# 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:
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 ( $1 \mathrm{~N}=21$ ), 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 1 N gametes. If you were to self a doubled haploid, could the F2 population be used to construct a genetic map? Explain your answer.
4. (10 points) Explain why most mutations that occur in eukaryotes are selectively neutral.
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 $\mathrm{A}, \mathrm{H}$ 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. $\mathrm{A} \times \mathrm{B}$ | II. A X C |
| :---: | :---: |
| segregating progeny --------------------->> |  |
| marker/ map posn. | marker/ |
|  | map posn. |
| g6844 HHAAAAABHHBAAAHBHHHHABHHHABBAHHBHAHHBAAHHA | g6844 HНАААААСННСАААНСННННАСНННАССАННСНАННСААННА |
| g3843 HHAAAAABHHBAAAHBHHHHABHHHAHBAHHBHAHHBAABAA | g3843 HHAAAAACHHCAAAHCHHHHACHHHAHCAHHCHAHHCAACAA |
| g2616 HHAAHHHBHHBAAAHBHННАВНННННННВВНВННАНННННHH | g2616 HНААНННСННСАААНСНННАСНННННННССНСННАНННННнН |
| m210 HНАННВНННННАААННВНННАННАНАНННААВННАНВНАВАА | m210 HНАННСННННАААННСНННАННАНАНННААСННАНСНАСАА |
| g 6837 HHAABHHAHBHHBAAHBHHHAHHAHAHHHAABHHAHBHABAA | g 6837 HHAACHHAHCHHCAAHCHHHAHHAHAHHHAACHHAHCHACAA |
| g10086 AНННААНННАНВННВАННННАННАНАНННААНННАНВННВАВ | g10086 АНННААНННАНСННСАННННАННАНАНННААНННАНСННСАС |
| g 4564 a НААННВНННННААННВНННАННАНАНННААНННАНВННВАА | g4564a НААННСННННАААННСНННАННАНАНННААНННАНСННСАА |
| g3845 HAHHHBHHHAHAAAAHBHHAHBAHAHHHAAHHAHBHHHAHH | g3845 НАНННСНННАНААААНСННАНСАНАНННААННАНСНННАНН |
| g4539 AHHHAAHHHAHBHHHAHHHAAHBAHAHHHHAHHBAHBHHHAH | g4539 AHHHAAHHHAHCHHHAHHHAAHCAHAHHHHAHHCAHCHHHAH |
| m557 HAHHHBHHHAHAAAAHBHHAAHBAHAHHHHAHHBAHBHHHAH | m557 НАНННСНННАНААААНСННААНСАНАННННАННСАНСНННАН |
| g3883 HAHHHBHHHAHAAAAHBHHHAHBAHAHHHHAHHBAHBHHHAH | g3883 НАНННСНННАНААААНСНННАНСАНАННННАННСАНСНННАН |
| g19833 HAHAHBHHAHAAAAHBHHAHBAHHHHAHHHABAHHAHHBBAH | g19833 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA |
| g19838 HAHHAHBHHAHAAHBHAHHBAAHBHHAHHBAAHHHHABHHAH | g 19838 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA |
| m272 HAHAHBHHHAHAAHBHAHHBAAHBHHAHHBAAHHHHABHHAB | m272 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA |
| g4513 HAHAHBHHHAHAAAAHBHAHHHBAAAHBHHAHBBAAHHHHAB | g 4513 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA |

6. (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?
7. (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 ' $\mathrm{GC}^{\wedge} \mathrm{GGCCGC} 3 '$ ). What is the advantage of the NotI sites, versus, for example, Eco RI ( 5 ' $\mathrm{G}^{\wedge}$ AATTC $3^{\prime}$ ) or Bam HI ( $5^{\prime} \mathrm{G}^{\wedge}$ 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

$$
\begin{gathered}
\text { i) } N=\frac{G}{L} \\
\text { ii) } \quad N=\frac{\ln (1-P)}{\ln \left(1-\frac{L}{G}\right)}
\end{gathered}
$$

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 pDm 73 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 $\mathbf{d}$ centiMorgans away, it is necessary to construct a contig of overlapping YAC or BAC clones spanning $\mathbf{d}$ 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 <br> map (Mb) | Genetic map (cM) |  |  | Number of markers |
|  |  | Male | Female | Sex Avg. |  |
| 1 |  |  | 345 | 270 | 8 |
| 2 | 282 | 195 | 325 | 257 | 468 |
| 3 | 252 | 190 | 276 | 218 | 407 |
| 4 | 225 | 161 | 259 | 203 | 369 |
| 5 | 205 | 147 | 260 | 206 | 302 |
| 6 | 199 | 151 | 242 | 190 | 334 |
| 7 | 191 | 138 | 230 | 179 | 293 |
| 8 | 169 | 128 | 210 | 159 | 246 |
| 9 | 158 | 108 | 198 | 158 | 247 |
| 10 | 150 | 117 | 198 | 176 | 193 |
| 11 | 146 | 134 | 218 | 176 | 256 |
| 11 | 153 | 109 | 196 | 171 | 260 |
| 12 | 153 | 136 | 207 156 | 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 | 106 89 | 109 | 162 | 135 | 181 |
| 18 | 89 89 | 109 99 | 143 | 121 | 158 |
| 19 | 69 | 93 | 127 | 110 | 120 |
| 20 | 69 59 | 75 | 122 | 98 | 141 |
| 21 | 30 | 47 | 76 | 62 | 67 |
| 22 | 30 31 | 49 | 83 | 66 | 66 |
| X | 31 156 | 49 | 179 | 179 | 177 |
| TOTAL | 3191 | 2591 | 4460 | 3615 | 5136 |

