

Name: \_\_\_\_\_KEY\_\_\_\_\_

## 7.03 Exam One -- 2005

Name: \_\_\_\_\_KEY\_\_\_\_\_

Exam starts at 11:05 am and ends at 11:55 am.

There are 7 pages including this cover page.

Please write your name on each page.

Only writing on the **FRONT** of every page will be graded.  
(You may use the backs, but only as scratch paper.)

**Question 1**      **24 pts**\_\_\_\_\_

**Question 2**      **30 pts**\_\_\_\_\_

**Question 3**      **30 pts**\_\_\_\_\_

**Question 4**      **16 pts**\_\_\_\_\_

**TOTAL**      **out of 100**\_\_\_\_\_

**1. (24 pts)** You are studying two recessive mutations in the fruit fly *Drosophila melanogaster*. The  $hb^-$  mutation causes flies to have hairy backs (wild-type flies have hairless backs). The  $tl^-$  mutation causes flies to have 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 500 **MALE** progeny in the F2 generation, how many flies of each possible phenotypic class would you expect, given that:

**(a, 8pts)** The two traits are determined by two unlinked autosomal genes

**P generation:**  $hb^- hb^- tl^+ tl^+$  X  $hb^+ hb^+ tl^- tl^-$   
**F1:**  $hb^+ hb^- tl^+ tl^-$  X  $hb^- hb^- tl^- tl^-$   
**F2:**  $hb^- hb^- tl^+ tl^-$  OR  $hb^+ hb^- tl^- tl^-$  OR  $hb^- hb^- tl^- tl^-$  OR  $hb^+ hb^- tl^+ tl^-$   
 hairy thick: **125**  
 hairy thin: **125**  
 hairless thick: **125**  
 hairless thin: **125**

**(b, 8pts)** The two traits are determined by two completely linked genes on the X chromosome

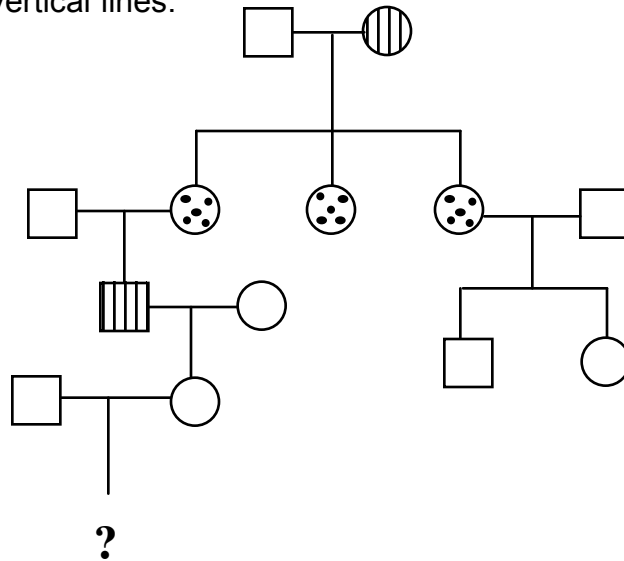
**P generation:** X  $hb^- tl^+$  X  $hb^- tl^+$  X  $hb^+ tl^-$  Y  
**F1:** X  $hb^- tl^+$  X  $hb^+ tl^-$  X  $hb^- tl^-$  Y  
**F2:** X  $hb^- tl^+$  Y OR X  $hb^+ tl^-$  Y  
 hairy thick: **0**  
 hairy thin: **250**  
 hairless thick: **250**  
 hairless thin: **0**

**(c, 8pts)** The two traits are determined by two autosomal genes that are 20 cM apart

**P generation:**  $hb^- tl^+ / hb^- tl^+$  X  $hb^+ tl^- / hb^+ tl^-$   
**F1:**  $hb^- tl^+ / hb^+ tl^-$  X  $hb^- tl^- / hb^- tl^-$   
**F2:**  $hb^- tl^+ / hb^- tl^-$  OR  $hb^+ tl^- / hb^- tl^-$  OR  $hb^+ tl^+ / hb^- tl^-$  OR  $hb^- tl^- / hb^- tl^-$   
 -----parentals-----  
 hairy thick: **50**  
 hairy thin: **200**  
 hairless thick: **200**  
 hairless thin: **50**

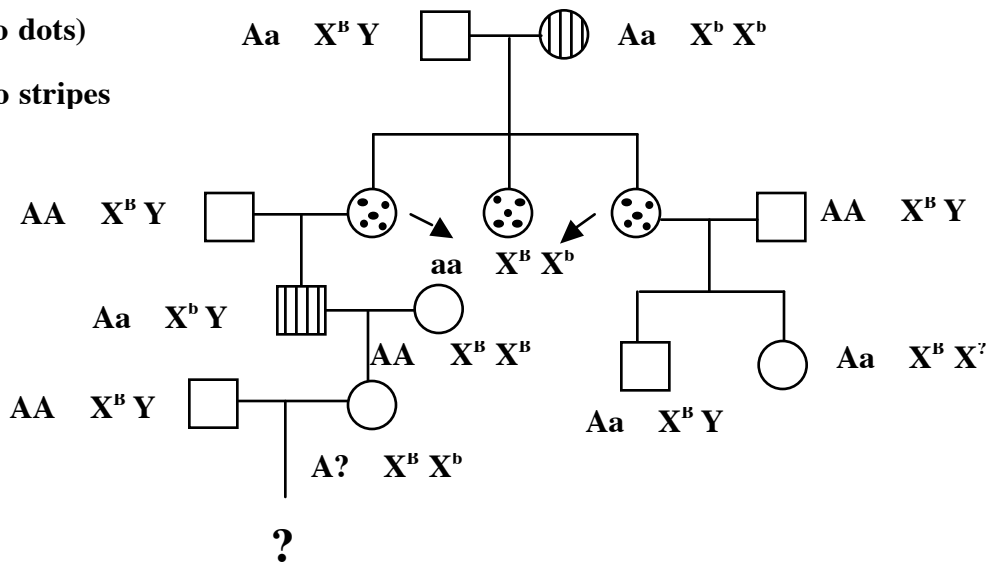
**2. (30 pts)** The following pedigree shows the inheritance two different **rare** traits. Each trait is determined by a different gene. The presence of Trait 1 is indicated by dots, and the presence of Trait 2 is indicated by vertical lines.

(Note that no single individual displays both traits.)



**(a, 6pts)** What mode(s) of inheritance is/are consistent with each of the traits segregating in this pedigree? (Your choices are: autosomal recessive, autosomal dominant, X-linked dominant, X-linked recessive.) Assume no new mutations and complete penetrance.

**Dots:** a (A is no dots)  
**Stripes:** X<sup>b</sup> (X<sup>B</sup> is no stripes)



Trait 1 (dots): **autosomal recessive**

Trait 2 (vertical lines): **X-linked recessive**

**Note that the fact that the traits are RARE implies that anyone marrying into the family carries no alleles associated with the trait. This makes autosomal recessive inheritance inconsistent with trait #2.**

**(b, 6pts)** State whether the two traits in the pedigree are **linked** or **not linked**, or if it is inconclusive given these data.

**Not linked (because one is encoded on the X chromosome and the other is encoded on an autosome; thus the two different genes MUST be on different chromosomes)**

**Please note that your conclusion had to be consistent with your answer to part A.**

**(c, 6pts)** What is the probability that the child indicated with a question-mark will show at least one of the two traits? Show your work.

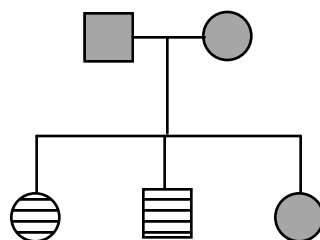
**25%**

**The probability that the child will get Trait 1 is zero because the father is AA.**

**The probability that the child will get Trait 2 is 25%, because the child first must be a boy for it to show Trait 2 (and the probability of having a boy is 50%), and then, if the child is a boy, he will have a 50% chance of showing Trait 2. This is because the mom is a carrier. Thus the final probability is  $50\% * 50\% = 25\%$ .**

Consider this new pedigree, which shows the inheritance of two different rare traits. Each trait is determined by a different gene. The presence of Trait 3 is indicated by horizontal lines, and the presence of Trait 4 is indicated by shading.

(Note that no single individual displays both traits.)

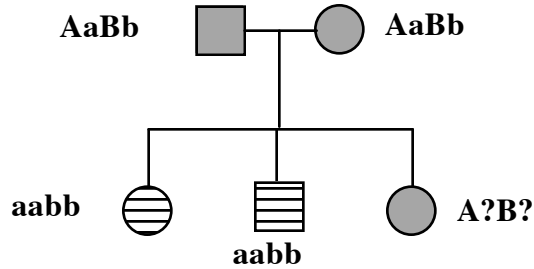


Name: \_\_\_\_\_ KEY \_\_\_\_\_

(d, 6pts) What mode(s) of inheritance is/are consistent with each of the traits segregating in this pedigree? (Your choices are: autosomal recessive, autosomal dominant, X-linked dominant, X-linked recessive.) Assume no new mutations and complete penetrance.

**IF UNLINKED**

Stripes: a (A is no stripes)  
 Shading: B  
 b is no shading

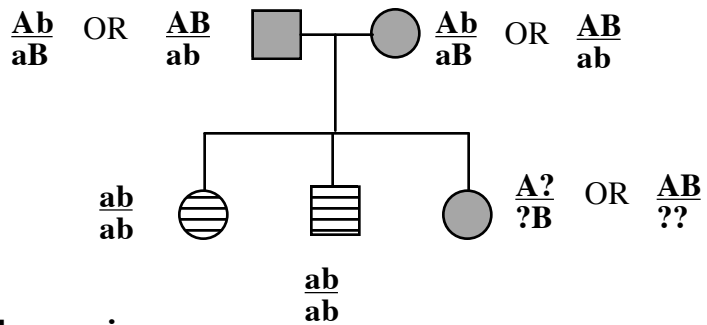


Trait 3 (horizontal lines): **autosomal recessive**

Trait 4 (shading): **autosomal dominant**

**IF LINKED**

Stripes: a (A is no stripes)  
 Shading: B  
 b is no shading



Trait 3 (horizontal lines): **autosomal recessive**

Trait 4 (shading): **autosomal dominant**

(e, 6pts) State whether the two traits in the pedigree are **linked** or **not linked**, or if it is inconclusive given these data.

**Inconclusive**

Please note that your conclusion had to be consistent with your answer to part D.

**3. (30 pts)** You are studying three mutations in yeast. The first mutation causes the Ser<sup>-</sup> phenotype of being unable to grow without serine in the medium. The second mutation causes the His<sup>-</sup> phenotype of being unable to grow without histidine in the medium. The third mutation causes a small colony phenotype. Wild-type yeast are Ser<sup>+</sup> His<sup>+</sup> and big. You mate a Ser<sup>-</sup> haploid mutant yeast to a His<sup>-</sup> small haploid mutant yeast. You induce sporulation of the resulting diploid, and obtain the following tetrad types. (The number of tetrads of each type that you get (out of a total of 100) are shown after the tetrad type.)

Tetrad Type A                    }
   
Ser<sup>-</sup> His<sup>+</sup> big
   
Ser<sup>-</sup> His<sup>+</sup> small
   
Ser<sup>+</sup> His<sup>-</sup> big
   
Ser<sup>+</sup> His<sup>-</sup> small                }       9 tetrads of this type

Tetrad Type B                    }
   
Ser<sup>-</sup> His<sup>+</sup> big
   
Ser<sup>-</sup> His<sup>+</sup> big
   
Ser<sup>+</sup> His<sup>-</sup> small
   
Ser<sup>+</sup> His<sup>-</sup> small                }       90 tetrads of this type

Tetrad Type C                    }
   
Ser<sup>+</sup> His<sup>-</sup> big
   
Ser<sup>-</sup> His<sup>+</sup> small
   
Ser<sup>-</sup> His<sup>-</sup> big
   
Ser<sup>+</sup> His<sup>+</sup> small                }       1 tetrad of this type

**(a, 4pts)** Which Tetrad Types are TTs, NPDs, and PDs with respect to the His and size genes?

TT: **Type A**

NPD: **Type C**

PD: **Type B**

**(b, 4pts)** Are the His and size loci linked? If so, what is the genetic distance between them?

**Yes they are, at 7.5 cM**

**Use the formula**

$$\text{map distance} = \frac{6 \text{ NPD} + \text{TT}}{2 \times (\# \text{ tetrads})} \times 100 = \frac{6(1) + 9}{2(100)} \times 100 = 7.5 \text{ cM}$$

Name: \_\_\_\_\_ KEY \_\_\_\_\_

**(c, 4pts)** Which Tetrad Types are TTs, NPDs, and PDs with respect to the Ser and size genes?

TT: **Type A and Type C**

NPD: **none**

PD: **Type B**

**(d, 4pts)** Are the Ser and size loci linked? If so, what is the genetic distance between them?

**Yes they are, at 5 cM**

Use the formula

$$\text{map distance} = \frac{6 \text{ NPD} + \text{TT}}{2 \times (\# \text{ tetrads})} \times 100 = \frac{6(0) + 10}{2(100)} \times 100 = 5 \text{ cM}$$

**(e, 4pts)** Which Tetrad Types are TTs, NPDs, and PDs with respect to the Ser and His genes?

TT: **Type C**

NPD: **none**

PD: **Type A and Type B**

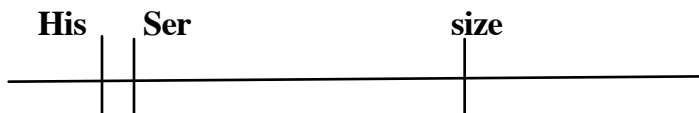
**(f, 4pts)** Are the Ser and His loci linked? If so, what is the genetic distance between them?

**Yes they are, at 0.5 cM**

Use the formula

$$\text{map distance} = \frac{6 \text{ NPD} + \text{TT}}{2 \times (\# \text{ tetrads})} \times 100 = \frac{6(0) + 1}{2(100)} \times 100 = 0.5 \text{ cM}$$

**(g, 6pts)** Draw a genetic map showing the correct relative order of the Ser, His, and size loci. If one of the loci is unlinked from the other two, draw it on a separate chromosome.



**His and Ser are the closest together, both based on the distance calculated and the fact that they only have one TT (and 99 PDs). His and size are the farthest apart, both based on the distance calculated and the fact that they are the only two loci between which you saw double crossovers.**

**Please note that your map had to be consistent with your answers to parts A-F.**

**4. (16 pts)** You are studying a recessive trait in a diploid rodent species in which XX organisms are female and XY organisms are male. This trait is determined by a single gene, but you have no idea where in the genome this gene is located. This rodent has 20,000 distinct genes in its genome, 400 of which are found on the X chromosome.

**(a, 4pts)** Given this information, give your best estimate of the probability that the trait you are studying is X-linked.

$$\frac{400}{20,000} = 0.02$$

**(b, 12pts)** You mate a female rodent displaying the trait to a wild-type male. You then mate an F1 female to a wild-type male to produce F2 offspring, and analyze only the F2 males. The first three F2 male offspring display the wild-type phenotype.

Given that the first three male F2 offspring show the wild-type phenotype, determine the probability that the trait you are studying is X-linked. Show **all** steps of your work, using clear labels.

**X = trait is X-linked**

**notX = trait is not X-linked and is therefore autosomal**

**Y = the first three males analyzed are wild-type (note that only males were analyzed, so the gender of the offspring should not be taken into account in your probability calculation)**

$$p(X) = 0.02 \text{ (see part a)}$$

$$p(\text{notX}) = 1 - 0.02 = 0.98$$

$$p(Y|X) = p(\text{1}^{\text{st}} \text{ egg contained "X"}^{\text{A}} \text{ allele}) * p(\text{2}^{\text{nd}} \text{ egg same}) * p(\text{3}^{\text{rd}} \text{ egg same}) \\ = 1/2 * 1/2 * 1/2 = 1/8$$

**(Note that the father donates his Y chromosome and is thus irrelevant.)**

$$p(Y|\text{notX}) = p(\text{1}^{\text{st}} \text{ sperm contained "A"} \text{ allele}) * p(\text{2}^{\text{nd}} \text{ sperm same}) * p(\text{3}^{\text{rd}} \text{ sperm same}) \\ = 1 * 1 * 1 = 1$$

**[Note that the father is wild-type (AA) and this makes the mother irrelevant.]**

$$p(X|Y) = \frac{p(Y|X) * p(X)}{[p(Y|X) * p(X)] + [p(Y|\text{notX}) * p(\text{notX})]}$$

$$p(X|Y) = 1/393 = 0.25\%$$