Week 7 Handout

BIO1A Discussion Section

Week 7 Key Topics

- 1) Genes and chromosomes
 - a) Genes can be physically linked on chromosomes
 - b) Gene linkage scenarios
 - i) Unlinked
 - ii) Linked (no recombination)
 - iii) Linked (<50 cM apart)
 - iv) Linked (>50 cM apart)
 - c) Recombination is proportional to distance between genes
 - d) Gene maps
 - e) Sex-linked traits will appear more frequently in one sex than another
- 2) Nucleic acid structure and synthesis
 - a) Nucleic acid structure
 - i) Properties
 - (1) Chemical components
 - (2) Base pairing
 - (3) Thermodynamics
 - (4) Polarity
 - ii) Difference between RNA and DNA: T vs U, deoxyribose vs ribose
 - b) DNA synthesis
 - i) Enzymes involved: helicase, primase, DNA polymerase III DNA polymerase I, ligase
 - ii) Replication bubble: leading vs. lagging strand
- 3) Transcription and translation
 - a) Transcription
 - i) RNA polymerase
 - ii) Different genes can be on different strands
 - b) Translation
 - i) Genetic code
 - ii) Specific tRNAs have unique aminoacyl tRNA synthetases

Genes and Chromosomes

 What stage of meiosis results in Mendel's law of segregation? Mendel's law of assortment? Explain how the biology of meiosis results in the genetics laws that Mendel observed.

Mendel's first law (the law of segregation) results from the separation of homologous chromosomes during anaphase I. Mendel's second law (the law of independent assortment) results from the random arrangement of homologous pairs during metaphase I.

2. Imagine a cross between two organisms involving genes G, T, and R. The dominant form of the gene is upper case, and the recessive form of the gene is lower case. You cross two parents with genotypes ggTTrr and GGttRR to generate F1 offspring, and then use the F1 offspring in a testcross. You observe the formation of the gametes in the following frequency:

| Gametes | Frequency | | | |
|-------------|-----------|--|--|--|
| gTr and GtR | 282/318 | | | |
| gTR and Gtr | 106/94 | | | |
| gtr and GTR | 74/76 | | | |
| gtR and GTr | 27/23 | | | |

a. Are the three genes linked or unlinked? How can you tell?

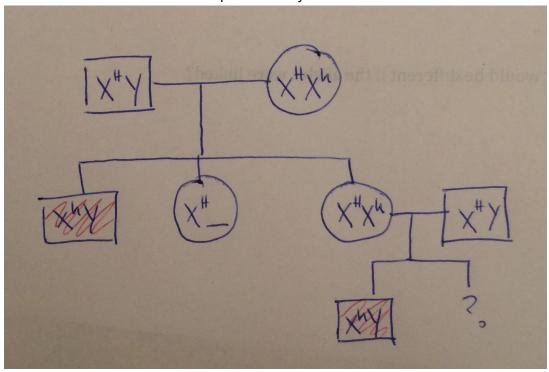
The genes are linked; if they were unlinked, you would expect all types of gametes to appear with equal frequency.

| b. | What is the percent recombination between each pair of genes? | | | | | | | | |
|----|---|----------|-------|-----------|------------|-----------|-----------|------------|-------------|
| | i. | G and | T = _ | 20% | _ | | | | |
| | ii. | T and | R = _ | 35% | _ | | | | |
| | iii. | G and | R = _ | 25% | _ | | | | |
| C. | Draw | a geneti | c map | of the pa | art of the | chromosor | ne contai | ning these | three genes |
| | | | | | | | | | |
| | | | R | _25cm | G | 20cm | T | | |
| | | | | | | | | | |

d. Why don't the two smaller recombination frequencies add up to the larger recombination frequency?

This discrepancy results from double crossover events that cancel each other out.

- 3. Hemophilia is a sex linked trait that is inherited via the X chromosome in parents. Two grandparents, with the genotypes X^HX^h and X^HY, have two daughters and one son. The son is affected but the daughters are not. One of these daughters then mates with an unaffected male. They have two offspring, including one affected son.
 - a. Draw the pedigree described. Remember that males are represented by squares and females are represented by circles. Affected individuals are shaded



b. What is the probability the other offspring is a son with hemophilia?

Probability of having a son x Probability of son having hemophilia = $\frac{1}{2} * \frac{1}{2} = \frac{1}{4}$ A son will inherit either a wildtype or hemophiliac X chromosome from his mother.

c. If the other offspring is a daughter, what is the probability she will have hemophilia?

Probability of daughter having hemophilia = 0
Any daughter will inherit an wildtype X chromosome from their father.

Translation and Transcription

4. (a) Fill in the blanks. Use the attached codon chart. You will know if you made it right.

DNA Sense Strand

5'- A T G G C C G A C G A G A T C A C C C G C A T C G G C C A C A C C T A G

DNA Template Strand

3' - T A C C G G C T G C T C T A G T G G G C G T A G C C G G T G T G G A T C mpNa

5'- A U G G C C G A C G A G A U C A C C C G C A U C G G C C A C A C C U A G

Protein Three Letter

N - Met Ala Asp Glu Ile Thr Arg Ile Gly His Thr * Single Letter $N - \ \underline{M} \quad \underline{A} \quad \underline{D} \quad \underline{E} \quad \underline{I} \quad \underline{T} \quad \underline{R} \quad \underline{I} \quad \underline{G} \quad \underline{H} \quad \underline{T} \quad \underline{*}$

The DNA is replicated such that the bottom DNA strand is the leading strand. Which of the following sequences is a possible primer for an Okazaki fragment?

1)5'-TGGCCGA-3'

2) 5' -GAGAUCA-3'

3)5'-UCCACAC-3'

4)5'-CCGGCUG-3'

5)5'-UAGGUGU-3'

Standard genetic code

| 1st base | | 2nd base | | | | | | | |
|-------------|--------------------|-----------------------|-----|-------------------|----------------------|-----------------------|----------------------|--------------------|------|
| | U | | | С | | Α | G | | base |
| U | UUU | | | UCU | | (T0.0) T | UGU (Q. 10) Q. 11 | | U |
| | UUC | (Phe/F) Phenylalanine | UCC | /O/O\ C | UAC (Tyr/Y) Tyrosine | | UGC (Cys/C) Cysteine | | С |
| | UUA | (Leu/L) Leucine | UCA | (Ser/S) Serine | UAA | Stop (Ochre) | UGA | Stop (Opal) | Α |
| | UUG | | UCG | | UAG | Stop (Amber) | UGG | (Trp/W) Tryptophan | G |
| С | CUU | | CCU | (Pro/P) Proline | CAU | (His/H) Histidine | CGU | | U |
| | CUC | | ccc | | CAC | | CGC | (Arg/R) Arginine | С |
| | CUA | | CCA | | CAA | (0) (0) (0) | CGA | | Α |
| | CUG | | CCG | G | | (Gln/Q) Glutamine | CGG | | G |
| А | AUU | | ACU | (Thr/T) Threonine | AAU | (Asn/N) Asparagine | AGU | (Ser/S) Serine | U |
| | AUC | (lle/l) Isoleucine | ACC | | AAC | | AGC | | С |
| | AUA | | ACA | | AAA | (Lvs/K) Lvsine | AGA | (Arg/R) Arginine | Α |
| | AUG ^[A] | (Met/M) Methionine | ACG | | AAG | | AGG | | G |
| G | GUU | | GCU | (Ala/A) Alanine | GAU | (Asp/D) Aspartic acid | GGU | | U |
| | GUC | (Val/V) Valine | GCC | | GAC | | GGC | (01-(0)-01 | С |
| | GUA | | GCA | | GAA | 101 (5) (6) | GGA | (Gly/G) Glycine | Α |
| | GUG | | GCG | | GAG | (Glu/E) Glutamic acid | GGG | | G |

5. RNAse H is required to specifically degrade the RNA from DNA+RNA hybrid duplexes. Which part of the DNA replication process would be interfered with if you prevented this activity? Why?

This would prevent the removal of the RNA primers used to initiate replication at the origin for the leading strand and for the individual origins of the Okazaki fragments.

6. The "TATA box" is an AT rich DNA motif that is present in many promoter regions. During transcription initiation, it is bound by the TATA binding protein (TBP) which then bends and unwinds the DNA, facilitating the binding of the rest of the transcription machinery. What physical properties of the motif facilitate this function?

A-T pairs only have two hydrogen bonds, which means that it is easier to separate.

- 7. This is the translated region of an mRNA for a hypothetical small peptide:
- 5'- AUG GCC AAG GAG AUG UAC GAC GCC UAC TAG -3'

Are the two AUG codons recognized by the same type of tRNA? Why or why not?

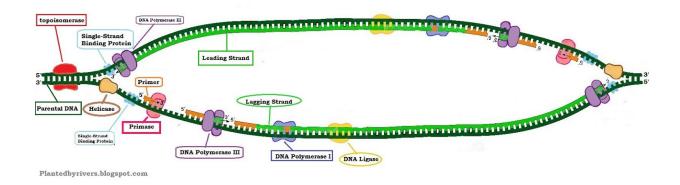
They are not recognized by the same type of tRNA. The first AUG is recognized by the special "Initiator tRNA" which is required for translation initiation, while the second is recognized by the normal Methionine tRNA.

DNA Replication

8. Do it yourself diagram! The more you draw yourself, the better it sticks, we swear.

Diagram a replication bubble. Include and label the replication initiation site, 5' and 3', helicase, primase, DNA polymerase III, DNA polymerase I, ligase, Leading Strand, Lagging Strand, Okazaki Fragment. Major bonus points if you manage to do it while showing DNA pol III as a homodimer.

It should come out somewhat like this, though without topoisomerase or the ssbps.



If you go for the homodimer, the ends will probably look something like this.

