Hannah-Alava, Aloha. Department of Genetics, University of Turku, Turku, Finland. Localization of Pc and Scx.

Inasmuch as the positions for 12 of the 17 loci mapped on p. 462-63 in the "Revision" of the Mutants of D. melanogaster (Lindsley & Grell, 1968) are given in tenths of a unit, it might be presumed that there is a high level of accuracy in genetic localization of the genes in the centric region of chromosome-3. On the contrary, recent linkage studies have so consistently shown such great variance in recombination values for the genes in the st-p interval, that there is now a tendency for some authors to even refrain from giving the map positions of these loci. Furthermore, although ri has long been considered as an "accurately" located gene, in spite of the fact that its position has been listed as either 47.0 or 47.1, both it and the "less accurately" located in gene have been accurately mapped only recently (e.g., Arajärvi & Hannah-Alava, this issue of DIS). The linkage results obtained in a series of experiments for locating the Pc and Scx alleles have been even more deviant, with the result that the positions of these loci have been listed as both 47 and 48. It is not unlikely that attempts to relocalize at least some of the other mutants in the in-p interval will reveal similar ambiguities in genetic position.

As pointed out by Lindsley & Grell (l.c., p. 5) reliance upon "accurate" locations in mapping may result in inaccuracy with respect to both position and order of the genes. Disregarding other evidence when mapping the "less accurately" located genes not only leads to confusion, but may even result in erroneous assumptions in subsequent investigations. Thus, for example, there probably will be misconceptions concerning the positions of Pc and Scx. Even though it was stated in two different places in the mutant descriptions that Scx is located between Pc and p^P, due to the fact that its genetic position was considered to be 47, it was placed in the cytogenetic map between in and ri in the left arm, while Pc, which was listed as 48, was located in the right arm and, probably correctly, next to the Antp locus. Regardless of the ambiguity in genetic localization of these mutants, it has at least been established that their order is Pc - Scx, and not the reverse order as suggested in the cytogenetic map.

In her description of Pc (subsequently referred to as Pc^1) P. Lewis (1947, DIS 21) only stated that this mutant was in chromosome-3 and between th and p. Later, Hannah & Stromnaes (1955 DIS 29) reported that Pc^1, as well as Scx, was between st and p^P, but because the localizations were based only on the males with extra sexcombs, their positions were given, tentatively, as 48±. They were considered as pseudoalleles, but recombination was obtained only in subsequent linkage tests.

With the discovery of Pc^2, in 1961, relocalization of all three of the 'Extra-sexcomb' mutants was undertaken. Linkage tests were first made with the 'thrie' (th st cp in ri p^P bx sr e^s) and '3ple' (ru h st p^P ss e^s) mutant-marked tester chromosomes, and later with strains having various combinations of the 'Extrasexcomb' mutants and recessive marker genes. Although none of the linkage tests involved large numbers of flies (because of the necessity for progeny testing) many tests were made, from which some 20 strains, with various combinations of Scx and/or Pc^1 or Pc^2 and the recessive genes, were extracted and (because they were homozygous lethal) have been maintained by balancing with either T(2;3)Mé or TM1, Mé ri sbd^1.

The linkage results were exceptionally variable with the consequent wide range in recombination values, and hence locations, for all three of the 'Extra-sexcomb' mutants. The linkage results were more variable with one 'Extra-sexcomb' mutant than with two, and with two in the coupling phase than two in the repulsion phase. Only part of the variance, e.g., inequality in reciprocal classes, could be related to viability factors associated with specific genes or combinations of genes. There was frequently a marked deviation from the standard value of 4.0 for recombination in the st-p interval, but the range in values was no greater than in other crosses (e.g., Arajärvi & Hannah-Alava, l.c.). Examples of the variance in linkage values for the st-p region obtained in experiments involving two 'Extra-sexcomb' mutants are summarized in the following table for five different experiments: #1: Pc^1 Scx/'3ple'; +/+ ♀♀ and #2: Pc^1 Scx / '3ple'; Cy/+ ♀♀ (sibs of #1) X '3ple' ♂♂; #3: ru h st Scx p^P ss e^s/ru h Pc^2 ♀♀ X 'thrie' ♂♂; #4: Pc^2 Scx p^P sr / 'thrie' ♀♀ X 'thrie' ♂♂; #5: (for locating the lethal associated with Scx) Pc^1/ru h st Scx p^P ss e^s ♀♀ X ru h st Scx p^P ss e^s ♂♂:

Cross	Offspring	Crossover %: Region			Map length	Position*	
		st-Pc	Pc-Scx	Scx-p	st-p	Pc	Scx
# 1	1333 ♂	0.8	0.2	0.6	1.65	46.0	46.5
# 2	1504 ♂	2.6	0.1	0.3	3.13	47.4	47.6
# 3	1649 ♂	1.2	0.4	0.2	1.82	46.7	47.5
# 4	239 ♂	2.5	0.8	-	>3.3	46.5	47.3
# 5	296 ♀&♂	2.7	1.7	0.7	5.07	46.4	47.4
	151 ♂	3.3	2.0	0.7	5.96	46.2	47.6

*Corrected for deviation from the standard value of 4.0 for the st-p interval for all except # 4.

These examples of the variance in linkage results clearly show the difficulties encountered in an attempt to accurately localize the 'Extra-sexcomb' mutants. It might even be concluded that Pc could be to the left of ri; but the types of recombinants recovered in Exp. # 4 (and others similar to it) established that all three mutants were between ri (47.0) and p^P (48.0), with the linear order being st cp in ri Pc^1 (or Pc^2) Scx p^P. The more recent tests also revealed that Scx was considerably more to the left of p^P than had been indicated by the earlier linkage results (Hannah & Strömnaes, 1955 DIS 29). The linkage values for Pc and Scx usually ranged from 0.1 to 0.8 of a unit with an average of 0.3 of a unit. Consequently when the map location for the 'Extra-sexcomb' mutants was submitted for inclusion in the "Revision of the Mutants" it was given as 47± (rather than 48± for all three. Since either value is completely ambiguous, the most reasonable tentative position is probably 47.5±, at least until there is better genetic mapping for the whole of the ri-p section.

Exp. # 5 is included to show an example of exceptionally deviant results and because it reveals some of the sources of error that may be encountered in mapping the 'Extra-sexcomb' mutants. All of the other tests made for mapping the lethal, associated with Pc^1, Pc^2 or Scx, showed that it was in the same region of the chromosome as the 'Extra-sexcomb' mutant. The recovery of an apparent double crossover (genotypically ru h st p^P ss e^s) in the st-p region, in # 5, could also mean that the lethal was not in the same position as Scx. An alternative and more likely explanation is that a small number of the presumed ru h st Scx p^P ss e^s chromosomes did not contain the Scx factor.

With the exception of the one questionable double crossover found in Exp. # 5, no double crossovers in the st-p region have been recovered in either these experiments or in similar experiments by Arajärvi (Arajärvi & Hannah-Alava, l.c.). Nevertheless, there is rather frequent "loss" of the 'Extra-sexcomb' mutants, particularly Scx, from the strains which are balanced with T(2;3)Mé or TM1,Mé ri sbd^1, presumably through double crossing-over with the Mé chromosome. Although it has been possible to insert p^P into the Mé chromosome by double crossing-over such an event is relatively rare. Not only is the loss of an 'Extra-sexcomb' factor more frequent, but if it is due to double crossing-over, it can take place in a region presumably of less than one map unit, because in one case at least, Scx was lost from a chromosome with the following combination of genes: th st cp in ri Pc^2 Scx p^P without loss of either Pc^2 or p^P, and of course the other recessives. A similar "loss" of two Antp mutants ($Antp^B$ and $Antp^{50}$) has also occurred. Thus the section of the chromosome containing the 'Extra-sexcomb' and 'Antennapedia' loci may have special cytogenetic properties which under certain conditions responds with enhanced crossing-over, or an event resembling crossing-over.

Because there is apparently no chromosomal change associated with Pc^1, Pc^2 or Scx, their location in 3R is on the basis of indirect evidence, i.e., lethality of Scx/Antp compounds and semilethality of $Pc^2/Antp^{49}$. Exact mapping of the Pc and Scx loci awaits the discovery of alleles associated with a cytologically identifiable chromosomal change. Resolution of the nature of the functional allelism between the 'Antennapedia' and 'Extra-sexcomb' mutants might be facilitated by means of the working-hypothesis that they are in a region of repeats, in which the replicated (triplicate?) 'Antennapedia' or 'Extra-sexcomb' genes have retained only part of their genetic and functional homology. A "triplicate" would explain the stickiness of the 83E-84D section of the salivary chromosomes, the relatively wide spread in the breaks associated with 'Antennapedia' and account for the fact that a large number of inversions and translocations with breaks in the 83E-84B region do not have an associated antennapedia or extra-sexcomb phenotype.