Momma, Eizi. Hokkaido University, Sapporo, Japan. Domestic Drosophila in Hawaii.

From Jan. 19 to Feb. 11, 1967, Drosophila populations were sampled from six main islands in Hawaii. Collections were made with the use of traps containing usually fermented banana (guava fruit was used at Hana) at one hour intervals from sunrise to sunset for two days in each island excepting in Oahu (for one day) by the help of Prof. E. Elmo Hardy, Univ. of Hawaii. We were interested in distribution of immigrant species, and therefore copses near human habitations limited to the lower altitudes (below 2000 ft.) were chosen as collecting sites. Collection sites in each island were as follows: Kauai - 2 miles northward from Lihue, Oahu - Campus of the Univ. of Hawaii, Molokai - 7 miles northeastward from Kaunakakai, Lauai - 2 miles northeastward from Lanai City, Maui - 2 miles southeastward from Kakawao and 3 miles northward from Hana, Hawaii - 6 miles westward from Hilo.

A total of 67,566 flies represented by 3 genera, 15 species (except 12 specimens of unknown spp.) was obtained as given in Table 1. All specimens excepting only 3 individuals were of immigrant species. D. nasuta was the most abundant species in every island excepting in Molokai. The most predominant species in Molokai was D. simulans. D. hydei was the second dominant species in Lanai, though few or no fly of this species were found in other islands.

Table 1. Number of flies collected by trapping in Hawaii (Jan.-Feb., 1967)*

Island	Kauai	Oahu	Molokai	Lanai	Maui	Hawaii	Total
(Immigrant species)							
Chymomyza							
procnemis	-	-	-	101	1	-	102
Drosophila							
ananassae	36	48	2	-	295	3	384
busckii	1	-	3	-	1	1	6
carinata	1	-	414	1711	858	-	2984
hydei	-	1	-	7063	3	-	7067
immigrans	298	28	388	726	1460	507	3407
kikkawai	41	12	2	-	15	104	174
melanogaster	-	-	-	203	33	2	238
nasuta	13201	2402	3502	17049	2208	3974	42336
polychaeta	690	19	-	1	-	-	710
simulans	1775	458	3935	1344	1424	1237	10153
(Endemic species)							
Scaptomyza							
confusa	-	-	1	-	-	-	1
varifrons	-	-	1	-	-	-	1
palmae?	-	-	1	-	-	-	1
Drosophila							
crassifemur	-	-	-	-	2	-	2
(Unknown species)	3	-	1	-	1	7	12
Total	16026	2968	8250	28198	6301	5835	67578
No. of species collected	11	7	11	8	12	12	25?

* Identification of the flies was confirmed by Hardy's descriptions (1965, 1966).

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Lifschytz, E. and R. Falk. The Hebrew University, Jerusalem, Israel. A system for fine structure analysis of chromosome segments.

In a previous note (DIS 42:89) we presented a complementation map of recessive lethals which were induced in the segment of the X-chromosome that was covered by a w^+•Y-chromosome. It was shown that most lethals were multi-genic and that even those, for which there was no direct evidence that they were aberrations, interfered with recombination in their vicinity.

We present here a complementation map of recessive lethals which were induced in the segment of the X-chromosome covered by the ma-l^+•Y (#2) chromosome. Of the 413 lethals induced with an X-ray dose of 3200r 10% (42) were covered by the ma-l^+•Y-chromosome. 34 of these lethals have already been mapped; none was covered by the w^+•Y-chromosome, they extended thus distally to the su-f region. Included in the map were also 4 lethals of the previously mentioned series (X 1, X 2, X 3, X 4) which were covered by w^+•Y, and two lethals (81,AA33) which were induced by alkylating mutagens.

Twenty eight mutations proved to be multi-genic and for only 6 mutations there was no evidence for more than one affected gene. These results indicate to us that practically all the induced lethals were aberrations: even if a couple of the 6 "single gene" mutations will prove to be affected in more than one gene - they probably represent that end of the distribution curve of aberration-sizes which are smaller than one gene (intra genic aberrations).

As expected the map includes also bigger aberrations which extend into the heterochromatin. Some of the aberrations reach as far as the bb-region, as determined by allelism with the sc^4-sc^8 lethal effect, but even they must have at least one other lethal effect in the euchromatin. There must be at least 18 genes in the studied euchromatic segment of the X-chromosome in which lethal mutations may occur.

Some lethals were sterile in males. Even if we exclude those sterile lethals that extend into the heterochromatin (in which the sterile effect could be also in the heterochromatin) it appears as if sterile lethals A200, B155 and B179 all encompass a specific locus (No. 13 in the map) that determines fertility. It is not sure whether flies deficient for the fertility locus alone would be viable. On the other hand it seems that a deficiency of ma-l is not lethal: females heterozygous for lethals A118 and B214 are viable and have an eye-color phenotype akin if not identical to that of ma-l.

With the aid of the more extensive lethal aberrations in the ma-l region we started a modified system for the detection of induced lethals, in which it is possible to recover in F_2 both lethals outside the ma-l region (detected by the absence of one class of males) and lethals within (part of) the ma-l region (detected by the absence of one of the female classes). This technique is now used for studies on the effects of mutagens on the induction of "point" mutations and aberrations as well as for fine structure analysis of a preselected segment of the X-chromosome.