2005 7.03 Problem Set 2

Due before 5 PM on FRIDAY, September 30, 2005.
Turn answers in to the box outside of 68-120.
PLEASE WRITE YOUR ANSWERS ON THIS PRINTOUT.

1. A single gene determines coat color in a fuzzy creature you have discovered. The males of this species are either gray or brown, and the females are either gray, brown, or gray-and-brown striped.

(a) What is the most likely mode of inheritance for coat color in this creature?

(b) A very large litter of pups is produced, and every brown pup in the litter is male. What are all of the possible combinations of parents that produced this litter? (Include both the phenotype and genotype of both the mother and father for each possible mating.)

2. You are studying three X-linked recessive mutations in flies. Two of these mutations are in the same gene, the bl gene. The bl-1 mutation causes the phenotype of black bodies (wild-type flies have brown bodies). The bl-2 mutation also causes the phenotype of black bodies. The cw mutation causes the phenotype of curly wings (wild-type flies have straight wings). You cross true-breeding bl-1 curly-winged females to bl-2 males to obtain an F1 generation. You then cross female F1 flies to wild-type males. You analyze 5000 resulting males, and find the following numbers of flies:

Phenotype		Number of flies
Brown bodies	Straight wings	1
Brown bodies	Curly wings	6
Black bodies	Straight wings	2505
Black bodies	Curly wings	2488

(a) What are the phenotype(s) and genotype(s) of the F1 females?

(b) What are the phenotype(s) and genotype(s) of the F1 males?

(c) Why is it not necessary to cross the F1 females to homozygous recessive males (as it is in other three factor crosses we discussed in class)?

(d) Why do we only see four phenotypic classes in the F2 generation, instead of eight (as we saw in other three factor crosses we discussed in class)?

(e) Draw a map showing each of the possibilities for the relative order of the bl-1, bl-2, and cw loci. Draw any orders that are possible <u>before</u> you analyze the number of F2 flies.

(f) For each of your possible maps above, state the minimum number of crossovers required (during meiosis in the F1 female) to create a brown straight-winged male, and the minimum number of crossovers required to create a brown curly-winged male.

(g) Draw the map that shows the correct relative locations of the bl-1, bl-2, and cw loci.

3. Consider the above problem, in which we discussed how you have two mutations in the bl gene of Drosophila. Each mutation on its own (bl-1 or bl-2) or both mutations together will cause flies to have black bodies instead of brown bodies (like wild-type flies). Say you mate a true-breeding bl-1 female to a bl-2 male to generate the F1 generation.

(a) Draw a cell in an F1 female that is neither going through mitosis or meiosis (but is rather dormant in the G0/G1 stage of the cell cycle). Make sure to draw the X chromosome as being long, so that it would be much longer than the Y chromosome. Also please draw one other chromosome of an intermediate length that is an autosome. Also be sure to mark the alleles present on each chromosome at the bl-1 and bl-2 loci.

You cross an F1 female with a wild-type male, and obtain one brown-bodied male after much searching. Draw one cell from the F1 female gonad going through the various stages of meiosis to generate an egg cell that could have produced this brown-bodied male fly following fertilization. Each time you draw a step, follow the format described in part **(a)**. Draw the following steps only.

(b) The cell after DNA replication, but before the first cell division of meiosis has begun.

(c) The cell in metaphase I with its chromosomes lined up, after any recombination events have occurred, but before the crossing-over has been resolved.

(d) The two cells in metaphase II with their chromosomes lined up.

(e) The four final products of the meiosis. (Please indicate the gamete that led to the creation of the brown-bodied male with a star.)

4. You are studying two different mutations in yeast that both give the same phenotype. Either the Ts-1$^-$ mutation or the Ts-2$^-$ mutation alone causes the phenotype of temperature sensitivity, in the sense that each single mutant yeast is able to grow at 30°C and 33°C as usual, but is not able to grow at 36°C.

You are interested in determining whether the Ts-1 and Ts-2 loci are linked to each other, and whether the Ts-1$^-$ and Ts-2$^-$ mutations are in the same gene or not.

You mate a Ts-1$^-$ haploid mutant strain to a Ts-2$^-$ haploid mutant strain, producing a diploid strain. You can then starve these diploid yeast to induce meiosis and produce tetrads, each of which is a group of four haploid spores bundled together. Theoretically, you could get three different types of tetrads out of this experiment. You know what phenotype to expect from a wild-type spore and a single mutant spore, but not a double mutant spore.

(a) Given what you know, fill out the three tables below. Note that a few lines are already filled in for you. **Remember, the three tetrad types should all be distinct from one another.**

Tetrad Type One

Type of Tetrad (circle one): PD or NPD or TT

	Genotype		**Phenotype**	
	at Ts-1 (+ or −)	at Ts-2 (+ or −)	Growth at 33°C (yes or no)	Growth at 36°C (yes or no)
Spore A				
Spore B			**no**	**no**
Spore C				
Spore D			**no**	**no**

Tetrad Type Two

Type of Tetrad (circle one): PD or NPD or TT

	Genotype		**Phenotype**	
	at Ts-1 (+ or −)	at Ts-2 (+ or −)	Growth at 33°C (yes or no)	Growth at 36°C (yes or no)
Spore A				**no**
Spore B				**no**
Spore C				**yes**
Spore D				**no**

Tetrad Type Three

Type of Tetrad (circle one): PD or NPD or TT

	Genotype		**Phenotype**	
	at Ts-1 (+ or −)	at Ts-2 (+ or −)	Growth at 33°C (yes or no)	Growth at 36°C (yes or no)
Spore A				
Spore B				
Spore C				
Spore D				

State how many PDs, NPDs, and TTs would result (out of a total of 36 tetrads), given that each of the three different scenarios are true:

(b) The Ts-1 and Ts-2 loci lie extremely close to each other in the same gene.

(c) The Ts-1 and Ts-2 loci are unlinked.

(d) The Ts-1 and Ts-2 loci are about 3 cM apart and are in different genes.