PLNT3140 INTRODUCTORY CYTOGENETICS

MID-TERM EXAMINATION

1 p.m. to 2:20 p.m. Tuesday, October 22, 2009

Answer any combination of questions totalling to exactly 100 points. If you answer questions totalling more than 100 points, answers will be discarded at random until the total points equal 100. This exam is worth 15% of the course grade.

Hand in these question sheets along with your exam book.

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1. (20 points) Fill in the blanks. (Don't bother rewriting the question in the exam book, just write the answer.)

a. When you want to examine mitotic chromosomes, the single most important factor is to choose a source of cells with _____ .

b. Chromosome bands are the result of variations in _____ , which in turn cause a variation in stain retained by chromosomes.

c. Cells that give rise to gametes are referred to as _____ .

d. Cells that form most of the structure of multicellular organisms, but do not directly lead to gametes are referred to as _____.

e. To obtain a synchronous culture of cells, such that all cells undergo mitosis at the same time, colchicine is often added to the media to _____ .

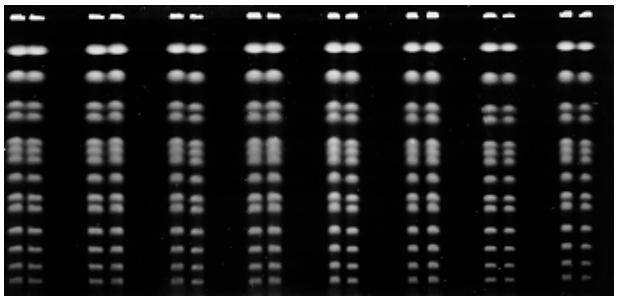
2. (15 points) Draw a simple figure illustrating the four main steps in mitosis, as well as interphase. The figure should include chromosomes, the nuclear envelope, and spindle fibers, with labels to indicate the features of the cells being shown.

3. (10 points) Why does crossing over occur in meiotic prophase I, as opposed to meiotic prophase II? That is, what would not occur if crossing over happened in meiotic prophase II?

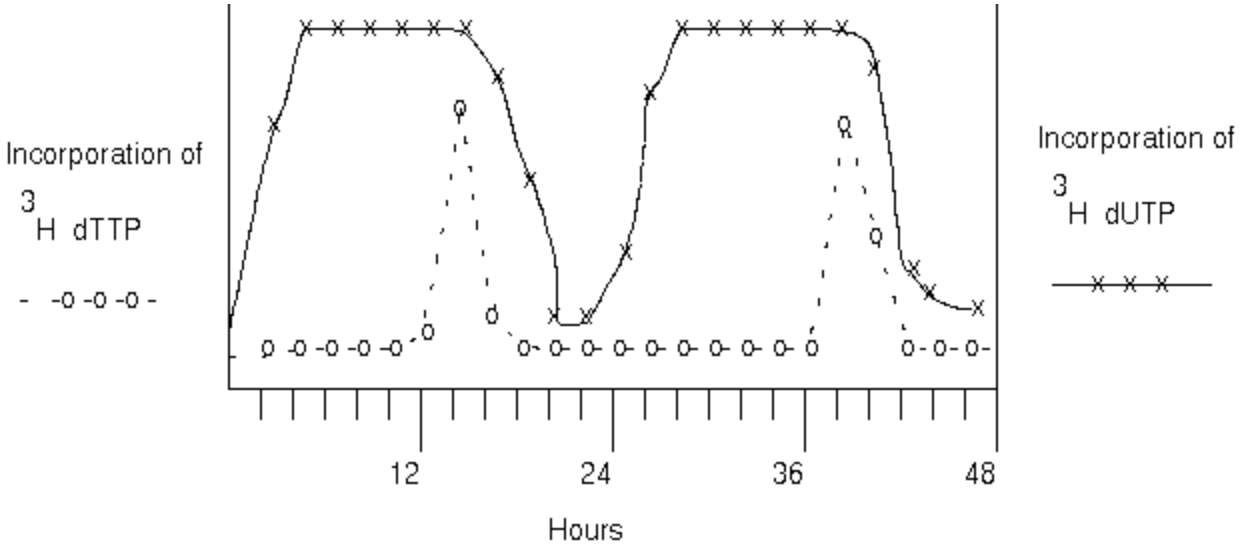
4. (20 points) Eukaryotic genomes can be several orders of magnitude larger than prokaryotic genomes. List 5 characteristics of the eukaryotic chromosome, or the eukaryotic cell in general, which can be considered adaptations to having a larger genome, and briefly explain why.

5. (5 points) The figure below shows Pulsed Field Gel Electrophoresis (PFGE) of yeast (*Saccharomyces ceriviscea*) chromosomal DNA. Each band corresponds to a chromosome, and the sizes of the chromosomes are all known.

Suppose you had a cloned sequence for a gene from the ascomycete fungus, *Neurospora crassa*. What would be a simple way to find out which chromosome has the corresponding yeast gene?



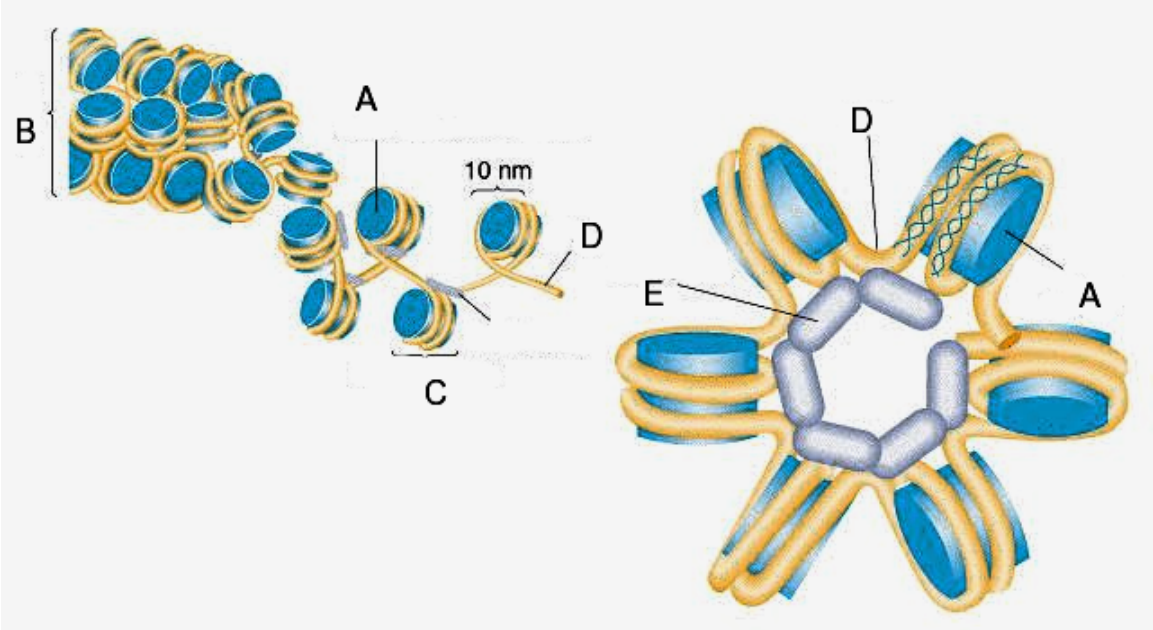
6. (10 points) Mamalian cells were grown in synchronous culture with a 24 hour cell cycle. In two parallel experiments, cells were labeled using either ^{3}H-dTTP or ^{3}H-dUTP. To measure the incorporation of isotope, a sample of cells were centrifuged every two hours, and ^{3}H was measured in the pellets using a scintillation counter. The results are shown below:



Explain the results.

7. (10 points) Name the chromatin components labeled in the image below. Where a label is used twice, you can assume it is the same structure.

A.
B.
C.
D.
E.



8. (10 points) Maize cells were grown in synchronous culture. That is, all cells in the culture were at the same point in the cell cycle, at any given time. To study the expression of the alcohol dehydrogenaseI gene (AdhI), Argon gas was bubbled into the culture, creating an anerobic condition that induces AdhI expression. One batch of cells was harvested during G1 and nuclei were isolated. Another batch was harvested just at the beginning of prophase of mitosis (ie. condensed chromosomes are beginning to be visible, but the nuclear envelope is still intact). Nuclei were isolated from these cells as well. DNAse sensitivity experiments were conducted using each nuclei prep. In nuclei from G1, the AdhI gene was degraded. Using the nuclei from early prophase, the AdhI gene remained intact. In 1 or 2 sentences, explain the reason for this difference.

9. (10 points) Telomerase (telomere terminal transferase) adds repeat units of a specific DNA sequence to the 3' protruding ends of telomeres.

a. Where does the sequence information come from to add these repeats?

b. Why can't DNA polymerase simply fill in the gaps left during DNA replication, after RNA primers are removed?

10. (10 points) Prokaryotic genomes could be thought of as one big domain, whereas eukaryotic genomes are divided into many hundreds or thousands of domains. At the same time, prokaryotes are generally single-celled, whereas eukaryotes have evolved into multicellular organisms with highly-differentiated tissues. What would be a possible connection between these two observations?