# Mutation Notes — *Drosophila melanogaster*

## Saturation mutagenesis of region 82F.

**Carpenter, Adelaide T. C.** Department of Genetics, University of Cambridge, Downing Street, Cambridge CB2 3EH, UK.

In an attempt to isolate mutations in the 82F gene responsible for the late puff there, an X ray and an ENU mutagenesis were run, starting with an isogenic *mwh red e* chromosome and testing against *Df(3R)3-4* (82F3-4;82F10-11, my cytology, does remove the puff) for lethals and visibles in the $F_2$. Out of 5756 fertile $F_1$ tests of X-rayed chromosomes (78% of males were fertile, 97% of females) there were 21 lethals = $3.6 \times 10^{-3}$ for ca 9 bands; out of 3130 fertile $F_1$ tests of ENU-treated chromosomes (92% of males fertile, 95% of females) there were 14 lethals and one semi-lethal = $4.8 \times 10^{-3}$. These were then sorted into three regions by complementation testing against *Df(3R)6-7* (82E3;82F3-7, not my cytology, does remove the puff) and *Df(3R)110* (82C4;82F3-7, not my cytology, does not remove the puff). All mutations within a region were crossed to each other and also to all mutations in the adjacent region(s); 11 compementation groups resulted, with only one (*l(3)82Fh*) being at all complicated, and one deficiency was recovered: *Df(3R)ME15,* 81F3-6;82F5-7. All X-ray induced mutations had their cytology checked; if no aberration is indicated below, then the 82F region had no obvious cytological defect.

**In group 1 (lethal over all four deficiencies):**

*l(3)82Fa:* X ray alleles 1 and 2, ENU alleles 3 and 4. Larval-pupal lethals with inclusions; mitotic index low.

*l(3)82Fb:* ENU alleles 1 and 2. Both alleles are only semi-lethal; escapers have small heads and broad abdomens.

**In group 2 (lethal over *Df(3R)6-7, Df(3R)ME15,* and *Df(3R)3-4;* viable over *Df(3R)110):***

*l(3)82Fc:* X ray alleles 1, 2, and 3, ENU allele 4. *In(3R)82Fc*$^{1}$, het;82F3-11; *In(3R)82Fc*$^{2}$, het;82F3-7. Pre-larval lethals.

*l(3)82Fd:* X ray alleles 1, 2, 4, 5, 6, 7, 8; ENU allele 3. *Tp(3;Y)82Fd*$^{1}$, 82F3-11;98F8-14; *T(2;3)82Fd*$^{1}$, 42E3-7;82F5-7; *Tp(3;3)82Fd*$^{7}$, 82F5-7;92D1+;92F3-5, new order 61A1-82F5|92D2-92F5|82F5-92D1|92F5-100. All alleles are eclosion lethals over deficiencies; flies assisted from their pupal cases are alive, and weaker combinations give significant levels of escapers who had been wing-stuck. Alleles 2 and 3 have brown eyes over deficiencies and allele 1 has variegated brown eyes (since the parent chromosome carries *red,* this phene has not been assayed in the heteroallelic combinations); the rest have wild-type eyes. Allele 3 is homozygous viable and fertile; all other alleles are stronger, with roughly the order (strongest) 1, 2; 4, 7; 8; 5, 6 (weakest) based on relative viabilities over deficiencies and each other, although slightly different orders result from different comparisons, suggesting that the gene may be somewhat complex -- as indeed is already suggested by the variation in eye color effects. Allele 4 does not puff the 82F puff, suggesting that *l(3)82Fd* is the puff gene itself.

*l(3)82Fe:* X ray allele 1, ENU allele 2. *In(3)82Fe*$^{1}$, het;82F3-7. Pre-larval lethals.

**In group 3 (lethal over *Df(3R)3-4* only; viable over *Df(3R)110, Df(3R)6-7* and *Df(3R)ME15):***

*l(3)82Ff:* one allele induced with ENU, early pupal lethal

*l(3)82Fg:* one allele induced by X rays, mid-pupal lethal

*l(3)82Fh:* alleles 1, 2, and 5 induced with X rays; alleles 3, 4, 6, 7, and 8 induced with ENU. *T(2;3)82Fh*$^{2}$, 57F3-11;82F7-11. Alleles 1 and 2 appear to be amorphic (from stages of death of hypomorphs over them) and are pre-larval lethals; the rest of the alleles are increasingly hypomorphic, with alleles 6, 7, and 8 complementing each other in all combinations. Lethal phases of hypomorphic

combinations range from pre-larval lethality through hanging up as wandering third instars to late pupal lethality.

*l(3)82Fi:* alleles 1 and 2 induced with X rays, allele 3 with ENU. *T(2;3)82Fi*$^{2}$, 57A10-B1;82F10-83A1. Pre-larval lethal.

*l(3)82Fj:* one allele induced with X rays, pre-pupal lethal. *Ab(het;3R)82Fj*$^{1}$, het;83A1+.

*l(3)82Fk:* one allele induced with ENU, leaky late pupal/eclosion lethal.

**Other mutations recovered from X rays:**

*Df(3L)ru-22,* 61F8;62A3-5. Detected because the *Df(3R)3-4* chromosome used carried *ru*$^{1}$ although this wasn't indicated on its label.

*In(3LR)Sai*$^{1}$, 69D2-6;84E12-F3. Dominant outheld wings, recessive lethal allele of the *mirr* complementation group = *mirr*$^{Sai1}$.

*Sai*$^{2}$, dominant outheld wings; no cytological defect, maps genetically to 3-37.9 relative to *h* and *th.* Recessive lethal allele of the *mirr* complementation group = *mirr*$^{Sai2}$.

*Sai*$^{1}$, *Sai*$^{2}$, *D*$^{1}$, *D*$^{3}$, and *mirr*$^{DH-1}$ (homozygous viable hypomorphic *mirr* allele) fail to complement each other; *Sai*$^{1}$ is the strongest allele, then *D*$^{1}$ = *Sai*$^{2}$, then *D*$^{3}$. *D*$^{3}$/*mirr*$^{DH-1}$ is nearly completely viable, though with mild head defects and missing bristles.

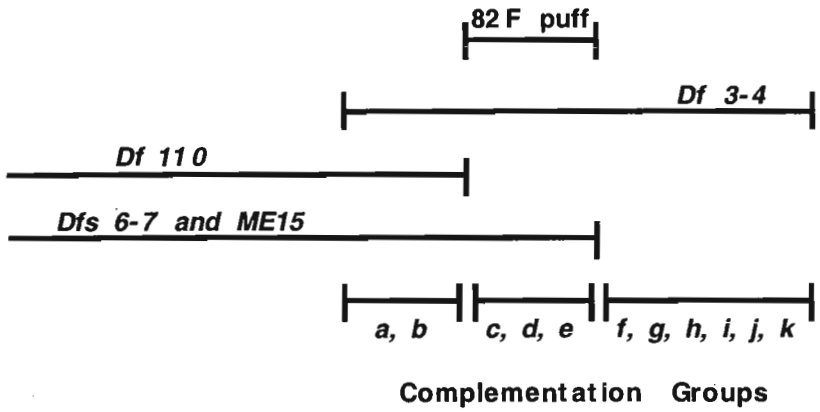


Figure 1.

Other mutations recovered from ENU: saw several, kept only a scarlet (= *st*$^{33}$), again detected because the *Df(3R)3-4* chromosome carried a *st* allele that wasn't indicated on its label.

Thirty-five mutations across 11 complementation groups = 3.2 hits per gene on average; although the distribution of numbers of hits per gene observed is very far off that expected from the Poisson distribution, that distribution predicts that the number of lethally- or visibly-mutable genes missed is 0.5.

## New lethal mutations in the 97B1-10 to 97D13 region of the *Drosophila melanogaster* 3rd chromosome.

**Ambrose R. Kidd III, Dhea Tolla, and Michael Bender.** Department of Genetics, University of Georgia, Athens, GA 30602.

In F2 EMS screens for mutations in the *dPC2* gene, we recovered sixteen lethal mutations and one visible mutation over *Df(3R)Tl-X* and *Df(3R)ro80b*. Together, the deficiencies cover the 97B1-10 to 97D13 region and overlap in the 97D1-2 region (Anderson *et al.*, 1985; Knibb *et al.*, 1993). Nine lethal mutations and the visible mutation fail to complement both deficiencies and thus map to the 97D1-2 region that includes the *dPC2* gene. These mutations are described elsewhere (D.T., A.R.K., and M.B., manuscript in preparation). Three (*dt6, dt12, dt14*) of the remaining 7 mutations recovered in our screens fail to complement *Df(3R)Tl-X* but complement *Df(3R)ro80b* and therefore are located beween 97B1-10 and 97D1 (Figure 1). The *dt6, dt12,* and *dt14* mutations fail to complement one another and also fail to complement *l(3)673*, a previously identified lethal in the region (K. Anderson, unpublished). These mutations have recently been shown to be allelic to