Beckenbach, A.T. Simon Fraser University, Burnaby, B.C., Canada. Map position of the esterase-5 locus of D. pseudoobscura: a usable marker for "sex-ratio".

Recently, Anderson and Norman (1977) published a map of D. pseudoobscura mutants. The purpose of this note is to add the esterase-5 (est-5) locus to that map. The primary impetus for the work was to determine whether the est-5 alleles would provide usable markers for the "sex-ratio" (SR) X-chromosome in laboratory population studies. Efforts to obtain recombinants between est-5 and SR have thus far failed (Beckenbach, unpubl.; Curtsinger and Feldman 1979). However, Sturtevant and Dobzhansky (1936) have provided a recombination map relating the SR and standard (ST) chromosomes for a number of visible markers. Thus by localizing est-5 with respect to the visibles on the ST chromosome, it was hoped to obtain a better estimate of the linkage relationship between that locus and the SR inversions.

Stocks used: (1) A marker strain of D. pseudoobscura carrying the visible mutants yellow (y), singed (sn), vermillion (v), compressed (co) and short (sh) was obtained from Dr. W.W. Anderson. This stock was found to be homozygous for the 1.07 allele of est-5. (2) A strain of the species, homozygous for the 0.85 allele, was obtained from Dr. G.A. Cobbs. This strain was originally derived from an isofemale line from a citrus grove in Riverside, California, and was made homozygous by recurrent inbreeding. Both strains carried the ST arrangement of the X-chromosome. Virgin females of the marker stock were crossed to est-5 males. A total of 887 F_2 progeny (431 females, 456 males) were examined for the presence of the visible markers and then tested for est-5 genotype, using polyacrylamide vertical slab gel electrophoresis and the technique described by Cobbs (1976).

Results: The results are given in the table. Esterase-5 maps to the position 111.8, just distal to co on the right arm of the X-chromosome. Graphic representation of the map of part of the X-chromosome, with comparison to recombination values in SR/ST heterokaryotypes (from Sturtevant and Dobzhansky 1936) is given in Fig. 1.

Region	Number Observed	Frequency
non-recombinants	297	0.335
y - sn	103	0.116
sn - v	18	0.020
v - co	194	0.219
co - est-5	54	0.061
est-5 - sh	418	0.471

Curtsinger and Feldman (1979) have placed the upper limit (95% confidence interval) of recombination between est-5 alleles and the SR chromosome in SR/ST heterokaryotypes at 1.5%. That value is based on 0 recombinants in 240 males examined. The results of this study suggest that their value is quite conservative. Comparison to Sturtevant and Dobzhansky's map suggests and upper limit of 0.5%. This value, too, may be excessive. SR differs from ST by three non-overlapping inversions and a considerable homosequential length of chromosome exists between the proximal pair of inversions and the distal one (Dob-

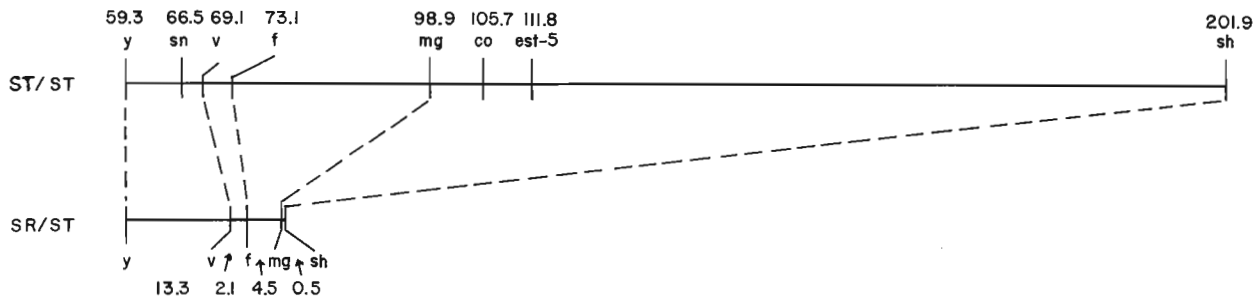

Fig. 1. Map positions for the visible markes and esterase-5 in the ST/ST homokaryotype and recombination frequency in the SR/ST heterokaryotype. Map positions (upper figure) are taken from Anderson and Norman (1977), Sturtevant and Tan (1937) and this study. The symbol f refers to "forked"; mg refers to "magenta"; other symbols are defined in the text. Recombination values (lower figure) are taken from Sturtevant and Dobzhansky (1936).

zhansky and Epling 1944). Recombinants between SR and ST are known from that region (Wallace 1948; Anderson, pers. comm.), isolating the small distal inversion. The "sex-ratio" phenotype is carried in the proximal pair of inversions (Wallace 1948). It is quite likely that the recombination in the homosequential region accounts for much of the recombination found by Sturtevant and Dobzhansky. Since over 90 map units separate est-5 from sh, it is likely that most recombinants occur distal to est-5, beyond the region conferring the "sex-ratio" phenotype.

References: Anderson and Norman 1977, DIS 52:11-12; Cobbs 1976, Genetics 82:53-62; Curtsinger and Feldman 1979, Genetics, in press; Dobzhansky and Epling 1944, Carnegie Inst. Wash. Publ. 554, Part II, Plate 4; Sturtevant and Dobzhansky 1936, Genetics 21:473-490; Sturtevant and Tan 1937, J. of Genetics 34:415-432; Wallace 1948, Evolution 2:189-217.

Carton, Y., J. Roualt and H. Kitano. Lab. Gén. Evolutive C.N.R.S., Gif-sur-Yvette, France. Susceptibility of the seven sibling species of sub-group melanogaster infected with a Cynipide parasite.

Specific parasites are an important component of the niche and it has been assumed that development of genetic defense mechanisms could play a role during the speciation process. The seven sibling species of the melanogaster sub-group appear to originate from West Africa where speciation process occurs (Tsacas 1979). The existence in this area of parasitic Cynipidae specific to Drosophila (Barbotin et al. 1979) might play a role in this process. Cothonaspis boulardi is a solitary, endophagous parasite (parasitoid) that oviposits into larvae of several species of Drosophila. We have tried to estimate the differential susceptibility of the seven sibling species of Drosophila towards this parasite. For this purpose we retained the following experimental procedure. Females of this solitary parasite lay their eggs (at 25°C) in the second instar larvae of the host; consequently, the exposure of host larvae to the parasite was limited to 24 hrs. Ten wasp females were introduced into a plexi-

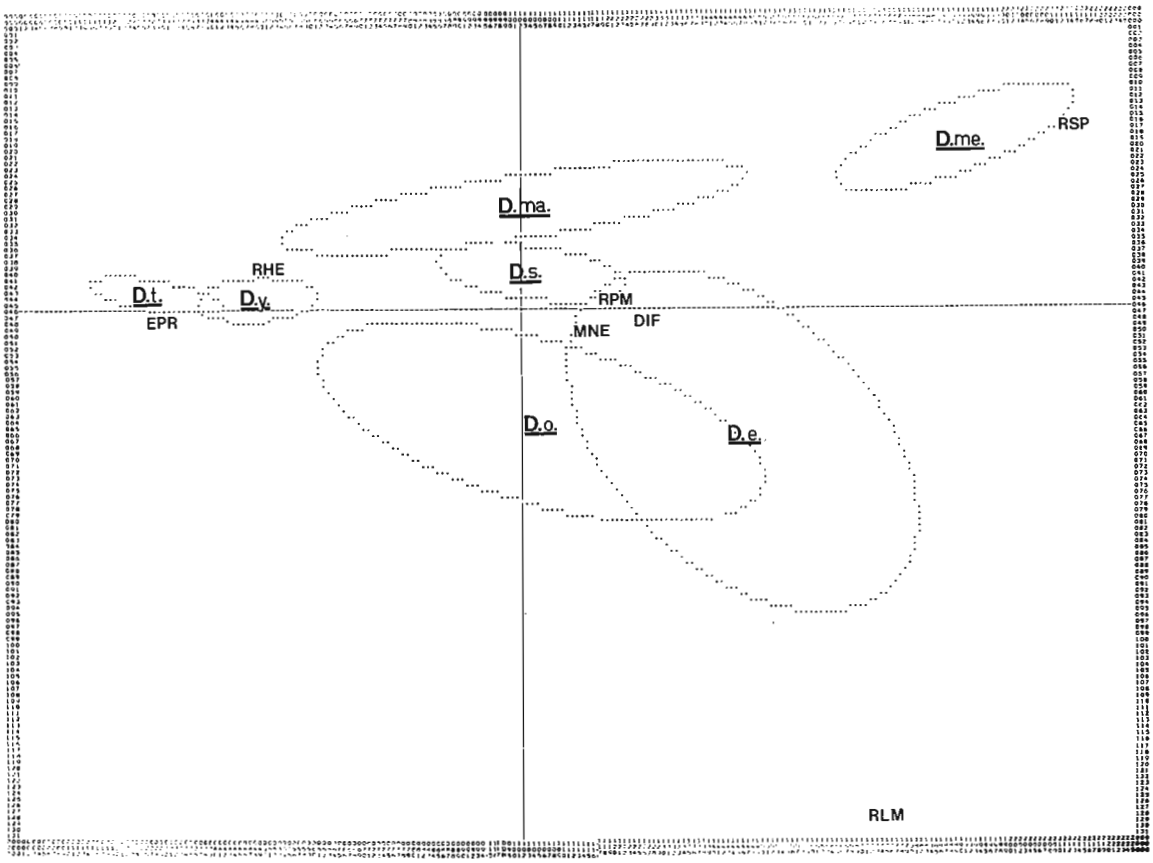

Fig. 1