PLNT3140 INTRODUCTORY CYTOGENETICS
FINAL EXAMINATION

December 10, 2009
Time: 9:00 - 11:00 pm
Location: Frank Kennedy Brown Gym, seats 361-379

Answer any combination of questions totalling to exactly 100 points. (There are 11 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.

---

1. (5 points) When haploids are produced in species such as wheat (1N = 21), one often sees that some chromosomes are partially paired with other chromosomes during meiosis. In principle, there is only one copy of each homologous chromosome. Why is pairing possible, in such an instance?

2. (10 points) Doubled haploids are produced when haploid zygotes are treated with chemicals such as colchicine, which causes chromosome numbers to double, resulting in diploid plants, which can flower and produce normal 1N gametes. If you were to self a doubled haploid, could the F2 population be used to construct a genetic map? Explain your answer.

3. (10 points) Explain why most mutations that occur in eukaryotes are selectively neutral.

4. (10 points)

a) Suppose you are working with a species for which chromosomes have never before been studied. Using simple staining techniques, how can you determine the number and identity of chromosomes in the genome? That is, what information can you use to distinguish chromosome 3 from 8, or 7 from 2 etc? (Assume that banding techniques have not yet been worked out, for this species.)

b) Some genomes have large numbers of small chromosomes. For example, there are salamanders with > 200 chromosomes. What unique problems do such genomes pose for identifying chromosomes?

5. (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) At each locus, what is the predicted ratio for seeing A, H or B?

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

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

marker/ map posn.	
g6844	HHAAAAABHHBAAAHBHHHHABHHHABBAHHBHAHHBAAHHA
g3843	HHAAAAABHHBAAAHBHHHHABHHHAHBAHHBHAHHBAABAA
g2616	HHAAHHHBHHBAAAHBHHHABHHHHHHHHBBHBHHAHHHHHH
m210	HHAHHBHHHHHAAAHHBHHHAHHAHAHHHAABHHAHBHABAA
g6837	HHAABHHAHBHHBAAHBHHHAHHAHAHHHAABHHAHBHABAA
g10086	AHHHAAHHHAHBHHBAHHHHAHAHHHAAHHHAHBHHBAB
g4564a	HAAHHBHHHHHAAAHHBHHHAHHAHAHHHAAHHHAHBHHBAA
g3845	HAHHHBHHHAHAAAAHBHHAHBAHAHHHAAHHHAHBHHHAH
g4539	AHHHAAHHHAHBHHHAHHHAAHBAHAHHHHAHHBAHBHHHAH
m557	HAHHHBHHHAHAAAAHBHHAAHBAHAHHHHAHHBAHBHHHAH
g3883	HAHHHBHHHAHAAAAHBHHHAHBAHAHHHHAHHBAHBHHHAH
g19833	HAHAHBHHAHAAAAHBHHAHBAHHHHAHHHABAHHAHHBBAH
g19838	HAHHAHBHHAHAAHBHAHHBAAHBHHAHHBAAHHHHABHHAH
m272	HAHAHBHHHAHAAHBHAHHBAAHBHHAHHBAAHHHHABHHAB
g4513	HAHAHBHHHAHAAAAHBHAHHHBAAAHBHHAHBBAAHHHHAB

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	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
g19838	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
m272	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
g4513	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

6. (10 points)

a) Kits for chromosome painting (spectral karyotyping) are tremendously difficult to construct, because you would have to start from scratch for each new species. One might be tempted, if working with gorillas for example, to use a human chromosome painting kit for karyotype analysis, investigating genetic diseases, and so forth. Is that likely to work? Why or why not?

b) Similarly, a lot of work goes into creating good gene chips for microarray analysis of gene expression. Affymetrix Inc. does not, as of yet, produce commercial gorilla arrays. Would it be possible to measure levels of gorilla mRNA expression using a human gene chip? Why or why not?

7. (10 points) Suppose that you wish to screen a genomic library for a BAC clone containing a specific gene. Consider following terms and equations:

N - the number of clones that must be screened
P - the probability of finding at least one clone containing the gene
G - the haploid genome size, in base pairs
L - the average length of a BAC clone, in base pairs

$$i) \qquad N = \frac{G}{L}$$

$$ii) \qquad N = \frac{\ln(1 - P)}{\ln\left(1 - \frac{L}{G}\right)}$$

a) To calculate the number of clones that must be screened to find your gene of interest in a library of randomly-chosen clones, why must you use formula ii, rather than formula i ?
b) Under which circumstances would it be appropriate to use formula i?

8. (20 points) Three of the statements below contain an error. One of the statements has no errors. Indicate which statement that is. For each erroneous statement, indicate which part is incorrect, and how the correct statement would read. (Don't rewrite the entire statement.)

Example: DNA sequences that intrinsically lend themselves to amplification are called shellfish DNA.

you could write the following:

... selfish DNA

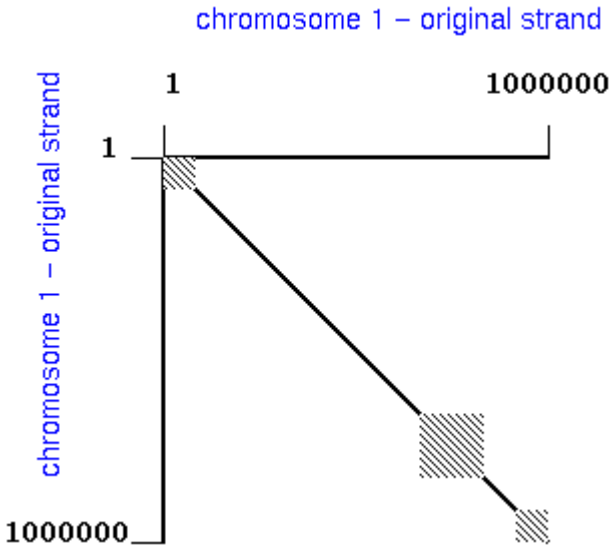
a) Prokaryotic genomes lack middle repetitive DNA. Thus, most crossover events must occur in non-coding DNA.

b) Some of the middle repetitive DNA sequences found in *Drosophila melanogaste*r are middle repetitive sequences in other species of the *Drosophila* subgroup. For example, when *D. melanogaster* fragment pDm73 is used as a probe on Southern blots, it lights up dozens of bands in *D. melanogaster*, but only one or a few bands in other *Drosophila* species.

c) RFLPs are an example of codominant markers, because the heterozygote has the same phenotype as one of the homozygotes.

d) When using end-labeled probes to "walk along the chromosome" from a marker to a gene that is **d** centiMorgans away, it is necessary to construct a contig of overlapping YAC or BAC clones spanning **d** centiMorgans.

9. (10 points) The structure and evolutionary history of entire chromosomes can be studied using dot-matrix programs such as DXHOM. For example, comparison of an entire chromosome with itself might give a plot like that shown below:



Explain why we see these 'diamond' arrays of parallel diagonals.

10. (10 points)

Otto SP, Whitton J (2000) Polyploid incidence and evolution. Ann. Rev. Genet. 34:401-437.

"*One of the biggest stumbling blocks to the successful establishment of polyploidy in sexual species is the requirement for a genetically compatible mate.*" (Otto SP, Whitton J (2000))

a) Explain what the authors mean.

b) Plants lend themselves to polyploidy more readily than do animals. One of the reasons appears to be that plants seem to have mechanisms that compensate for variations in gene dosage. Aside from that, what is it about the reproductive biology of plants that makes it easier for polyploid species to arise?

11. (10 points) Briefly discuss how the following drive speciation:

a) changes in chromosome number

b) changes in chromosome structure