Name: _____

7.03 - Genetics - Fall 2004
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1. You are studying three autosomal recessive mutations in the fruit fly *Drosophila melanogaster.* Flies that are homozygous for the hb⁻ mutation are "humpbacked" (wild-type flies are straight-backed). Flies that are homozygous for the bl⁻ mutation are "blistery-winged" (wild-type flies are smooth-winged). Flies that are homozygous for the st⁻ mutation are "stubby-legged" (wild-type flies are long-legged).

You mate flies from two true-breeding strains, and the resulting F1 flies are all are straight-backed, smooth-winged, and long-legged. F1 females are then mated to males that are humpbacked, blistery-winged, and stubby-legged. In the F2 generation, among 1000 progeny resulting from this cross, you observe the following phenotypes:

Phenotype	Number
humpbacked, blistery-winged, and stubby-legged	(26 flies)
humpbacked, blistery-winged, and long-legged	(455 flies)
humpbacked, smooth-winged, and long-legged	(24 flies)
straight-backed, blistery-winged, and stubby-legged	(27 flies)
straight-backed, blistery-winged, and long-legged	(4 flies)
straight-backed, smooth-winged, and stubby-legged	(442 flies)
straight-backed, smooth-winged, and long-legged	(22 flies)

(a, 6 pts.) The male flies that were bred to the F1 generation in order to produce the F2 generation were humpbacked, blistery-winged, and stubby-legged. On each of their chromosomes, they have the alleles hb⁻ bl⁻ st⁻. Using this notation, **state the genotype** of each of the two true-breeding parental strains (i.e. the two strains in the **P generation**).

Genotype of one parental strain:

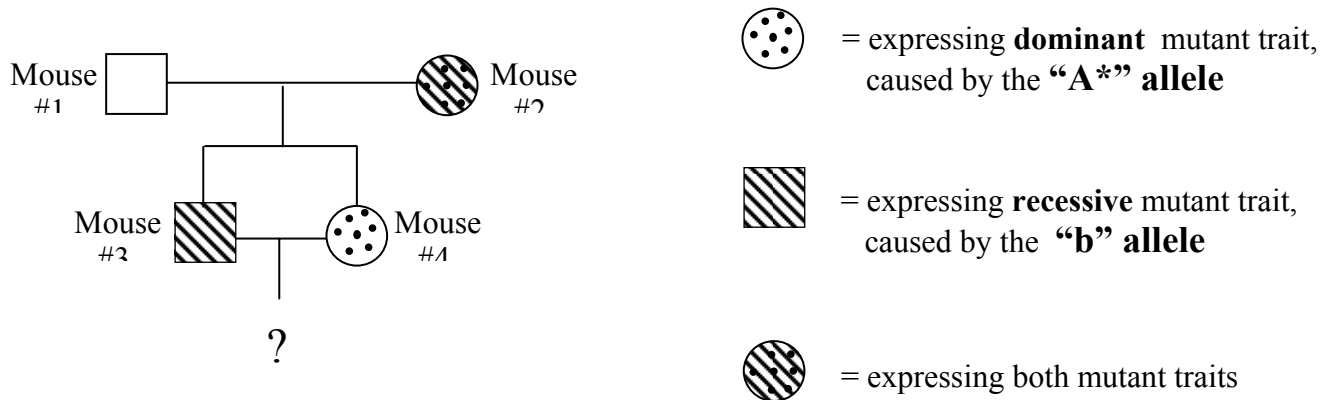Genotype of the other parental strain:

(b, 6 pts.) How many flies are found in the class that is the reciprocal class of the humpbacked, blistery-winged, and stubby-legged flies?

(c, 7 pts.) What is the genetic distance between the **hb** and **bl** loci? (Label your answer with the proper units.)

(d, 7 pts.) What is the genetic distance between the **bl** and **st** loci? (Label your answer with the proper units.)

(e, 6 pts.) Draw a genetic map showing the correct order of the **hb**, **bl**, and **st** loci.

2. The following mouse pedigree shows the segregation of two different mutant traits. The mutant trait indicated by the dots is dominant, whereas the mutant trait indicated by the stripes is recessive. Assume 100% penetrance and no new mutations.
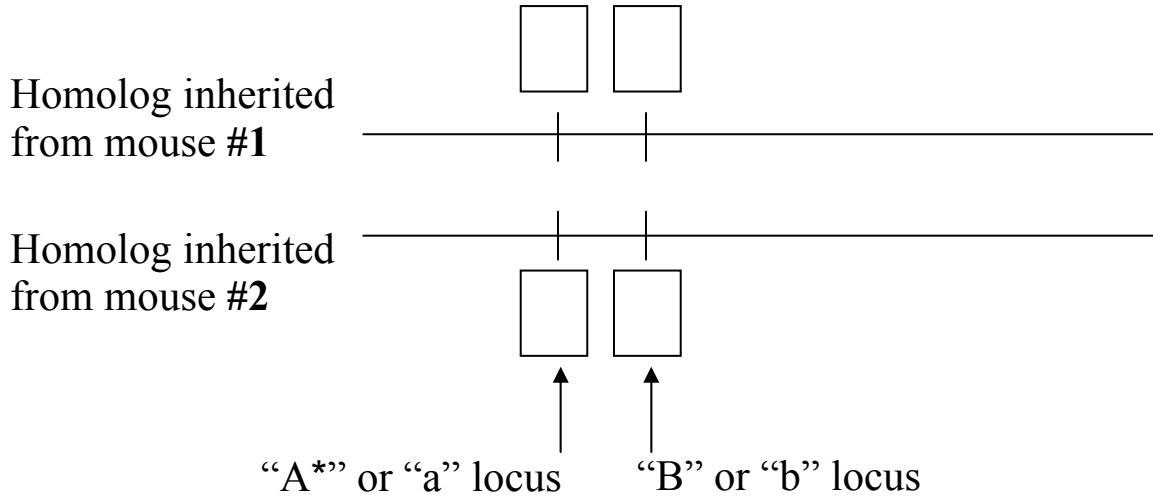(Squares = males, circles = females.)

Mouse #1   Mouse #2

Mouse #3   Mouse #4

?

= expressing **dominant** mutant trait, caused by the **"A*" allele**

= expressing **recessive** mutant trait, caused by the **"b" allele**

= expressing both mutant traits

(a, 6 pts.) Assuming that both mutant traits are due to linked autosomal genes that are 6 cM apart, **fill in** the following chart using the allele notation indicated by the key above. Blocks in the chart that cannot be filled in conclusively should be indicated as "*inconclusive*."
<u>NOTE:</u> One line of the chart is already filled in correctly for you.

	Number of "A*" alleles	Number of "a" alleles	Number of "B" alleles	Number of "b" alleles
Mouse #1				
Mouse #2				
Mouse #3	0	2	0	2
Mouse #4				

(b, 6 pts.) Assuming that both mutant traits are due to linked autosomal genes that are 6 cM apart, fill in the boxes with the alleles possessed by mouse #4 on each of the two homologs of this autosome that are depicted in the diagram below.

Homolog inherited from mouse **#1**

Homolog inherited from mouse **#2**

"A*" or "a" locus   "B" or "b" locus

(c, 7 pts.) Assuming that both mutant traits are due to linked autosomal genes that are 6 cM apart, what is the probability that the mouse indicated by a question mark will show **both** mutant traits (the trait encoded by "A*" **and** the trait encoded by "b")?

(d, 8 pts.) Assuming that the **recessive** mutant trait is caused by a gene on an autosome and the **dominant** mutant trait is caused by a gene on the X chromosome, **fill in** the following chart using the allele notation indicated by the key above. Blocks in the chart that cannot be filled in conclusively should be indicated as "*inconclusive*."

	X-linked		autosomal	
	Number of "A*" alleles	Number of "a" alleles	Number of "B" alleles	Number of "b" alleles
Mouse #1				
Mouse #2				
Mouse #3				
Mouse #4				

(e, 6 pts.) Assuming that the **recessive** mutant trait is caused by a gene on an autosome and the **dominant** mutant trait is caused by a gene on the X chromosome, what is the probability that the mouse indicated by a question mark will show **only** the recessive mutant trait **assuming that the mouse is born female**?

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3. You are working with a mutant strain of yeast that is dark tan (wild-type yeast are white). The "dark tan" phenotype of the haploid cells you are working with is caused by two different mutations in the same strain. The two mutations are designated drk1⁻ and drk2⁻.

(a, 6 pts.) Mating of the **drk1⁻ drk2⁻** double mutant to **wild-type** yeast produces diploids that are white. Sporulation of these diploids yields 50 tetrads. 4 of these tetrads (called "Type One") contain four light tan spores. 37 of these tetrads (called "Type Two") contain two dark tan spores and two white spores. 9 of these tetrads (called "Type Three") contain one dark tan spore, two light tan spores, and one white spore.
Categorize **each** of the tetrad types as parental ditype (PD), tetratype (TT), or nonparental ditype (NPD).

(b, 6 pts.) Are the drk1⁻ and drk2⁻ mutations linked? **If so,** give the distance between them. (Label your answer with the proper units.)

(c, 6 pts.) In yeast, 1 cM of genetic distance corresponds to 3,500 base pairs of physical distance. An average yeast gene is about 1,400 base pairs long, and the longest yeast gene is 14,700 base pairs. Keeping this information in mind, you select a "Type Three" tetrad from part **(a)** and mate the two light tan spores from that tetrad to each other. Can you deduce the color of the resulting diploids? **If so**, what color would the diploids be?

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Next you isolate a mutant strain of yeast that cannot grow on medium lacking leucine. This strain contains a single mutation you call leu1⁻. The leu1⁻ mutation is near to drk1⁻ on the same chromosome. When the leu1⁻ mutant is mated to wild-type yeast, the resulting diploids cannot grow on medium lacking leucine.

(d, 9 pts.) You mate **leu1⁻** yeast to **drk1⁻** yeast and sporulate the resulting diploid. You grow the resulting spores on medium containing leucine. You then test for growth on medium lacking leucine. It is apparent that you have isolated only two types of tetrads, 10 tetrads of Type A and 10 tetrads of Type B. On medium lacking leucine, only two spores from each Type A tetrad can grow; both are light tan in color. Complete the chart below so as to indicate: **How many** spores from each Type B tetrad can grow on medium lacking leucine, **and what color** is each spore that can grow?

	# of spores that can grow on medium lacking leucine	color of each spore that can grow on medium lacking leucine
Type A tetrad	2	both are light tan
Type B tetrad		

(e, 8 pts.) What are the genotypes at the leu1 and drk1 loci of each of the two light tan spores from the Type A tetrads that grew on medium lacking leucine?

Genotype of one light tan spore:

Genotype of the other light tan spore: