## MCB 140 GENERAL GENETICS, Fall 2006 LECTURE 9, SOLUTIONS TO PROBLEMS

- 1. Perform a complementation test. Mate a bulging eye1 heterozygous fish (blg1+ / blg1-) with a bulging eye2 heterozygous fish (blg2+ / blg2-). If blg1 and blg2 are mutant alleles of the same gene, then approximately 25% of the embryos of this cross should display the bulging eye phenotype.
- 2. (a) About 50 embryos will be wildtype and about 50 embryos will display the ntl phenotype. (b, c) The number of wildtype and mutant embryos is almost equal, meaning there is very little crossing over between the ntl gene and the centromere. The ntl gene is very near to its centromere. The distance of a gene to its centromere is  $[(1/2) \times (total-2q) / total] \times 100$ , which in this example is  $[(1/2) \times (100-96) / 100] \times 100 = 2$  map units.
- 3. The distance of a gene to it's centromere is  $[(1/2) \times (\text{total-}2q) / \text{total}] \times 100$ , where q is the number of mutant embryos. The small proportion of mutant embryos tells us that the golden gene is located far from its centromere. Plugging in the numbers...  $[1/2 \times (100-10) / 100] \times 100 = 45$  map units. Of the wildtype fish, 90 carry recombinant chromosomes.
- 4. (a) Since the spt gene is 40 map units from its centromere, we can figure out the number of mutants to expect by distance =  $[1/2 \times (total-2q) / total] \times 100$ , where total = 100 and the distance is 40 map units. Equation:  $40 = (1/2)(100-2q)/100 \times 100$ ; therefore q (number of mutants observed) should be about 10 and the number of wild-type embryos should be about 90. (b) Expect about 50 wild-type and 50 spt mutant embryos among the heat-shock gynogenetic progeny.
- 5. (a) The genotype of fish carrying recombinant chromosomes is slv/+. Of the 200 total progeny, 160 fish carry recombinant chromosomes. Math: Recombinants (r+s) = total 2 mutants (q) = 200 2(20) = 160

(b) Distance between *slv* and centromere = ([1/2 (total - 2q)] / 200) \* 100= ([1/2 (200 - 40)] / 200) \* 100 = (80/200) \* 100 = 40 m.u.

(c) If two zfish genes are linked, the only way to get a doubly homozygous mutant halftetrad from a transheterozygous female is with a 4-strand double crossover. Double crossovers are rare in zebrafish (high interference). If two zebrafish genes are unlinked, then we expect to see double mutants due to independent assortment during meiosis. Since no double mutants are observed, we can say that the *slv* and *gdy* genes are linked.

Distance between gdy and centromere = ([1/2 (total - 2q)] / 200) \* 100= ([1/2 (100 - 40)] / 100) \* 100 = 30 m.u.

-----*gdy*-----*slv* -----<------30 m.u.----> <-----> 40 m.u.--->