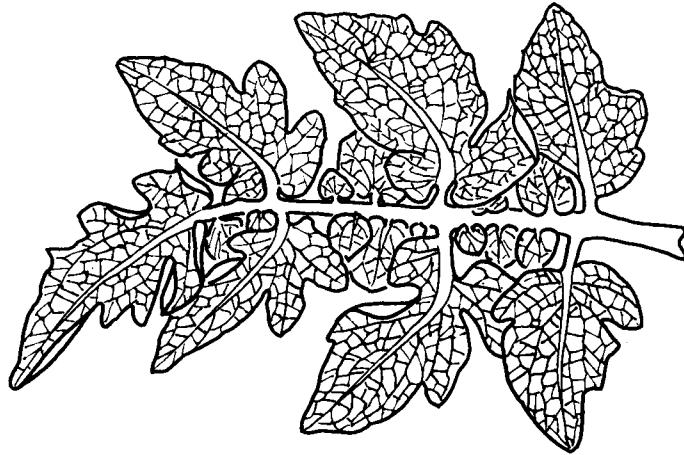


REPORT
of the
TOMATO GENETICS
COOPERATIVE



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DEPARTMENT OF VEGETABLE CROPS
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This report is a medium of exchange among members of information and stock relating to tomato genetics. None of the information herein may be used in publications without consent of the respective authors.

FOREWORD

The Tomato Genetics Cooperative is a group of workers who have a common interest in tomato genetics and who are organized informally for the purpose of exchanging information and stocks. Participation is voluntary, and costs of activities are met by assessments to members.

Membership as of December 31, 1968 stood at 321. It is interesting to note that the enrollment of foreign members has increased to 163, now constituting the majority (50.7%) of our membership. Our financial situation has improved, thanks largely to the increase in membership assessments that took effect last year. At the end of 1968 the financial balance was \$358.51.

The regular annual meeting was held under the auspices of the American Society for Horticultural Science at Davis, California on August 19, 1968. Minutes appear on this page. Arrangements have been completed and notices sent for the 1969 meeting to be held with the Tomato Breeders Round Table in Denver, Colorado on February 20. The current tendency toward splintering the AIBS convention into separate meetings of the member societies diminishes the opportunity for holding our annual session with a national meeting attended by a good cross section of our membership. Our present policy is to rotate TGC meetings among the societies in which most of our membership is represented.

We are deeply grateful to several workers whose assistance was essential for progress of the TGC during the past year. Dora Hunt again shouldered a major share of the operations. As Executive Secretary, she was in charge of all membership affairs, and, as Editor, she skillfully compiled the bibliography and revisions of the membership list, prepared the financial statement, and edited all copy for TGC 19. Virginia Vanderhoff was responsible for the masterful job of typing the stencils. Many other willing workers assembled the Report and assisted with other details.

Five hundred copies of this Report have been issued.

Coordinating Committee

L. Butler	C. M. Rick, Chairman
G. B. Reynard	Department of Vegetable Crops
R. W. Robinson	University of California
M. L. Tomes	Davis, California 95616

MINUTES OF THE DAVIS MEETING

August 19, 1968

The annual meeting of the TGC was held in Room 1066 Engineering Building on the Davis campus of the University of California in conjunction with the national meeting of the American Society for Horticultural Science.

Chairman C. M. Rick called the meeting to order. The question of where and with what society future meetings will be held was brought up, but no decisions were made at this time. Membership was reported to be well over 300 and the financial balance, \$208.

Shig Honma introduced a brief discussion about classifying mutants according to plant parts affected. No published work has appeared. C. M. Rick suggested classification might be done conveniently in a table.

An unsolved problem was laid before the group—the proposal to put mutants in a common genetic background. The difficult hurdle is finding a genotype that is universally satisfactory. No one offered his favorite variety, so no debate ensued, and the meeting adjourned.

D. G. Hunt, Secretary, pro tem

PART IRESEARCH NOTES

Butler, L. A partial map of chromosome 2.

The three-point data given in my note on coincidence and recombination values can be used to confirm the linear order and map distances for eight of the genes in this group. In view of the marked differences of the recombination values for the aw - d section, it is necessary to accept one value as standard. The crosses made to 706 sel. d p o s bk gave recombination values near 10% for this section, and this will be adopted as standard for the present. Applying this standard, then the cross Wo aw d must be discarded because its 22.3% puts it into a different class. The genes Wo Cu and Me are close together and within 6 units of wv in contrast to the 15 units found in other crosses. The two values for the cross Wo m d are much too large, giving a total distance of 40.1% instead of 29.3% as in the other cross. There is some doubt about the position of dil, but most of the evidence indicates that it is between Me and aw. It does not seem worthwhile to turn these recombination units into map units until we can refer all values to the "standard" background, or some other background. In the meantime we can hypothesize that the background genes controlling recombination are affecting the whole chromosome in the same manner, and that, if we select for the minimum values in each case, we are mapping one end of the spectrum which we can designate standard. The order and standard values are given below.

5.0	9.5	11.8	
wv 3.1 Wo 3.2 Cu Me	10 dil	aw 9.2 suf	d

Butler, L. Recombination and coincidence in chromosome 2.

Examination of the accumulated linkage data reveals significant heterogeneity. The recombination values depend on the genetic background. We are now beginning to place the genes on a uniform genetic background, but it will be several years before data are available from this source. In the meantime, some of the best data available are given by the three-point backcrosses listed below. The recombination values obtained map fairly consistently except in the case of dil, which gives larger values for the distances Me dil and d dil than are expected. The coincidence values show that recombination in one region does interfere with recombination in the adjacent region. There are two cases of significant positive interference. In the one case this is probably because of the difficulty of classification of mottled, but the other case needs further investigation. The column headings a_1 and a_2 refer to recombinants in regions 1 and 2. The headings p_1 and p_2 refer to recombination percentage in regions 1 and 2.

Genes	a ₁	a ₂	a _{1,2}	N	C	P ₁	P ₂
wv-aw-d	84	76	4	659	0.37	13.3	12.1
wv-aw-d	710	527	71	5194	0.99	15.0	11.5
wv-Me-aw	44	107	9	1260	1.80	4.2	9.2
wv-Me-aw	186	563	32	5194	1.28	4.2	11.5
wv-Me-d	21	135	7	488	0.86	5.7	29.0
wv-Me-d	164	1090	54	5194	1.56	4.2	22.0
Wo-aw-suf	30	22	1	291	0.41	10.6	7.9
Wo-aw-d	23	45	6	229	0.92	12.7	22.3
Wo-Me-d	41	189	9	843	0.77	5.9	23.4
Wo-dil-d	20	65	6	368	1.20	7.0	19.2
Wo-Me-dil	7	24	1	230	1.15	3.5	10.9
Wo-m-d	161	59	12	609	0.59	28.5	11.6
Me-aw-d	63	78	2	659	0.25	9.8	12.1
Me-dil-d	41	54	10	349	1.07	14.6	18.3
Cu-aw-suf	35	55	3	502	0.68	7.5	11.5

Butler, L. The interaction of rosette (ro) and white virescent (wv).

Linkage studies indicated that ro and wv were not closely linked, but it seemed impossible to

recover ro wv segregates from repulsion crosses. A number of these F₂ plants which were wv were grown and seed collected. Several of these wv plants were heterozygous for ro, but the ro segregates did not show virescence. Four-week-old ro plants were transplanted and grew very slowly because of their poor root development. At seven weeks they showed typical wv characteristics. Previous ro plants which had grown for three months failed to show any wv segregates. It is suggested that the leaves of the non-transplanted wv ro do not become virescent.

Butler, L. The linkage of gf and al.

In 1960 I was working with a fruit color modifier which I had obtained from Philippine tomato stocks.

This gene was called "muddy fruit color." Subsequently, E. A. Kerr showed it to be identical with gf. A large backcross was grown which was homogeneous and gave excellent monogenic ratios. The data were:

Al Gf	Al gf	al Gf	al gf
36	880	856	34

These data give a recombination value of 3.8%, which is significantly different from the map distance of 23%. Perhaps the identity of these genes should be rechecked.

Contant, R. B., and K. Verkerk
Confusion in fruit shape terminology.

On the terminology of fruit shape there seems to be some confusion.

The fruit shape of the obl mutant (TGC 17:56-58 and TGC 18:42-43) was called "oblate" in agreement with Butler's description of the fruit shape resulting from o (J. Hered. 43:25-35; 1952). The same term is used extensively for fruit types with a ratio of polar to

equatorial diameters of less than 0.95 (cf. Zielinski in Genetics 33:405-428; 1948). Strictly speaking, "oblate," meaning "flattened at the poles," does not define the length/width ratio of a fruit. Therefore, this term is inadequate for describing the fruit shape of the obl mutant and also seems incorrect for denoting a fruit that is shorter than its width, unless it is agreed that this term replaces correct descriptions such as "oblate-spherical" or "oblate-spheroid." An elongated fruit may be correctly called "elongate(d)," "ellipsoidal," "ovoid," possibly "ovate." However, there is also difficulty in finding suitable terms to distinguish clearly a strongly elongated shape with flattened poles such as obl from a smooth ellipsoid type. The obl mutant would be well described as having an oblong longitudinal cross-section.

We welcome a glossary of fruit shape terms which would facilitate classification in genetical studies and the assignment of gene symbols.

Contant, R. B., and K. Verkerk
Development of selection and breeding methods adapted to irradiated plant populations.

The potential use of mutation induction for the improvement of quantitative traits cannot be evaluated properly without knowledge of optimal procedures

of selection and breeding in mutagen-treated material. This problem is studied in tomato by comparing the advance under selection for earliness and yielding capacity in three different groups of M_2 material derived from seed irradiation treatments: (1) "major" mutants of approximately normal vigor and good fertility; (2) normal appearing plants in the same progenies as (1); (3) plants selected from non-segregating progenies obtained from the same mutagenic treatments; and (4) plants selected from the unirradiated control.

The possible importance of group (1) is suggested by the following considerations: (a) certain "major" mutations may by themselves confer improvements in quantitative traits; (b) "major" mutations are likely to be accompanied by other mutations, including those affecting quantitative traits; (c) the abrupt induction of "major" mutations in a formerly stabilized genotype may cause genetic unbalance, leading via an increased rate of "spontaneous" mutation to an increased genetic variability for quantitative traits. In the latter two cases, the visible mutation acts as an "indicator." It seems insufficient to consider only group 2 while omitting group 1, as the desirable genes may be genetically linked to the "major" mutation in question. Hypothesis (c) is, to our knowledge, novel in its application to higher organisms, but finds support in the work of S. I. Alikhanian on microorganisms (TGC 17: 16-18).

Of each group, 43 pairs of M_2 plants were grown to maturity, each pair selected from a different M_1 plant progeny. Groups 1, 2, and 3 were all derived from the same mutagenic (fast neutron) treatments. Several characteristics were recorded per plant; the within-group means + standard deviation of single observations are shown below; for standard deviation of the mean, divide by 9.3.

Group	Flowering date	No. of leaves below 1st cluster	Length 3rd leaf (mm)	Fertility (weight of seeds per fruit)
1	15.02+8.95	10.02+1.18	155.1+28.3	52.1+22.3
2	8.55+3.00	9.72+0.84	173.6+17.6	61.7+16.0
3	8.75+3.20	9.53+0.84	172.3+17.6	60.2+15.4
4	8.01+2.48	9.77+0.74	176.6+13.8	73.0+12.8

Group 1, composed of mutants with fairly normal phenotype, showed a 13% lower average leaf length, a 29% lower fertility, an increased number of leaves below the first inflorescence, and a concomitant flowering delay of 7 days compared with the control group 4. Groups 2 and 3 were virtually identical in respect to means and variances. In contrast to group 1, the means of the vegetative criteria in these groups were only slightly affected by irradiation, whereas fertility was reduced by 18%. Within-group variation for the different traits was increased by 14 to 29% in groups 2 and 3 and by 60 to 260% in the mutant group. Groups 1, 2, and 3 contained individuals that, in respect to any single character, equalled or even exceeded the most favorable control values. There was no within-group correlation between flowering date, length of the 3rd leaf, and fertility ($r < 0.1$). From each population 12 individuals were selected on the basis of the most favorable combination of the above characteristics, viz. early flowering, long 3rd leaf, and high fertility. Their offspring is subjected to selection for earliness and yield under early season greenhouse conditions.

The most promising lines within each group will also be intercrossed in the M_3 generation in order to create optimal opportunities for genetic recombination before proceeding to further inbreeding with its inherent risk of gene losses.

Contant, R. B., and K. Verkerk

On the genetics of fruit shape in 'San Marzano' and the obl mutant of 'Money Maker.'

The long-fruited variety 'San Marzano' (SM), the round-fruited variety 'Money Maker' (MM), and the long-fruited obl mutant of the latter were crossed in all

combinations (TGC 18:42-43). The F_1 and the F_2 were grown in 1968 to examine fruit shape and its segregation. The data on the reciprocal hybrid were pooled, as no cytoplasmic differences could be ascertained.

The F_1 (MM x obl) was round; its F_2 segregated 26 round : 7 long. This is consistent with the expected 3 : 1 ratio for the segregation of obl; the + allele behaved as completely dominant in this genetic background.

The segregation ratios for the other crosses are shown in the table. The distinction in fruit shape between F_1 (MM x SM) and F_1 (obl x SM), slightly ovate (round-ovate) versus ovate, indicates that obl in heterozygous condition, though by itself unable to affect the round phenotype, does have a detectable expression in combination with the heterozygous condition of the fruit shape genes of SM. Whereas this suggests non-allelic interaction, it is not excluded that in respect to their primary products the genes involved would act additively.

In the F_2 of both crosses the proportion of long-fruited individuals (SM type), which is about 1/4, suggests that only one recessive factor determines the characteristic long-fruit shape of SM; the apparent heterogeneity of intermediate phenotypes on the other hand indicates the presence of at least one other factor with less marked expression. Furthermore, at least one gene seems to have intermediate inheritance.

On this basis the existence is postulated of at least two genes for fruit shape in SM, $el_2^*/+$ and $o_2^*/+$. The expression of each gene, in combination with the + alleles of the other genes, may be as follows:

obl/obl	long	$obl/+$	round	$+/+$	round
el_2/el_2	long	$el_2/+$	round	$+/+$	round
o_2/o_2	ovate	$o_2/+$	round-ovate	$+/+$	round

However, the heterozygotes $obl/+$ and $el_2/+$, though individually unable to show an intermediate phenotype, may produce in combination round-ovate fruits. Similarly, the triple heterozygote would become ovate instead of round-ovate as conferred by $o_2/+$ alone.

The segregation ratios expected on the basis of this hypothesis were consistent

* Tentative symbols

with the observed values (see table). All alternative hypotheses tested provided less satisfactory agreement with the data. There was no evidence of linkage. Further tests on larger F₂'s and subsequent generations are required for obtaining more conclusive evidence. The major fruit shape gene in 'San Marzano,' which we refer to as el₂ according to Butler (J. Hered. 43:25-35; 1952), probably differs from el(e) and o. The connection between the genes obl and o₂ on the one hand and el and o on the other is still unknown.

		Observed	Expected	Genotype(s)		
				<u>obl</u>	<u>el</u> ₂	<u>o</u> ₂
F ₁ (MM x SM)	round-ovate	All	All	+/+	<u>el</u> ₂ /+	<u>o</u> ₂ /+
F ₂ (MM x SM)*	round	8	6.2	+/+	./+	+/+
	round-ovate	11	12.4	+/+	./+	<u>o</u> ₂ /+
	ovate	7	6.2	+/+	./+	<u>o</u> ₂ / <u>o</u> ₂
	long	7	8.2	+/+	<u>el</u> ₂ / <u>el</u> ₂	./.
F ₁ (<u>obl</u> x SM)	ovate	All	All	<u>obl</u> /+	<u>el</u> ₂ /+	<u>o</u> ₂ /+
F ₂ (<u>obl</u> x SM)*	round	1	1.8	./+	+/+	<u>o</u> ₂ /+
				+/+	./+	+/+
	round-ovate	5	5.0	<u>obl</u> /+	<u>el</u> ₂ /+	+/+
				./+	+/+	<u>o</u> ₂ /+
				+/+	./+	<u>o</u> ₂ /+
	ovate	8	6.1	<u>obl</u> /+	<u>el</u> ₂ /+	<u>o</u> ₂ /+
			./+	./+	<u>o</u> ₂ / <u>o</u> ₂	
long <u>obl</u>	4	4.3	<u>obl</u> / <u>obl</u>	./.	./.	
long SM	5	5.8	./.	<u>el</u> ₂ / <u>el</u> ₂	./.	

* Chi² F₂ (MM x SM) = 0.96 (n.s.)
 F₂ (obl x SM) = 1.06 (n.s.)

. = either allele

Contant, R. B., and K. Verkerk

Successful selection for earliness and yielding capacity amongst the offspring of visibly mutated plants.

The following hypothesis was tested: that M₂ plants with slight morphological aberrations but of approximately normal vigor and fertility might be

suitable as basic material for selection for quantitative traits in subsequent generations. Nineteen such mutant seedlings were retained from a total M₂ population of about 60,000. First results of selection for earliness and yield were reported in TGC 17:16-18 and TGC 18:43-45. In 1968, the best selections were re-examined in 3 identical experiments sown at 2-month intervals through winter and spring. There were 6 x 10 plants per object. Only the first 5 clusters were harvested. This trial largely confirmed the results of the 1967 experiment (2 sowings), as shown in the table for cumulative yields of those lines that were superior to the control.

L₁ and L₅ were earlier than the mother variety 'Glorie,' but ultimate yields were only slightly higher. In contrast, M and its reselection M₁ had a higher yield over the whole harvesting period, but no improved earliness. In 1967, M₁ was superior to M, while the opposite was true in 1968; for this

