Name:	KEY	

2006 7.012 Problem Set 2 KEY

Due before 5 PM on FRIDAY, September 29, 2006.

Turn answers in to the box outside of 68-120.

PLEASE WRITE YOUR ANSWERS ON THIS PRINTOUT.

1. You are doing a genetics experiment with the fruitfly *Drosophila melanogaster*. In the "P" generation, you cross two true-breeding flies. The two flies are a large-winged hairless female and a puny-winged hairy male. All of the flies in the F1 generation are large-winged and hairy.

Indicate the alleles associated with dominant phenotypes by a capital letter and alleles associated with recessive phenotypes by a lowercase letter. Assume the two traits you are following are autosomal. Indicate the hair alleles by the letters "H" and "h" and indicate the wing alleles as "G" and "g."

(a) The ge	(a) The genotypes of the flies in the P generation are:			
(GGhh	_ females and	ggНН	males.
The genoty	pes of the flies in the	e F1 generation a	re:	
	GgHh	_ females and	GgHh	males.
hairless ma This male's (b) You co	ike an F1 generation ale. s genotype is: unt 1600 offspring in ou would expect to c	gghh_ the F2 generatio	·	
400	_# of large-winged h	airy flies (of the g	enotype	GgHh)
400	_# of large-winged h	airless flies (of the	e genotype	Gghh)
400	_# of puny-winged h	airless flies (of the	e genotype	gghh)
400	_# of puny-winged h	airy flies (of the g	enotype	_ggHh

Unlinked genes assort independently from each other, this means that the GgHh female would create the four possible gametes (GH, gh, Gh, and gH) each 25% of the time. Each of these 4 different kinds of eggs would be fertilized by a sperm containing gh from the father (as he is doubly homozygous, there is only one kind of gamete he can produce).

Name:	KEY	•

(c) Instead, when you count the F2 generation, you really get:

85 large-winged hairy flies

712 large-winged hairless flies

75 puny-winged hairless flies

728 puny-winged hairy flies

What is the genetic distance between the hair and wing genes?

It is 10% or 10 cM. In the mother's chromosomes, the G and h allele go together and the g and H allele go together. (This is because of who her parents were; see the diagram below.) Therefore any gametes that she produces that are Gh or gH will be "parental type" and any gametes that she produces that are "GH" or "gh" will be recombinants. The two recombinant types of gametes produce puny-winged hairless flies and large-winged hairy flies. There are 85 large winged-hairy flies produced and 75 puny-winged hairless flies.

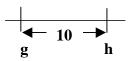
So the recombination frequency = $\frac{\text{\# of recombinants}}{\text{Total progeny}} \times 100$

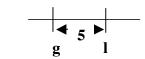
$$= \frac{85+75}{85+75+712+728} \times 100 = \frac{160}{1600} = 10\%$$

Therefore, the distance between the hair and wing genes is 10 cM.

(d) A series of fruit fly matings shows that the recombination frequency between the gene for wing size and the gene for antenna length is 5% (i.e. the genetic distance between them is 5 centimorgans). List all possible recombination frequencies between the gene for amount of hair and the gene for antenna length.

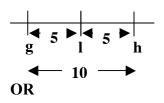
It could be 5% or 15%. This is because we know that:



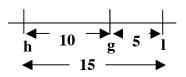


(l = antenna length)

These genes can be arranged in two ways:



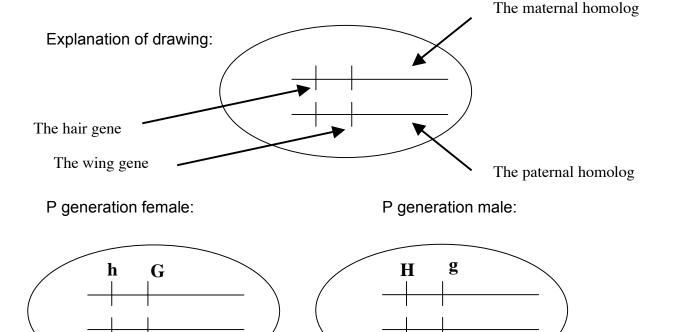
Distance between 1 and h = 10 - 5 = 5 cM Therefore, the recombination frequency would be 5 %.



Distance between l and h = 10 + 5 = 15 cM Therefore, the recombination frequency would be 15 %.

Name:	KEY	•

(e) Draw out the arrangement of the hair and wing genes in the nucleus of a randomly selected eye cell in the following flies (which are the same flies that were described above). Draw the genotype inside the circles below, which indicate a nucleus of an eye cell. The long lines represent the pair of homologous chromosomes that have the genes for the hair and wing traits on them. The tick marks indicate the position of the two genes. Write in a letter next to each tick mark in each cell to indicate which alleles exist at each of the two genes on each of the two homologs.



F1 generation female:

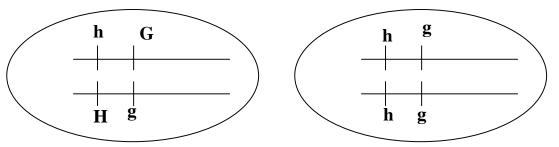
 \mathbf{G}

h

puny-winged hairless male (who was crossed to the F1 female):

H

g

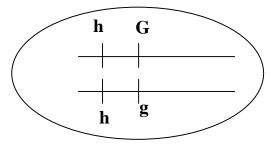


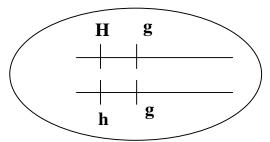
The F1 female must look like this because she had to get one chromosome from each of her parents.

Name:	KEY	•	
_			

The four possible F2 generation flies created by the cross of the F1 female to the puny hairless male:

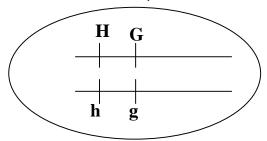
-- the two possible non-recombinants:

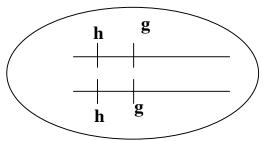




These F2s are non-recombinants because they received a chromosome from mom that did not require recombination to form. The other chromosome was received from their father.

-- the two possible recombinants:

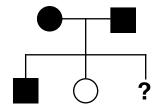


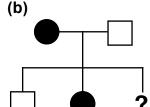


These F2s are recombinants because the chromosome they received from their mother does not exist in that arrangement in the mother's cells. Thus it must have required recombination to have formed. The other chromosome was received from their father.

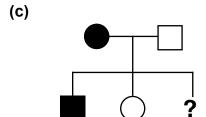
2. Each of the families below exhibits a different very rare genetic disorder where individuals expressing the disorder are shown by solid symbols. Give all possible modes of inheritance that are consistent with each pedigree (your choices are: autosomal recessive, X-linked recessive, X-linked dominant, or autosomal dominant). Also calculate the probability that the next child indicated by a (?) will be affected given each possible mode of inheritance. In the case of X-linked inheritance, calculate separate probabilities for sons and daughters.

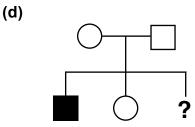
(a)





Name:	KEY	•
•		





(a) This pedigree <u>cannot represent a disorder following an autosomal recessive or X-linked recessive inheritance</u> because, if either of those were the case, all the progeny will be affected, because both parents would have only possessed the mutant alleles so that they would both show a recessive mutant disorder.

It <u>cannot be an X-linked dominant disorder</u> because all daughters would have been affected since all of them would have received a mutant allele from dad. Thus, <u>the only possible mode of inheritance is autosomal dominant</u>. Both parents are heterozygous (Aa) so the probability that the next child will be affected is ³/₄.

(b) This disorder cannot be X-linked recessive. If it had been, then no F1 females would have ever been affected because they would always receive a normal allele from dad. However, the disorder can be X-linked dominant, in which case the father would be X^aY (if we use the capital letter to indicate the allele that gives the dominant phenotype) and the mother would be X^aX^a. This would lead to a half of the daughters and a half of the sons being affected. Thus, the probability that the next child is affected is: ½ for females and ½ for males. This disorder can also be autosomal dominant. For this to be true, mom have to be heterozygous (Aa) and dad homozygous (aa), so ½ of the progeny will receive mutant allele from mom and will be affected.

The two possible modes of inheritance listed above are equally likely to be correct, since only 1 mutant allele total needs to be present in the parents in order to be consistent with the pedigree. In contrast, given that the disorder is very rare (as stated in the introduction), it is very unlikely (although formally possible) that the mode of inheritance is autosomal recessive. For this to occur, the mom would have to be homozygous for the mutant allele (aa) and the dad a carrier (Aa.) Therefore, 3 mutant alleles would have to be present in the P generation, which is improbable given that the disorder is very rare. If it were to occur that an affected female would happen to start a family with a carrier male, then the probability of having another affected child is ½.

(c) This pedigree most likely tracks an autosomal dominant disorder or an X-linked dominant disorder. For autosomal dominant to be true, mom has to be heterozygous (Aa) and dad homozygous (aa) so the probability of having an affected child is $\frac{1}{2}$. This pedigree can also represent an X-linked dominant disorder, in which case mom will be X^AX^A and dad X^AY . A half of the sons and a half of the daughters will receive the mutant allele from mom and will have the disorder. These 2 patterns of inheritance are the most likely (and are equally likely) since the presence of only 1 mutant allele in the P generation is enough to produce the pedigree as we see it.

Although less likely, X-linked recessive inheritance is also consistent with the pedigree, in which case mom will be homozygous (X^aX^a) and dad will have the normal allele (X^AY) . All

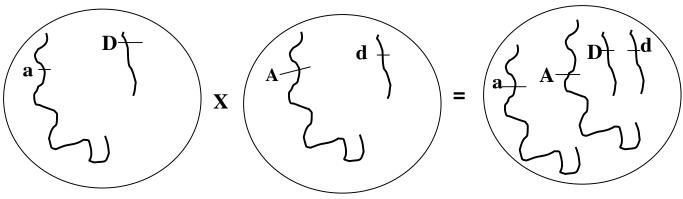
Name:	KEY	•

the sons will receive a mutant allele from mom; therefore the probability of a male child to be affected is 1. Since all daughters will receive a normal allele from dad, the probability of having a female child with the disorder is 0. This mode is less likely since it requires mom to have two mutant alleles, which is rare for an X-linked recessive trait. (Most people affected with an X-linked trait are male.)

It is also formally possible but very unlikely that the mode of inheritance is autosomal recessive; this mode is very unlikely since 3 mutant alleles would have to have met in the P generation to have this pedigree work with this mode of inheritance (mom would have to be aa and dad would be Aa). If this were the case, then the probability of having an affected child would be ½.

- (d) This disorder can neither be autosomal dominant nor X-linked dominant, otherwise one of the parents of an affected offspring should be affected. The disorder is most likely X-linked recessive. This would mean that mom is a carrier (XAXa) and dad is not (XAY). Thus, ½ of the sons will be affected. There will never be an affected daughter, since she will always receive an X chromosome from dad carrying the normal allele. It is formally possible that this disorder can also be autosomal recessive, with both parents being heterozygous (Aa). This would make the probability of having an affected child of ¼. However this mode of inheritance is less likely than X-linked recessive because it requires a male carrier and a female carrier to happen to meet, which is unlikely given how rare the allele is that confers the disorder.
- **3.** You are studying a type of yeast that has two different chromosomes in its genome. You have isolated three mutations, "a," "b" and "d," each of which causes the same phenotype. When you mate a strain containing any one of these three mutations to wild-type, the resulting diploid exhibits the wild-type phenotype. You are in the process of doing complementation tests with these mutants. You discover that "a" and "d" do complement each other, but "a" and "b" do not. The corresponding wild-type alleles are "A," "B" and "D." **Draw in the correct alleles** that exist at each of these loci (A, B, and D) in each of the six yeast cells drawn below. Make sure to put the alleles in their correct locations, as determined by those already drawn in for you. Also make sure to **draw in the chromosomes** to any cell whose chromosome(s) is/are missing.

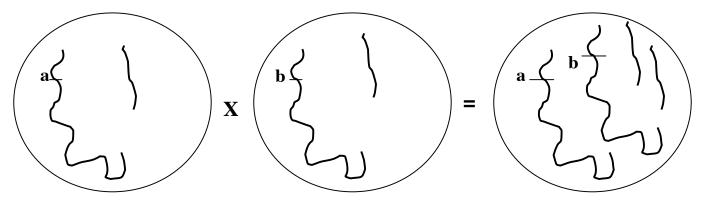
First cross: You mate haploid yeast of genotype "a" to haploid yeast of genotype "d."



Name:	KEY

Mutations "a" and "d" do complement, indicating that the two mutations lie in different genes. Each mutation is in one of two genes necessary for the wild-type phenotype. Two separate genes are involved; each mutant will have a lesion in one gene while maintaining a wild type copy of the second gene. When the diploid cell is produced, it will express the mutant allele a and the wild-type allele D. The diploid will also express the wild-type allele A and the mutant allele d. Because the diploid is expressing both of the necessary wild-type alleles, the wild-type phenotype is observed.

Second cross: You mate haploid yeast of genotype "a" to haploid yeast of genotype "b."



Mutations "a" and "b" do not complement, indicating that these two mutations occur in the same gene. Each homolog will express a mutant version of the gene in the diploid cell. Without any normal functioning gene product in the cell, a mutant phenotype occurs. The A/a alleles and the B/b alleles must be in the same location in the genome because they are in the same gene.

4. Shown below is a hypothetical scheme for the formation of eye pigment in *Drosophila*.



The enzyme encoded by the **Pr** gene converts a purple pigment into the normal red pigment in the eye. The **pr** allele causes the recessive phenotype of purple eyes. The enzyme encoded by **BI** gene converts a blue pigment into the purple pigment. The **bI** allele causes the recessive phenotype of blue eyes. Both the **Pr** and **BI** genes are on the X chromosome. A male from a true-breeding blue-eyed strain is crossed to a female from a true-breeding purple-eyed strain.

(a) All of the F₁ female progeny from this cross have normal eyes. What colored eyes should the F₁ male progeny have?

Name:_____KEY____

They should have purple eyes.

F1
$$\frac{pr^-bl^+}{Y}$$
 \xrightarrow{pr} and $\frac{pr^-bl^+}{pr^+bl^-}$ \bigcirc +

All males inherit the mutant pr- allele from the P female, so they will have purple eye color.

(b) An F₁ female fly (with normal eyes) is crossed to a wild-type male, and a large number of male progeny from this cross are examined. Among the male progeny, there are flies with normal red eyes, flies with purple eyes, and flies with blue eyes. You notice that significantly more male progeny have blue eyes than have purple eyes. In one sentence or less, state why this should be the case.

There are two acceptable ways to phrase this:

- 1) There are more blue eyed flies than purple flies because purple eyed flies can only result from a single mutant class of offspring, whereas blue eyed flies result from a single mutant class and from a double mutant class.
- 2) There are more blue eyed flies than purple flies because purple eyed flies can only result from a parental class of offspring, whereas blue eyed flies result from a parental class and from a recombinant class.

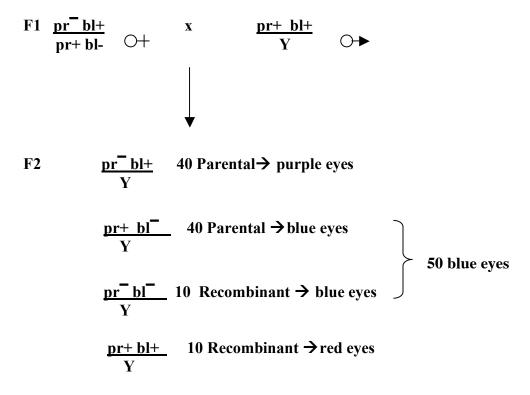
See the cross drawn out below part (c) for an explanation of why this statement is true.

(c) Given that the **Pr** and **BI** genes are 20 cM apart on the X chromosome (i.e. the recombination frequency between them is 20%), determine the number out of 100 <u>male</u> progeny from the cross in part (**b**) that should have purple eyes, blue eyes, or normal red eyes.

•	<u>Number</u>
Purple-eyed males:	40
Blue-eyed males:	50
Red-eyed males:	10
	Total = 100

Name:	KEY

Since the recombination frequency is 20%, there are 20% X 100 = 20 recombinants present out of 100 offspring. There will be two recombinant classes, each of which will exist in equal frequencies, so there will be 10 of one recombinant class and 10 of the other recombinant class. That leaves us with 80 parental offspring, which will fall into two equally probable classes, so there will be 40 of one parental class and 40 of the other parental class.



We are only looking at sons, and the male always gives the Y to his sons. So the sons' eye colors are determined by the mother. The mother will give one of her chromosomes to 40% of the males, the other of her chromosomes to 40% of the males, and recombinant chromosomes that she herself does not possess to 20% of her sons.

- **5.** In many of the classic experiments we discussed in lecture, scientists use different radioisotopes to label different components of the cell. Be as specific as possible in your answers below regarding these radioisotopes.
- (a) Which specific part of DNA is radioactively labeled by N¹⁵?

The nitrogen-containing bases.

(b) Which specific part of protein is radioactively labeled by S³⁵?

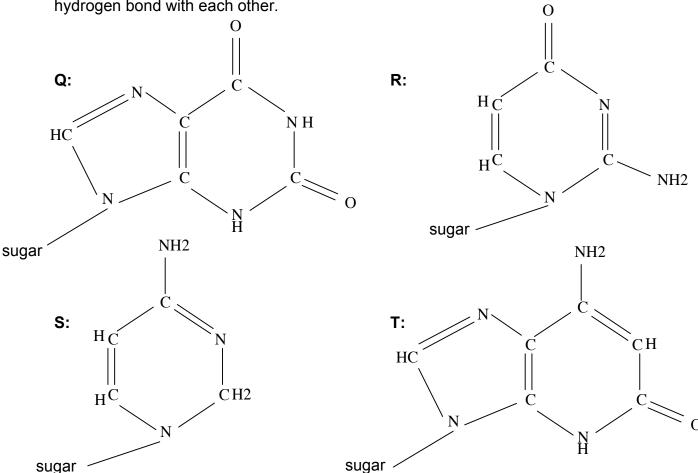
Name:	KEY	•	
_			

The two R groups of the 2 amino acids that contain sulfur – namely, Cysteine and methionine.

(c) Which specific part of DNA is radioactively labeled by P³²?

The phosphorous that is part of the phosphate group(s) that hang off the 5' carbon of the sugar that makes up the nucleotide.

6. Imagine an organism that uses the four following nitrogenous bases, drawn below. Other than the identity of the bases, assume that every other aspect of the structure and function of this organism's DNA is the same as the DNA of organisms that use A, G, C, and T. Just as with the usual A, G, C, and T, there are two exclusive pairs of bases that hydrogen bond with each other.



Name:KEY_	
-----------	--

(a) Which base do you think pairs with each base below? Circle one base for each
--

Q base pairs with...? (circle one) Q R Т R base pairs with...? (circle one) Q R S S base pairs with...? (circle one) (Q) R S Т T base pairs with...? (circle one) Q (R) S Т

We know that, in DNA, one purine always basepairs with one pyrimidine, so when we look at T (a purine, because it has two rings), we know it will base-pair with either R or S, the two pyrimidines (because they have one ring). If we flip S over and line it up with T as it would in DNA, three sets of chemical groups line up with each other:

Two NH2 groups

An N and a CH

A CH2 with a C ==O

None of these three pairs of chemical groups can hydrogen bond with each other.

Therefore, T must bind with R. If you flip R over and line it up with T, you get the following chemical groups lined up with each other:

C=O and NH2

N and CH

NH2 and C=O

The top and the bottom sets can Hydrogen bond with each other, so R forms 2 H bonds with T.

Now you can flip S over and line it up with Q. The chemical groups that align are:

C=O and NH2

NH and N

C=O and CH2

The top two sets can Hydrogen bond with each other, so S forms 2 H bonds with Q.

(b) Draw one pair of bases, aligning them as they would in a double stranded DNA molecule, and showing the hydrogen bonds that could occur between them. (You do not have to draw the entire nucleotides; you only have to draw the nitrogenous bases.)

Name:_____KEY____

Draw each hydrogen bond as a series of short dashes:

(c) Draw the other pair of bases, aligning them as they would in a double stranded DNA molecule, and showing the hydrogen bonds that could occur between them. Draw the hydrogen bonds as a series of short dashes.

 \mathbf{T}