7.E: Linkage and Mapping (Exercises)

These are homework exercises to accompany Nickle and Barrette-Ng’s "Online Open Genetics” TextMap. Genetics is the scientific study of heredity and the variation of inherited characteristics. It includes the study of genes, themselves, how they function, interact, and produce the visible and measurable characteristics we see in individuals and populations of species as they change from one generation to the next, over time, and in different environments.

Study Questions

7.1 Compare recombination and crossover. How are these similar? How are they different?

7.2 Explain why it usually necessary to start with pure-breeding lines when measuring genetic linkage by the methods presented in this chapter.

7.3 If you knew that a locus that affected earlobe shape was tightly linked to a locus that affected susceptibility to cardiovascular disease human, under what circumstances would this information be clinically useful?

7.4 In a previous chapter, we said a 9:3:3:1 phenotypic ratio was expected among the progeny of a dihybrid cross, in absence of gene interaction.

a) What does this ratio assume about the linkage between the two loci in the dihybrid cross?

b) What ratio would be expected if the loci were completely linked? Be sure to consider every possible configuration of alleles in the dihybrids.

7.5 Given a dihybrid with the genotype CcEe:
a) If the alleles are in coupling (cis) configuration, what will be the genotypes of the parental and recombinant progeny from a test cross?

b) If the alleles are in repulsion (trans) configuration, what will be the genotypes of the parental and recombinant progeny from a test cross?

7.6 Imagine the white flowers are recessive to purple flowers, and yellow seeds are recessive to green seeds. If a green-seeded, purple-flowered dihybrid is testcrossed, and half of the progeny have yellow seeds, what can you conclude about linkage between these loci? What do you need to know about the parents of the dihybrid in this case?

7.7 In corn (i.e. maize, a diploid species), imagine that alleles for resistance to a particular pathogen are recessive and are linked to a locus that affects tassel length (short tassels are recessive to long tassels). Design a series of crosses to determine the map distance between these two loci. You can start with any genotypes you want, but be sure to specify the phenotypes of individuals at each stage of the process. Outline the crosses similar to what is shown in Figure 7.8, and specify which progeny will be considered recombinant. You do not need to calculate recombination frequency.

7.8 In a mutant screen in *Drosophila*, you identified a gene related to memory, as evidenced by the inability of recessive homozygotes to learn to associate a particular scent with the availability of food. Given another line of flies with an autosomal mutation that produces orange eyes, design a series of crosses to determine the map distance between these two loci. You do not need to calculate recombination frequency.

7.9 Image that methionine heterotrophy, chlorosis (loss of chlorophyll), and absence of leaf hairs (trichomes) are each caused by recessive mutations at three different loci in Arabidopsis. Given a triple mutant, and assuming the loci are on the same chromosome, explain how you would determine the order of the loci relative to each other.

7.10 If the progeny of the cross *aaBB* x *AAbb* is testcrossed, and the following genotypes are observed among the progeny of the testcross, what is the frequency of recombination between these loci?

\[
\begin{align*}
AaBb & \quad 135 \\
Aabb & \quad 430 \\
aaBb & \quad 390 \\
aabb & \quad 120
\end{align*}
\]

7.11 Three loci are linked in the order B-C-A. If the A-B map distance is 1cM, and the B-C map distance is 0.6cM, given the lines *AaBbCc* and *aabbcc*, what will be the frequency of *Aabb* genotypes among their progeny if one of the parents of the dihybrid had the genotypes *AABBCC*?

7.12 Genes for body color (B black dominant to b yellow) and wing shape (C straight dominant to c curved) are located on the same chromosome in flies. If single mutants for each of these traits are crossed (i.e. a yellow fly crossed to a curved-wing fly), and their progeny is testcrossed, the following phenotypic ratios are observed among their progeny.
black, straight  17  
yellow, curved  12  
black, curved  337  
yellow, straight  364

a) Calculate the map distance between B and C.

b) Why are the frequencies of the two smallest classes not exactly the same?

7.13 Given the map distance you calculated between B-C in question 12, if you crossed a double mutant (i.e. yellow body and curved wing) with a wild-type fly, and testcrossed the progeny, what phenotypes in what proportions would you expect to observe among the F₂ generation?

7.14 In a three-point cross, individuals AAbbcc and aaBBCC are crossed, and their F₁ progeny is testcrossed. Answer the following questions based on these F₂ frequency data.

\[
\begin{align*}
aaBbCc & \quad 480 \\
AaBbcc & \quad 15 \\
AaBbCc & \quad 10 \\
aaBbcc & \quad 1 \\
aabbCc & \quad 13 \\
Aabbcc & \quad 472 \\
AabbCc & \quad 1 \\
aabbcc & \quad 8
\end{align*}
\]

a) Without calculating recombination frequencies, determine the relative order of these genes.

b) Calculate pair-wise recombination frequencies (without considering double cross overs) and produce a genetic map.
c) Recalculate recombination frequencies accounting for double recombinants.

7.15 Wild-type mice have brown fur and short tails. Loss of function of a particular gene produces white fur, while loss of function of another gene produces long tails, and loss of function at a third locus produces agitated behaviour. Each of these loss of function alleles is recessive. If a wild-type mouse is crossed with a triple mutant, and their F₁ progeny is test-crossed, the following recombination frequencies are observed among their progeny. Produce a genetic map for these loci.

Chapter 7 - Answers

7.1

Crossovers are defined cytologically; they are observed directly under the microscope.
Recombination is defined genetically; it is calculated from observed phenotypic proportions.
Some crossovers lead to recombination, but not all crossovers result in recombination.
Some recombinations involve crossovers, but not all recombinations result from crossovers.
Crossovers happen between sister and non-sister chromatids. If the chromatids involved the crossover have identical alleles, there will not be any recombination.
Crossovers can also happen without causing recombination when there are two crossovers between the loci being scored for recombination.
Recombination can occur without crossover when loci are on different chromosomes.

7.2

The use of pure breeding lines allows the researcher to be sure that he/she is working with homozygous genotypes. If a parent is known to be homozygous, then all of its gametes will have the same genotype. This simplifies the definition of parental genotypes and therefore the calculation of recombination frequencies.

7.3

This would suggest that individuals with a particular earlobe phenotype may also carry one or more alleles that increased their risk of cardiovascular disease. These individuals could therefore be informed of their increased risk and have an opportunity to seek increased monitoring and reduce other risk factors.

7.4 a)

It assumes that the loci are completely unlinked.

b)
If the parental gametes were \( AB \) and \( ab \), then the gametes produced by the dihybrids would also be \( AB \) and \( ab \), and the offspring of a cross between the two dihybrids would all be genotype \( AABB: AaBb:aabb \), in a 1:2:1 ratio.

If the parental gametes were \( Ab \) and \( aB \), then the gametes produced by the dihybrids would also be \( Ab \) and \( aB \), and the offspring of a cross between the two dihybrids would all be genotype \( AAbb:AaBb:aaBB \), in a 1:2:1 ratio.

### fur tail behaviour

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</table>

7.5 a) Parental: \( CcEe \) and \( ccee \); Recombinant: \( Cee \) and \( ccEe \).

b) Parental: \( Cee \) and \( ccEe \); Recombinant: \( CcEe \) and \( ccee \).

7.6 Let \( WwYy \) be the genotype of a purple-flowered (\( W \)), green seeded (\( Y \)) dihybrid. Half of the progeny of the cross \( WwYy \times wwyY \) will have yellow seeds whether the loci are linked or not. The proportion of the seeds that are also either white or purple flowered would help you to know about the linkage between the two loci only if the genotypes of the parents of the dihybrid were also known.

7.7

Let \( tt \) be the genotype of a short tassels, and \( rr \) is the genotype of pathogen resistant plants. We need to start with homozygous lines with contrasting combinations of alleles, for example:

P: \( RRtt \) (pathogen sensitive, short tassels) \( \times rrtT \) (pathogen resistant, long tassels)
F₁: \( RrTt \) (sensitive, long) \( \times \) \( rtt \) (resistant, short)

F₂: parental \( Rrtt \) (sensitive, short), \( rrTt \) (resistant, long)

Recombinant \( rtt \) (resistant, short), \( RrTt \) (sensitive, long)

7.8 Let \( mm \) be the genotype of a mutants that fail to learn, and \( ee \) is the genotype of orange eyes. We need to start with homozygous lines with contrasting combinations of alleles, for example (wt means wild-type):

P: \( MMEE \) (wt eyes, wt learning) \( \times \) \( mmee \) (orange eyes, failure to learn)

F₁: \( MmEe \) (wt eyes, wt learning) \( \times \) \( mmee \) (orange eyes, failure to learn)

F₂: parental \( MmEe \) (wt eyes, wt learning), \( mmee \) (orange eyes, failure to learn)

Recombinant \( Mmee \) (wt eyes, failure to learn), \( mmEe \) (orange eyes, wt learning)

7.9 Given a triple mutant \( aabbcc \), cross this to a homozygote with contrasting genotypes, i.e. \( AABBCC \), then testcross the trihybrid progeny, i.e.

P: \( AABBCC \) \( \times \) \( aabbcc \)

F₁: \( AaBbCc \) \( \times \) \( aabbcc \)

Then, in the F₂ progeny, find the two rarest phenotypic classes; these should have reciprocal genotypes, e.g. \( aBbCc \) and \( AAbbcc \). Find out which of the three possible orders of loci (i.e. \( A-B-C \), \( B-A-C \), or \( B-C-A \)) would, following a double crossover that flanked the middle marker, produce gametes that correspond to the two rarest phenotypic classes. For example, if the rarest phenotypic classes were produced by genotypes \( aBbCc \) and \( AAbbcc \), then the dihybrid’s contribution to these genotypes was \( ABC \) and \( Abc \). Since the parental gametes were \( ABC \) and \( abc \) the only gene order that is consistent with \( ABC \) and \( Abc \) being produced by a double crossover flanking a middle marker is \( B-A-C \) (which is equivalent to \( C-A-B \)).

7.10 If the progeny of the cross \( aaBB \times AAbb \) is testcrossed, and the following genotypes are observed among the progeny of the testcross, what is the frequency of recombination between these loci?

\[
\begin{align*}
   \text{AaBb} & \quad 135 \\
   \text{Aabb} & \quad 430 \\
   \text{aaBb} & \quad 390 \\
   \text{aabb} & \quad 120 \\
\end{align*}
\]

\[
\frac{(135 + 120)}{(135+120+390+430)} = 24\%
\]

7.11
Based on the information given, the recombinant genotypes with respect to these loci will be $Aabb$ and $aaBb$. The frequency of recombination between A-B is 1cM=1%, based on the information given in the question, so each of the two recombinant genotypes should be present at a frequency of about 0.5%. Thus, the answer is 0.5%.

7.12

a) 4cM

b) Random sampling effects; the same reason that many human families do not have an equal number of boys and girls.

7.13

There would be approximately 2% of each of the recombinants: (yellow, straight) and (black, curved), and approximately 48% of each of the parentals: (yellow, curved) and (black, straight).

7.14

a) Without calculating recombination frequencies, determine the relative order of these genes.

A-C-B

b)

A-B 4.6%
A-C 2%
B-C 3%
B C A

|--------|--------|

3cM 2cM

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c) Recalculate recombination frequencies accounting for double recombinants
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7.15

A is fur color locus

B is tail length locus

C is behaviour locus

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B C A

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4.1cM 1.5cM

Pairwise recombination frequencies are as follows (calculations are shown below):

A-B 5.6%
A-C 1.5%
B-C 4.1%

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5.6% 1.5% 4.1%

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