

PLNT3140 INTRODUCTORY CYTOGENETICS FINAL EXAMINATION

December 6, 2008

Time: 1:30 - 3:30 pm

Location: E2-150 EIT Complex, seats 1-18

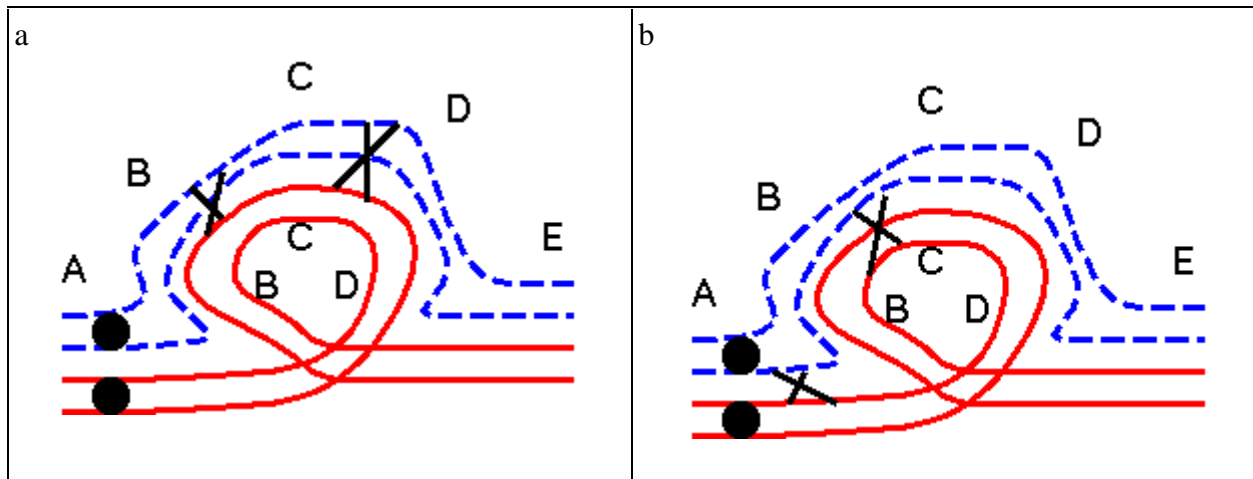
Answer any combination of questions totalling to exactly 100 points. (There are 11 questions to choose from, totaling 120 points.) This exam is worth 35% of the final grade.

Ways to write a readable and concise answer:

- 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.
- 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.
- Point form, diagrams, tables, bar graphs, figures are welcome. Often they get the point across more clearly than a long paragraph.
- Your writing must be legible. If I can't read it, I can't give you any credit.

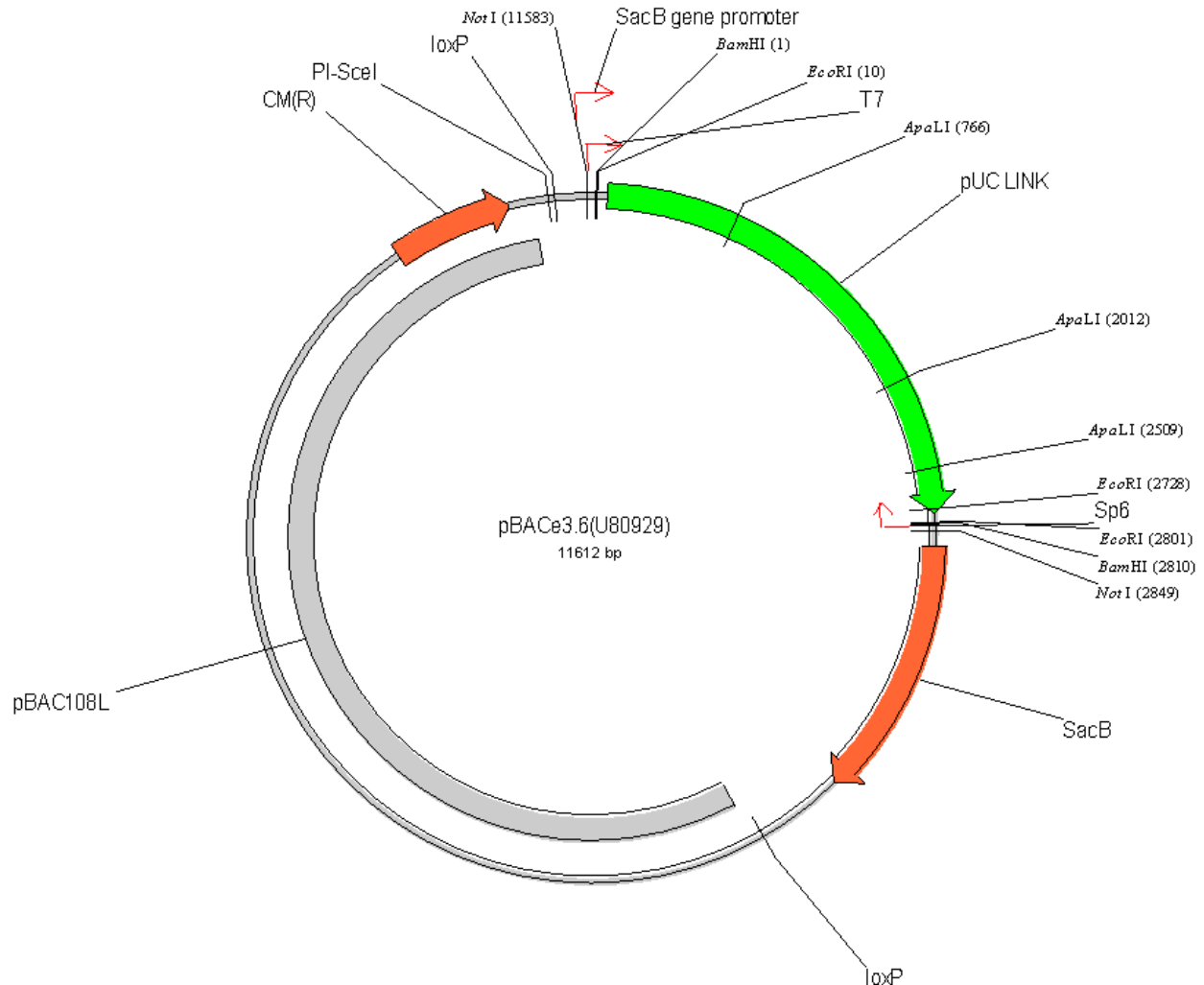
1. (5 points) When haploids are produced in species such as wheat ($1N = 21$), one often sees that some chromosomes are partially paired with other chromosomes during meiosis. In principle, there is only one copy of each homologous chromosome. Why is pairing possible, in such an instance?

2. (10 points) For each of the following diagrams, indicate the outcome of double crossovers in meiosis by listing the number of normal, inverted, dicentric, or acentric chromosomes.



3. (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 F_2 population be used to construct a genetic map? Explain your answer.

7. (15 points) The figure below shows a typical BAC vector.



a) The *sacB* gene encodes levansucrase, which converts sucrose to levan, which is toxic to *E. coli*. The coding sequence for levansucrase 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 advantage of the NotI sites, versus, for example, EcoRI (5'G[^]AATTC3') or BamHI (5'G[^]ATCC3')?

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

8. (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

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

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

- 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?

9. (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.)

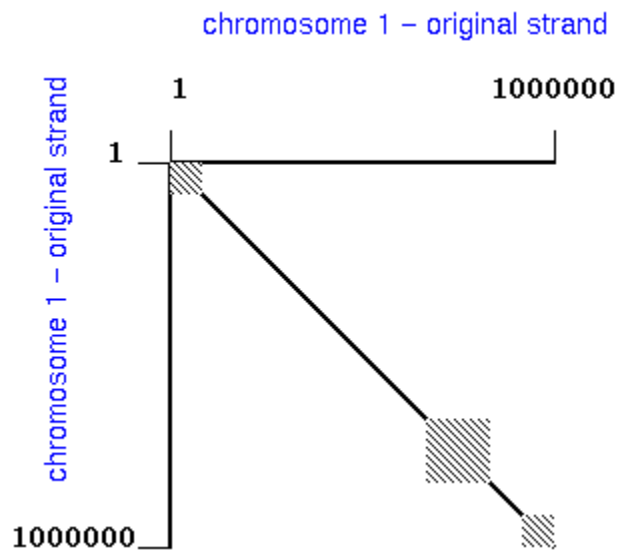
Example: DNA sequences that intrinsically lend themselves to amplification are called shellfish DNA.

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 melanogaster* 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.

10. (10 points) The structure and evolutionary history of entire chromosomes can be studied using dot-matrix plots 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.

11. (5 points) In the table below, the genetic lengths are given for all human chromosomes, with the exception of Y. Why are no results shown for the Y chromosome?

Physical and Genetic lengths of human chromosomes					
	Physical map (Mb)	Genetic map (cM)			Number of markers
		Male	Female	Sex Avg.	
1	282	195	345	270	468
2	252	190	325	257	407
3	225	161	276	218	369
4	205	147	259	203	302
5	199	151	260	206	334
6	191	138	242	190	293
7	169	128	230	179	246
8	158	108	210	159	247
9	150	117	198	158	193
10	146	134	218	176	256
11	153	109	196	152	260
12	153	136	207	171	239
13	100	101	156	129	175
14	87	94	142	118	161
15	87	103	155	129	125
16	106	108	150	129	151
17	89	109	162	135	181
18	89	99	143	121	158
19	69	93	127	110	120
20	59	75	122	98	141
21	30	47	76	62	67
22	31	49	83	66	66
X	156		179	179	177
TOTAL	3191	2591	4460	3615	5136