

May 6 - **Paper 5** -- Metzstein and Krasnow. 2006. "Functions of the Nonsense-mediated mRNA Decay Pathway in *Drosophila* Development." PLoS 2: e180.

Presentations and review. Look for more detail online (download the presentation from [www.clfs.umd.edu/classroom/CBMG688I/private/PresentationPPTs/Figs-Metzstein.ppt](http://www.clfs.umd.edu/classroom/CBMG688I/private/PresentationPPTs/Figs-Metzstein.ppt)).

- 1) Introduction/Synopsis.
- 2) Identification of mutants: the screen (1<sup>st</sup> ten lines of the results and Fig. 1A).
- 3) Identification of mutants: photoshop mutants (the remainder of that section).
- 4) Photoshop mutations are loss-of-function alleles in NMD genes: *Upf2* alleles
- 5) Photoshop mutations are loss-of-function alleles in NMD genes: *Upf1*, *Smg1*.
- 6) Photoshop mutations abolish or reduce NMD in a mutant transcript in vivo.
- 7) The SV40 3' UTR is targeted by NMD.
- 8) Targets of the NMD pathway during development.
- 9) *Drosophila* NMD genes are dispensable for many developmental processes but provide cells an advantage
- 10) Discussion: The role of NMD genes in *Drosophila* development, *Smg1*
- 11) Discussion: Targeting of a specific 3' UTR by the *Drosophila* NMD pathway

-----  
**Review:**

Define perdurance

Are *sp* and *Sp* alleles of the same gene?

Are *wg* and *Sp* alleles of the same gene?

**Types of allele (Muller's tests):**

For each of the following, select hypomorph, hypermorph, antimorph, neomorph, or null (haploinsufficient) as the best way of classifying the dominant allele (designated *Dom*). In each case, *Df* refers to a deficiency for the region including the dominant gene.

- 1) *Dom* / + has a phenotype that differs from wild-type, and *Dom* / + / + is more severe than *Dom* / + . *Dom* / *Df* / + is phenotypically equivalent to *Dom* / + . *Df* / + is normal (does not differ from +/+).
- 2) *Dom* / + has a phenotype which is phenotypically equivalent to *Df* / + and *Dom* / *Df* / + . *Dom* / + / + is normal (does not differ from +/+).
- 3) *Dom* / + has a phenotype, and *Dom* / + / + is less severe than *Dom* / + . *Dom* / *Df* / + is phenotypically equivalent to *Dom* / + . *Df* / + is normal (does not differ from +/+).
- 4) *Dom* / + has a phenotype. That phenotype is equivalent to those seen with both *Dom* / + / + and *Dom* / *Df* / + . *Df* / + is normal (does not differ from +/+).

**General *Drosophila* questions.** These questions test your new knowledge of *Drosophila* nomenclature, serve as a review of basic mendelian genetics, and give you experience using online resources. Some of the information you need to answer these questions was presented in the fly handout. For some questions you will also need to consult the online resources flybase ([flybase.bio.indiana.edu](http://flybase.bio.indiana.edu)).

5. In crosses among flies in a balanced stock such as *l(2)gl* / *SM5*, *In(2LR)SM5*, *Cy*, (in other words, when the flies in the stock mate among themselves) what fraction of embryos survive to adulthood?
6. In a cross between two strains carrying the *SM5* balancer: *l(2)gl* / *SM5*, *In(2LR)SM5*, *Cy* females X *Sp* / *SM5*, *In(2LR)SM5*, *Cy* males what fraction of embryos survive to adulthood?
7. In this same cross, what fraction of the resulting adults will have curly wings?

**Questions about your gene.** You should be able to get to flybase gene pages from NCBI using your gene accession number (e.g. the GenBank page for NP\_477205 will take you to [flybase.bio.indiana.edu/reports/FBgn0016978.html](http://flybase.bio.indiana.edu/reports/FBgn0016978.html)). You will also want to look at your gene in other *Drosophila* species on the [UCSC browser](#). I also encourage you to look at the alignment with other *Drosophila* species and otherwise explore a bit. For example, snRNP70K is at chr2L:6,969,825-6,971,736.

8. What protein refseq accession number are you using for your gene in *Drosophila*?
9. What is the cytological position of your gene (e.g. 27D or 93D)?
10. Is there a P insertion in your gene? If not, what is the nearest P element to your gene (e.g. l(2)02107). What phenotypes (if any) are observed in mutant alleles of your gene?