Solutions to 7.014 Problem Set 4

Question 1

Because you have not read much scientific literature, you decide to study the genetics of garden peas. You have two pure breeding pea strains. One that is tall and has fuzzy leaves, and one that is short and has hairless leaves. You cross these plants and find that the F\(_1\) plants are short and fuzzy.

a) Which phenotypes are dominant? Which are recessive?
*Short and fuzzy are the dominant phenotypes, tall and hairless are the recessive phenotypes.*

b) Among wild peas, tall plants outnumber short plants by a factor of 10. Does this contradict your answer to part a? Explain.
*No, this is not a contradiction. Although tall is a recessive phenotype, that does not mean the same as rare. If the established population has a large majority number of tall (tt) plants, then that trait will continue to be seen. As long as there is not an advantage to being short, the tt plants will persist.*

c) You now cross two short and fuzzy F\(_1\) plants together. For the remainder of this problem use T for the allele associated with the dominant phenotype and t for the allele associated with the recessive phenotype (either tall or short from above). Use H for the allele associated with the dominant phenotype and h for the allele associated with the recessive phenotype (either fuzzy or hairless from above).

i) What phenotypes do you expect in the progeny?
*You would expect short & fuzzy, short & hairless, tall & fuzzy, and tall & hairless*

ii) What ratios of genotypes would you expect if these traits are unlinked?

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iii) What ratios of phenotypes would you expect if these traits are unlinked?
*(9) Short and Fuzzy : (3) Short and hairless : (3) Tall and fuzzy : (1) Tall and hairless*

d) In contrast to your prediction (hopefully), the F\(_1\) cross yields only the following phenotypic classes in the following numbers:

*Short fuzzy (93), Short hairless (30), Tall Fuzzy (28)*

Explain this finding in genetic terms.
*It appears that the plants showing both recessive phenotypes, the tall and hairless plants, are missing. You might assume that this is a lethal condition.*
Question 2

You are a scientist studying mice. You come across a mutant mouse missing gene M. The phenotype associated with the loss of gene M function is inherited in the following manner.

mutant male $\times$ wt female $\rightarrow$ P$_0$

All wild type (WT) $\rightarrow$ F$_1$

F$_1$ male $\times$ F$_1$ female $\rightarrow$ F$_2$

among females: all WT and among males: 1/2 mutant 1/2 WT

a) Given the ratios of WT and mutant progeny observed in the F$_2$ generation. What is the mode of inheritance of your mutation?

$X$-linked recessive

The phenotype of your mutation is rather strange. The mice appear completely normal and are just as healthy as WT mice. The mutant phenotype only becomes apparent when you attempt to map genes in your mutant mice. For example:

The loci for coat color and eye color are normally 26 map units apart, meaning that there is a recombination frequency of 26% between these two loci. In mutant mice, however, these loci are only 4 map units apart. Yet all of the genes that normally separate these markers on the chromosome of a normal mouse are still in the normal order.

b) Propose a genetic explanation for the change in mapping data among your mutant mice.

This mutation must reduce recombination or the frequency of crossover events.

c) Where would you expect the protein encoded by the gene deleted in your mutant to be active in a WT mouse?

Because the lack of this protein only affects recombination, you would expect the wildtype version of this protein to be found in the germ line cells that form gametes.

d) In terms of mitosis and meiosis, when would you expect it to be active? Be as specific as possible.

Because the lack of this protein affects recombination, you would expect the wildtype version of this protein to be active in Meiosis I.
Question 2, continued

e) You examine the gametes produced by your mutant mice, and find that a larger than normal fraction of them are either missing a chromosome, or have an extra chromosome. You are able to look at the products of an individual meiosis in your mutant. You find that in a meioses that produces gametes with extra or too few chromosomes there are always two gametes with an extra chromosome, and two missing that same chromosome. Diagram the meiosis that causes this, draw each copy of the affected chromosome at each step in meiosis.

![Diagram of meiosis in mutant and normal meiosis]

Question 3

You conduct a genetic screen for mutant fruit flies that have abnormal eyes. You isolate 3 separate recessive mutants in *Drosophila* with affected eye development. In each case, the defect causes the eyes to be too large. You call these mutations *bugeye* 1, 2 and 3.

a) Describe how you would determine if these mutations are in separate genes. Give brief details of the experiment or test you would do, and what the outcome would be if the mutations are in the same gene as compared to if the mutations are in different genes.

You would need to perform a complementation test for each pair. You would cross flies that are homozygous for *bugeye* 1 with flies that are homozygous for *bugeye* 2. If the mutations are in the same gene, the progeny will be affected. If the mutations are in separate genes then the progeny will all be heterozygous at both loci, and thus be unaffected.
Question 3, continued

b) You carry out your scheme and determine that bugeye1 and 2 are mutations in the same gene, but bugeye3 is in a different gene. You make a double mutant fly homozygous for both bugeye1 and bugeye3. This fly has giant eyes, even larger eyes than either single mutant.

You cross a fly heterozygous for both bugeye1 and bugeye3 with a fly homozygous for both bugeye1 and bugeye3. The following phenotypes of progeny are observed in the following numbers:

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<th>Phenotype</th>
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<td>WT (normal eyes)</td>
<td>24</td>
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<tr>
<td>Big Eyes</td>
<td>53</td>
</tr>
<tr>
<td>Giant Eyes</td>
<td>23</td>
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i) What genotypes are represented by each of the phenotypic classes above? Use $b1^+$ and $b3^+$ for the wild-type alleles of bugeye1 and bugeye3. Use $b1^-$ and $b3^-$ for the mutant alleles of bugeye1 and bugeye3.

- **WT** = $b1^+/b3^+$, $b1^-/b3$
- **Big Eyes** = $b1^+/b3^-$, $b1^-/b3^-$ or $b1^-/b3^-$, $b1^-/b3$
- **Giant Eyes** = $b1^-/b3^-$, $b1^-/b3$

ii) Are bugeye1 and bugeye3 linked? Justify your answer.

With independent assortment, you would predict (1) WT : (2) Big eyes : (1) Giant eyes. That is what is seen, so these two gene are not linked.

c) You cross a fly homozygous for the mutant bugeye1 allele and homozygous for wildtype peepers allele to a fly that is homozygous for the wildtype bugeye1 allele and homozygous for mutant peepers allele. This gives you F1 flies that are heterozygous for each of these mutations.

You then take an F1 heterozygote and cross it to a bugeye1, peepers homozygote

$p^+/b1^-, p/b1^+ \times p/b1^-, p/b1$

The phenotypes of the progeny are as follows: WT (normal eyes) 6, Big Eyes 94

i) What genotypes are present in each one of the phenotypic classes shown above?

- **WT** = $p^+/b1^-, p/b1$
- **Big Eyes** = $p^+/b1^-, p/b1$ or $p/b1^-, p/b1$ or $p/b1^+, p/b1$

ii) Are bugeye1 and peepers linked? If so, what is their distance in map units?

Yes, bugeye1 and peepers are linked. If these two loci were unlinked, you would expect (3) big eyes : (1) WT. That is not what is seen, so you infer linkage.

The 6 normal-eyed progeny ($p^+/b1^-, p/b1$) represent recombinant progeny. There would be 6 big-eyed progeny of the genotype ($p/b1^-, p/b1$) which are also recombinant. However, based on phenotype they are grouped with the non-recombinant progeny.

Thus, the map distance between these loci is $\#$ recombinant/total or $6 + 6/100 = 12$ map units.
Question 4

Geneticists studying humans rely upon the analysis of pedigrees to determine the cause of certain traits such as genetically heritable diseases. In the following pedigrees, shaded symbols represent affected individuals. Assume all individuals from outside these families are homozygous for the wild type allele.

a)

i) What is the mode of inheritance?
*Autosomal recessive*

ii) What is the genotype of the following individuals?
- Individual 1: +/-
- Individual 2: +/-
- Individual 3: +/-

iii) Suppose individuals 2 and 3 have another child. What is the chance that it will be affected?
1/4
b)

i) What is the mode of inheritance here?  
*Autosomal dominant*

ii) What is the genotype of the following individuals?  
- Individual 1: +/+  
- Individual 2: +/−  
- Individual 3: +/−  
- Individual 4: +/+  

iii) Suppose individual 5’s parents have another child. What are the chances that this child will be affected?  
1/2

iv) This pedigree represents a disorder that is both lethal and relatively common in the population. Explain how this is possible?  
*This condition may be characterized as late onset. Affected individuals do not show the phenotype until after they reach sexual maturity. This allows affected individuals to reproduce prior to death and maintains the disease allele in the population. Such is the case with Huntington’s disease, a lethal neurological condition that strikes around the age of 40.*

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c) The pedigree below represents the inheritance of a recessive skin condition in cats.

i) Why are the cats in generation 3 unaffected? Explain in genetic terms.  
*In one family, this condition is caused by a mutation in one gene, where in the other family, this condition is caused by a mutation in a different gene. In the third generation where the individuals are heterozygous at each loci, the two mutations complement each other.*

ii) Suppose cats 1 and 2 had kittens, what fraction of them would you expect to suffer from the condition?  
*7/16 would show the skin condition because they are homozygous for at least one mutant allele.*