PLNT3140 INTRODUCTORY CYTOGENETICS
FINAL EXAMINATION

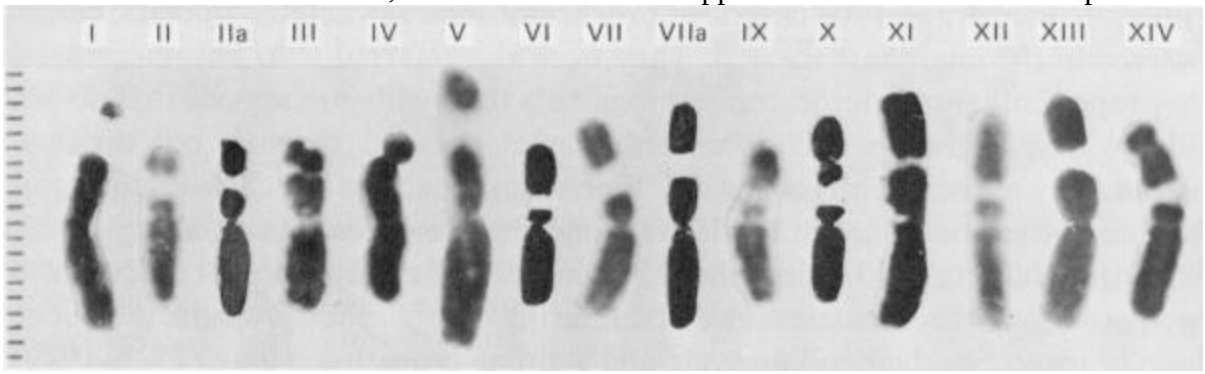
December 10, 2007
Time: 9:00 a.m. to 11:00 a.m.
Location: Frank Kennedy Brown Gym, Seats 345 - 363

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.

---

1. (5 points) In many organisms, chromosomes appear to have "satellites", as pictured below. What are chromosome satellites, and what causes their appearance under the microscope?



2. (15 points) Fill in the blanks.

ESTs are cDNA clones for which partial sequence is available, usually from a single sequencing reaction. This question distinguishes between what ESTs can tell you, and what they can't. Complete the sentence for ANY 5 of the following:

a) Map position: An EST, by itself doesn't tell you the map position of a gene, but it can be used to find the position by _____.
b) Amino acid sequence: An EST tells you some of the amino acid sequence of a protein, if you can determine _____.
c) Locations of introns: An EST can tell you the location of some of the introns if you also know _____.
d) Gene function: An EST can't tell you the function of gene from the sequence alone, but that sequence can be used to infer function if _____.

e) Gene copy number: If a gene exists as a multigene family, a large EST population can tell you a minimal estimate of copy number but _____.
f) Gene expression: ESTs can tell you whether or not a gene is expressed in a given tissue or developmental stage, but if you want to know _____ the ESTs must be used in gene array experiments.

3. (15 points) The pairwise distances in cM between five loci are shown in Table 1.

Table 1

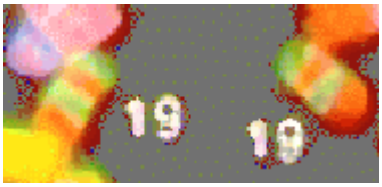
	T175	C35	T93	C66
C35	4.2			
T93	18.7	15.6		
C66	26.1	25.5	12.1	
T50B	30.4	30.5	21.1	12.2

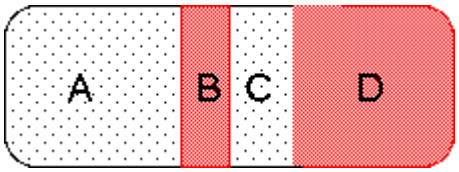
a) Draw a map, showing the order of markers and the distances between adjacent markers.

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?

c)Can you suggest a potential solution to this problem?

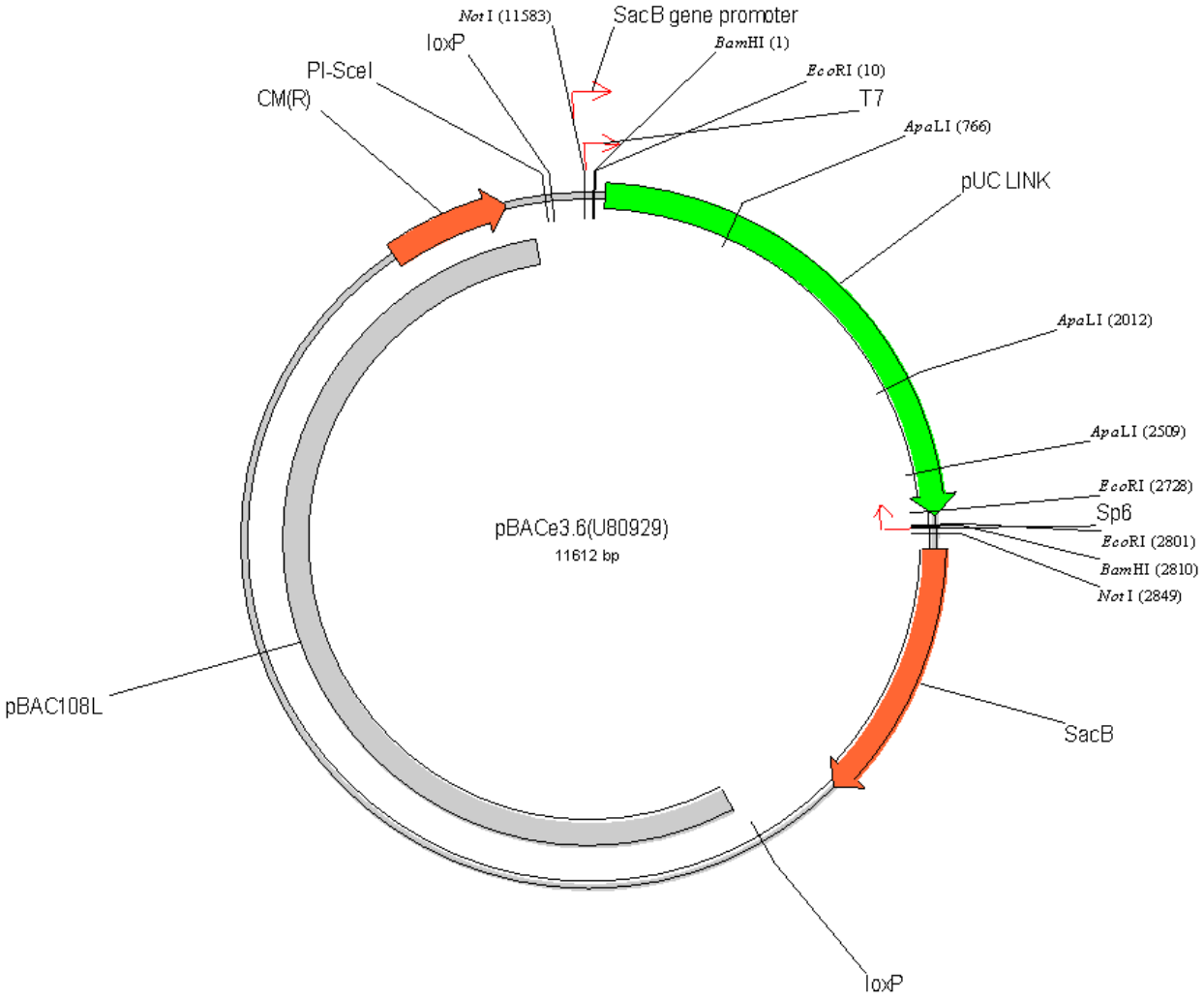
4. (10 points) When gibbon chromosomes are hybridized using a chromosome painting kit of human chromosomes. Most chromosomes show several segments in different colors, indicating that a number of independent events (eg. translocations) have brought together two or more ancestral segments which are found 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?

5. (15 points) The figure below shows a typical BAC vector.



a) The sacB gene encodes levanosucrase, which converts sucrose to levan, which is toxic to to *E. coli*. The coding sequence for levanosucrase is interrupted in the BAC vector by the presence of the pUCLINK stuffer fragment. What is the purpose of sacB in this vector?

b) The vector includes sites for the restriction endonuclease NotI (5'GC^GGCCGC3'). What is the purpose of these sites?

c) BACs are circular, while YACs are linear. In what way is being circular an advantage when working with BACs, compared to YACs?

6. (10 points) The accompanying table shows data from an experiment in which various relatives of wheat were crossed, followed by selfing, to create amphiploid hybrids. The amount of DNA in nuclei was measured by flow cytometry of chromosomes. DNA amounts are given in picograms (pg) per nucleus.

a) From these data, what can you conclude about genome size in resynthesized amphiploid hybrids?

b) Propose a mechanism that could account for these observations.

Parents and amphiploids	Generation	2*n*	Genome	Observed DNA value	Expected DNA value
T. turgidum ssp. *carthlicum*		28	BBAA	23.64 ± 0.23	
Ae. tauschii		14	DD	10.16 ± 0.02	
T. turgidum ssp. *carthlicum–Ae. tauschii*	S_1	42	BBAADD	32.13 ± 0.13	33.80
	S_2	42	BBAADD	31.23 ± 0.06	33.80
	S_3	42	BBAADD	31.44 ± 0.06	33.8
T. turgidum ssp. *dicoccoides*		28	BBAA	23.97 ± 0.04	
Ae. tauschii		14	DD	10.16 ± 0.06	
T. turgidum ssp. *dicoccoides–Ae. tauschii*	S_2	42	BBAADD	31.80 ± 0.11	34.13
Ae. longissima		14	S^lS^l	14.35 ± 0.09	
Ae. umbellulat		14	UU	10.87 ± 0.11	
Ae. longissima–Ae. umbellulata	S_2	28	S^lS^lUU	23.21 ± 0.04	25.22
Ae. sharonensis		14	S^hS^h	14.65 ± 0.07	
Ae. umbellulata		14	UU	10.80 ± 0.09	
Ae. sharonensis–Ae. umbellulata	S_1	28	S^hS^hUU	23.15 ± 0.06	25.45
	S_3	28	S^hS^hUU	23.17 ± 0.10	25.45
T. turgidum ssp. *durum*		28	BBAA	23.91 ± 0.12	
Ae. sharonensis		14	S^hS^h	14.66 ± 0.07	
T. turgidum ssp. *durum–Ae. sharonensis*	S_3	42	BBAASS	36.52 ± 0.10	38.57
T. urartu		14	AA	11.76 ± 0.07	
Ae. tauschii		14	DD	10.16 ± 0.13	
T. urartu–Ae. tauschii	S_1	28	AADD	19.67 ± 0.26	21.92
	S_2	28	AADD	19.80 ± 0.07	21.92

S - selfing generations

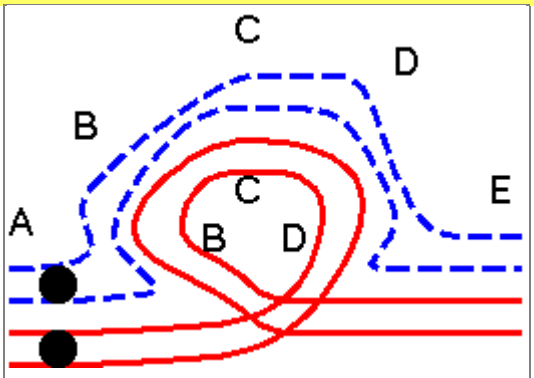
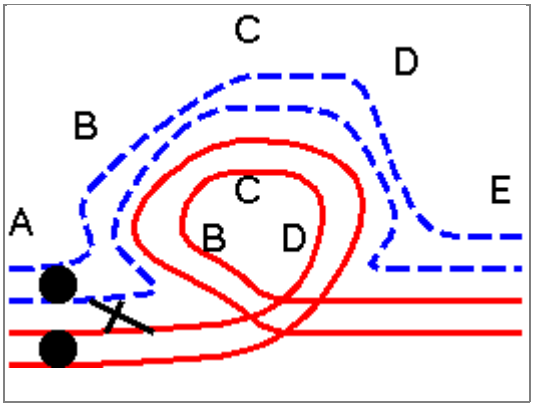
7. (15 points) For genetic engineering of complex traits, it is usually necessary to transform a plant with several different genes, all of which are necessary for expression of a trait. For example, these could be different enzymes in a biochemical pathway. Traditionally, this would have to be done by transforming plants with each gene one at a time, until all genes are present, usually on different chromosomes 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 different 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) One artificial chromosome 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?

8. (15 points) The table illustrates the effects of crossovers in individuals heterozygous for a paracentric inversion. For each case, list the number of normal, inverted, recombinant, dicentric or acentric chromosomes that would be found in gametes from each meiosis.

Paracentric Inversions	
No crossover	
Single crossover outside inversion	
Single crossover within inversion