Botany 132
Final exam
2002 Name
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Please show all of your work in answering the questions below.

1. F- bacterial cells of genotype met^{-} thi^{-} pur^{-} were conjugated with F+ cells with the genotype met^{+} thi^{+} pur^{+}. After the conjugation reaction was interrupted, cells containing met^{+} were selected and tested for the unselected markers thi and pur. The number of met^{+}colonies with the following genotypes determned:

thi^{+} pur^{+}	400
thi^{+} pur^{-}	0
thi^{-} pur^{+}	8
thi^{-} pur^{-}	52

(a) What is the gene order?

The gene order is Met – Pur - Thi

(b) Draw a genetic linkage map showing map distances between met, thi, and pur.

Met – Pur: 52/460 x 100 = 11.3% recombination = 11.3 map units

Pur – Thi: 8/460 x 100 = 1.7% recombination = 1.7 map units

____Met____11.3 mu______________Pur__1.7 mu_Thi_____

2. Three testcrosses with combinations of three linked genes were performed. The crosses and the inferred gametes produced by the tested parent were as follows:

AB/ab X ab/ab: 40% AB, 40% ab, 10% Ab, 10% aB

AD/ad X ad/ad: 46% AD, 46% ad, 4% Ad, 4% aD

BD/bd x bd/bd: 44% BD, 44% bd, 6% bD, 6% Bd

What is the probable genetic map of the three genes? Show your work.

A- B: 20% recombination
A-D: 8% recombination
B-D: 12% recombination

|-----------20 mu--------------|
__A______D_____________B__
8 mu 12 mu

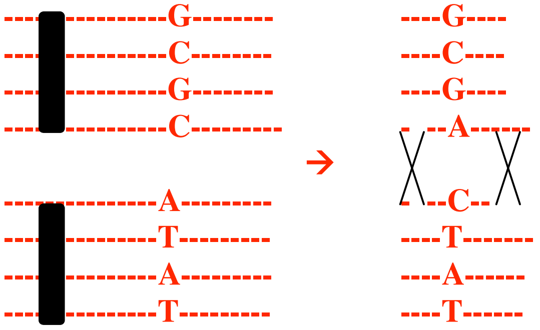
3. Crosses were made between two strains of yeast. Each strain of carried a different allele of the a gene. While most of the tetrads formed as a product of this cross were normal, one unusual tetrad was observed. Explain (using figures) how this tetrad could have been generated.

Cross: $a1\ a3^{+}$ X $a1^{+}\ a3$

Abnormal tetrad:
$a1^{+}a3$
$a1^{+}a3$
$a1^{+}\ a3^{+}$
$a1\ a3^{+}$

Assume that a wild type allele for a1 (a1+) is A/T and the mutant allele is G/C. The abnormal tetrad has 3 copies of the wt allele and only one of the mutant allele – this suggests that a heteroduplex was created during recombination and that the mutant allele was repaired to wild type.

For example: for a1 at meiosis, there would be four chromatids:



Recombination between one strand of chromatid 2 and 3 results in 2 heteroduplexes. If these are repaired, then the repair process can generate a wild allele (A/T0 or a mutant allele (G/c). In this case, both duplexes were repaired to generate the wt allele.

4. If a woman and a man are heterozygous for a gene, and if they have three children, what is the chance that all three will also be heterogygous?

0.5 x 0.5 x 0.5 = 0.125

5. In *Drosophila*, the three gene pairs for red eyes (cn^+) vs. cinnabar (cn), normal bristle number (rd^+) vs. reduced (rd), and long wings (vg^+) vs. vestigial (vg) are known to map to X chromosome. A female heterozygous for all three genes was crossed against a male fly with cinnabar eyes, reduced bristle number and vestigal wings. Map the position of these three genes to one another draw a map. Show your work.

cinnabar, reduced, vestigial	406
cinnabar, reduced, long	46
cinnabar, normal vestigial	28
cinnabar, normal, long	3
red, normal, long	438
red, normal, vestigial	45
red, reduced, long	33
red, reduced vestigial	1

a) Calculate the map distances between the genes, and construct a linkage map of these loci. Show your work.

Cn – Vg: 46 + 45 + 1 + 3/1000 = 0.095 x 100 = 9.5 mu

Cn – Rd: 28 + 33 + 1 + 3/1000 = 0.065 x 100 = 6.5 mu

Vg – Rd: 33 + 28 + 45 + 46 + 2(1 + 3)/1000 = 0.160 x 100 = 16 mu

Vg ---6.5 mu------------ Cn------------9.5 mu -------------------------- Rd

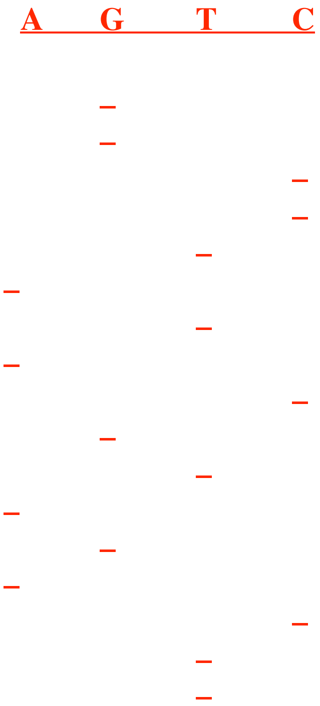
|-------------------------------16 mu--|

b) Determine the coefficient of coincidence for this set of loci.

COC = obs. # of DCO/exp.# of DCO
= 4/0.095 (0.065) (1000) = 0.65

6. Draw the banding pattern you would expect to see on a DNA-sequencing gel if you annealed the primer 5’-CTAGG-3’ to the following single-stranded DNA fragment and carried out a dideoxy sequencing reaction.

3’-G-A-T-C-C-A-A-G-T-C-T-A-C-G-T-A-T-A-G-G-C-C-5’



7. Use the supplied figure of the genetic code to complete the following table. Assume that reading is from left to right and that the columns represent transcriptional and translational allignments.

T	A	C	A	C	C	A	T	G	A	C	G	**DNA**
A	T	G	T	G	G	T	A	C	T	G	C	**double helix**
A	U	G	U	G	G	U	A	C	U	G	C	**mRNA**
U	A	C	A	C	C	A	U	G	A	C	G	**tRNA**
Met			Trp			Tyr			Cys			**amino acids**

8. Consider the inducible regulation of the lac operon. For both for β-galactosidase (z) and permease (y), is enzyme production by each of the following genotypes constitutive, uninducible or inducible?

	β-galactosidase	permease
a) $I^+\ p^+\ o^c\ z^+\ y^+$	**constitutive**	**constitutive**
b) $I^+\ p^+\ o^+\ z^-\ y^- / i^-\ p^+\ o^c\ z^-\ y^+$	**uninducible**	**constitutive**
c) $I^+\ p^+\ o^+\ z^+\ y^- / i^-\ p^+\ o^c\ z^-\ y^+$	**inducible**	**constitutive**
d) $I^+\ p^+\ o^c\ z^+\ y^- / i^S\ p^+\ o^+\ z^-\ y^+$	**constitutive**	**uninducible**
e) $i^S\ p^+\ o^+\ z^+\ y^- / I^+\ p^+\ o^+\ z^-\ y^+$	**uninducible**	**uninducible**

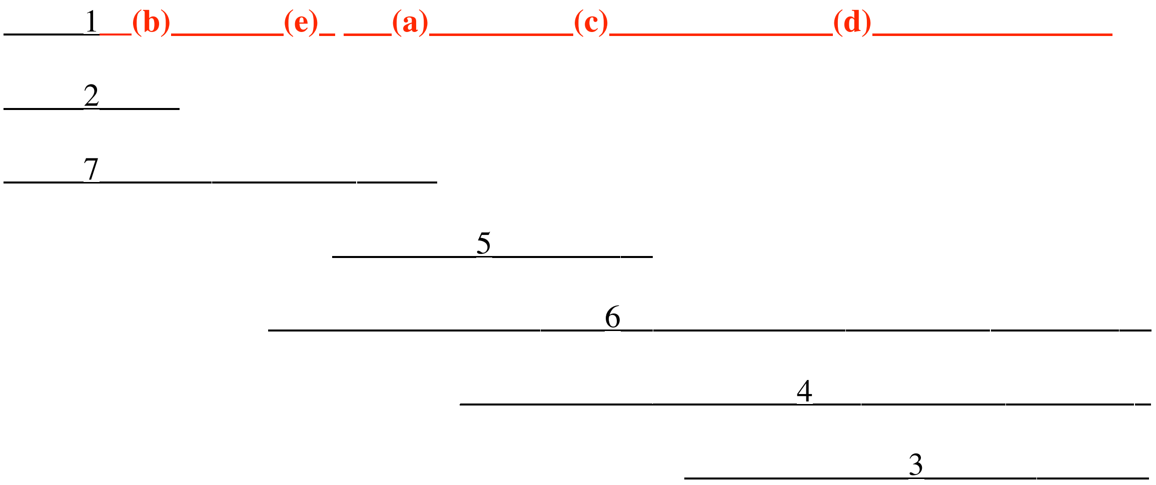
9. The molecule 2-aminopurine is an analog of adenine that pairs with thymine. It also occasionally pairs with cytosine. What types of mutations will be induced by 2-aminopurine after two rounds of replication? (Show your reasoning)

10.

-----A--------		**----2AP----**		**-----2AP-----**		**-----2AP-----**		**----G-----**
-----T---------	**→**	**------T-----**	**→**	**-----C---------**	**-→**	**-----C or T--**	**+**	**----C-----**

Results in an A/T - > G/C transition

A set of seven different rII deletion mutants of bacteriophage T4, 1-7, were mapped, with the following result: (the lines indicate the extent of the deletion)



Five rII point mutants were crossed with each of the deletions, with the following results, (+ = r^+ recombinants and 0 = no r^+ recombinants)

Point Mutants	Deletion Mutants 1	2	3	4	5	6	7
a	0	+	+	+	0	0	0
b	0	0	+	+	+	+	0
c	0	+	+	0	0	0	+
d	0	+	0	0	+	0	+
e	0	+	+	+	+	0	0

Map the locations of the point mutations.

10. In the Meselson and Stahl experiment, ^{15}N-labeled bacterial cells were shifted to ^{14}N medium, at what we can designate as generation 0. What proportion of ^{15}N-^{15}N, ^{15}N-^{14}N and 1^{14}N-^{14}N DNA would you expect to find at generations 1, 2 and 3?

Generation 1: All of the DNA will be 15N/14N

Generation 2: Half of the DNA would be 15N/14N and half will be 14N/14N

Generation 3: ¼ of the DNA will be 15N/14N and ¾ of the DNA will be 14N/14N