PLNT3140 INTRODUCTORY CYTOGENETICS 2016
FINAL EXAMINATION

Wednesday January 11, 2017
Time: 12:30 - 14:30
Location: Engineering E2-130, Seats 1 -27

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 12 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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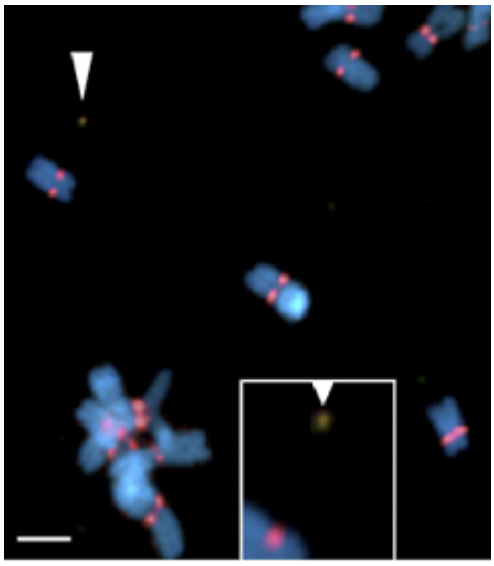
1. (10 points) We have spent a lot of time describing how chromosomal abnormalities such as translocations, inversions, deletions and duplications can help drive speciation, through their effects on pairing at meiosis.

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

2. (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.)



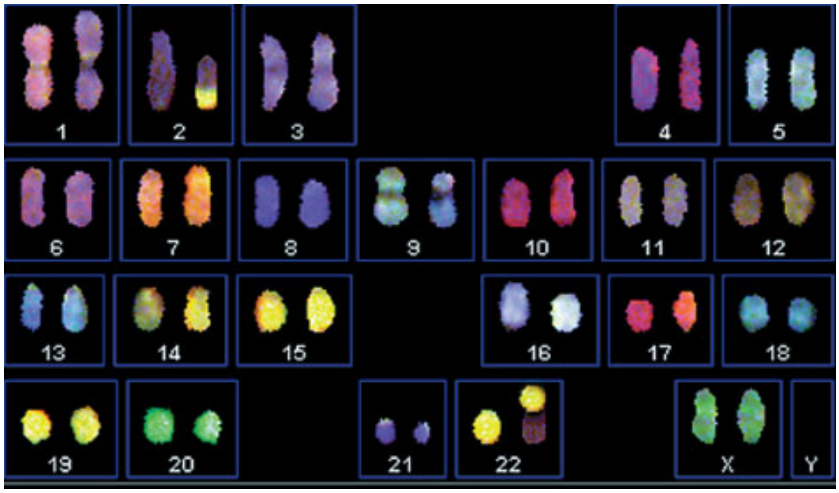
3. (5 points) Explain the concept of microsynteny, in the context of comparing genomes between two related species.

4. (15 points)

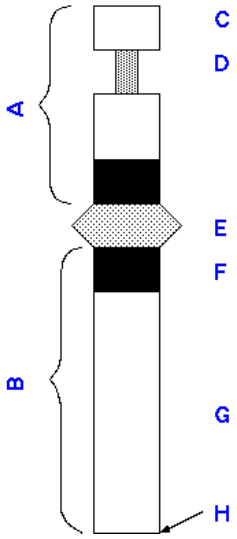
a) State in one sentence the Hardy-Weinberg law.
b) Briefly describe any four of the components of evolution discussed in class.

5. (5 points) Unequal crossing over can generate in a single step both a deletion and a duplication. Draw a simple diagram to illustrate the mechanism by which this occurs.

6. (10 points) The spectral karyotype below shows a set of human chromosomes. What sex is the person from which the chromosomes were imaged? What is the other important finding that is apparent from this data?



7. (10 points) What is the term for the diagram at right?
For A - H, name each part.



8. (15 points) In a cross between two *Arabidopsis* lines, A and B, a map of one chromosome was constructed 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

```
        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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9. (10 points) The pairwise distances in cM between five loci are shown in Table 1.

Table 1

	T175	C35	T93	C66
C35	4.2			
T93	18.7	15.6		
C66	26.1	25.5	12.1	
T50B	30.4	30.5	21.1	12.2

a) Draw a map, showing the order of markers and the distances between adjacent markers.

b) The distances between markers do not appear to be additive. That is, if the map order was BCA, the BA distance is not equal to BC + CA. What is the most likely reason for this observation? Can you suggest a potential solution to this problem?

10. (10 points) The accompanying table lists the lengths of chromosomes in the duck-billed platypus (*Ornighorhynchus anatinus*).

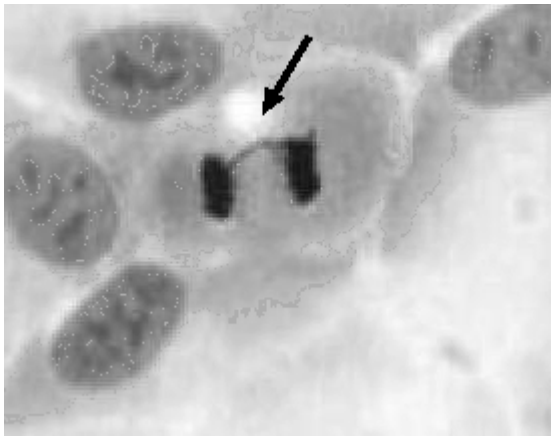
Loc	*Type*	*Name*	*RefSeq*	*INSDC*	*Size (Mb)*
Nuc	Chr	1	NC_009094.1	CM000409.1	47.59
Nuc	Chr	2	NC_009095.1	CM000410.1	54.8
Nuc	Chr	3	NC_009096.1	CM000411.1	59.58
Nuc	Chr	4	NC_009097.1	CM000412.1	58.99
Nuc	Chr	5	NC_009098.1	CM000413.1	24.61
Nuc	Chr	6	NC_009099.1	CM000414.1	16.3
Nuc	Chr	7	NC_009100.1	CM000415.1	40.04
Nuc	Chr	10	NC_009103.1	CM000416.1	11.24
Nuc	Chr	11	NC_009104.1	CM000417.1	6.81
Nuc	Chr	12	NC_009105.1	CM000418.1	15.87
Nuc	Chr	14	NC_009107.1	CM000419.1	2.7
Nuc	Chr	15	NC_009108.1	CM000420.1	3.79
Nuc	Chr	17	NC_009110.1	CM000421.1	1.4
Nuc	Chr	18	NC_009111.1	CM000422.1	6.61
Nuc	Chr	20	NC_009112.1	CM000423.1	1.82
Nuc	Chr	X1	NC_009114.1	CM000424.1	45.54
Nuc	Chr	X2	NC_009115.1	CM000425.1	5.65
Nuc	Chr	X3	NC_009116.1	CM000426.1	5.95
Nuc	Chr	X5	NC_009118.1	CM000427.1	27.79
MT	Chr	MT	NC_000891.1	X83427.1	0.017019
	Un	-	.	-	1,558.51

a) Using the Clark and Carbon formula, calculate the number of BAC clones needed to ensure a 99% chance of finding at least one clone for any given gene. Assume that the BAC library has an average insert size of 100 kb.

$$N = \frac{\ln(1-P)}{\ln(1-f)}$$

b) Suppose that you didn't care about getting a complete genomic library, but rather were only interested in getting genes from chromosome 18. (Assume flow cytometry is not an option.) Does that make any difference to your cloning strategy? Explain why or why not.

11. (10 points) The cell indicated by the arrow is in anaphase of mitosis. What is atypical about the chromosomes shown in this cell, compared to a normal mitosis? What is one possible mechanism that could explain this result?



12. (10 points) Explain one reason why eukaryotic genomes sequenced by Whole Genome Sequencing usually give incomplete sequences for most chromosomes. Illustrate your answer using one or more diagrams.