

3F05

BIOL 2500 FALL 2005

GENETICS

EXAMINATION 3

Prof Finger

NAME [REDACTED]

RIN # [REDACTED]

THIS PAGE IS RESERVED FOR GRADING.

YOU MAY USE THE REVERSE SIDE OF EACH PAGE AS SCRATCH PAPER. THERE ARE 7 QUESTIONS AND 3 BONUS QUESTIONS.

Question 1 12 (max 12)

Question 2 8 (max 10)

Question 3 21 (max 28)

Question 4 18 (max 18)

Question 5 5 (max 8)

Question 6 5 (max 10)

Question 7 4 (max 14)

Bonus 3 (max 3 bonus)

TOTAL: 76

Name: Emily Germain

Question 1 (12 points).

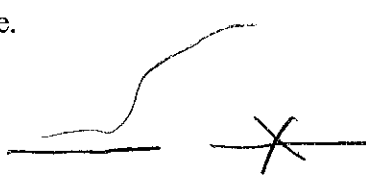
In a bacterial operon, regions *a*, *b*, *c*, and *d* represent the repressor gene, the promoter sequence, the operator region, and the structural gene encoding an enzyme, but not necessarily in that order. This operon regulates the metabolism of a molecule (*m*). From the data given below, assign *a*, *b*, *c*, and *d* to the four parts of the operon.

12

Genotype	<i>m</i> present	<i>m</i> absent
$a^+ b^+ c^+ d^+$	active enzyme	no enzyme
$\textcircled{a} b^+ c^+ d^+$ <i>repressor can't bind</i>	active enzyme	active enzyme
$a^+ b^- c^+ d^+$ <i>promoter</i>	no enzyme	no enzyme
$a^+ b^+ c^- d^+$ <i>structural</i>	inactive enzyme	no enzyme
$a^+ b^+ c^+ \textcircled{d}$ <i>operator?</i>	active enzyme	active enzyme
$\textcircled{a} b^+ c^+ d^+ / F' a^+ b^+ c^+$ <i>constitutive</i>	active enzyme	active enzyme
$a^+ \textcircled{b} c^+ d^+ / F' a^+ b^+ c^+ d^+$ <i>necessary still works</i>	active enzyme	no enzyme
$a^+ b^+ c^- d^+ / F' a^+ b^+ c^+$	active enzyme + inactive enzyme	no enzyme
$a^+ b^+ c^+ d^- / F' a^+ b^+ c^+$	active enzyme	no enzyme

~~a~~ d is the repressor gene. *B-*

b is the promoter sequence.

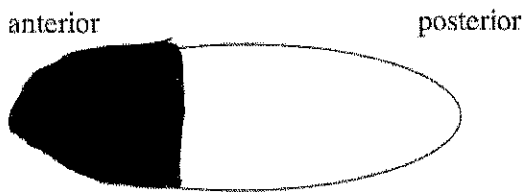
~~a~~ a is the operator region. 

~~a~~ c is the structural gene encoding an enzyme.

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**Question 2 (10 points).**

The *Drosophila* gene *bicoid* exemplifies a maternal-effect gene that, when mutated produces embryos that lack anterior structures, but have posterior structures duplicated. The Bicoid protein is a morphogen that establishes the domain of expression of the gap gene *hunchback* by activating *hunchback* transcription in a concentration-dependent manner. The Bicoid protein is usually present in an anterior-to-posterior gradient with the highest concentration at the anterior end of the early embryo. Diagrammed below is the major domain of expression of *hunchback* in an embryo from a wildtype mother.



What are the expected domains of *hunchback* expression in embryos from mothers with the following genotypes. Draw diagrams similar to the one shown here, and predict the phenotype of each embryo.

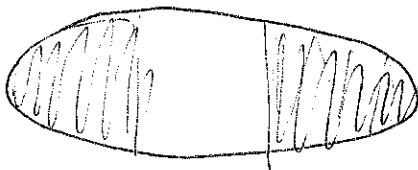
- Homozygous for a *bicoid* null mutation.
- Homozygous for a transgene that causes *bicoid* to be localized at both poles of the embryo.

a.



2 posterior ends

b.



2 anterior ends

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**Question 3 (28 points).**

Classify each of the following mutations based on the information given (more than one term may be necessary):

- a. A *C. elegans* cell that normally undergoes programmed cell death develops into an extra neuron.

4  
cell lineage mutation  
~~homeotic mutation~~

- b. Yeast cells that grow normally at 25°C are unable to divide when shifted to 37°C.

4  
temperature-sensitive mutation

- c. *Drosophila* have legs at the normal site of antennae.

4  
cell lineage mutation  
homeotic mutation

- d. Homozygous *Drosophila* females are normal but produce larvae that have a head at each end and no distal ends. Homozygous males produce normal offspring, assuming that the mate is not a homozygous female.

3  
imprinted paternally  
~~pair wise mutation~~  
cell lineage mutation  
homeotic

- e. The most anterior and posterior regions of the *Drosophila* embryo are eliminated.

cell lineage mutation  
pairwise mutation  
terminal mutation  
coordinate gene mutation

- f. A <sup>ACC</sup>TGG codon is converted to a <sup>GCC</sup>CGG codon.

4  
base substitution mutation  
amino acid change in protein  
missense or transition

- g. A *Drosophila* gene normally expressed in the eye is expressed in the leg, causing eye structures to develop on the leg.

2  
~~homeotic mutation~~  
\*gain of function  
cell lineage  
partial credit for homeotic

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**Question 4** (18 points).

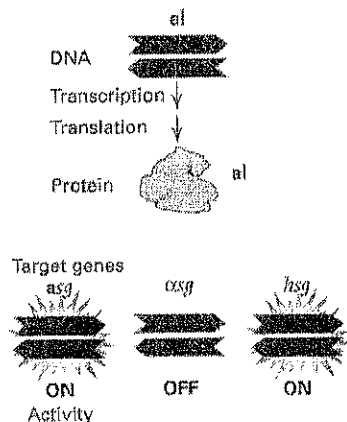
A geneticist decides to use yeast DNA microarrays to study effects on transcription of strains of different mating types and deletion mutants in the MAT mating-type locus. To perform these experiments, RNA is extracted from two strains of yeast to be compared, and labeled cDNA probes are prepared from each strain by reverse transcription of the RNA in the presence of either green or red fluorescent labels. The differently labeled cDNA solutions are mixed and applied to a microarray with spots for each of the types of genes shown in the table. *MAT $\alpha$ 1*, *MAT $\alpha$ 2*, and *MAT $\alpha$ 1* are DNAs for the possible coding sequences present at the MAT locus, *asg* and *asg* spots contain DNA for genes expressed specifically in  $\alpha$  and *a* cells, respectively, and *hsg* spots contain DNA of genes expressed in haploid cells. The figure of transcriptional regulation of mating type given below is provided for your reference. The symbol  $\Delta$  indicates a deletion.

For each of the hybridizations in the table, indicate the expected color of the hybridizations (red, green, yellow or none). Yellow indicates equal amounts of both fluorescent labels, none indicates lack of expression in both strains.

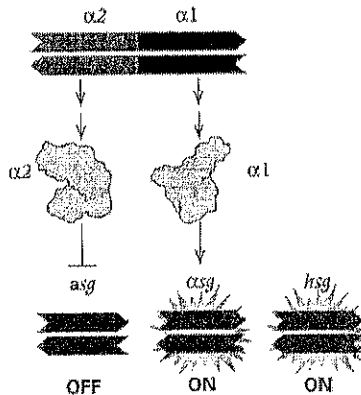
Red	Wildtype <i>a</i> cells	$\Delta$ <i>MAT<math>\alpha</math>1</i> cells	$\Delta$ <i>MAT(<math>\alpha</math>1<math>\alpha</math>2)/MAT<math>\alpha</math>1</i>
Green	Wildtype <i>a/a</i> cells	Wildtype $\alpha$ cells	Wildtype <i>a</i> cells
<i>MAT<math>\alpha</math>1</i>	None	Green	None
<i>MAT<math>\alpha</math>2</i>	Green	Yellow	None
<i>MAT<math>\alpha</math>1</i>	Yellow	None	Green
<i>asg</i>	None	Green	None
<i>asg</i>	Red	None	Yellow
<i>hsg</i>	Red	Yellow	Yellow

← makes none of these proteins

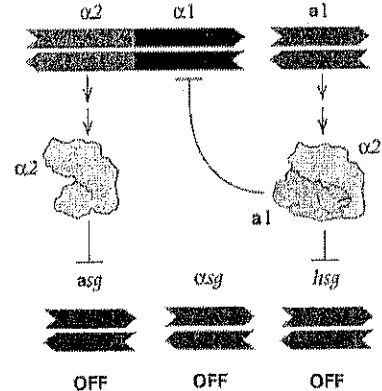
(A) An *a* cell



(B) An  $\alpha$  cell



(C) An *a/a* diploid cell



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**Question 5 (8 points).**

For each situation, write the term for the mechanism of gene regulation described:

- a. V-J joining of antibody genes.

2 <sup>somatic</sup>  
gene recombination

programmed  
DNA rearrangement

- b. Polycomb group proteins bind to a DNA sequence preventing transcription.

3 repression transcriptional silencing

**Question 6 (10 points)**

The human genome has about 300,000 copies of a transposon-like repetitive element known as an *Alu* repeat. These elements have recently been shown to be the source of genetic disease. Describe two mechanisms by which *Alu* elements could cause disease.

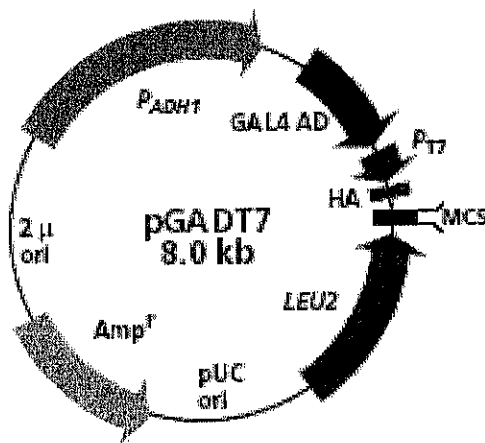
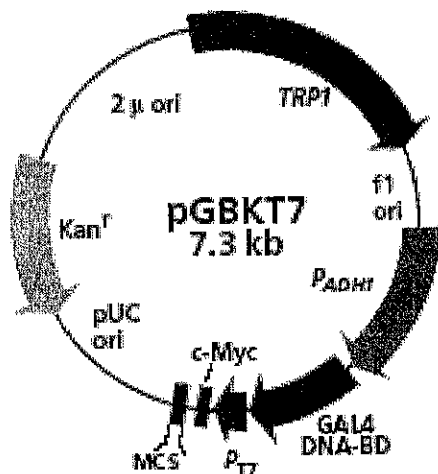
✓ An <sup>Alu</sup> <sub>element</sub> could transpose into the middle of ~~a~~ a necessary gene and disrupt production of its protein. The gene could be split or excised out during transposition.

If it transposes into an intron it could make the gene too long ~~for~~ for RNA polymerase to stay on over the length of it so transcription doesn't finish often enough.

inserts in gene and disrupts:  
ectopic recombination

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**Question 7** (14 points). Refer to the plasmid maps to answer the questions below.



- a. What features of the plasmid pGADT7 enable it to function as a shuttle vector?

can be selected with antibiotics

has enzyme splice site for restriction enzymes to come in and splice in a selected sequence. The MCS site has numerous different restriction enzyme splice sites

origin of replication for two species  
bc replicated and selected for in two species

- b. How is the GAL4 transcriptional activator used in the pGBKT7 and pGADT7 plasmids to facilitate the discovery of interactors with a protein of interest?

If the DNA of interest is properly spliced in in the correct orientation, production of the GAL4 protein can be induced.

the protein of interest can be attached to the protein product of GAL4. Other proteins can be attached to another protein that binds the DNA in this region. If the two proteins in question interact, the DNA will be bent in such a way as to allow access to the promoter region and the ~~GAL4~~ proteins regulated by GAL4 will be produced.

used for two-hybrid screen, GAL4 separated into two domains and can't interact need to screen a library

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**Bonus questions** (1 point each).

Explain in 1-2 sentences, using only the space provided, the significant contributions of each geneticist(s).

1. John Sulston ~~mapped~~ mapped the lineages of cell differentiation in *C. elegans*
2. Eric Wieschaus and Christiane Nusslein-Volhard discovered genes important for determining body segments in fruit flies.
3. Joshua Lederberg designed the method of replica plating so copies of plates can be made and different things selected for, mapping the original plate

**Optional:** Check one answer for each question.

This test was \_\_\_\_\_ too short \_\_\_\_\_ too long X about right.

This test was \_\_\_\_\_ too easy X too hard \_\_\_\_\_ about right.



		Second Position					
First Position (5' end)		U	C	A	G		
	U	UUU ] Phe UUC ] UUA ] Leu UUG ]	UCU ] Ser UCC ] UCA ] UCG ]	UAU ] Tyr UAC ] Stop UAA ] Stop UAG ]	UGU ] Cys UGC ] UGA ] Stop UGG ] Trp	U C A G	Third Position (3' end)
	C	CUU ] CUC ] Leu CUA ] CUG ]	CCU ] CCC ] Pro CCA ] CCG ]	CAU ] His CAC ] CAA ] Gln CAG ]	CGU ] CGC ] Arg CGA ] CGG ]	U C A G	
	A	AUU ] Ile AUC ] AUA ] Met AUG ]	ACU ] ACC ] Thr ACA ] ACG ]	AAU ] Asn AAC ] AAA ] Lys AAG ]	AGU ] Ser AGC ] AGA ] Arg AGG ]	U C A G	
	G	GUU ] GUC ] Val GUA ] GUG ]	GCU ] GCC ] Ala GCA ] GCG ]	GAU ] Asp GAC ] GAA ] Glu GAG ]	GGU ] GGC ] Gly GGA ] GGG ]	U C A G	