

Name: _____

2007 7.013 Problem Set 2

Due before 5 PM on FRIDAY, March 2, 2007.

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

PLEASE WRITE YOUR ANSWERS ON THIS PRINTOUT.

1. Wild-type flies are brown in color. You have discovered a gene that controls body color in flies called gene A. You have two true-breeding mutant strains, both of which have black bodies.

Strain One (a_1/a_1) is homozygous for a mutation in gene A that causes a dominant mutant phenotype.

Strain Two (a_2/a_2) is homozygous for a mutation in gene A that causes a recessive mutant phenotype.

Group Three are flies that result from mating Strain One to Strain Two.

Group Four are flies that result from mating Strain One to wild-type (A/A).

Group Five are flies that result from mating Strain Two to wild-type (A/A).

Predict the genotypic ratio and the phenotypic ratio of the offspring resulting from the following crosses. Make sure to label each class in each of your ratios.

(a) Group Three and Group Five
Genotypic ratio:

Phenotypic ratio:

(b) Strain Two and Group Three
Genotypic ratio:

Phenotypic ratio:

(c) Group Four and Strain Two
Genotypic ratio:

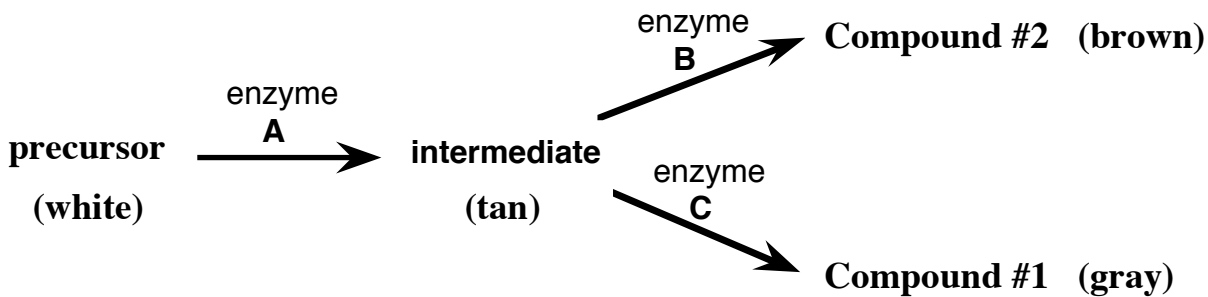
Phenotypic ratio:

(d) Group Four and Group Five
Genotypic ratio:

Phenotypic ratio:

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2. Consider a fictitious pathway that controls coat color in the mouse. The mouse genome contains gene A, which encodes enzyme A, an enzyme that converts the precursor (a white compound) to the intermediate (a tan compound). The mouse genome contains gene B, which encodes enzyme B, an enzyme that converts the intermediate to Compound #2 (a brown compound). The mouse genome contains gene C, which encodes enzyme C, an enzyme that converts the intermediate to Compound #1 (a gray compound). Mice that produce both compound #1 and compound #2 are brownish-gray. Genes A, B, and C are all autosomal genes that lie on different mouse chromosomes. Loss-of-function mutations in both homologous versions (maternal and paternal) of any one gene (A, B, or C) causes a recessive phenotype.



(a) Which color coat would each following mouse have? Some are filled in for you.

AABBCC =

aaBBCC =

AaBbcc = brownish-tan

AabbCc = grayish-tan

Aabbcc = tan

aaBBcc =

aabbCc =

aabbcc =

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(b) Two different true-breeding strains of mice have been isolated; neither strain can produce compound #1 or compound #2. When an individual from one strain is crossed with an individual from the other strain, all of the F1 mice produce both compounds. Write out the genotypes for both P generation strains, and the genotype for the F1 generation. (Use "A," "B," and "C" to designate the wild-type alleles and "a," "b," and "c" to designate the defective alleles of the three genes.) Also write out the coat color of each group of animals.

	Genotype	Coat Color
P generation, one strain		
P generation, other strain		
F1 generation		

(c) Two of the F1 mice are crossed to one another. The possible phenotypes for the F2 progeny are shown below. What fraction of the F2 generation will be represented by each phenotype on average? (Note: some fractions in the table may be zero.)

Coat Color	Fraction of F2 that is this coat color
white	
tan	
brown	
brownish-gray	
brownish-tan	
grayish-tan	

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3. You are studying two recessive traits in the fruit fly *Drosophila melanogaster*. The “h” allele causes flies to have the recessive phenotype of hairy backs (wild-type flies have hairless backs). The “t” allele causes flies to have the recessive phenotype of thick legs (wild-type flies have thin legs). You mate females from a true-breeding strain with hairy backs and normal legs to males from a true-breeding strain with normal backs and thick legs. F1 females are then mated to males that have hairy backs and thick legs to produce F2 progeny. If you analyzed 1000 **MALE** progeny in the F2 generation, how many flies of each possible phenotypic class would you expect, given that:

(a) The two traits are determined by two unlinked autosomal genes

hairy thick:

hairy thin:

hairless thick:

hairless thin:

(b) The two traits are determined by two completely linked autosomal genes

hairy thick:

hairy thin:

hairless thick:

hairless thin:

(c) The two traits are determined by two autosomal genes that are 10 cM apart

hairy thick:

hairy thin:

hairless thick:

hairless thin:

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(d) The two traits are determined by two completely linked genes on the X chromosome

hairy thick:

hairy thin:

hairless thick:

hairless thin:

(e) The two traits are determined by two genes that are 20 cM apart on the X chromosome

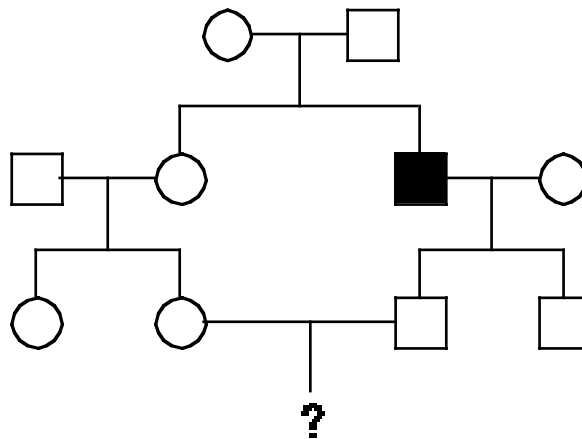
hairy thick:

hairy thin:

hairless thick:

hairless thin:

4. You have just been hired as a genetic counselor for a royal family that still engages in a significant amount of inbreeding. As your first assignment, you are presented with the following pedigree where the filled symbol represents a male in the royal family who has a rare disease.



Name: _____

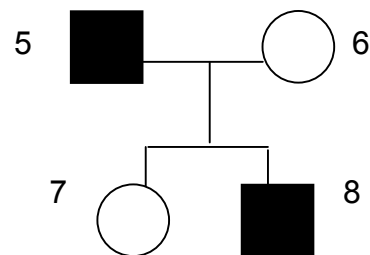
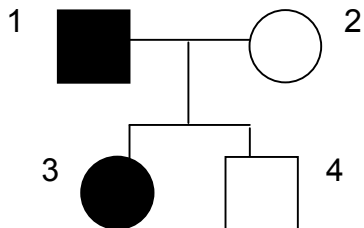
Your job is to calculate the probability that the child indicated by ? will have the disease. To do this, assume that no new mutations arise within the pedigree and that no unrelated individual is a carrier (because this is a very rare disease). Also assume complete penetrance.

(a) If the disease is autosomal recessive, what is the probability that the child indicated by the ? will have the disease?

(b) If the disease is X-linked recessive, what is the probability that a child will be born with the disease if that child is born **male**?

(c) If the disease is X-linked recessive, what is the probability that a child will be born with the disease if that child is born **female**?

5. This problem involves two families, each of which contains individuals that express the same rare trait due to having the same rare mutation. The families are diagrammed below — individuals are numbered, and those expressing the rare trait are represented by the filled symbols. For each possible mode of inheritance listed below, state what the probability is that the child will express the rare trait. Assume that no new mutations arise within the pedigree, and assume complete penetrance.



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(a) Assume that the rare trait is **autosomal recessive**. Consider the possible matings described below. For each, calculate the probability that the child will have the rare trait.

Female 6 and Male 4

Female 6 and Male 1

Female 7 and Male 1

Female 3 and Male 5

(b) Now assume that the rare trait is **autosomal dominant**. Again for each of the possible matings given below, calculate the probability that the child will have the rare trait.

Female 6 and Male 4

Female 6 and Male 1

Female 7 and Male 1

Female 3 and Male 5

(c) Finally, assume that the rare trait is **X-linked recessive**. For each of the possible matings given below, calculate the probability that the child will have the rare trait. Explicitly give a probability for sons and a probability for daughters in any case where the probabilities for a boy or a girl having the trait differ.

Female 6 and Male 4

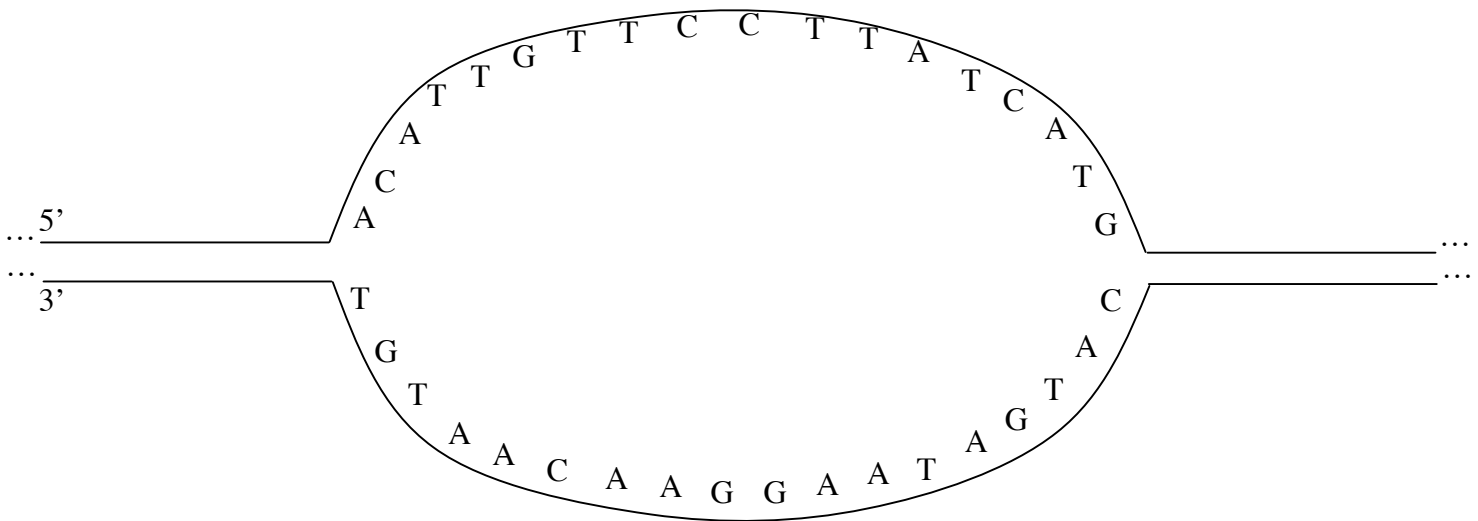
Female 6 and Male 1

Female 7 and Male 1

Female 3 and Male 5

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6. Below is shown a picture of a replication bubble.



(a) The primer 5'-GAA-3' is being used to replicate this piece of DNA. Would that primer anneal to the upper strand of DNA in the picture or the lower strand?

(b) Write what the product of DNA replication would be if the first five nucleotides had been added onto this primer by DNA polymerase. Label the 5' and 3' ends. Make sure to include the primer.

(c) Would that strand that you have drawn in part (b) be a leading strand or a lagging strand?