PLNT3140 INTRODUCTORY CYTOGENETICS
FINAL EXAMINATION

December 16, 2013
Time: 18:00 - 20:00
Location: Frank Kennedy Gold Gym, Seats 149-176

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) What is the distinction between the terms evolution and speciation.

2. (5 points) When cells are transformed with an artificial chromosome, there is always a concern that the artificial chromosome might have incorporated into one of the host chromosomes, rather than segregating on its own as an independent chromosome. How you distinguish between these two possibilities?

3. (15 points) Describe the three kinetic classes of DNA in a eukaryotic genome, as defined in a C_0t experiment. Roughly how many copies of sequences are found in each class? What types of sequences are found in each class? Answer in point form.

4. (10 points) We learned that the three basic components of eukaryotic chromosomes are centromeres, telomeres and origins of replication. Yet, it has been possible to transform cells in a number of species with artificial chromosomes whose main chromosomal component is nothing more than a section of centromeric satellite sequences. These constructs function as independent chromosomes. What cellular mechanisms are thought to account for these observations?

5. (10 points) What does the data in this table tell us about the relationship between life history and genome evolution?

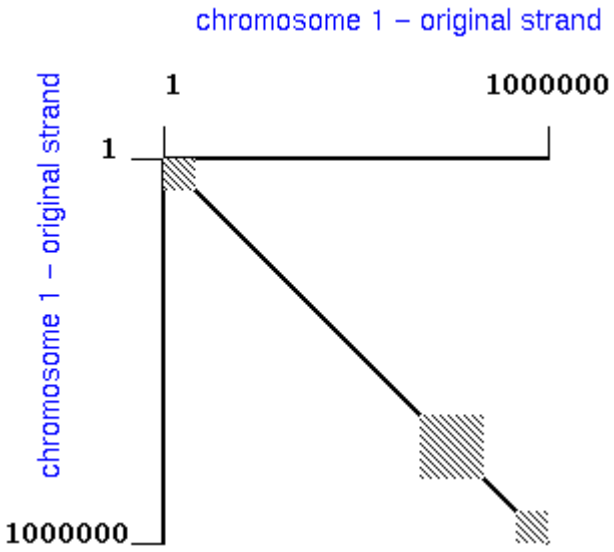
Table 9.6. Duration of mitosis and meiosis in a number of plant species, together with their DNA values in picograms and their annual or perennial habit; where the DNA values are different, both are given.

Species	**Picograms per Haploid Genome**	**Mitosis in Hours**	**Meiosis in Hours**	**Plant Habit**
Crepis capillaris	1.20	10.8	--	Annual
Haplopappus gracillis	1.85	10.5	36.0	Annual
Pisum sativum	3.9, 4.8	10.8	--	Annual
Ornithogalum virens	6.43	--	96.0	Perennial
Secale cereale	8.8, 9.6	12.8	51.2	Annual
Vicia faba	13.0, 14.8	13.0	72.0	Annual
Allium cepa	14.8, 16.25	17.4	72.0	Perennial
Tradescantia paludosa	18.0	18.0	126.0	Perennial
Endymion nonscriptus	21.8	--	48.0	Perennial
Tulipa kaufmanniana	31.2	23.0	--	Perennial
Lillium longiflorum	35.3	24.0	192.0	Perennial
Trillium erectum	40.0	29.0	274.0	Perennial

Source: Van't Hof, 1965, and Bennett, 1972.

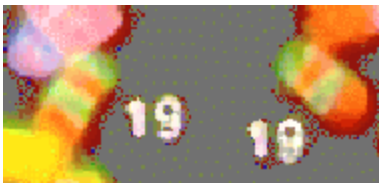
6. (10 points) The structure and evolutionary history of entire chromosomes can be studied using dot-matrix programs such as DXHOM. For example, comparison of an entire chromosome with itself might give a plot like that shown at right.

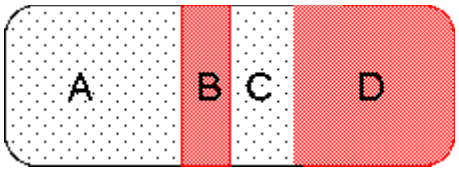
Explain why we see these "diamond" arrays of parallel diagonals.



7. (10 points) How are doubled haploid plants produced in the lab? What advantages to doubled haploid plants offer to geneticists and plant breeders?

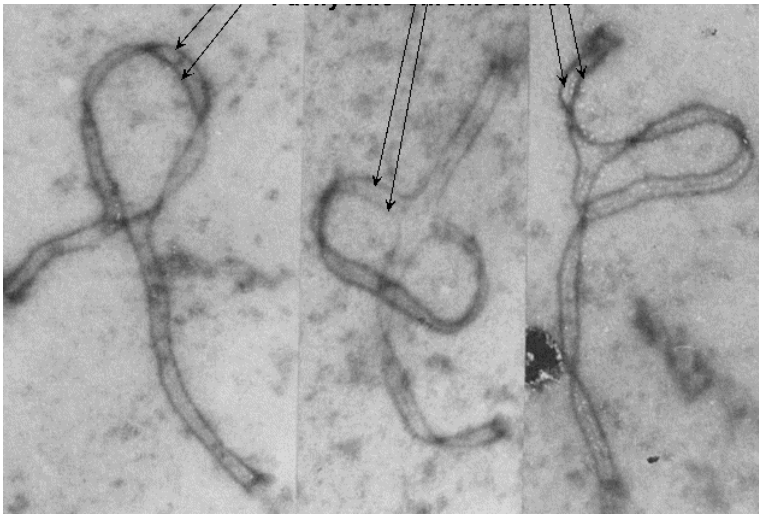
8. (10 points) When gibbon chromosomes are hybridized using a chromosome painting kit of human chromosomes. Most chromosomes show several segments in different colors, indicating that a number of independent events (eg. translocations) have brought together two or more ancestral segments which are found on different chromosomes in human, but on the same chromosome in gibbon. An example is chromosome 19, shown at right in both an actual photo, and in a diagram. The diagram shows that four segments, labeled A - D, are homologous to sequences from two human chromosomes. A and C are homologous to sequences from one human chromosome, and B and D are homologous with sequences from a different human chromosome.





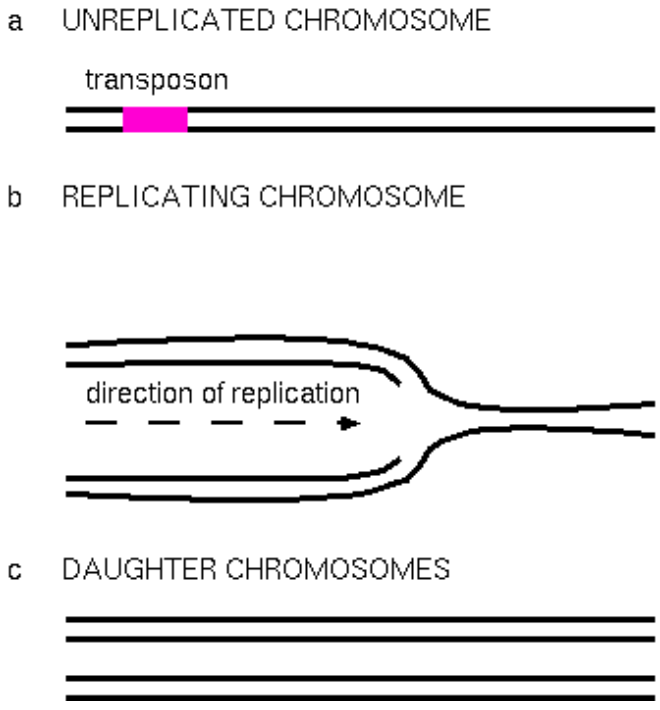
It is easy to imagine how such a composite chromosome might arise from 3 or four translocation events. However, there is a simpler explanation, involving only 2 steps. How could such a chromosome have arisen in two steps?

9. (10 points) The chromosomes below are from cells at pachytene.
a) Why do the chromosomes appear as two threadlike-structures, rather than four?
b) What is the most likely explanation for the loops seen in each?



10. (15 points) Most molecular markers used for mapping in eukaryotes are selectively neutral. Cite two independent reasons why this is true. Also, explain why this matters in genetic mapping.

11. (5 points) Redraw the picture below, showing how transposition of a transposon during DNA replication can result in a net increase in the number of transposons.



12. (10 points) Bacterial artificial chromosomes (BAC) are plasmids designed to facilitate the cloning and manipulation of _____a_____. A BAC vector will typically have cloning sites for enzymes such as Not I (5'GC^GGCCGC3'), which is expected to cut once every _____b_____ base pairs. The cloning site in the vector usually contains a _____c_____ that interrupts a selectable marker. For example, some BAC vectors contain a gene such as SacB, whose expression is toxic to bacterial cells grown on sucrose. When used for cloning, the SacB gene is removed by a restriction digest. Thus, one can select for clones containing inserts by _____d_____. One advantage of BACs, compared to linear YACs, is that BACs are circular, which are less susceptible to _____e_____ than linear chromosomes would be.

13. (5 points) When designing a microarray, the goal is to create 60-mer oligonucleotides, each of which recognizes a specific gene. Given that a gene may consist of coding sequences, introns, and 5' and 3' non-coding regions, which regions would be the best choice as the source of the 60-mer sequence for a gene? Explain your reasoning.