Saturation mutagenesis of region 82F.

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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 F2. Out of 5756 fertile F1 tests of X-rayed chromosomes (78% of males were fertile, 97% of females) there were 21 lethals = 3.6 x 10^-3 for ca 9 bands; out of 3130 fertile F1 tests of ENU-treated chromosomes (92% of males fertile, 95% of females) there were 14 lethals and one semi-lethal = 4.8 x 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 complementation 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)82Fe', het;82F3-11; In(3R)82Fc', 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', 82F3-11;98F8-14; T(2;3)82Fd', 42E3-7;82F5-7; Tp(3;3)82Fd', 82F5-7;92D1+;92F3-5; T(2;3)82Fd', 57F3-11;82F7-11. 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(3R)82Fe', 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', 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.

\( In(3LR)Sa^d, 69D2-6;84E12-F3. \) Dominant outheld wings, recessive lethal allele of the \( mirr \) complementation group = \( mirr^{304}. \)

\( Sa^b, \) 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 = \( mirr^{304}. \)

\( Sa^d, \) \( Sa^f, D^1, D^3, \) and \( mirr^{Ph-1} \) (homozygous viable hypomorphic \( mirr \) allele) fail to complement each other; \( Sa^d \) is the strongest allele, then \( D^1 = Sa^f, \) then \( D^3. \) \( D^1/mirr^{Ph-1} \) is nearly completely viable, though with mild head defects and missing bristles.

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.

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In F2 EMS screens for mutations in the \( dPC2 \) gene, we recovered sixteen lethal mutations and one visible mutation over \( Df(3R)Ti-X \) 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 \( Df(3R)Ti-X \) but complement \( Df(3R)ro80b \) and therefore are located between 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