

# MCB 142 Discussion

Hana Lee

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## 1 Announcements

Exams will be handed back this week. If you wish to submit your exam for a regrade, you have one week to submit the exam to me or Prof. Amacher with a cover sheet of one page explaining why you believe your answer should be reevaluated.

Please don't hesitate to come talk to me if you are concerned about your grade.

## 2 Practice Problems

### 2.1 *C. elegans* Portrait: C-10

The *unc-54* (uncoordinated) and *daf-8* (dauer constitutive) genes are 18 m.u. apart on chromosome I of *C. elegans*. You want to construct a worm strain homozygous for mutations in both genes. Stocks of wild-type males and *unc-54*<sup>-</sup> / *unc-54*<sup>-</sup> hermaphrodites and *daf-8*<sup>-</sup> / *daf-8*<sup>-</sup> hermaphrodites are available for your use. The first cross is wild-type males x *unc-54*<sup>-</sup> / *unc-54*<sup>-</sup> hermaphrodites.

- What progeny of this first cross will you use for the second cross?
- What progeny arise from your second cross?
- What worms will you use for the final cross to get the desired double homozygote?
- What event has to happen to get a double homozygote?
- What proportion of the progeny will have the desired genotype?

### 2.2 Lecture 9 Problem

Mutations in the *him-8* gene give rise to a recessive High incidence of males (Him) phenotype; hermaphrodites that are homozygous for *him-8* mutations produce almost 40% male self-progeny. Surprisingly, *him-8* mutations do not

produce high numbers of inviable progeny (dead embryos), in contrast to mutations in most other *him* genes.

- Why might this be?

You are interested in determining which gene is *him-8*. You decide to map the gene. You first cross *him-8* males to the mapping strain *unc-5 IV; dpy-11 V; lon-2 X*. About 1/4 of the Lon F<sub>2</sub> progeny and 1/4 of the Dpy F<sub>2</sub> progeny that you pick after the initial cross are Him, but only 4 out of the Unc F<sub>2</sub> progeny show the Him phenotype.

- What is the map distance between *him-8* and *unc-5*?

Next, you mate *him-8* males to *unc-24 dpy-20 IV* hermaphrodites and pick the cross progeny (nonUnc nonDpy) hermaphrodites. You let these self-fertilize, pick a bunch of F<sub>3</sub> to individual plates, and determine which of them are homozygous for the recombinant chromosome (only Unc or only Dpy). Because *unc-24* and *dpy-20* are genetically quite close together, you can assume that recombination in this interval is negligible in the F<sub>2</sub> generation.

You determine that of the homozygous Unc nonDpy F<sub>3</sub>s, 11 are nonHim and 19 are Him. Of the homozygous nonUnc Dpy F<sub>3</sub>s, 38 are nonHim and 20 are Him.

- *unc-24* is at genetic map position 3.5 on chromosome IV, and *dpy-20* is at 5.2. What genetic map position would you assign to the *him-8* gene based on these data?