PLNT3140 INTRODUCTORY CYTOGENETICS
FINAL EXAMINATION

Monday December 14, 2015
Time: 13:30 - 15:30
Location: Engineering E2-229, Seats 130 - 157

Answer any combination of questions totaling to exactly 100 points. If you answer questions totaling more than 100 points, answers will be discarded at random until the total points equal 100. There are 10 questions to choose from, totaling 120 points. This exam is worth 35% of the final grade.

Ways to write a readable and concise answer:
i. Just answer the question. Save time by specifically addressing what is asked. Don't give irrelevant background if it doesn't contribute to the question that was asked.
ii. Avoid stream of consciousness. Plan your answer by organizing your key points, and then write a concise, coherent answer. Make your point once, clearly, rather than repeating the same thing several times with no new information.
iii. Point form, diagrams, tables, bar graphs, figures are welcome. Often they get the point across more clearly than a long paragraph.
iv. Your writing must be legible. If I can't read it, I can't give you any credit.

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1. (5 points) Stable triploids are not found in sexually-reproducing species, but are found in parthenogens. Explain why.

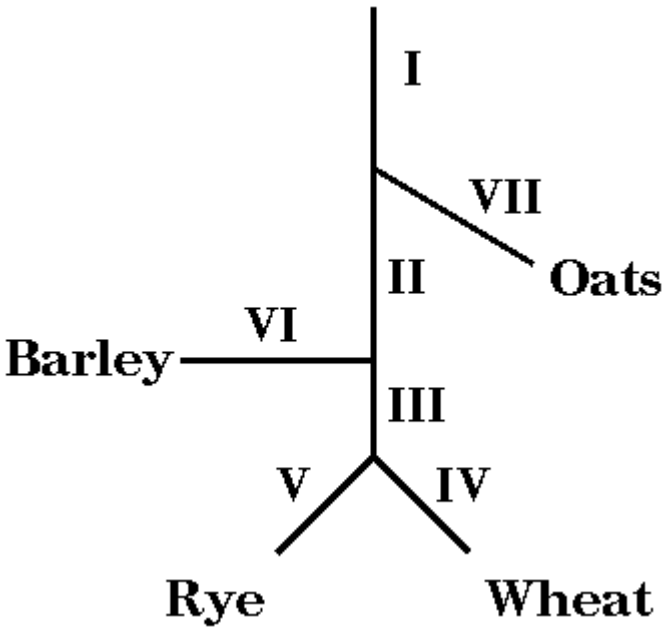
2. (10 points) Explain how changes in chromosomal structure, such as duplications, deletions, translocations and inversions, help drive the process of speciation. You do not need to go into detail on defining what these changes are eg. don't bother drawing diagrams of meiotic products resulting from translocations. Rather, concentrate on the evolutionary consequences of these changes.

3. (10 points) You are beginning a new project studying ribosomal RNA genes, which are typically present in > 200 copies per haploid genome. The project will involve a lot of Southern blots, which normally require a 20 hour hybridization time to detect a single copy gene. You realize that it should be possible to do your Southern blots in a shorter time, because of the fact that rRNA genes are present in high copy numbers. If you want to get bands with the same intensity as you would get for a single copy gene, how long should you hybridize? Hint: Consider the definition of C_0t.

4. (10 points) We have spent a lot of time describing how chromosomal abnormalities such as translocations, inversions, deletions and duplications can help drive speciation, through their effects on pairing at meiosis.

Describe a mechanism by which amplification or deletion of middle-repetitive sequence familes might also create reproductive barriers between populations within a species?

5. (15 points) In the experiments of Flavell and co-workers, C_0t analysis was employed to compare the relative amounts of interspersed repetitive DNA families in four cereal species. As we discussed, the authors defined seven distinct classes of repetitive sequence families, I - VII. For example, Class I refers to repetitive sequences found in the common ancestor of all 4 species, while Class VII refers to repetitive sequences that arose after the divergence of Oat from its common ancestor with Barley, Wheat and Rye. They performed C_0t curves to determine, for example, the percentage of Class II sequences present in Rye, Wheat and Barley, or the percentage of Class III sequences found in Rye or Wheat.



In principle, you obtain the same information using 60-mer microarrays. Oligos in such an array would represent the entire genome, including repetitive sequences, and not just transcribed sequences. A critical consideration in this case is that while a substantial percentage of the wheat and barley genomes have been sequenced, there is relatively little sequence available from rye and oat genomes, at this writing. Notwithstanding, it should at least be possible to construct microarrays containing 60-mers representative of a substantial percentage of the Wheat and Barley genomes.

a) In your exam booklet, rewrite the table below, filling in roman numerals of any class of sequences that would show up as repetitive using either the Wheat or Barley microarrays, when hybridized with labeled genomic DNA from Wheat, Rye, Barley or Oat.

	microarray:	Wheat	Barley
labeled-DNA:			
Wheat			
Rye			
Barley			
Oat			

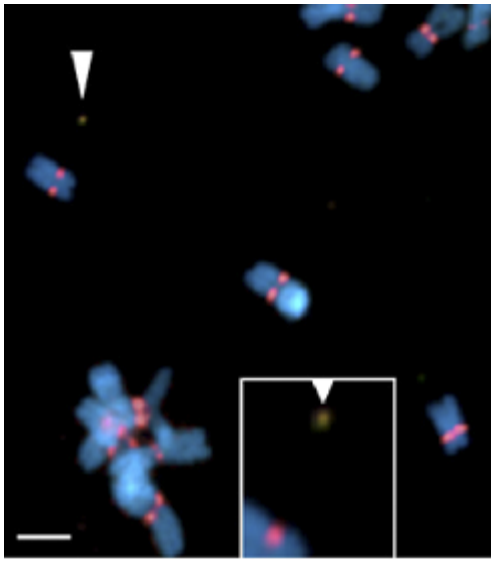
b) What additional things about the wheat and barley genomes would you learn from microarrays that you wouldn't learn from C_0t analysis?

6. (10 points)

a) Draw a diagram illustrating how chromosomes pair during meiosis in cells heterozygous for a reciprocal translocation. Feel free to use colors, shading or hatching to represent homologous chromosomes.

b) Draw a diagram illustrating the orientation of reciprocal translocation products from a), at metaphase, assuming an Alternate configuration.

7. (10 points) In the accompanying figure, the arrow points to an MMC artificial chromosome in T_0 maize plants, visualized using Fluorescent In-situ Hybridization (FISH). To prove that these chromosomes are stably-inherited like naturally-occurring chromosomes, this transgenic line was selfed for two generations. If the chromosome was stably-inherited, draw the expected FISH results as seen in the T_2 generation. (Just draw the MMC, and not the natural chromosomes.)



8. (15 points)

a) State in one sentence the Hardy-Weinberg law.

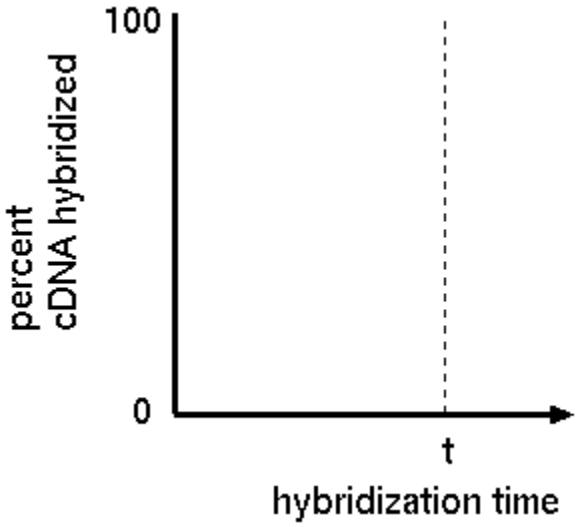
b) Briefly describe any four of the components of evolution discussed in class.

9. (5 points) Explain the mechanism by which unequal crossing over can generate in a single step both a deletion and a duplication. Draw a simple diagram to illustrate the point.

10. (15 points) Microarrays attempt to measure the concentration of mRNAs by hybridizing cDNA populations to oligonucleotides on the array. The accuracy of the measurement is dependent on the time **t** of the hybridization. In other words, **t** is the time at which we stop hybridizing the slide and begin washing off unhybridized cDNA. Recall that the equation relating hybridization time to concentration can be represented in two equivalent forms:

$$-dC = \frac{kC^2}{dt} \qquad \frac{C}{C_0} = \frac{1}{1 + kC_0 t}$$

Draw a graph, similar to the one below, with three curves, representing the percent cDNA hybridized to the array for a highly-expressed transcript, a moderately-expressed transcript, and a weakly-expressed transcript.



Based on these three curves, how does our choice of time **t** affect the accuracy of measurement of each of these three categories of transcript?

11. (15 points) In a cross between two *Arabidopsis* lines, A and B, a map of one chromosome was constucted using a set of co-dominant markers. An excerpt of the mapping data for this cross is shown in panel I. At each locus, the marker is scored as being homozygous for the allele from parent A, homozygous for the allele from parent B, or heterozygous. The order of loci shown in the table corresponds to the order of those loci on the chromosome.

a) What is the predicted ratio for seeing A, H or B, at any given locus?

b) In cross II, parent A was crossed with another *Arabidopsis* line, C. Thus, the expected phenotypes would be either A, H or C. In this cross, the mapping data look similar to that found in cross I. However, all loci distal to g3883 exhibit only the A phenotype, in all progeny. What is a simple explanation for this result?

c) Based on your answer to b, how could you test your hypothesis?

I. A x B

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        segregating progeny ------------------->

marker/
map posn.
g6844   HHAAAAABHHBAAAHBHHHHABHHHABBAHHBHAHHBAAHHA
g3843   HHAAAAABHHBAAAHBHHHHABHHHAHBAHHBHAHHBAABAA
g2616   HHAAHHHBHHBAAAHBHHHABHHHHHHHBBHBHHAHHHHHHH
m210    HHAHHBHHHHHAAAHHBHHHAHHAHAHHHAABHHAHBHABAA
g6837   HHAABHHAHBHHBAAHBHHHAHHAHAHHHAABHHAHBHABAA
g10086  AHHHAAHHHAHBHHBAHHHHAHHAHAHHHAAHHHAHBHHBAB
g4564a  HAAHHBHHHHHAAAHHBHHHAHHAHAHHHAAHHHAHBHHBAA
g3845   HAHHHBHHHAHAAAAHBHHAHBAHAHHHAAHHHAHBHHHAHH
g4539   AHHHAAHHHAHBHHHAHHHAAHBAHAHHHHAHHBAHBHHHAH
m557    HAHHHBHHHAHAAAAHBHHAAHBAHAHHHHAHHBAHBHHHAH
g3883   HAHHHBHHHAHAAAAHBHHHAHBAHAHHHHAHHBAHBHHHAH
g19833  HAHAHBHHAHAAAAHBHHAHBAHHHHAHHHABAHHAHHBBAH
g19838  HAHHAHBHHAHAAHBHAHHBAAHBHHAHHBAAHHHHABHHAH
m272    HAHAHBHHHAHAAHBHAHHBAAHBHHAHHBAAHHHHABHHAB
g4513   HAHAHBHHHAHAAAAHBHAHHHBAAAHBHHAHBBAAHHHHAB
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II. A x C

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        segregating progeny ------------------->

marker/
map posn.
g6844   HHAAAAACHHCAAAHCHHHHACHHHACCAHHCHAHHCAAHHA
g3843   HHAAAAACHHCAAAHCHHHHACHHHAHCAHHCHAHHCAACAA
g2616   HHAAHHHCHHCAAAHCHHHACHHHHHHHCCHCHHAHHHHHHH
m210    HHAHHCHHHHHAAAHHCHHHAHHAHAHHHAACHHAHCHACAA
g6837   HHAACHHAHCHHCAAHCHHHAHHAHAHHHAACHHAHCHACAA
g10086  AHHHAAHHHAHCHHCAHHHHAHHAHAHHHAAHHHAHCHHCAC
g4564a  HAAHHCHHHHHAAAHHCHHHAHHAHAHHHAAHHHAHCHHCAA
g3845   HAHHHCHHHAHAAAAHCHHAHCAHAHHHAAHHHAHCHHHAHH
g4539   AHHHAAHHHAHCHHHAHHHAAHCAHAHHHHAHHCAHCHHHAH
m557    HAHHHCHHHAHAAAAHCHHAAHCAHAHHHHAHHCAHCHHHAH
g3883   HAHHHCHHHAHAAAAHCHHHAHCAHAHHHHAHHCAHCHHHAH
g19833  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
g19838  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
m272    AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
g4513   AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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