

Table 2. Transmissibility of mutations and their relation to parental pattern

Pattern of parental eyes	Non-transmitted	Transmitted
both eyes full mutant	2	2
one eye full mutant, one eye normal	6	1
one eye full mutant, one eye sector	2	0
both eyes sector	5	1
one eye sector, one eye normal	5	4
total	20	8

The induction of single strand lesions in sperm leads to mosaics which tend to remain separated by a left-right symmetry along the anterior-posterior axis. Only a few ($8/40 = 0.20$) of the mosaics represented mixed distributions of mutant and normal cells to each eye. Table 2 presents the transmitted mutations and their relation to the pattern of mosaicism in the initial mutant parent.

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Tsakas, S. and E. Diamantopoulou-Panopoulou. Agricultural College of Athens. Is the "hidden heat sensitive polymorphism" (crude extract) polymorphism of the structural examined locus in all cases? Experiments with *D. subobscura*.

132 isogenic lines for the O chromosome extracted from two natural Greek populations, Parnes (P) and Crete (C), were studied. In our samples composed of the crude extract of 12 flies we tested whether the observed heat-sensitive "alleles" were new hidden alleles of the tested loci, A.O, M.E and Xdh, located on the O chromosome.

The main conclusion from this experimental work is that in our tested cases the new hidden heat-sensitive polymorphism doesn't belong solely to the tested locus but is the result of interaction among the "enzymatic products of different loci". The evidence for this is: (a) non-repeatable heat-sensitive phenotypes within some tested strains; (b) the heat-sensitive phenotypes within F_1 crosses didn't give one pattern in most of the tested cases; (c) in single crosses by using null-strains and single fly analysis (new technique applied by us), we did not observe one locus Mendelian segregation within the offspring.

The report of this work has been submitted to the Biochemical Genetics magazine.

Wakimoto, B.T., R.A. Lewis and T.C. Kaufman. Indiana University, Bloomington, Indiana. Genetic analysis of the Antennapedia gene complex: mutant screen of proximal 3R, bands 84A-84B1.

In order to extend our knowledge of the genetic and functional relationships of the members of the Antennapedia gene complex (ANT-C), we have utilized a proximal 3R deficiency chromosome Df(3R)Scr in a mutant screen. This chromosome was generously provided for our use by Dr. D. Sinclair. It is deficient for bands 84A1

through 84B1. Like the previously described Df(3R)Antp^{Ns+R17} (Duncan and Kaufman; Kaufman), Df(3R)Scr is associated with a dominant reduced sex comb phenotype and fails to complement the recessive lethality of the dominant homoeotics Msc, Antp and Antp^{Scx}. However, Df(3R)Scr extends more proximally than Df(3R)Antp^{Ns+R17} and exposes the proboscipedia (pb) locus. The recovery and characterization of mutants derived from the present screen would establish if the previous screen utilizing Df(3R)Antp^{Ns+R17} had saturated the 84B1,2 region of the ANT-C (see Lewis, R.A., this volume). Furthermore, we could extend the limit imposed by the Df(3R)Antp^{Ns+R17} chromosome to include more proximal regions including the pb locus.

EMS mutations were induced according to the method of Lewis and Bacher. Using a third chromosome marked with red and ebony, a total of 2,832 chromosomes were screened for visible, lethal and semi-lethal mutations exposed by Df(3R)Scr. The mutants recovered were designated by the letters Ef followed by an identification symbol. Results of inter se complementations are summarized by Fig. 1.

<i>Df(3R)Antp^{Ns+R17}</i>									
<i>Df(3R)Scr</i>									
			<i>pb</i>		<i>EbR11</i>		<i>Scr</i>	<i>Antp-Hu-Scr</i>	<i>EdR16</i>
<i>EfW5</i>	<i>EfW36</i>	<i>EfR9</i>	<i>EfW1</i>	<i>EfW4</i>	<i>XaK2</i>	<i>EfR1</i>	<i>EfW17</i>	<i>EfW10</i>	
<i>EfW9</i>			<i>EfW14</i>	<i>EfW19</i>	<i>EfW20</i>	<i>EfR3</i>	<i>EfW22</i>	<i>EfW15</i>	
<i>EfW27</i>						<i>EfW6</i>		<i>EfW24</i>	
						<i>EfW21</i>		<i>EfR4</i>	

Fig. 1. Complementation map of proximal 3R mutants derived from a screen utilizing *Df(3R)Scr*. The mutant sites *EbR11*, *XaK2* and *EdR16* were defined by the previously described *Df(3R)Antp^{Ns+R17}* screen (see text).

The *Df(3R)Scr* screen failed to define any new lethal sites within the region that is also exposed by *Df(3R)Antp^{Ns+R17}*. However, several new members have been added to the complementation groups originally established in the *Df(3R)Antp^{Ns+R17}* screen. Specifically, in the *Antp^{Scx}* complementation group, four new lethal mutations have been recovered. One of these, *EfW15*, is a new allele of *Antp^{Scx}*. It appears to be more extreme than the original allele in producing extra sex combs on the meso- and metathoracic legs and in removing the sternopleural bristles. Other mutants derived from the screen include two new lesions in the *Scr* group. Both of these new mutations show reduced sex comb phenotypes and are entirely consistent with the earlier interpretation that the function of the *Scr⁺* site is to promote prothoracic leg development.

In addition, four new members of the *EbR11* complementation group and two new *pb* alleles have been recovered. The *pbEfw4* allele transforms the labial palps into distal arista and proximal leg tissue. *pbEfw19* appears to transform labial palps completely into antennal structures.

We have defined four new lethal sites exposed by the *Df(3R)Scr* chromosome. The linear order of these sites and their position with respect to the *pb* locus is arbitrary at this point. We are continuing genetic and developmental studies of these newly induced mutations. Further analyses will investigate the possibility that the new lethal sites are members of the ANT-C whose function is in the determination of anterior segmentation in *Drosophila*.

References: Duncan, I.W. and T.C. Kaufman 1975, *Genetics* 80:733-752; Kaufman et al. 1979, *Genetics* (submitted); Lewis and Bacher 1968, *DIS* 43:193.

Watabe, H., E. Momma and M.T. Kimura.
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Changes in drosophilid fauna at the University Botanical Garden in Sapporo, Japan.

Through the serial papers "Drosophila Survey of Hokkaido", Momma and his collaborators have revealed the distribution and abundance of Drosophilidae in Hokkaido. The authors have studied the dynamic aspects of drosophilid populations at the University Botanical Garden (UBG) in Sapporo. This preliminary report deals with

changes in the species composition of the drosophilid assemblages in this semi-natural area.

A weekly collection during the active season was made by exposing fermenting banana, using two "retainer" traps in 1975 and six from 1976 to 1978. Momma (1965) had previously surveyed the drosophilid fauna of UBG in the ten successive years from 1953 to 1962, using "open" traps. The constitutions of the relative frequencies of the assemblage are different for "retainer" and "open" traps. For example, *D. immigrans* is more frequent in the former than in the latter, while for *D. auraria* the opposite is true. Therefore it is difficult to make a quantitative comparison between the present data and Momma's. For this reason, the survey was also carried out using "open" traps in 1972 and 1977. It would be possible to compare these data with Momma's for the number of species collected and the constitutions of the populations (Beppu and Toda, 1976). Except for *D. suzukii*, *D. lutescens* and *D. immigrans*, the relative frequencies of the common species did not significantly vary between Momma's collection and 1972. Thereafter, domestic species such as *D. immigrans*, *D. melanogaster*, *D.*