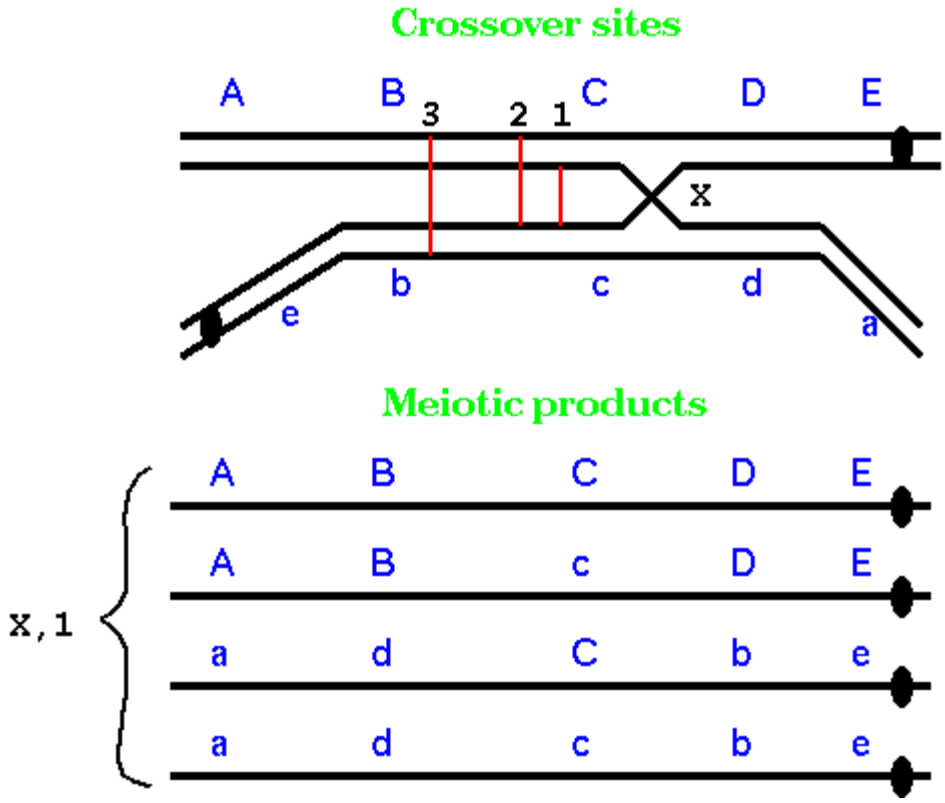
PLNT3140 INTRODUCTORY CYTOGENETICS
FINAL EXAMINATION

December 22, 2022, 1:30 pm - 3:30 **E2-160 seats 1 - 27**

Answer any combination of questions totaling to exactly 100 points. If you answer questions totaling more than 100 points, answers will be discarded at random until the total points equal 100. There are 13 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.) (10 points) Chromosome pairing in a heterozygote for an inversion is shown below. (For simplicity, an inversion loop is avoided by drawing the termini unpaired.) Consider a set of possible double crossovers. In all cases, one crossover event occurs at position X. The example shows meiotic products resulting from a second crossover at site 1. Draw the meiotic products for the crossover site was at either 2 or at 3.



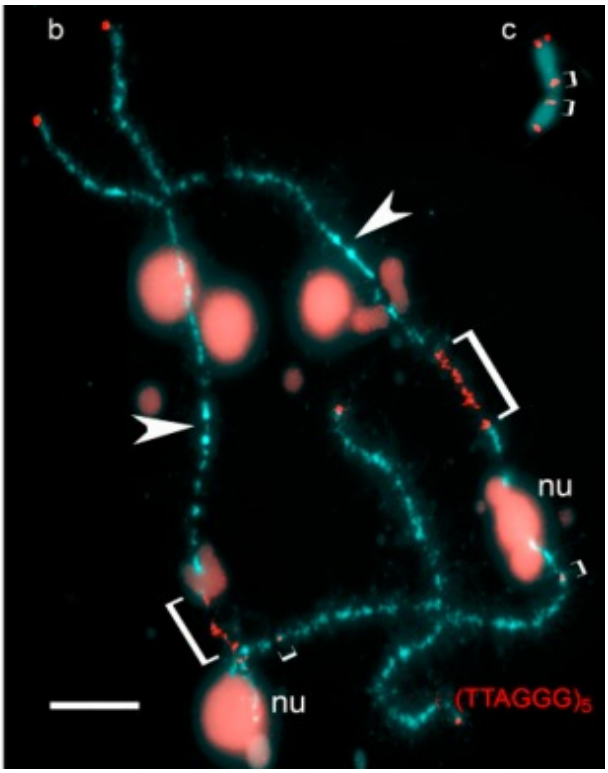
2. (10 points) Suppose you have agreed to review a manuscript for a journal. The authors report a new mutant for the Histone H2a gene. The mutation results in an inactive H2a protein which prevents formation of a histone core particle. When homozygous h2a mutants are crossed with the wild type, the progeny segregate 3:1 for the wild type to mutant phenotype:

	wild type		mutant
P genotype	H2a/H2a	X	h2a/h2a
		↓	
F1 phenotype		H2a	
		↓	
F2 phenotype	H2a		h2a
	3		1

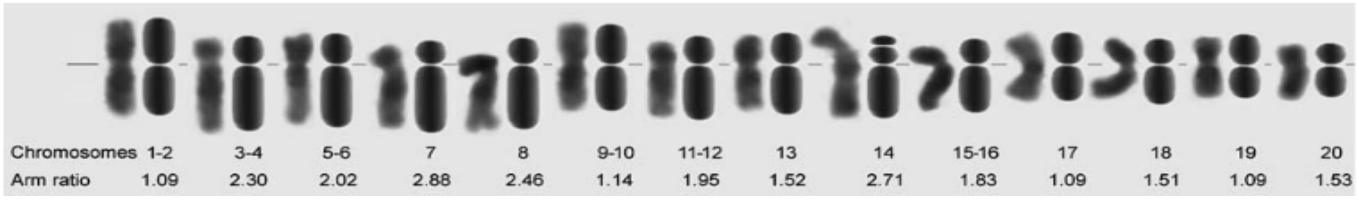
Would you accept or reject the paper? Briefly state your reasons.

3. (5 points) In some bird species, oocytes are arrested in diplotene of meiosis, during which they partially uncoil to allow transcription to occur. These so-called lampbrush chromosomes allow for high-resolution imaging of chromosomes. In the figure at right, the bright region indicated by the brackets indicates hybridization of a telomeric FISH probe to a site within the chromosome arm. Arrowheads show the positions of centromeres. The inset c) shows the condensed metaphase chromosomes, also hybridized with telomeric probe.

Propose a genetic mechanism by which telomeric sequences occur within a chromosome.



4. (5 points) On which chromosome would you expect to find ribosomal RNA genes?



5. (10 points, multiple choice) The 20 chromosomes of the oilseed plant Camelina sativa have been arranged in a circle to facilitate easy comparison of homologous blocks of sequences between chromosomes. In this example, homologous sequences shared by both chromosomes 3 and 7 are shown. The density of repetitive sequences is shown in the outer (red) circle, while the density of genes is shown in the inner circle (blue).

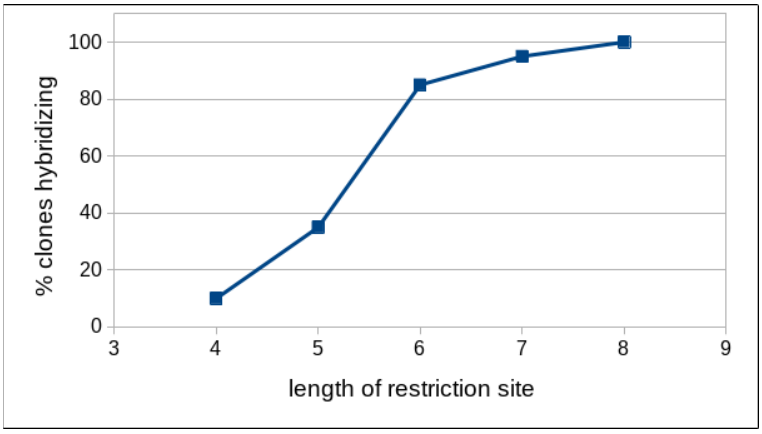
Based on data in the map, select one of the following for each statement below:

- SUPPORTED - consistent with the map, with some direct evidence
- CONSISTENT- consistent with the map, but no direct evidence from the map
- INCONSISTENT - contradicted by map

a) Gene rich regions tend to have a high repeat density
b) Chromosome 7 is derived from part of chromosome 3
c) The intergenic regions in chromosome 3 have lost copies of repetitive sequences that are present in chromosome 7
d) The intergenic regions in chromosome 7 have gained copies of repetitive sequences that are not present in chromosome 3
e) Camelina sativa is an allotetraploid

6. (10 points) Five libraries of genomic DNA fragments were constructed using DNA cut with five different restriction enzymes.

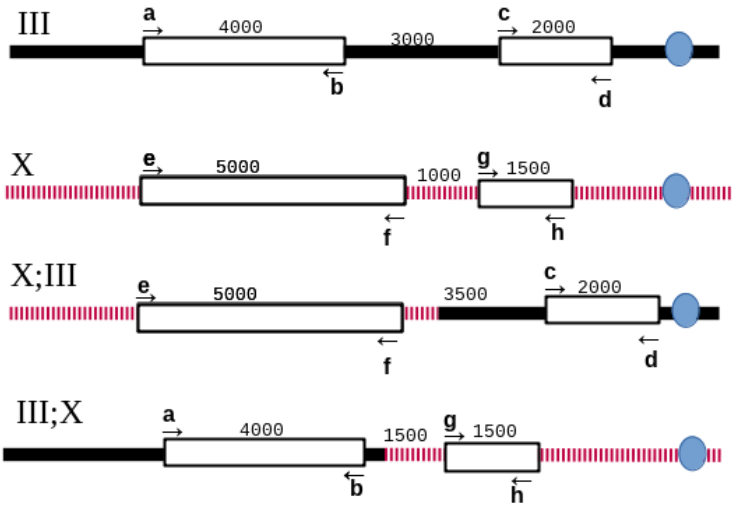
Enzyme	Recognition Sequence	length of rest. seq.	avg. insert size
TaqI	TCGA	4	256
MboII	GAAGA	5	1024
BamHI	GGATCC	6	4096
AbeI	CCTCAGC	7	16384
NotI	GCGGCCGC	8	65536



Each of the libraries was probed with a sequence from a 300 bp middle repetitive sequence, and the percentage of clones hybridizing was estimated for each library. For example, a library of TaqI fragments would have an average insert size of 256 bp. When the library of TaqI fragments was probed, about 10% of the clones showed hybridization. When the library of MboII fragments was probed, about 35% of the clones showed hybridization, and so on.

Briefly explain why these results were seen.

7. (10 points) The map shows two genes on chromosomes III and X, and PCR primers available for these genes. The goal is to detect individuals carrying the translocations. Choose pairs of primers that would give distinct bands for each of the two normal and two translocated chromosomes.



a) III
b) X
c) X;III
d) III;X
e) null control*

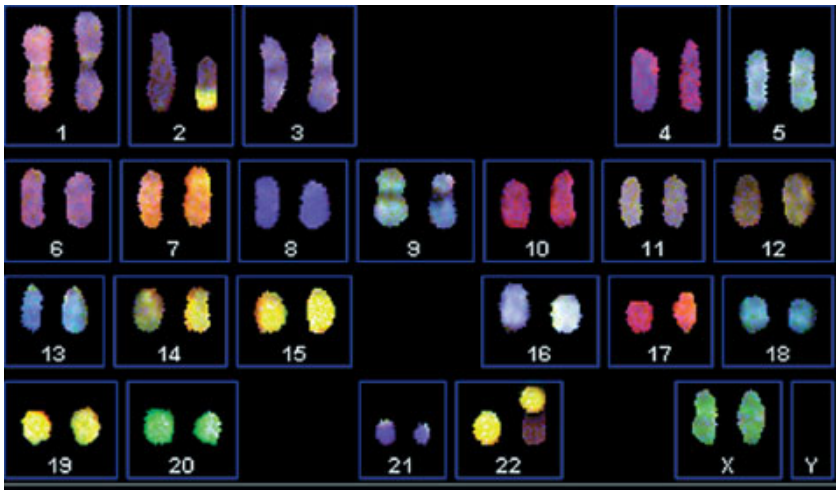
* - choose any primer combination that would not give any bands

8. (10 points, multiselect)

In maize, the Ds element inserted into the C locus, inactivating that gene, and giving yellow kernels. When the yellow maize (cc) was crossed with a line bearing the Ac locus, the kernels displayed blue sectors. Which of the following is true?:

a) The Ac element carried a wild type C allele.
b) The Ds element carried a gene for transposase.
c) The Ac element carried a gene for transposase.
d) In some kernels, excision of the Ds element early in kernel development resulted in large blue sectors.
e) In some kernels, excision of the Ds element early in kernel development resulted in small blue sectors.

9. (10 points) The spectral karyotype below shows a set of human chromosomes. What sex is the person from which the chromosomes were imaged? What is the other important finding that is apparent from this data?



10. (10 points) Given the following cases,

a) diploid which has undergone a autopolyploidization to autotetraploid
b) two diploids which have hybridized to form an allotetraploid

match the following statements

i) C_0t curve will not change
ii) C_0t curve will shift to the right
iii) Genome size (bp) will stay the same
iv) Genome size (bp) will double
v) homeologous pairing will occur in meiosis

11. (10 points) Fill in the blanks. (Don't re-write the paragraphs. Just list answers for a - j)
You might think that genome size shouldn't affect mitotic cycle time. If the number of ____a____ per Mb stays the same, all genomes should replicate at the same rate. There must be other limiting factors eg. nuclear or cytoplasmic volume probably doesn't double when genome size doubles. For example, the concentration of dNTPs could be a major limiting factor.

In nature, annual plants tend to have ____b____ genomes and ____c____ mitotic cycles. Perennial plants tend to have ____d____ genomes and ____e____ cell cycles. Annuals have to grow very rapidly in spring, requiring rapid ____f____. Therefore, ecological ____g____ with other species forces annuals to have ____b____ genomes.

Question: Is the perennial habit more tolerant of a ____e____ mitotic cycle or ____d____ genome? Periennials pay a large metabolic price in their first year in the development of extensive root systems and above ground shoots. However, these features make them more ____h____ in subsequent years.
____d____ genomes are probably better tolerated when habitat is not limiting, in terms of food, water, light and space. The prediction would be that ____b____ genomes are favored when resources are ____i____.

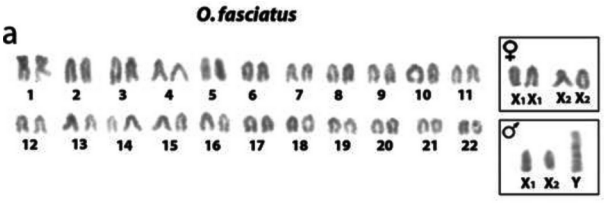
Interestingly our annual crops such as wheat and corn tend to have ____d____ genomes. We pamper them with fertilizers and water, and eliminate ____g____ through weed control. Domesticated crops are ____j____ competitors outside of cultivation.

a)
b)
c)
d)
e)
f)
g)
h)
i)
j)

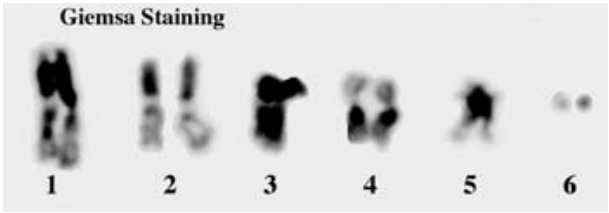
12. (10 points) Karyotypes of the fish *Oplegnatiathus* and the fruit fly *Scaptodrosophila* are shown below.

For which of the two species would it be more difficult to create a chromosome painting kit that distinguishes each chromosome with a unique fluorescent spectrum.? Explain your reasoning, based on what you know about about the steps that go into creating such a kit.

A *Oplegnatiathus fasciatus*



B *Scaptodrosophila hibisci*



13. (10 points) The accompanying table lists the lengths of chromosomes in the rat (*Rattus norvegicus*).

Loc	*Type*	*Name*	*RefSeq*	*INSDC*	*Size (Mb)*
Nuc	Chr	1	NC_005100.4	CM000072.5	282.76
Nuc	Chr	2	NC_005101.4	CM000073.5	266.44
Nuc	Chr	3	NC_005102.4	CM000074.5	177.7
Nuc	Chr	4	NC_005103.4	CM000075.5	184.23
Nuc	Chr	5	NC_005104.4	CM000076.5	173.71
Nuc	Chr	6	NC_005105.4	CM000077.5	147.99
Nuc	Chr	7	NC_005106.4	CM000078.5	145.73
Nuc	Chr	8	NC_005107.4	CM000079.5	133.31
Nuc	Chr	9	NC_005108.4	CM000080.5	122.1
Nuc	Chr	10	NC_005109.4	CM000081.5	112.63
Nuc	Chr	11	NC_005110.4	CM000082.5	90.46
Nuc	Chr	12	NC_005111.4	CM000083.5	52.72
Nuc	Chr	13	NC_005112.4	CM000084.5	114.03
Nuc	Chr	14	NC_005113.4	CM000085.5	115.49
Nuc	Chr	15	NC_005114.4	CM000086.5	111.25
Nuc	Chr	16	NC_005115.4	CM000087.5	90.67
Nuc	Chr	17	NC_005116.4	CM000088.5	90.84
Nuc	Chr	18	NC_005117.4	CM000089.5	88.2
Nuc	Chr	19	NC_005118.4	CM000090.5	62.28
Nuc	Chr	20	NC_005119.4	CM000091.5	56.21
Nuc	Chr	X	NC_005120.4	CM000092.5	159.97
Nuc	Chr	Y	NC_024475.1	CM002824.1	3.31
MT	Chr	MT	NC_001665.2	AY172581.1	0.016313
	Un	-	.	-	88.16
TOTAL					2870.2063

a) Using the Clark and Carbon formula, calculate the number of BAC clones needed to ensure a 99% chance of finding at least one clone for any given gene. Assume that the BAC library has an average insert size of 100 kb.

$$N = \frac{\ln(1-P)}{\ln(1-f)}$$

b) Suppose that you didn't care about getting a complete genomic library, but rather were only interested in getting genes from chromosome 18. (Assume flow cytometry is not an option.) Does that make any difference to your cloning strategy? Explain why or why not.