**MCB 140, Fall 2006**
**LECTURE 9 PRACTICE PROBLEMS:**

(1) You have done a genetic screen in zebrafish and have identified two recessive embryonic lethal mutations with a similar phenotype – "bulging eyes". You map the mutations and they are linked. How will you know whether the two mutations identify the same or different genes? Describe what you will do and the expected results.

(2) You have isolated a recessive zebrafish mutation in a gene called *no tail* (*ntl*). (a) If one hundred haploid progeny of a *ntl* heterozygote (+ / *ntl*) female are scored, approximately how many haploids will be mutant and how many will be phenotypically normal? (b) When eggs from a *ntl* heterozygote female are treated with UV-inactivated sperm followed by pressure treatment to block the second meiotic division, one observes about 48 *ntl* mutant and 52 phenotypically normal gynogenetic individuals. (c) Is *ntl* located near or far away from the centromere? How did you figure that out?

(3) When creating gynogenetic diploid progeny from a female zebrafish heterozygous for a recessive pigment mutation *golden*, you observe 5 embryos with the *golden* mutant phenotype and 95 with a wild-type phenotype. How far is the *golden* locus from its centromere? How many of the wild-type fish carry recombinant chromosomes?

(4) Zebrafish gynogenetic diploids can be made in two ways: (1) pressure application of activated haploid eggs to block the second **meiotic** division and (2) heat shock of activated haploid eggs to block the first **mitotic** division. Gynogenetic diploid progeny are made from a female heterozgous at the *spadetail* (*spt*) locus (+ / *spt*) using both techniques. (a) If 100 pressure-treated haploids are scored, how many mutants and wild-type fish do you expect to see among the progeny? (b) If 100 heat-shock-treated haploids are scored, how many mutants and wild-type fish do you expect to see among the progeny? (The *spt* locus is about 40 cM from its centromere).

(5) You find a recessive zebrafish mutation, *silver* (*slv*), that causes extra iridiphores (silver pigment cells) to accumulate on the body. In order to map the *silver* gene, you score the early-pressure (EP)-induced half-tetrad progeny of a heterozygous *slv*/+ female. *(Hint: EP blocks the second meiotic division).* You observe 180 wild-type fish and 20 silver fish.
   (a) What is the genotype of fish carrying recombinant chromosomes? How many fish carry recombinant chromosomes?
   (b) What is the distance between the *silver* gene and its centromere?
   (c) You isolate a second mutation, *goldilocks* (*gdy*), that causes extra xanthophores (gold pigment cells) to accumulate on the fins. Zebrafish with silver bodies and golden fins would be highly prized, so you cross *slv*/*slv* fish to a *gdy*/*gdy* fish to generate an FI stock in which both genes are segregating. You then examine the EP-induced half-tetrad progeny from an F1 female. Among the progeny, you observe 20 goldilocks, 10 silver, and 70 wild-type fish. Using this data alone, can you say anything about the linkage relationship of the *silver* and *goldilocks* genes? Why or why not? Draw the best genetic map to explain the observed results. Indicate all relevant genetic distances, both between genes and between each gene and its centromere.