7.013 Problem Set 1 Answers – Spring 2003

The completed problem set must be turned into the wood box outside 68-120 by 4:40 pm, Thursday, February 20. Problem sets will not be accepted late.

Solutions will be put on the web after the due time.

Question 1

You have identified a new, rapidly reproducing species of bird that you have named the “mitquat”. The mitquat is diploid and has only two autosomal chromosomes. Chromosome I carries gene $A$ with two alleles designated $A$ and $a$. Chromosome II carries gene $B$ with two alleles designated $B$ and $b$.

a) Diagram mitosis in a heterozygous ($AaBb$) mitquat cell shown below. Include the alleles in your diagram.
Indicate the genotype of cells that would result after telophase. _____AaBb______
b) Starting with metaphase I cell shown below, diagram, note where the crossover takes place and diagram anaphase I, metaphase II, and anaphase II of meiosis. Designate the alleles, the spindle.

![Diagram of meiosis stages](image)

Metaphase I → Anaphase I → Metaphase II → Anaphase II

c) You determine that Chromosome I has in addition to gene A, another gene, gene D, with two alleles designated D and d. Gene A and gene D have been shown to be 20 cM apart.

i) Given the cell with chromosome configuration below, what would be the recombinant genotypes of the gametes?

\[
\begin{array}{cc}
A & d \\
\hline
a & D
\end{array}
\]

\[
\begin{array}{cc}
A & D \\
\hline
a & d
\end{array}
\]

\[
\begin{array}{cc}
a & D \\
\hline
A & d
\end{array}
\]

ii) At what frequency do you expect each of the recombinant genotypes to occur? 0.10 or 10%
Question 2

You have two pure-breeding mutant mitquat strains. The first mutant has green eyes (the wildtype strain has yellow eyes). The second mutant strain has bumpy beaks (the wildtype strain has smooth beaks).

a) You cross green-eyed females with bumpy beaked males and obtain all wildtype F1 progeny (as shown below).

Parents  green-eyed smooth beaked females  X  yellow-eyed bumpy beaked males

F1  all wildtype

Circle any recessive phenotype.

<table>
<thead>
<tr>
<th>Green eyes</th>
<th>Yellow eyes</th>
<th>Bumpy beaks</th>
<th>Smooth beaks</th>
</tr>
</thead>
</table>

b) You mate pairs of F1 siblings and see the following phenotypic classes in the F2 generation.

<table>
<thead>
<tr>
<th>Phenotypic Class</th>
<th>Genotypes</th>
</tr>
</thead>
<tbody>
<tr>
<td>green eyes, smooth beaks</td>
<td>GG bb  gg BB</td>
</tr>
<tr>
<td>yellow eyes, bumpy beaks</td>
<td>Gg bb  GG bb</td>
</tr>
<tr>
<td>yellow eyes, smooth beaks</td>
<td>GgBb  GG Bb  Gg BB</td>
</tr>
<tr>
<td>green eyes, bumpy beaks</td>
<td>g g bb</td>
</tr>
</tbody>
</table>

i) On the adjacent lines above, write out the genotypes corresponding to the phenotypic classes. (Using conventional nomenclature (capital letters denote allele conferring dominant phenotype), designate the eye color alleles as G and g, and the beak texture alleles as B and b.)

ii) Based on the F2 progeny results above, the eye color and beak texture genes are....

Linked  Unlinked  Indeterminable
(Linkage can’t be determined)

iii) Based on F2 progeny results above, draw out the chromosomal configuration (see 1, c, i) of an F1 mitquat. (Use G/g and B/b.)

G  g  B  b

c) What if instead of the result shown in b) above, you see the following phenotypic classes in the F2 generation.

<table>
<thead>
<tr>
<th>Phenotypic Class</th>
<th>Genotypes</th>
</tr>
</thead>
<tbody>
<tr>
<td>green eyes, smooth beaks</td>
<td>g g BB</td>
</tr>
<tr>
<td>yellow eyes, bumpy beaks</td>
<td>Gg bb</td>
</tr>
<tr>
<td>yellow eyes, smooth beaks</td>
<td>Gg Bb</td>
</tr>
</tbody>
</table>
i) On the adjacent lines above, write out the genotypes corresponding to the phenotypic classes (Using the conventional nomenclature, designate the eye color alleles as $G$ and $g$, and the beak texture alleles as $B$ and $b$.)

ii) Based on the F2 progeny results above, the eye color and beak texture genes are....

<table>
<thead>
<tr>
<th>Linked</th>
<th>Unlinked</th>
<th>Indeterminable</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>(Linkage can’t be determined)</td>
</tr>
</tbody>
</table>

iii) Based on F2 progeny results above, draw out the chromosomes and corresponding alleles of an F1 mitquat. (Use $G/g$ and $B/b$.)

```
g B                                               G b
```

**Question 3**

In addition to gene $B$ (that specifies beak texture) on Chromosome II, there is a gene that specifies beak hue (mutants have orange beaks while wildtype mitquats have red beaks). You cross pure-breeding bumpy red beaked birds to a pure breeding smooth yellow beaked birds and obtain F1 progeny with hot pink, smooth beaks as shown below.

```
Parents      bumpy, red beaks  X  smooth, yellow beaks
            \                       
            F1        ALL  smooth, hot pink beaks
```

a) What mode of inheritance does beak color exhibit?

*Codominance* or *Partial dominance*

b) If you were to cross the F1 progeny, what phenotypes and what ratios would you expect in the F2 generation if the genes are unlinked?

```
<table>
<thead>
<tr>
<th>6:</th>
<th>3:</th>
<th>3:</th>
<th>2:</th>
<th>1:</th>
<th>1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Smooth hot pink</td>
<td>Smooth Red</td>
<td>Smooth Yellow</td>
<td>Bumpy Hot pink</td>
<td>Bumpy Red</td>
<td>Bumpy Yellow</td>
</tr>
</tbody>
</table>
```
c) But, you have determined that the genes are indeed linked and thus you’d like to know the genetic distance between the two. You therefore cross an F1 female to a pure-breeding bumpy, yellow beaked male. You obtain the following phenotypic classes.

<table>
<thead>
<tr>
<th>Progeny</th>
<th>Phenotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>123</td>
<td>bumpy, yellow beaks</td>
</tr>
<tr>
<td>110</td>
<td>smooth, hot pink beaks</td>
</tr>
<tr>
<td>275</td>
<td>bumpy, hot pink beaks</td>
</tr>
<tr>
<td>280</td>
<td>smooth, yellow beaks</td>
</tr>
</tbody>
</table>

**F1 female  \( \times \) bumpy, yellow-beaked male**

d) What is the genetic distance between beak texture and hue genes.

30 map units or centimorgans
Question 4
The following is a pedigree of a family with exhibiting a very rare disease. Assume ALL people marrying into the family have wildtype alleles at the disease gene.

a) What is the mode(s) of inheritance of this disease? Circle all that apply.

- autosomal dominant
- autosomal recessive
- mitochondrial inheritance
- X-linked dominant
- X-linked recessive
- Y-linked

b) Assign genotypes to the following individuals in this pedigree. Where the full genotype cannot be determined, provide what information you can.

1 _______ A? _______  4 _______ Aa _______  7 _______ Aa _______  10 _______ aa _______

2 _______ A? _______  5 _______ AA _______  8 _______ Aa _______  11 _______ A? _______

3 _______ Aa _______  6 _______ A? _______  9 _______ A? _______  12 _______ aa _______

c) What is the probability that individual 9’s offspring (#14) will develop the disease?
d) What is the probability that individual 12’s offspring (#15) will develop the disease?

0%

d) What information would you gain if you discovered that individual 4 were affected?

That both individuals 1 and 2 were carriers.