PLNT3140 INTRODUCTORY CYTOGENETICS
FINAL EXAMINATION

December 13 , 2006
Time: 1:30 p.m. to 3:30 p.m.
Location: E2 - 150 EITC, Seats 1 - 18

This exam consists of 8 questions totaling 100 points, and 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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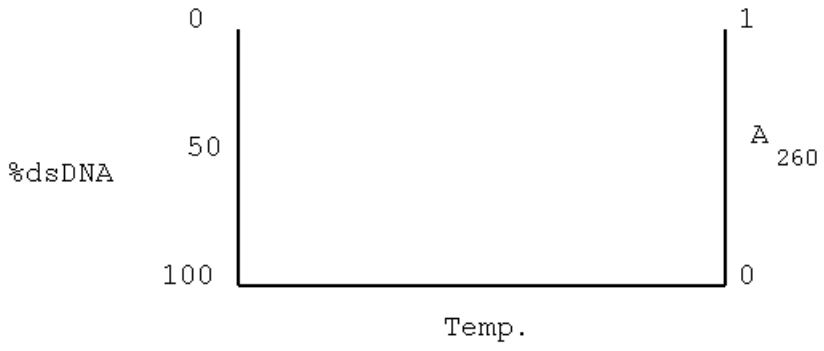
1. (20 points) Define ANY 5 of the following:

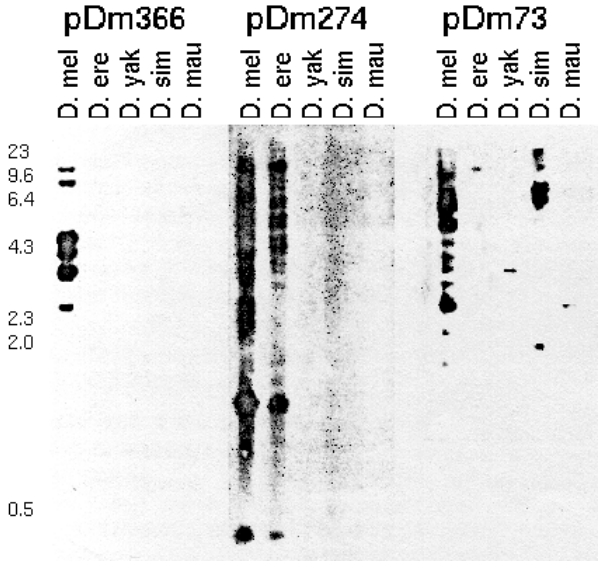
a) amphidiploid
b) nullisomic
c) p and q arms (human nomenclature)
d) aneuploid
e) secondary trisomic
f) metacentric

2. (10 points) Complete the following graph, showing melting curves for three types of DNA duplexes: polyA:polyT, polyG:polyC and heterogeneous DNA.



3. (10 points)

A southern blot with genomic DNA for five *Drosophila* speices is shown at right. Species include *D. melanogaster* (D. mel), *D. erecta* (D. ere), *D. yakuba* (D. yak), *D. simulan*s (D. sim), and *D. mauritiana* (D. mau). For each of the 3 probes from *Drosophila melanogaster*, (pDm366, pDm274 and pDm73), bands are seen in some closely-related *Drosophila* species, but not in others.



Cite two different mechanisms that could account for these observations. To keep things simple, assume that these sequences were present in the common ancestor of all *Drosophila* species.

4. (10 points) Using HAP chromatography, DNA from a C_0t experiment was isolated so that only sequences annealing between $\log C_0t = 0$ and $\log C_0t = 3$ were obtained. This fraction contains some of the middle repetitive fraction, excluding the most repetitive sequences. This DNA was labeled, and used as a probe on a Northern (RNA) gel blot. Hundreds of bands were seen. Explain the results.

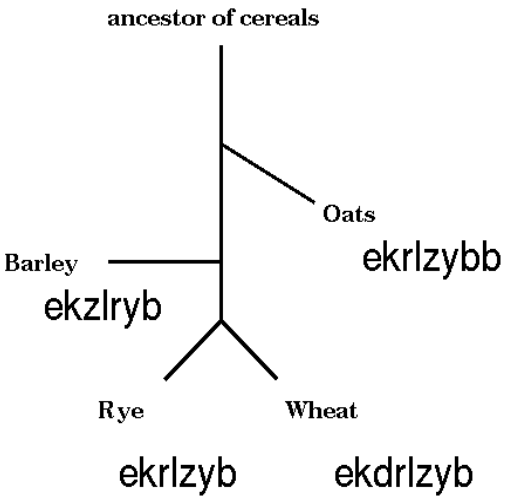
5. (15 points) For genetic engineering of complex traits in plants, it is usually necessary to transform a plant with several different genes, all of which are necessary for expression of a trait. For example, these could be different enzymes in a biochemical pathway. Traditionally, this would have to be done by transforming plants with each gene one at a time, until all genes are present in a single transgenic line.

a) The goal is to get a line that breeds true for the trait. Assuming that each gene goes into a diffferent chromosomal location, what would you have to do to get a line that breeds true for the trait? (Assume that each gene only goes in as a single copy insertion at a single chromosomal location.)

b) Artificial chromosomes can accept many genes. In terms of genetics, how would artificial chromosomes help in engineering of complex traits?

c) One concern with transgenic plants is "escape" of the traits by spontaneous crossing between transgenic and non-transgenic plants, either non-transgenic crops or wild relatives of the crop. To prevent the escape of novel traits into wild populations, which is better, transgenic lines with artificial chromosomes, or transgenic lines in which each gene has gone into a different chromosomal location?

6. (10 points) Just by looking at any pair of sequences or chromosomes, it is impossible to determine evolutionary history. For example, it is not possible to distinguish between an insertion in one sequence versus a deletion in another. However, when examples are available from several species whose evolutionary histories are known, it is possible to reconstruct the sequence of events that have led to the modern day chromosomes that we observe. The figure below shows the relationships between four cereal species. For each species, the order of a set of loci on a chromosome is indicated.



Reconstruct the order of mutational events, (eg. insertion, deletion, inversion, duplication etc.) and show the order of these loci in the common ancestor of the four cereals.

7. (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?

8. (15 points) Discuss how changes in chromosomal structure such as tranlocations and inversions influence the process of evolution.