Question 3 35 points
Question 2 33 points
Question 1 32 points

State any assumptions that you make.

To help us give partial credit, show your work and check your answers to make sure that they make sense.

Questions left unanswered or questions leaving easy questions unanswered.

Look over the entire exam so you don't spend too much time on hard questions.

Please:

Only writing on the front of every page will be graded.

Please write your name on each page.

There are eight pages including this cover page.

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

Section Time:

Padmini Gunada
Radhika Jegannathan
Thomas Carville
MichelleMiscake
Colin Chu
Bhav Bose

TA: Name:

7.03 Exam 1
Genotype of one parental strain:

Genotype of the other parental strain:

Using this notation, state the genotype of each of the two true-breeding parental strains (i.e. the two strains in the F1 generation that were bred to produce the F2 generation). The male flies that were bred in the F1 generation in order to produce the F2 generation were humpbacked, blister-eye-winged, and stubby-eggged. On each of their chromosomes, they have the alleles bp – bl – wr – eg.

<table>
<thead>
<tr>
<th>Phenotype</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>Straight-backed, smooth-winged, and long-eggged</td>
<td>22 flies</td>
</tr>
<tr>
<td>Straight-backed, smooth-winged, and stubby-eggged</td>
<td>42 flies</td>
</tr>
<tr>
<td>Straight-backed, blister-eye-winged, and long-eggged</td>
<td>4 flies</td>
</tr>
<tr>
<td>Humpbacked, smooth-winged, and long-eggged</td>
<td>27 flies</td>
</tr>
<tr>
<td>Humpbacked, blister-eye-winged, and long-eggged</td>
<td>24 flies</td>
</tr>
<tr>
<td>Humpbacked, blister-eye-winged, and stubby-eggged</td>
<td>455 flies</td>
</tr>
<tr>
<td>Humpbacked, blister-eye-winged, and stubby-eggged</td>
<td>26 flies</td>
</tr>
</tbody>
</table>

You have 1000 progeny resulting from this cross. You observe the following phenotypes:

- Humpbacked blister-eye-winged, and stubby-eggged
- Humpbacked smooth-winged, and long-eggged
- Humpbacked, blister-eye-winged, and long-eggged
- Humpbacked, blister-eye-winged, and stubby-eggged
- Humpbacked, blister-eye-winged, and stubby-eggged
- Humpbacked, blister-eye-winged, and stubby-eggged
- Humpbacked, blister-eye-winged, and stubby-eggged
- Humpbacked, blister-eye-winged, and stubby-eggged
- Humpbacked, blister-eye-winged, and stubby-eggged
- Humpbacked, blister-eye-winged, and stubby-eggged

You are studying three autosomal recessive mutations in the fruit fly Drosophila.

Name: [Signature]
(e, 6 pts.) Draw a genetic map showing the correct order of the \( Hb \), \( pl \), and \( st \) loci.

\[
\begin{align*}
\text{Distances (cm):} & \\
10.3 & = \left( \frac{100}{2.6 + 2.4 + 2.7 + 2.2 + 4 + 0} \right) \\
10.7 & = \left( \frac{100}{2.6 + 100} \right) \\
9.6 & = \left( \frac{100}{2.6 + 2.4 + 2.7 + 2.2 + 4} \right)
\end{align*}
\]

With the proper units (cm) label your answers.

(d, 7 pts.) What is the genetic distance between the \( Hb \) and \( st \) loci? (label your answer)

\[
5.5 \text{ cm} = \left( \frac{100}{2.6 + 2.4 + 2.7 + 2.2 + 4} \right)
\]

With the proper units (cm) label your answer.

(c, 7 pts.) What is the genetic distance between the \( Hb \) and \( pl \) loci? (label your answer)

\[
5.2 \text{ cm} = \left( \frac{100}{2.4 + 2.7 + 100} \right)
\]

With the proper units (cm) label your answer.

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

22

Name:
### Table

<p>| | | | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>Mouse #4</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>0</td>
<td>2</td>
<td>0</td>
<td>Mouse #3</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>Mouse #2</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>2</td>
<td>0</td>
<td>Mouse #1</td>
<td></td>
</tr>
</tbody>
</table>

### Key
- `p` alleles = expressing both mutant traits
- `q` alleles = causing the mutant trait
- `Q` alleles = expressing dominant mutant trait
- `q` alleles = expressing recessive mutant trait

### Diagram

2. The following mouse pedigree shows the segregation of two different mutant traits.
both mutant traits (the trait encoded by \( A \) and the trait encoded by \( p \)).

\[
\begin{array}{c}
447 \\
\end{array}
= 44 \times \frac{3}{1}
\]

(c) 7 pts. Assuming that both mutant traits are due to linked autosomal genes that are

\[ A \times \quad p \]

\[ \downarrow \quad \downarrow \]

\[ B \quad \text{or} \quad p \quad \text{Locus} \]

\[ A \quad \text{or} \quad A \quad \text{Locus} \]

\[ \text{from mouse} \ #2 \]

\[ \text{Homolog Inherited} \]

\[ \text{from mouse} \ #1 \]

\[ \text{Homolog Inherited} \]

homologs of this autosomal trait are depicted in the diagram below.

\[ \text{(q) 6 pts.} \]

Assuming that both mutant traits are due to linked autosomal genes that are
\[ \frac{1}{2} \times \frac{1}{2} = \frac{1}{4} \]

(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 trait? (\( p^2 \) or \( q^2 \))

<table>
<thead>
<tr>
<th>Mouse</th>
<th>( A^+ ) alleles</th>
<th>( A^- ) alleles</th>
<th>( B^+ ) alleles</th>
<th>( B^- ) alleles</th>
<th>( C^+ ) alleles</th>
</tr>
</thead>
<tbody>
<tr>
<td>9</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>4</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

X-linked X-linked

autosomal

Key

Name:
7

Yes, can deduce; white

You deduce the color of the resulting diploids? If so, what color would the diploids be?

Yes, linked

Yes, linked

1 2 3

Ⅲ

Ⅱ

Ⅰ

PD

Ⅰ

Type (NPD)

diploids (NPd).

Category eae the tetrad types as parental diploids (PD) and diploids (NPD) or nonparental

contain one dark and one white, two dark and two white, and one white and one white.

contain two dark and two white, and two white and two dark. There are two types of these tetrads (called "Type One") contain four dark and two white, and two white and two dark. There are two types of these tetrads (called "Type Two")

Allocation of these diploids yields 50 tetrads. 27 of these tetrads... 37 of these tetrads. 27 of these tetrads.

(a, 6 pts) Making of the dark-Δ10 double mutant to wild-type yeast produces
different mutations in the same strain. The two mutations are designated Δ10 and Δ12.

(b) Dark can "phenotype of the haploid cells you are working with is caused by two

3. You are working with a mutant strain of yeast that is dark can (wild-type yeast are white).
Next you isolate a mutant strain of yeast that cannot grow on medium lacking leucine. This strain contains a single mutation: 

(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 tetrad 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?

<table>
<thead>
<tr>
<th></th>
<th>Type A tetrad</th>
<th>Type B tetrad</th>
</tr>
</thead>
<tbody>
<tr>
<td># of spores that can grow on medium lacking leucine</td>
<td></td>
<td>2</td>
</tr>
<tr>
<td>color of each spore that can grow on medium lacking leucine</td>
<td>both are light tan</td>
<td>A WHITE</td>
</tr>
</tbody>
</table>

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

Genotype of one light tan spore: leu1+ drk1-
Genotype of the other light tan spore: leu1- drk1+