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?
X-linked codominant

The fact that the females (who have two alleles of an X-linked gene) can show both phenotypes (gray and brown) at the same time, but males (who have one allele only of an X-linked gene) can only either be gray or brown implies codominance. Note that incomplete dominance would have yielded the results that females could be either gray, brown, or one color spread evenly throughout their fur that is a color that is a blend of gray and brown.

X^GX^G: gray female
X^BX^G: brown-and-gray striped female
X^BY: brown male
X^GY: gray male

(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.)

mother: brown X^BX^B or X^BX^G
father: gray X^GY

The problem states that every brown pup is male, so we know that the mother carries allele X^B. The father does not, as if he did, some brown pups would be female. So we know the father's genotype is X^GY and the mother is $X^BX^?$. However, while we are given that every brown pup is male, this does not mean that every male pup is brown, so therefore some males could be gray. The mother can therefore have the genotype of X^BX^B or X^BX^G.

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?
cw+ = straight wings and cw = curly wings

The original P generation flies were $X^{bl\text{-}1\ cw}\ X^{bl\text{-}1\ cw}$ crossed to $X^{bl\text{-}2\ \ cw+}\ Y$

All female flies resulting from this cross would be:
$X^{bl\text{-}2\ \ cw+}\ X^{bl\text{-}1\ cw}$
black bodies, straight wings

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

The original P generation flies were $X^{bl\text{-}1\ cw}\ X^{bl\text{-}1\ cw}$ crossed to $X^{bl\text{-}2\ \ cw+}\ Y$

All male flies resulting from this cross would be:
$X^{bl\text{-}1\ \ cw}\ Y$
black bodies, curly wings

(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)?

We usually cross to a homozygous recessive male because we want to see in the F2 every contribution that the heterozygous mother made to the offspring. By crossing to a homozygous recessive male, any allele that the mother gives to her offspring automatically determines the offspring's phenotype. However, when the trait is X-linked, there is another way to ensure that the mother entirely controls the phenotype of her offspring, and this is to analyze only males in the F2 (which is what the introduction to this

question states that we do). If we are only looking at F2 males, and all of the loci we are examining are X-linked, then the mother automatically is the sole influence on the phenotype of her (male) offspring. Thus we can cross the F1 heterozygous mother to any male, as long as we only examine males in the F2.

(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)?

Two of the "factors" give the same phenotype. In other three factor crosses we did in class, each of the three "factors" controlled different aspects of phenotype, and there were two possible phenotypes (wild-type or mutant) resulting from each factor. Thus there were 2 X 2 X 2 = 8 possible phenotypic classes in the F2. Here there are only 2 X 2 = 4 phenotypic classes (because the flies can be either black or brown, and either straight or curly).

(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 before you analyze the number of F2 flies.

____bl-1 _bl-2 _____cw___ OR ____bl-2_bl-1_____cw___

The other putative order (cw in the middle) is not possible, knowing that bl-1 and bl-2 are alleles of the same gene. However, for typical three factor crosses in which all three mutations are alleles of distinct genes, all three putative orders could be true before you analyze the F2 progeny.

(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.

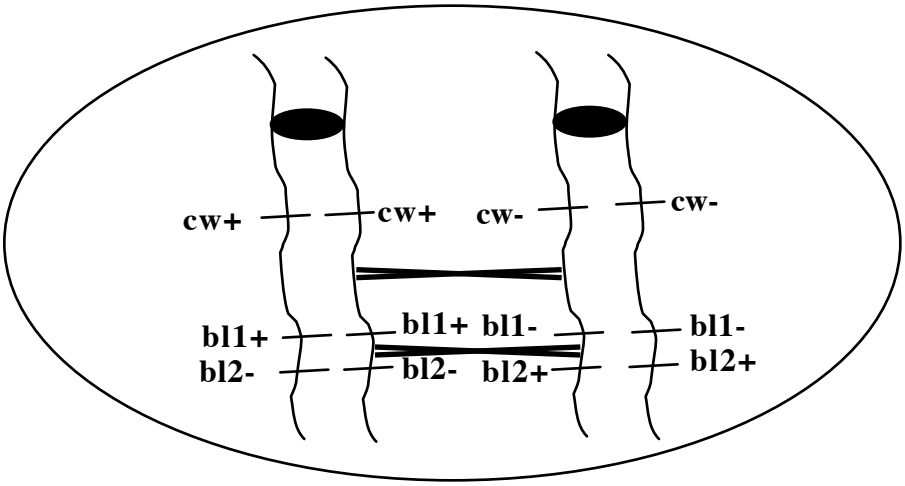
If bl-1 is in the middle:
2 crossovers for brown, curly-winged male
1 crossover for brown, straight-winged male

If bl-2 is in the middle:
1 crossover for brown, curly-winged male
2 crossovers for brown, straight-winged male

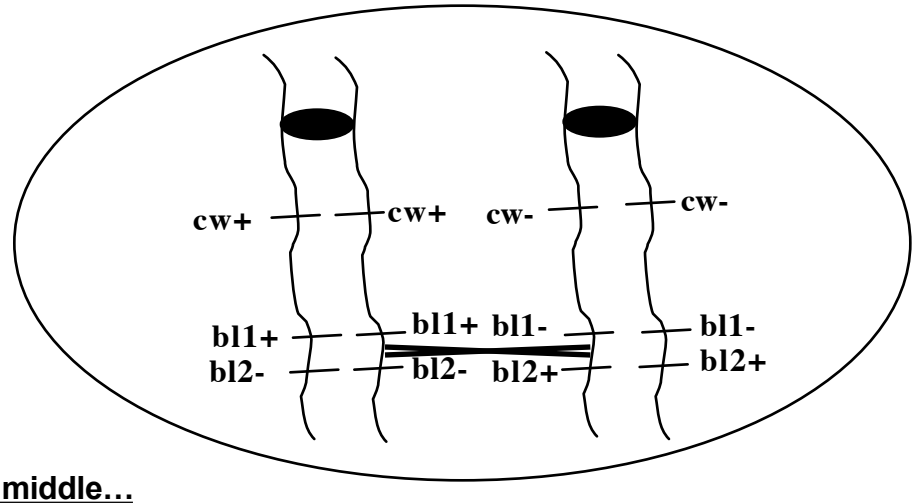
Consider the homologous chromosomes in the F1 female recombining during meiosis:

<u>If bl-1 is in the middle…</u>

To make a chromosome during meiosis that would generate a brown curly male, the following recombination events would have had to occur during meiosis I:

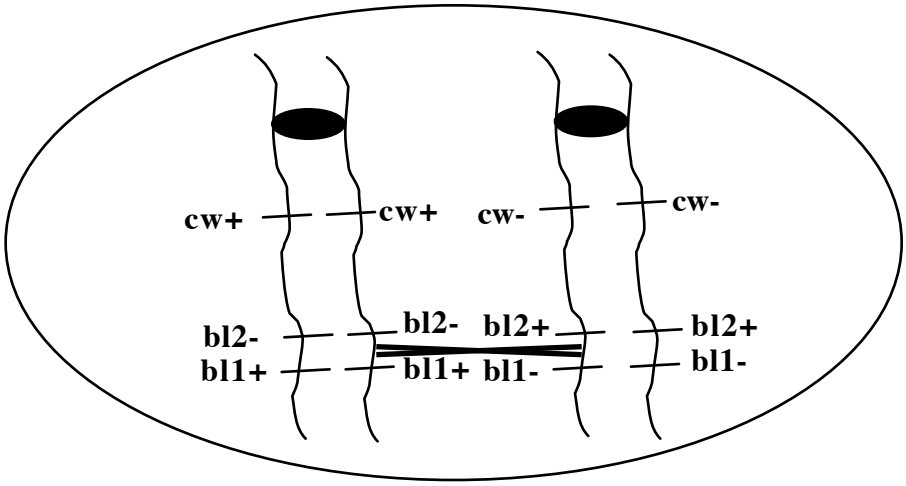


To make a chromosome during meiosis that would generate a brown straight male, the following recombination events would have had to occur during meiosis I:

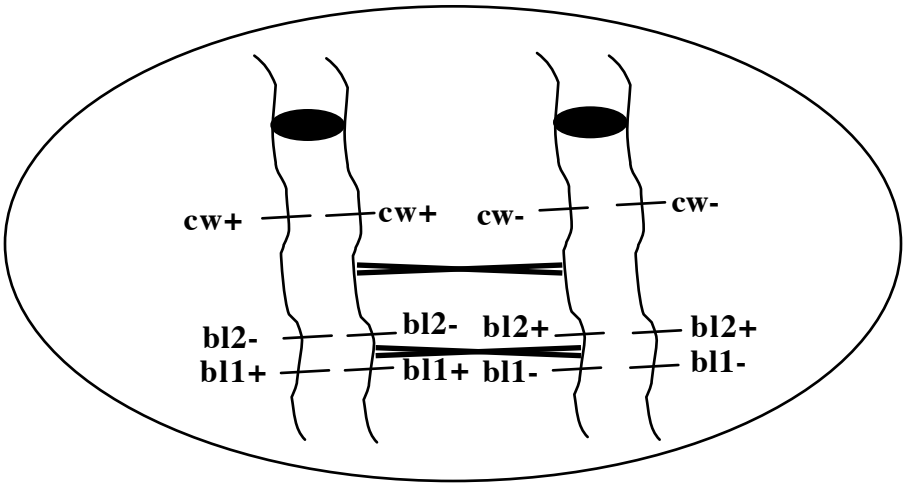


<u>If bl-2 is in the middle…</u>

To make a chromosome during meiosis that would generate a brown curly male, the following recombination events would have had to occur during meiosis I:



To make a chromosome during meiosis that would generate a brown straight male, the following recombination events would have had to occur during meiosis I:



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

Now, when you look at the data, you see that it was more frequent to get a brown curly male than a brown straight male. This data from the F2 is consistent with the order:

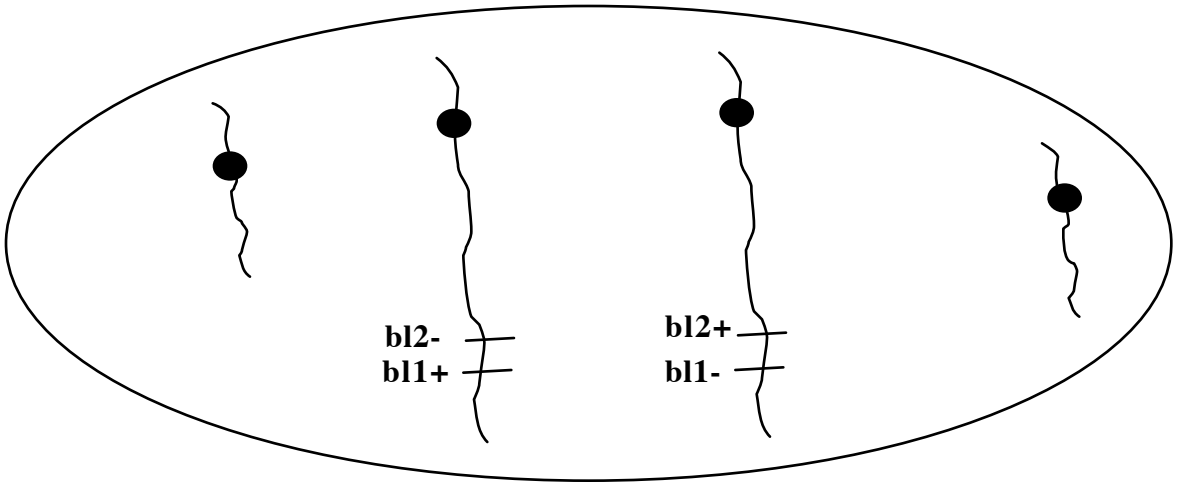
____bl-1 _bl-2 _____cw___

(bl-2 in the middle)

This is because single crossovers are more common than double crossovers. Thus, for the order with bl-2 in the middle, one would predict from part (f) that brown curly males would be more frequent than brown straight males. (Part (f) also tells you that, if the order had been that in which bl-1 is in the middle, you would expect brown straight males to be more frequent than brown curly males.)

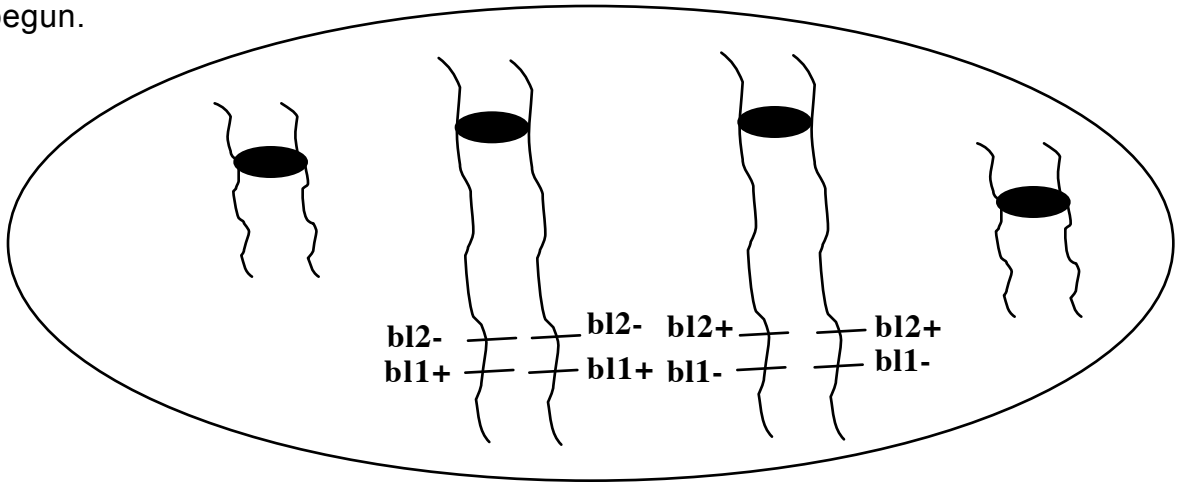
3. Consider the above problem, in which we discussed how you have two mutations in the bl gene of Drosophila. Each mutation on its own (bl-1 or bl-2) or both mutations together will cause flies to have black bodies instead of brown bodies (like wild-type flies). Say you mate a true-breeding bl-1 female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

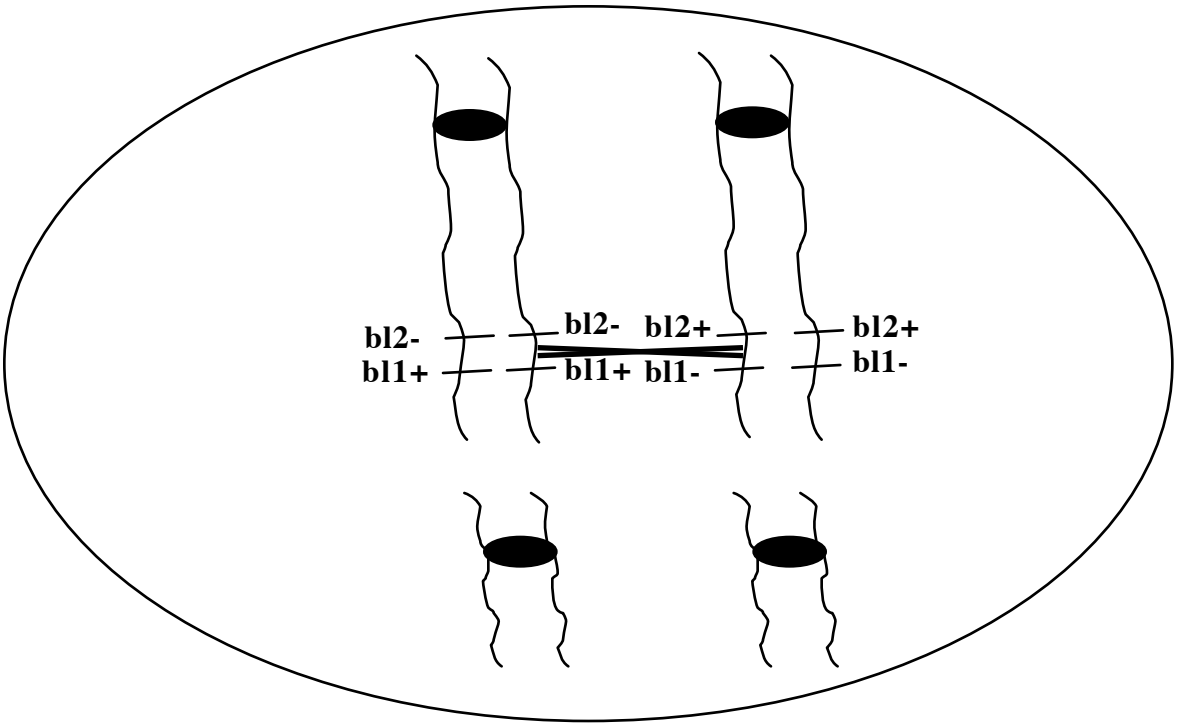


You cross an F1 female with a wild-type male, and obtain one brown-bodied male after much searching. Draw one cell from the F1 female gonad going through the various stages of meiosis to generate an egg cell that could have produced this brown-bodied male fly following fertilization. Each time you draw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

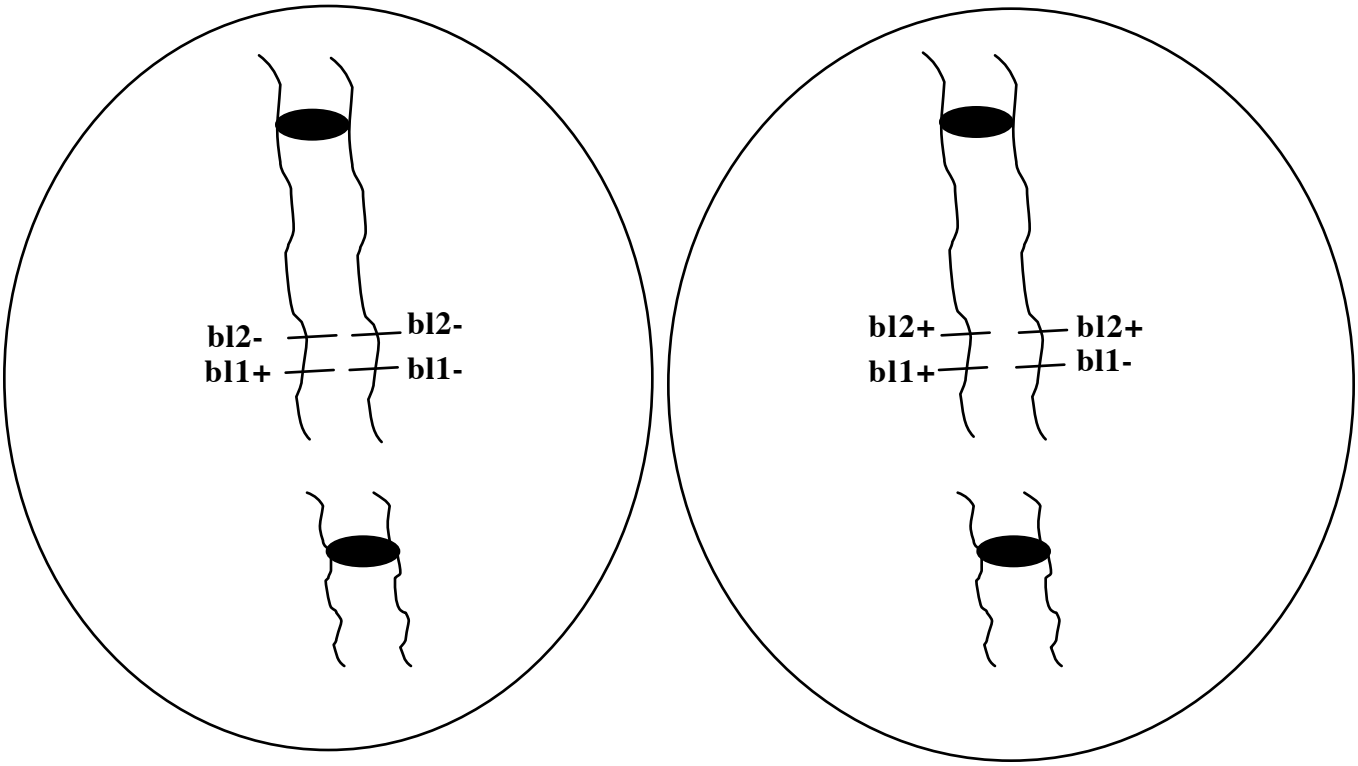
(b) The cell after DNA replication, but before the first cell division of meiosis has begun.



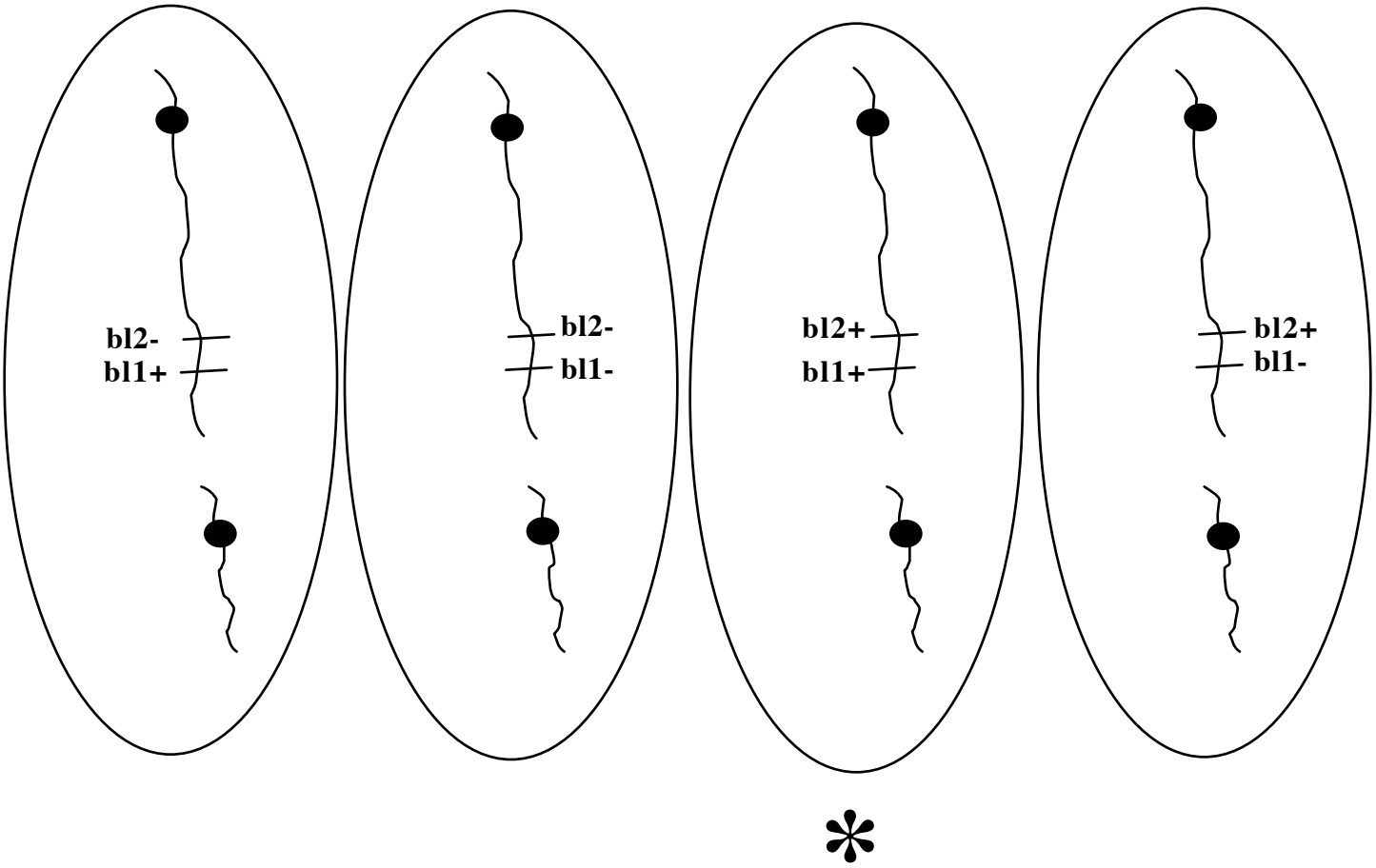
(c) The cell in metaphase I with its chromosomes lined up, after any recombination events have occurred, but before the crossing-over has been resolved.



(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.)



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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

Let "+" indicate wild-type and "-" indicate ts-1 or ts-2

	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	+	+	Yes	yes
Spore B	-	-	**No**	**no**
Spore C	+	+	Yes	yes
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	+	-	Yes	**no**
Spore B	-	+	yes	**no**
Spore C	+	+	Yes	**yes**
Spore D	-	-	No	**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	+	-	Yes	no
Spore B	+	-	Yes	no
Spore C	-	+	Yes	no
Spore D	-	+	Yes	no

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.

Almost entirely PDs (36 PDs).

An exact number cannot be calculated without more information. However, when two genes of interest are linked, PD is much greater than NPD. NPDs are products of double crossovers and TTs are products of single crossovers or double crossovers, so both would be rare or nonexistent for small samples sizes (i.e. 36 tetrads) in cases of extreme linkage.

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

6 PD, 24 TT, and 6 NPD

This follows the rule that, when two loci are unlinked, one sees a ratio of 1 PD : 4 TT : 1 NPD due to random segregation of Ts-1 with respect to Ts-2 during meiosis.

Given the following associations of Ts-1 with Ts-2, the resultant tetrad types are on the right. This gives us 1 PD to 4 TT to 1 NPD.

Ts-1	**Ts-1**	**+**	**+**	
Ts-2	Ts-2	+	+	NPD
Ts-2	+	Ts-2	+	TT
Ts-2	+	+	Ts-2	TT
+	Ts-2	+	Ts-2	TT
+	Ts-2	Ts-2	+	TT
+	+	Ts-2	Ts-2	PD

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

TT = 2 (or 3)
NPD = 0
PD = 34 (or 33)

Use the formula

$$\text{map distance} = \frac{6\,\text{NPD} + \text{TT}}{2 \times (\#\ \text{tetrads})} \times 100$$

you can see that, even if you got 1 NPD and no TTs, the distance you would calculate from your data would be much greater than 3cM. Thus you must have gotten no NPDs. Substituting 0 = # of NPDs, you then calculate:

$$\frac{\text{TT}}{72} \times 100 = 3$$

Thus TT = 2.16

This makes sense, because 3cM translates to a 3% chance of getting recombination between Ts-1 and Ts-2. This means that these two loci are quite close to each other, making the probability that you will see double crossovers very low, especially if you only look at 36 tetrads.