×10^{-7} for the two yg's. This suggests the presence of some mechanism that affords protection or acts as a buffer against genetic injury when seed is irradiated under partially hydrated conditions.

TABLE. Number of R_1 seedlings recovered after treating multiple heterozygote tomato seed with X-rays and/or moisture.

Moisture (Dose, r)	Phenotype of R_1 seedlings			
	Normal	Sectored*	md**	yg***
D(o)[1]	4104	32	1	0
D-W(o)[2]	4179	16	0	0
D(7500)[3]	1431	8866 (1.1×10^{-4})[4]	81 (1.1×10^{-6})	64 (8.2×10^{-7})
D-W(30,000)	247	10,253 (0.3×10^{-4})	143 (4.4×10^{-7})	163 (5.0×10^{-7})

[1]Dried over $CaCl_2$ for one day at 0°C.

[2]Dried over $CaCl_2$ for one day followed by 1/2 hour soak in distilled water at 0°C.

[3]X-irradiation (25°C) followed moisture treatments. All seeds were sealed in plastic bags after D, D-W and during irradiation.

[4]Frequency of affected seedlings less controls divided by the dose.

*Leaf sectors of light green tissue surrounded by normal tissue.
**Leaf sectors of yellow-green tissue surrounded by normal tissue.
***Leaf sectors of yellow tissue surrounded by normal tissue.

Shapiro, N., and A. B. Burdick.

Effects of X-ray on the frequency of mutations in hydrated wild-type pollen.

I. Analysis of R_1 data. A single, uniform pollen producing line 206, L. pimpinellifolium, was used. Fresh pollen composited from plants grown under controlled conditions was used as controls or dried over $CaCl_2$ (10-15% RH) in open gelatin capsules for 24 hours at 25°C or 0°C. Pollen samples, following drying, were hydrated over water, capped and irradiated. Pollinations were made using line 206 unirradiated flowers as females.

The R_1 data (see table) suggest the following:

1) The LD_{50} of pollen irradiated at 25°C, based on average seed set per fruit, is below 500r for D and a little above 1000r for D-W. The LD_{50} of pollen irradiated at 0°C is between 500r and 1000r for D and above 2000r for D-W.

2) Seed germination and pollen fertility of the R_1 show a decrease resulting from dry pollen irradiation at 25°C. At 0°C, there is a decrease in germination using 2000r and a decrease in pollen fertility using 1000r and 2000r.

3) When R_1 pollen fertility is broken down into 5 fertility classes (0-20% etc.), there is a decrease in the frequency of types with high fertility among the irradiated-dry progeny and an increase in such types among the irradiated-wet progeny.

4) Statistical analysis of the mutation data has not been made. However, there is a tendency for a higher percent of dominant mutations to be associated with the irradiated D and D-W pollen treatments. The average percent change is somewhat larger in the former treatment.

5) Seventy-one R_1 mutants have been classified according to phenotype and percent fertile pollen. There are 33 morphological mutants and 5 chlorophyll mutants classified as having high fertility (80% or above). The number of low fertility mutants (50% or below) which show changes in morphology, or chlorophyll, or both are 13, 7, and 13, respectively.

Pollen[1] treatment	Av. seed set per fruit	% germ.[2] of R_1 seed 25°C	Av. %[3] "Dominant mutations"	Av. % R_1 pollen[4] fertility
Control	20	95	1.31(5/379)	87
D	22	72	2.44(7/286)	79
D-W	25	62	2.85(7/245)	74
500r	21	86	1.74(6/343)	80
D(500r)	4	67	4.08(4/98)	69
D-W(500r)	17	88	3.07(6/195)	81
1000r	20	82	1.83(6/326)	87
D(1000r)	2	70	7.14(2/28)	78
D-W(1000r)	13	91	4.00(10/249)	83

Pollen[1] treatment	Av. seed set per fruit	% germ.[2] of R_1 seed 0°C	Av. %[3] "Dominant mutations"	Av. % R_1 pollen[4] fertility
D	27	78	3.20(10/312)	85
D-W	25	63	2.81(4/142)	87
D(500r)	21	97	0.68(1/145)	74
D-W(500r)	20	94	-	79
D(1000r)	9	85	4.92(12/243)	76
D-W(1000r)	24	88	2.82(10/354	85
D(2000r)	4	64	4.10(3/73)	67
D-W(2000r)	21	89	3.33(12/359)	81

[1]Dried over $CaCl_2$ for one day followed by humidification (W) for 1/2 hour at 25°C and 3 hours at 0°C. Irradiation followed the D and D-W treatments.

[2]A maximum of 400 R_1 seeds were planted in green house flats.

[3]Total number of mutant seedlings divided by total number of seedlings.

[4]Based on a maximum of 100 plants per treatment, 1 to 2 flowers per plant and 100 grains per flower.

II. Partial analysis of R_2 data.

A maximum of 100 R_1 seedlings per treatment were field grown during the summer of 1962. Ripe fruits of the first two inflorescences were harvested and the seed bulked. R_2 seedling mutations recovered from R_1 plants were noted. A summary of the data is given below:

Pollen treatment at 25°C	Number R_1 families[1]	% families segregating for mutations[1]
Control	100	3.
D	97	5.
D-W	97	4.
500r	100	3.
D(500r)	90	20.
D-W(500r)	98	5.
1000r	97	4.
D(1000r)	28	14.
D-W(1000r)	99	5.

[1]Mutations include lethals, leaf sectored seedlings, yellow green or light green cotyledons, or leaves, or both, and morphological mutations.

These data show that a high percent of the R_1 families segregating for mutations results from pollen irradiated dry.

The evidence suggests that pre-irradiation dry and wet pollen treatments cause different radiation damage.

Gröber, K. Genetical and physiological behaviour of a dominant chlorophyll mutant of the tomato. (Submitted by H. Stubbe)

X-irradiation of the variety "Condine Red" induced a mutant showing a segregation of 12 yellow, 24 yellowish-green and 35 normal green seedlings. The yellow seedlings were unable to live longer than 8-10 days after germination, but the yellowish-green seedlings proved able to grow as fast as the normal green sister-plants under favourable conditions. From this a dominant mutation with recessive lethal effect can be inferred. The mutant is identical with the mutant "Xanthophyllic$_1$" described by Butler and Chang (Can. J. Bot. 36, 1958) as far as the genetical behaviour is concerned and is symbolized with $\underline{Xa}_3$.

Analyses done later using larger seed material gave an unequivocal segregation ratio (table 1). Although the total number with P = 0.006 did not fit with the expected 1:2:1 segregation ratio, it is clear from the table that the difference is brought about only by the progeny of 1961. A similar deficit of yellow seedlings could be found also in the seeds harvested from the field in 1962. The summer was rather cool in 1961 as well as 1962 giving rather bad vegetation conditions for tomatoes.

A fundamental difference in the reaction to the growth factor light is evident for $\underline{Xa}_1$ on the one hand and $\underline{Xa}_3$ on the other. In contrast with the American type, our heterozygote tends to become green in midsummer. In extreme cases--growing with high light intensity and good temperature as well as food conditions--the heterozygote type cannot be distinguished from the homozygote recessive.

Table 1. Monogenic segregation in seeds, harvested in three different years.

Number	Seed quantity	Xa Xa yellow	Xa xa yellowish green	xa xa green	Average germination %	Chi^2	P for expectation 1:2:1
1186/59	200	52	99	39	95.00	2.12	0.34
249/60	400	86	186	103	93.75	1.56	0.44
224/61	300	30	160	75	88.33	26.85	$10^{-5}>P>10^{-6}$
	900	168	445	217	92.22	10.12	0.006
59 and 60 group only	600	138	285	142	94.17	0.10	0.75

Gröber, K. Green and yellow leaf-spotting of a yellowish-green shoot of the heterozygous chlorophyll mutation "$\underline{Xa}_3$" induced by X-irradiation.

Following X-irradiation of $\underline{Xa}_3\underline{xa}$ seeds, the X_1-plants H 189/1 and H 190/1 showed different types of shoots. Some branches were characterized by pure yellow as well as normal green spots on the yellowish-green leaves typical for the heterozygous plants. From both plants, 7 shoots

were grown. From these, 4 showed leaf-spotting in plant H 190/1, and the others were yellowish-green. Plant H 198/1 had a different and remarkable phenotype. Here 3 yellowish-green branches showed green and yellow leaf spotting, and the other 4 branches were normal green without spotting. The green colour of the branches without spots was identical with the pigmentation of "Condine Red"; the yellowish-green colour of the variegated branches was identical with the pigmentation of heterozygous control plants under the same environmental conditions.

Some details in connection with distribution and frequency of leaf spots from four different leaves of a variegated shoot are shown in table 1. The relation between yellow and green spots is in favour of the yellow ones. Generally the yellow spots are not only more frequent but also larger.

The variegated branches are characterized cytologically by a small fragment besides the 12 chromosome pairs in metaphase I. By the existence of a heteromorphic bivalent, it is clear that it is not an extra fragment but a piece of one of the normal chromosomes being reduced in size. The absence of the fragment in somatic tissue is followed by the complete bleaching of the cells manifested in the form of a yellow spot on yellowish-green ground. From the size and frequency of these spots in relation to the green ones, it can be concluded that the chromosome bearing the recessive allele is fragmented and the xa-locus localized on the fragment.

On the other hand the fragment in green cells was approximately double in size. Accordingly there seems to be a dosage effect in so far as two xa-alleles are compensating the effect of one Xa_3. The same effect is likely to be at work in the 4 green branches of plant H 189/1. But in this case it is not clear up to now what kind of mechanism is responsible for the stabilisation. Possibly the origin of an isochromosome in the initial cell of the 4 branches is connected with this effect.

The F_1 of the cross "tetraploid variety" (xaxa xaxa) x Xa_3xa was produced giving the possibility for testing the existence of dosage-effects for this gene. In contrast to expectation, only one of 23 F_1-plants is yellowish-green coloured.

Table 1. Comparison of the number of spots including yellow, green and twin-spots.

Leaf	Colour of spots		Twin spots	Ratio of green spots/yellow spots
	Yellow	Green		
A	1617	4	553	0.148
B	342	31	473	0.462
C	759	17	1315	0.476
D	614	2	769	0.387
	3332	54	3110	

Gröber, K. Connections between sample size and goodness of fit in case of a 3:1 segregation ratio of 7 chlorophyll mutations of the tomato.

Segregation analyses were done of 7 further recessive chlorophyll mutations of variety "Condine Red" from the Gatersleben sortiment (Table 1). Four of these independently arisen mutations have been called "xantha" because of their golden cotyledons; three further mutations are characterized by white and cream seed-leaves, thus belonging to the type "albina". $\underline{Xan}_{1-4}$ as well as $\underline{alb}_{1-3}$ are lethal under normal environmental conditions, although the effective lethal phases are quite different.

It is clear from the P-values found that the sample size is greatly influencing the goodness of fit with segregation values expected theoretically. Only in the case of $\underline{alb}_1$ nc statistically significant difference was found using the smallest P-value. But the general trend is unequivocal here also. From these findings some consequences are to be concluded which are of interest from a genetical, physiological and statistical point of view.

Table 1

Mutation	Observed Green	Observed Pale	Percent germination	Expected Green	Expected Pale	Chi square	P
xan_1	154	44	99.00	148.50	49.50	0.82	0.36
	1212	344	97.25	1167.00	389.00	0.94	0.008
	8284	2039	93.85	7742.25	2580.75	151.63	$<10^{-10}$
xan_2	150	46	98.00	147.00	49.00	0.25	0.62
	2557	789	98.41	2509.50	836.50	3.60	0.06
	24155	7619	96.87	23830.50	7943.50	17.67	0.00003
xan_3	163	28	95.50	143.25	47.75	10.89	0.001
	1846	272	96.27	1588.50	529.50	16.70	0.00005
	6987	1125	94.33	6084.00	2028.00	536.10	$<10^{-10}$
xan_4	144	56	100.00	150.00	50.00	0.96	0.32
	1211	358	98.06	1176.75	392.25	3.99	0.045
	4292	1193	94.57	4113.75	1371.25	30.91	$<10^{-7}$
alb_1	149	46	97.50	146.25	48.75	0.21	0.65
	715	218	93.30	699.75	233.25	1.33	0.25
	2705	853	88.95	2668.50	889.50	1.85	0.18
alb_2	140	42	91.00	136.50	45.50	0.36	0.55
	1683	481	98.36	1623.00	541.00	8.87	0.003
	3669	1028	97.85	3522.75	1174.25	12.95	0.00035
alb_3	151	44	97.50	146.25	48.75	0.62	0.43
	1249	361	89.44	1207.50	402.50	5.71	0.016
	3500	1020	94.17	3390.00	1130.00	14.28	0.00015

PART II

ADDITIONS AND CORRECTIONS TO LIST OF MEMBERS

(Last complete list issued in TGC 12)

Abdel-Al, Zidan, Department of Plant Production, College of Agriculture, Alexandria University, Alexandria, U.A.R.
Abe, Isamu, Morioka Branch, Horticultural Research Station, Shimokuriyagawa, Morioka, Japan
D'Amato, F., Instituto di Genetica, della Universita, Via del Borghetto, 35, Pisa, Italy
Andersen, W. R., Department of Vegetable Crops, University of California, Davis, California
Andras, Andrasvalvy, Tigris-utca 33, Budapest I, Hungary
Barnes, G. S. C., Box 173, Aguirre, Puerto Rico
Bell, William D., Department of Botany, Pennsylvania State University, University Park, Pennsylvania
Berry, Stanley, 1302 Oak Avenue, Davis, California
Bishop, Charles J., Program Directorate, Research Branch, Canada Department of Agriculture, Central Experimental Farm, Ottawa, Canada
Böklin, Åke, Caixa Postal 673, Campinas, S.P., Brazil
Boynton, John E., Department of Vegetable Crops, University of California, Davis, California
Brauer, Oscar, Colegio de Post-Graduados, Chapingo, Mexico
Broertjes, C., Tomato Mutation Breeding Group, Institute for Atomic Sciences, Postbus 48, Wageningen, Netherlands
Canada Department of Agriculture, Smithfield Experimental Farm, Research Branch, RR #4, Trenton, Ontario, Canada
Clark, Raymond L., U.S.D.A., A.R.S., Irrigation Experiment Station, Prosser, Washington
Colorado State University, The Libraries, Fort Collins, Colorado
Cottrell-Dormer, W., 71 Dell Road, Sta. Lucia, Brisbane, Australia
Frankel, Rafael, Agricultural Experiment Station, Bet Dagan, Israel
Freeman, J. E., Corn Products Company, P. O. Box 345, Argo, Illinois
Griffing, J. B., C.S.I.R.O., Canberra, Australia
Hardin, M., Box 351, Geary, Oklahoma
Hernandez Bravo, Guillermo, Department of Vegetable Crops, University of California, Davis, California
Hikida, H. R., Campbell Soup Co., Ltd., RR 6, Brampton, Ontario, Canada
Hirzel, R. W., Hirzel Canning Company, 411 Lemoyne Rd. at Woodville Rd., Toledo 5, Ohio
Howard, Gene S., Cheyenne Horticultural Field Station, Box 1250, Cheyenne, Wyoming
Kalia, Het Ram, Government Agricultural College, Leudhiana Punjab, India
Kyle, Jack H., Texas Agricultural Experiment Station, R.F.D. No. 3, Lubbock, Texas
Kim, Dwang Woo, Seoul Branch, National Institute of Horticulture, 43-1 Hikyong-Dong, Dongdaemoon-ku, Seoul, Korea
Lona, Jorge L., Estacion Exp. Agrop., Casilla 8 La Consulta, Mendoza, Argentina

Machado Tschusi, Eugenio, Estacion Experimental de Horticultura y Jard., Santa Cruz de Tenerife, Canary Island, Spain
Mandic, Ing. Slobodan, Institut za Povrtarstvo, Smederevska, Palanka, Jugoslavia
Menzel, Margaret Y., Department of Biological Science, Florida State University, Tallahassee, Florida
Moore, John F., Campbell Soup Co., Ltd., RR 6, Brampton, Ontario, Canada
Nassar, Sayed Hassan, Department of Horticulture, Louisiana State University, Baton Rouge 3, Louisiana
National Institute of Genetics, Yata IIII, Misima, Japan
Piovano, Abelardo, Via Posillipo 168-A, Naples, Italy
Platt, Ruth E., Western Washington State College, Bellingham, Washington
Pratt, David, Department of Bacteriology, University of Wisconsin, Madison 6, Wisconsin
Retig, Nira, Department of Field & Vegetable Crops, Hebrew University, P. O. Box 12, Rehovot, Israel
Richardson, Jr., R. W., Rockefeller Foundation, 49W 49th Street, New York 20, New York
Rumsey, Anthony E., Rumsey Seeds Pty. Ltd., 331 Church Street, Parramatta, N.S.W., Australia
Scowcroft, William R., Department of Agronomy, University of California, Davis, California
Stall, R. E., Indian River Field Laboratory, P. O. Box 1351, Ft. Pierce, Florida
Stubbe, Hans, Institut für Kulturpflanzenforschung, Gatersleben/Kreis Aschersleben, Germany
Tomes, M. L., Department of Botany and Plant Pathology, Purdue University, Lafayette, Indiana
Webb, Raymon E., Vegetables & Ornamentals Branch, Agricultural Research Service, U. S. Department of Agriculture, Beltsville, Maryland
Williams, Watkin, University School of Agriculture, King's College, Newcastle upon Tyne, England
Wittmeyer, E. C., Ohio State University, 1827 Neil Avenue, Columbus 10, Ohio
van Zanten, Jasper E. V., N. V. Sluis en Groot's Koninklijke, Zaadteelt en Zaadhandel, Enkhuizen, Netherlands

PART III

LIST OF AVAILABLE OR DESIRED STOCKS

STOCKS AVAILABLE

Andrus, C. F.

3238 *L. esculentum* homozygous for brittle-stem sub-lethal.

Bergh, B. O.

Twelve induced mutants affecting fruit size and shape reported in recent years by Hans Stubbe of Germany--seed of each in limited number.

Bohn, G. W.

Testers for chromosome 3 -- ms_9-r, wf-r.

Burdick, A. B.

001 2n Ex-Haploid D-y DBL_4
006 2n Ex-Haploid d_1 DBL_7 Lindstrom 1940
038 Agadir Cherry 4 gm. Fruit semi-wild from Morocco, F.A.

179 San Marzano aa?
206 2n Ex-Haploid pimpinellifolium DBL_3
216 4n Ex-Haploid pimpinellifolium DBL_3

240 Rosette-type
371 nd e Wo H
372 nd e Wo h
373 nd e H
376 af d c
377 af l
378 yc nd
379 yc md
380 af nd
381 af md
384 af d c l
387 nd md
425 nd yc af
467 nd ag l
470 nd md af

472 nd md yc
479 nd h Wo wf
487 nd ye
495 nd ag
421 md c
426 md yc af
446 md a hl j
486 md yc ye
488 md pl
490 md ye
492 md yo
455 ye d
456 ye c
489 ye yo
428 sy d c u

458 sy H u
459 sy d c
471 yo yc
493 yo pl
496 yo li
448 pt e H
461 pt d c H l
469 yc li
475 pg al wt
457 ae H l
465 ao d c H l
463 gl e
466 d_2 c H l
474 md c H

Ciccarone, A.

A stock of seeds of the tomato variety "Quarantino" (actually it is a population) which seems to be resistant to Sclerotium Rolfsii Sacc.

Denby, L. G.

Verticillium-resistant Ve Ve strains of the following established varieties. (Resistance from the variety Loran Blood, supplied by Dr. O. S. Cannon).

Ace
Bonny Best
Bounty
Break o' Day
Clark's Early (Dohler #7)
Earliest of All
Early Baltimore
Early Chatham
Early Harkness
Early Jersey
Early Lethbridge
Farthest North
Fireball
Firesteel
Geneva #6
Harris Gem
John Baer
Longred
Manasota
Marmande
Meteor
Morses 498
Non-acid

Pennheart	Sioux	Valiant
Pritchard	Speed	Valnorth
Puck	Splendid	Victor
Red Chief	Stokesdale #4	Wasatch
Red Cloud	Sugawara	Windowbox
Red Jacket	Summerland Gem	Wisconsin 55
Rutgers	Superior	Wisconsin (James)
Signet		

Frazier, W. A.

Various crack-resistant lines; early to medium early determinate lines with concentrated fruit set, fair crack resistance; early dwarf lines; fleshy (fl) calyx lines.

Gilbert, J. C.

Anahu - large fruited root knot resistant line. Also resistant to Stemphylium solani, Fusarium wilt and spotted wilt virus in Hawaii.

As spsp uu line with proven combining ability in F_1 hybrids (STEP trial results of 1959, 60, 61) in southern areas.

Fruitful lines combining resistance to tobacco mosaic virus, common races of root knot nematodes, Fusarium wilt, and Stemphylium solani. Adapted to southern latitudes.

Harrison, A. L.

Stocks available for exchange that carry combined resistance to fusarium wilt, collar rot and root knot. However, there is still some question as to whether these breeding stocks are resistant to all species of root knot nematode, although they are highly resistant to the species we have in this part of Texas.

Jenkins, J. A.

170	d_1 r y c a l_1	378	d_1-p-o-s r
171	d_1 f-j_1-lf-wt H al	767	br c j-lf-wt
234	d_1 c l_1 u-H dm	523	y at
		1504	La/La+

Kedar, N.

Low bushy lines with very short internodes, determinate or indeterminate, resistant to Fusarium wilt. Fruits globular or fasciated. (see Research Note in TGC 13).

Fusarium resistant high pigment (hp hp) lines. Plants determinate, fruits oblate, beaked or globular.

Kerr, E. A.

r-wf c-sp u
br wf c-sp n u f-j

Cf_1, Cf_2, Cf_3 and several other stocks with resistance to Cladosporium fulvum.

gf_1, l_2, and ls in combination with several other genes.

Lyall, L. H.

sl Stamenless stock available in limited quantity.

Martin, F. W.

Tiny Tim segregating 3:1 for self-fertility versus self-incompatibility. These lines have originated through 3 to 10 backcrosses from L. chilense or L. hirsutum.

Martin, M. W.

Loran Blood VeVe with Sp (Phytopath. 41: 986-990).
VR Moscow VeVe with sp
Some stocks partially resistant to curly top virus.

Peirce, L. C.

404 A-62-1 Sundwarf, determinate, uniform ripening (u), still segregating for resistance to fusarium wilt, small fruit size, prolific.

Piovano, A.

Determinate paste type tomato: San Pablo; CIRIO 49; San Marzano Chico.
Indeterminate paste type tomato: SMBI.4A; SMB.4B.

Rick, C. M.

2-72 Autodiploid San Marzano
2-95 4N San Marzano
2-227 4N Pearson

LA319 $\underline{ms}_{17}$ $\underline{Wo^m}$ $\underline{d}_1$ LA291 $\underline{ms}_2$ $\underline{a}$ $\underline{hl}$
LA321 $\underline{ms}_{17}$ $\underline{a}$ $\underline{d}_1$ $\underline{c}$ $\underline{l}_1$

Stocks of newly synthesized linkage testers (see Research Note in this report).

Stocks of various species of Lycopersicon and closely related species of Solanum.

Stocks of the primary trisomics can be supplied in limited quantity. Seed transmission is so poor in some that they must be sent as cuttings.

Clones of the following items are available. Cuttings are taken in May or later.

4-47 F_1 L. esculentum x S. lycopersicoides
4-2, 4-3 F_1 L. esculentum x L. chilense

Robinson, R. W.

ah-wd, nv-Tm_2

Skirdla, W.
Plant Introduction Station, Iowa State College, Ames, Iowa

Extensive tomato accessions of the Division of Plant Exploration and Introduction are maintained. The collections include species, species hybrids, and many lines of L. esculentum including some genetic marker strains.

Snoad, B.
(John Innes Inst.)

Tomato Translocations - The cytological identification of the chromosomes is not guaranteed in all cases.

a) Suttons Best of All selfed with irradiated pollen (4,000r):

T2 - 7	T7 - 11	T9 - 12
T3 - 9	T3 - 5	T5 - 7
T3 - 7	T4 - 9	T3 - 8
T7 - 11	T3 - 7	One unidentified
T3 - 12	T2 - 12	translocation
T2 - 9	T7 - 9	

b) d.p.o.s.r.y. x SBOA (after 4,000r to pollen):

06 (C2)	T2 - ?
06 (C2)	T2 - ?
	T1 - 2
T2 - 9	T2 - 9
T2 - 11	

c) Valiant selfed with irradiated pollen (4,000r):
T6 - 12
T2 - 4
Five unidentified translocations

d) d.aw.ps.o.a.y x 4,000r San Marzano O:
One unidentified translocation (not C2)

e) d.aw.ps x 4,000r San Marzano o:
T2 - ?

Tezier, C.

Varieties with medium-size fruits	Marmande, 1/2 lisse d'Alger, Hyb. F_1 TF60, Merveille des marches
Varieties with large fruits	Saint Pierre, Ballon Rouge

Thompson, A. E.

30-2-55	high pigment, determinate heavy set, green shoulders (u^+u^+?)
32-19-55	high pigment, determinate, heavy set, uniform color (u u ?) +/ab albescent

Young, P. A.

W935, 1482	wf, white flower.
G1074	Xa, Xantha.
S1447	Luxuriant cherry tomato that sets fruits in hot weather.
G1075, G1451, We, c	Wc, Woolly or Angora tomatoes.
G328, G912	pe, lg, vi, genes linked in group VII.
G1215, G1319	L. humboldtii, yellow cherry tomato with characteristic leaf type.
G1391	Pink gold tomato.
G1666, G1729	Cu, Curl or stick tomato.
G1105, G1128	wf wf/y y double recessive crossover; large, white flowers.
G1129, G1465	Protruding carpels on fruits.
G1458, G1738	Fruits ripen from green to yellow to orange to partly red as they become soft; unlike other tomatoes; red color in peel.
G2157, G2158	Smudge

STOCKS DESIRED

Alexander, L. J. Members are invited to send their exchange stocks to Dr. Alexander for screening by pathologists for disease resistance.

Bergh, B. O.

1. Lines that are s or bk, but not both.
2. Lines that are f or bi, but not both.
3. Any new genes linked with a.
4. Any new genes affecting fruit size and shape.

Currence, T. M.	Stocks earlier than Farthest North with fruit size equal to Farthest North. Lines known to transmit high yield, earliness, and large fruit; i.e., high in general combining ability for the combination of these three characteristics. Self pruning plant with beta orange fruit color, sp sp B B.
Frazier, W. A.	Early, determinate, crack-resistant material; early, deep red color lines; early lines resistant to fusarium, verticillium, phytophthora; combinations of genes conditioning these characters.
Hafen, L.	Breeding lines resistant to mosaic, lines resistant to cracking.
Harrison, A. L.	Breeding lines that carry resistance to any of the various types of mosaic.
Honma, S.	Breeding lines that carry resistance to any of the varied types of mosaic.
Johnson, K. W.	Seed stock having the following characteristics. 1. High pigment genes, either ph_1 or ph_2. 2. Any of the various dwarf genes.
Pearson, O. H.	Lines that have little or no gelatinous matter surrounding seeds.
Piovano, A. P.	Lines of determinate, paste type tomato. Lines with nematode resistance.
Pollack, B. L.	Any line that shows some degree of resistance to "gray wall."
Reynard, G. B.	u_2u_2 (u_gu_g) Any types with extra dark green unripe fruit.
Rick, C. M.	Any line that is jointless but not leafy (j-lf+).
Smith, J. J.	Stocks resistant to anthracnose.
Tezier, C.	Early dwarf lines that can be cultivated without staking. Lines resistant to radial and concentric cracking. Very early lines with medium fruit size. Lines resistant to Phytophthora infestans. Lines rich in dry weight and with good color for processing.
Williams, W.	List of tomato mutants wanted for stock blu M345 nd sl3 sl4

PART IV

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PART V

FINANCIAL STATEMENT

(to December 31, 1962)

		Total
Balance from 1961		$298.16
Receipts		
Assessments	$151.00	
Sale of back numbers	85.00	
Interest on savings	9.50	245.50
Assets		543.66
Expenditures		
TGC Report No. 12, 1962		
Multilithing and covers	192.50	
Stencils, envelopes, and clasps	17.50	
Postage	31.35	
Miscellaneous		
Postage for meeting notice	4.50	
Postage for newsletter	15.57	261.42
Balance		$282.24

MEMBERSHIP STATUS

Assessments paid for 1962	41
1963	147
1964	46
1965	15
1966	9
1967	3
1968	1
1970	1
Total members	263