adult survival rate (85.8% compared to 70.5%) at 25°C, and has a slightly higher survival at 18°C. At 30°C, however, the situation is reversed and not only are over twice as many flies surviving to the adult stage in line 3009, but line 3008 has a relative fecundity almost twice that of 3009 (the difference between strains for fecundity at 25°C and 30°C is significantly different, t = 3.59 and 3.03, p = 0.005). The fitness coefficients reflect the higher survival rates in line 3009 as well. Thus, it appears that the heat sensitive est-6^F allele in this study may be at an advantage with respect to individual survival and fecundity at temperatures around 25°C and lower but at a disadvantage in vivo at temperatures approaching 30°C. That this is an effect associated with the est-6^F heat sensitive allele is not entirely clear even though the study was initiated to determine if the ad hoc prediction would be met. The survey of additional lines fixed for est-6^S and the heat sensitive est-6^F alleles, which should differ in genetic background except at this locus, would aid in clarifying the relationship observed in this study. Examination of the relative allozyme activities in flies raised at different temperatures and delineation of the physiological role of esterase-6 would also help. Studies on certain aspects of these problems are continuing.

Table 2. Relative fecundity, survival and fitness within est-6 strains in flies kept at three different temperatures.

Line	Temperature °C	No. of eggs	No. of adults	Percent Relative Survival	Relative Fecundity	Fitness
3008 (est-6^F)	18	29	8	27.6	15.3	.32
	25	190	163	85.8	100.0	1.00
	30	155	42	27.1	81.6	.29
3009 (est-6^S)	18	40	10	25.0	14.5	.35
	25	275	194	70.5	100.0	1.00
	30	116	75	64.7	42.2	.96

References: Long, T. 1970, Genetics 66:401; Wright, T.R.F. and R.J. MacIntyre 1965, Elisha J. Mitchell Soc. -1:17.

Albornoz, J. and J. Rubio. University of Oviedo, Oviedo, Spain. Location of a region controlling the suppression of normal bristles in Drosophila melanogaster.

Repeated attempts to increase the number of missing dorsocentral and scutellar bristles (dc and sc) by selective crossing of the few deviant flies found in wild populations have failed. However, we found quite a number of missing dorsocentral and scutellar bristles in a population that had been intensively selected for increased number of bristles (dc and sc) and then let go without selection, where more than 95% of the flies had extra dc and sc bristles. The quick response to selection for increased number of missing bristles (line S) is shown in Figure 1 up to generation 11, when a plateau was reached; the 6 latest counts are included. Presently all the flies in the population lack some normal bristles in the dorsocentral and scutellar areas; other bristle systems, and occasionally some microchaetae, are also affected. The proportion of flies having extra bristles was drastically reduced from 95% to 6-8% at generation 11, but even now 4-8% of the flies in every generation have extra dc and sc bristles.

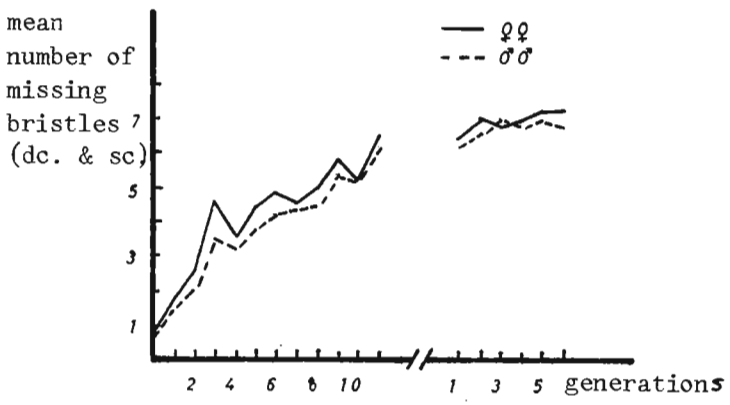

Fig. 1.

Chromosome contribution analysis: Conventional crossing of line S to balanced strain J-407 carrying dominant markers in all three major chromosomes indicates that the presence of chromosome III in homozygous con-

dition is quite fundamental, although chromosomes I and II also play a relevant role. The analysis of variance is shown in Table 1, together with the mean factorial effect of each chromosome given in missing bristles number.

Table 1. Analysis of Variance

Factor	d.f.	M. S.	F	P	Mean Factorial Effects
chromosome I	1	74	81.22	<0.01	0.50
chromosome II	1	471.25	517.24	<0.01	1.25
chromosome III	1	9976.33	10949.81	<0.01	5.77
interaction I-II	1	3.83	4.23	<0.05	-0.11
interaction I-III	1	79.05	86.77	<0.01	0.51
interaction II-III	1	453.87	498.16	<0.01	1.23
interaction I-II-III	1	3.20	3.52	n. s.	-0.10
residual (error)	1192	0.91			

In order to assess the specific effect of chromosomes II and III of line S, these chromosomes were substituted for the same chromosomes in inbred line Oregon-R, following the method used by Robertson (1954). Table 2 shows the mean number of missing bristles observed in each chromosomal type.

The phenotypic expression due to chromosome III (S) alone is low, but still this chromosome in homozygous condition causes by itself a quite distinct phenotype, so much so that the interaction with the chromosome II (S) is effective only when chromosome III (S) is homozygous.

Table 2. Mean number of missing bristles in each chromosomal type (O = Oregon-R wild type chromosome; S = chromosome from the S line.

		Chromosome III		
Chromosome II		S / S	S / O	O / O
S / S	f.	5.16 ± 0.07	0.002 ± 0.002	0.01 ± 0.04
	m.	4.15 ± 0.08	0.01 ± 0.05	0.01 ± 0.05
S / O	f.	4.24 ± 0.08		
	m.	3.22 ± 0.08	—	—
O / O	f.	1.58 ± 0.07		
	m.	1.03 ± 0.05	—	—

Location of the relevant region on chromosome III from the S line: Following the method used by Thompson and Thoday (1975), females from the S line were mated to an inbred marker stock carrying hairy (26.5 cM), scarlet (44.0 cM), curled (50.0 cM), ebony-sooty (70.7 cM) and claret (100.7 cM). F_1 females were backcrossed to h/st/cu/e^s/ca males, and the recombinants were picked up as males in the next generation. Twenty males of each recombinant class were mated individually to females from the S line. In their progeny recombinant chromosomes carrying factors contributing to bristle suppression could be identified by the occurrence of missing bristles. Table 3 gives, for each recombinant male class, the number of single-pair cultures showing missing bristles.

Table 3.

Males recombinant class	Number of cultures with missing bristles	Number of cultures without missing bristles
h st cu e^s ca	1	14
+ + + + +	12	0
h st cu e^s +	13	0
+ + + + ca	0	10
h st cu + +	11	0
+ + + e^s ca	3	8
h st + + +	5	0
+ + cu e^s ca	0	9
h + + + +	12	0
+ st cu e^s ca	1	10

The S region can be located on the distal part of chromosome III, after claret. Among a total of 109 recombinant males cross-tested, only 5 are recombinant between claret and the S region; this places the S region at about 4,6 cM away from claret, or 105 cM on the map. Due to the reduced number of progenies observed and the short distance left between claret and the chromosome end, this location is only approximate. We are now looking for any other mutant marker located in this region of chromosome III.

References: Robertson, F.W. 1954, J. of Genetics 52(3):494-520; Thompson, J.N. Jr. and J.M. Thoday 1975, Genet. Res. 26:149-162.