

# 7.014 Quiz III Solutions

**Class Average = 61.8**

**Median = 62**

<u>Grade</u>	<u>Range</u>	<u>%</u>
A	80 - 100	10
B	68 - 79	43
C	49 - 61	27
D	37 - 48	9
F	0 - 36	8

**Question 1 (20 points)**

The table below lists types of metabolism in the left column.

Type of metabolism	Electron source	Carbon source	Energy source
fermentation	<i>sugar</i>	<i>sugar</i>	<i>sugar</i>
sulfur oxidation chemosynthesis	$H_2S$	$CO_2$	<i>heat, <math>H_2S</math></i>
oxygenic photosynthesis	$H_2O$	$CO_2$	<i>light</i>
anaerobic respiration	<i>sugar</i>	<i>sugar</i>	<i>sugar</i>
nitrification chemosynthesis	$NH_3$	$CO_2$	<i>heat, <math>NH_3</math></i>
aerobic respiration	<i>sugar</i>	<i>sugar</i>	<i>sugar</i>
anoxygenic photosynthesis	$H_2S$	$CO_2$	<i>light</i>

a) For each type of metabolism,

i) use the following list to fill in Electron source (column 2) and Carbon source (column 3) in the table above.

- A. sugar (Note, "sugar" here is a generic term for any organic carbon compound  $(CH_2O)_n$ ).
- B. Water ( $H_2O$ )
- C. hydrogen sulfide ( $H_2S$ )
- D. methane ( $CH_4$ )
- E. carbon dioxide ( $CO_2$ )
- F.  $NH_3$

ii) fill in Energy source (column 4) in the table above. For this part, you are not limited to the list above.

b) For a number of the metabolisms above, the electron source is the same as the energy source. Explain why they are not the same for photosynthesis.

*The energy source in photosynthesis is light. While other energy sources are also sources of electrons (e.g. sugar), the energy source of photosynthesis, light, does not contain electrons. Therefore, organisms using light as an energy source must use a different source of electrons.*

c) Organisms carrying out respiration need a final electron <sup>donor</sup> acceptor to keep the electron transport chain (ETC) functional. (Circle the correct term above.)

Explain how this compound enables the ETC to remain functional.

*The final electron acceptor removes the electrons after they have traveled the length of the ETC. This then frees the last protein in the ETC to pull the next pair of electrons from the next to last protein in the chain. The newly freed protein can in turn pull the electrons from (only slightly) less electronegative protein.*

*If no final acceptor existed, the ETC would get "backed up" by accumulating electrons to capacity on ever less electronegative proteins. This back up would propagate to eventually saturate all proteins in the chain.*

*Having a final electron acceptor relieves this potential problem.*

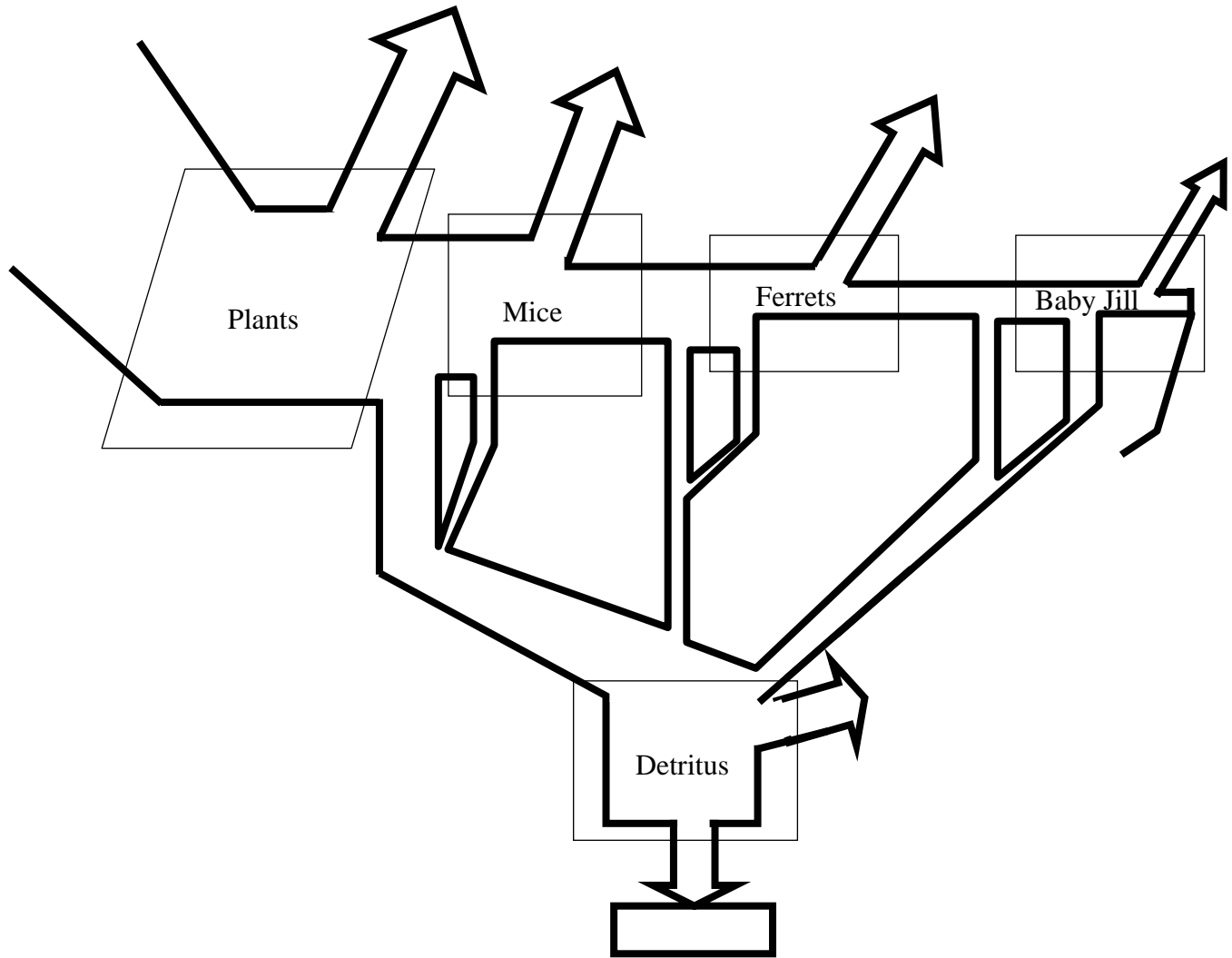
**Question 1, continued**

d) Using an argument based on redox and energetics, explain how aerobic respiration generates more ATP per molecule of glucose than anaerobic respiration.

*O<sub>2</sub> is the electron acceptor used in aerobic respiration. All the possible electron acceptors used in anaerobic respiration are less electronegative than O<sub>2</sub>. That means that each of these acceptors would operate with a shorter electron transport chain than O<sub>2</sub>. A shorter chain would include fewer proton pumps, so a smaller number of protons will be pumped in such a chain per molecule of NADH (and, consequently, per molecule of glucose). ATP synthase makes a new molecule of ATP for each proton pumped by the ETC. Therefore, a chain with as a final acceptor will produce more ATP per molecule of glucose than a chain with any acceptor used in anaerobic respiration.*

**Question 2 (22 points)**

Baby Jill is stuck on an uninhabited island. The food web quickly comes to look like this:



In this web,  
 NPP (plants)=200 kg/day  
 Mice AE (assimilation efficiency) = 20%  
 Ferret EE (exploitation efficiency) = 50%  
 Baby Jill EE = 40%

$I_M$  (Mice ingestion) = 20kg/day  
 Mice PE (production efficiency) =10%  
 Ferret AE = 80%                      Ferret PE = 10%  
 Baby Jill AE = 80%                      Baby Jill PE =10%

**Question 2, continued**

a) Suppose that shortly after baby Jill’s arrival the flow into the refractory carbon pool in the system decreased. Why was there a decrease?

*Jill starts consuming ferrets, which prevents these ferrets from ending up in detritus. Jill herself spends much of the energy she gets from the ferrets in respiration, so that energy is lost to the system. Since the detritivores now have less biomass to start with, less ends up in refractory carbon.*

*Note that this analysis works only in the short term. Longer term, mice not eaten by ferrets eaten by Jill may provide enough biomass to the detritus trophic level to increase the flow to refractory carbon.*

b) How many grams/day of carbon are stored in the form of ferrets? Show your work.

$$I_M \times AE_M \times PE_M \times EE_F \times AE_F \times PE_F = 20,000 \text{g/day} \times .2 \times .1 \times .5 \times .8 \times .1 = 16 \text{ g/day}$$

c) Given only the information on the previous page, is it possible to calculate the mean residence time of carbon in the ferret trophic level? Why or why not?

*Mean Residence Time (MRT) is defined as pool/flux. While it is possible to calculate flux (as we did above), we do not know how big the ferret biomass pool is. Therefore, we can not calculate MRT given only the information on the previous page.*

Suppose baby Jill gave ferrets a drug that lets them increase biomass faster on the same amount of food.

d) What system parameter(s) could have changed as a result? (circle all that apply)

NPP            PE<sub>J</sub>            AE<sub>J</sub>            GPP            EE<sub>F</sub>            PE<sub>F</sub>            AE<sub>F</sub>

Why?

*Ferrets are consuming the same amount of food as before, so their Exploitation efficiency, or any other parameter that precedes it in the web would not be affected. The two possibilities are that the drug enables the ferrets to assimilate the food they consume more efficiently (AE<sub>F</sub>) or that it enables the ferrets to utilize the energy derived from food more efficiently (PE<sub>F</sub>).*

Baby Jill finds some squash seeds and plants them on a previously vegetation-free lot. She is tired of eating ferrets, so she plans to eat squash exclusively when it is ready. Note that Jill is the only one on the island who will get to eat squash.

e) In the table below, for each system parameter listed, circle Yes or No to indicate whether that parameter will change once Jill plants and begins eating squash. For ONLY the parameters you believe will change, explain why in the space provided.

Parameter	Change?	Justify
NPP	<u>Yes</u> No	<i>There is a new primary producer in the system, so the NPP increases.</i>
EE <sub>J</sub>	<u>Yes</u> No	<i>Jill can consume entire squash, as opposed to portions of ferrets.</i>
PE <sub>J</sub>	Yes <u>No</u>	
AE <sub>J</sub>	<u>Yes</u> No	<i>Ferrets are closer in composition to Jill than squash is, so AE should decrease.</i>
GPP	<u>Yes</u> No	<i>There is a new primary producer in the system, so the GPP increases.</i>
EE <sub>F</sub>	Yes <u>No</u>	
AE <sub>F</sub>	Yes <u>No</u>	
EE <sub>M</sub>	Yes <u>No</u>	
AE <sub>M</sub>	Yes <u>No</u>	

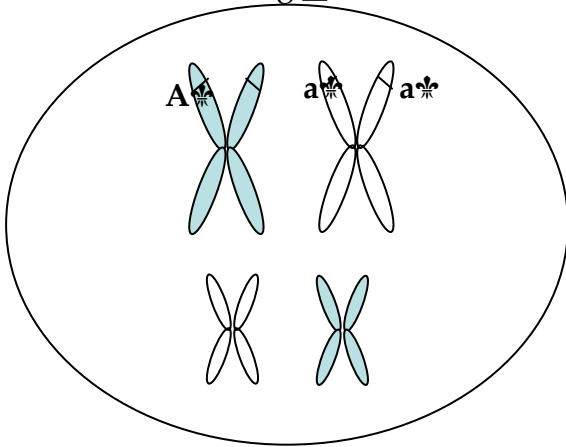
**Question 3 (30 points)**

You hope to use your hard-won 7.014 knowledge to make some extra cash over the summer, so you adopt two Chinchillas to start a Chinchilla breeding business.

Your Chinchillas are Standard male and a rare Velvet female. Chinchillas with Velvet coats have especially thick, soft hair.

Your first hypothesis is that the Velvet (coat thickness) is an autosomal trait.

- a) Draw and label a diagram of a Chinchilla cell right before the first meiotic division. Pretend for the moment that chinchillas only have two pairs of chromosomes both of which are autosomal. Your cell should be heterozygous at the Velvet locus. Make sure to label each allele, using A to indicate the dominant allele and a to indicate the recessive allele.



You reason that the rare Velvet coat phenotype of your female is recessive to the Standard coat phenotype of your male. Your male comes from a long line of show quality Standards, so you feel safe assuming that he is homozygous at the Velvet locus.

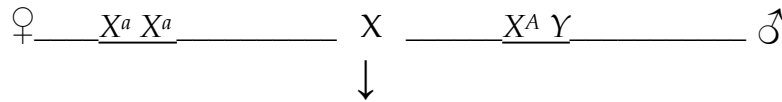
- b) You cross you Standard male and Velvet female. If your assumptions are correct, what coat phenotypes would you expect to see in the
- i. F1 generation?  
*All Standard*
  - ii. F2 generation?  
*3 Standard to 1 Velvet*

In your F1 offspring you find chinchillas of both sexes with Standard coats and a lot of males with Velvet coats. Your buddy from 7.014 suggests that, in contrast to your previous hypothesis, the Velvet phenotype is recessive and sex-linked. Chinchilla sex chromosomes are named X and Y and behave like human sex chromosomes.

**Question 3, continued**

- c) Suppose that your buddy is right and the Velvet gene is on the X chromosome. For the parental cross below, fill in the parental genotypes of your Velvet female and Standard male. Use  $X^A$  and  $X^a$  notation.

In the F1, fill in genotypes and phenotypes of the expected offspring.



F1:

♀  $X^a X^A$       *all Standard*

♂  $X^a Y$       *all Velvet*

Among the F1 progeny, you find a lone Velvet female.

- d) Is the recessive sex-linked inheritance pattern still possible given this data? Why or why not?

*As shown in the predictions above, all females in F1 should be heterozygous for the Velvet allele, and, therefore, should display Standard phenotype. Presence of Velvet female disproves the sex-linked recessive hypothesis.*

You confirm with the use of internet that only one autosomal gene is involved in the Velvet coat phenotype. Your friend now suggests two more hypotheses consistent with this fact:

- (1) your Standard is actually heterozygous at the velvet locus (Aa), while your Velvet is homozygous (aa).
- (2) your Velvet is actually heterozygous (Aa), and your Standard is homozygous (AA).

Recall that the parental cross (Standard X Velvet) gave a mix of Standard and Velvet coats. To determine which hypothesis above is correct, you do the following two crosses and get the following results:

Cross 1:      F1 Standard X P Standard

↓

Offspring: All Standard

Cross 2:      F1 Velvet X P Velvet

↓

Offspring: Velvet and Standard

- e) These results support hypothesis number 2

Explain your choice.

*Hypothesis 1 would predict that cross 1 would produce some individuals with Velvet phenotype, and cross 2 would produce all Velvet offspring. The data do not support this hypothesis.*

*Hypothesis 2 would predict all Standard progeny in cross 1 and a mix in cross 2, so hypothesis 2 agrees with the data.*

Name: \_\_\_\_\_

TA: \_\_\_\_\_

### Question 3, continued

- f) After repeating cross 2 a number of times, the overall ratio of progeny is 1 Standard to 2 Velvet. Explain this result.

*The ratio indicates that the homozygous aa genotype is lethal. We would expect 1AA:2Aa:1aa ratio of genotypes. That ratio can only correspond to the 1Standard : 2 Velvet ratio of phenotypes if the aa genotype is lethal and is not observed in the cross.*

Since Standard coat animals do not sell for as much as Velvet animals, you buy several females with Brown Velvet coats to mate with your Grey Velvet males. Brown is dominant over Grey. However, you are not sure whether the Brown Velvet females you bought are pure breeding at the coat color locus.

You know that two unlinked genes are involved with these phenotypes – one for coat color (B/b), and one for Velvet coat thickness (A/a). After a few years of mating the original pairs, you find they have produced the following offspring:

10 Standard Grey  
28 Grey Velvet  
13 Standard Brown  
24 Brown Velvet

- g) For the parental cross above, fill in the parental genotypes at the coat color and coat thickness loci of your Brown Velvet females and your Grey Velvet males.

♀ BbAa X bbAa ♂

- h) Give the phenotype for each of the possible F1 genotypes below:

BbAA    *Standard Brown*

bbAA    *Standard Grey*

BbAa    *Brown Velvet*

bbAa    *Grey Velvet*

Bbaa    *dead (never born – embryonic lethal)*

Bbaa    *dead (never born – embryonic lethal)*

Name: \_\_\_\_\_

TA: \_\_\_\_\_

### Question 4 (28 points)

You are studying a small experimental plant known as *Cactusus experimentalis*.

You would like to create a genomic library of *Cactusus experimentalis* so you can find the gene responsible for touch sensitivity, called TOU.

a) List the three features your cloning vector must contain to be useful in construction of a genomic library.

1. *Origin of replication*
2. *Antibiotic resistance gene*
3. *Restriction enzyme cut site*

b) After isolating the genomic DNA, what enzymes and reagents would you need to buy for the remaining steps of constructing a genomic library? (Circle ALL that apply.)

Enzymes

DNA Polymerase

RNA Polymerase

Ligase

Restriction enzyme

Reverse Transcriptase

Reagents

dATP, dCTP, dGTP, dTTP

ddATP, ddCTP, ddGTP, ddTTP

Primers

E. Coli

Human Cells

Cloning Vector

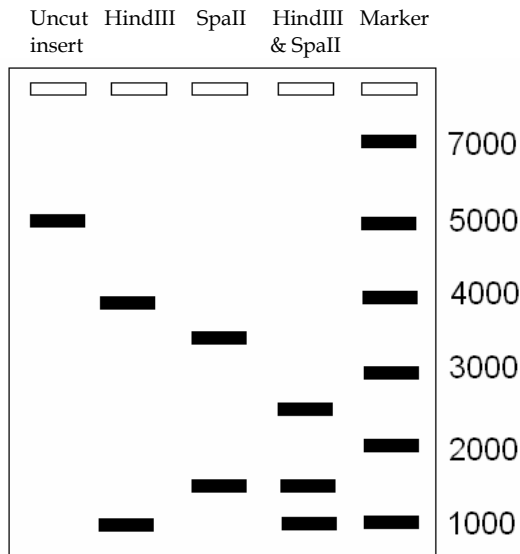
DNA template

ATP, CTP, GTP, TTP

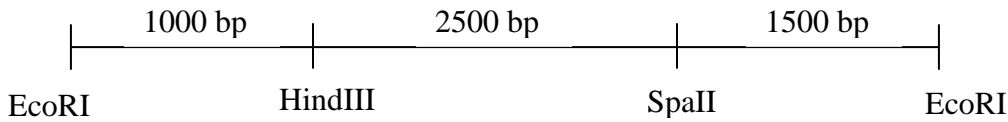
You create the genomic library (starting with an EcoRI digesting of the DNA), and identify one vector that contains your TOU gene. You decide to analyze this vector further. You cut the vector with EcoRI and purify the genomic insert. You then digest the insert with 2 different restriction enzymes SpaII and HindIII. You obtain the following results:



**Question 4, continued**



c) Draw a map of the genomic insert indicating restriction sites for the enzymes *SpaII* and *HindIII*. *EcoRI* sites are already shown for you. Be sure to include distances.



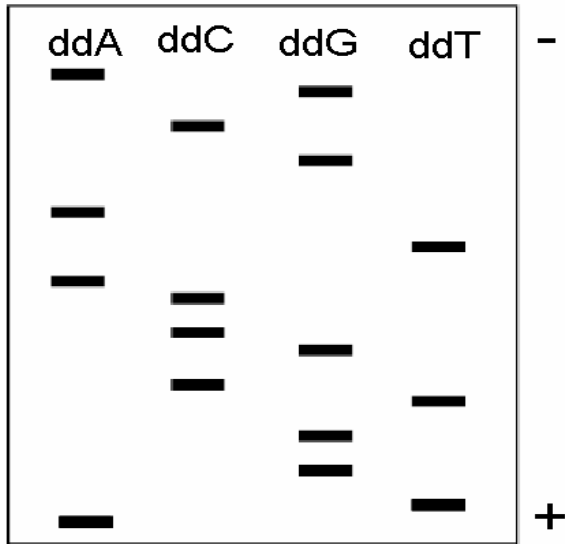
You then decide to sequence a small portion of the *TOU* gene found on your insert.

d) Circle ALL the enzymes and reagents on the following list that you would need to perform a sequencing experiment.

- | <u>Enzymes</u>        | <u>Reagents</u>                   |
|-----------------------|-----------------------------------|
| <u>DNA Polymerase</u> | <u>dATP, dCTP, dGTP, dTTP</u>     |
| RNA Polymerase        | <u>ddATP, ddCTP, ddGTP, ddTTP</u> |
| Ligase                | <u>Primers</u>                    |
| Restriction enzyme    | <i>E. Coli</i>                    |
| Reverse Transcriptase | Human Cells                       |
|                       | <u>TOU gene insert</u>            |
|                       | ATP, CTP, GTP, TTP                |

**Question 4, continued**

You obtain the following gel after amplification.



e) What is the sequence represented on the gel? Be sure to indicate the 5' and 3' ends.

5' ATGGTCGCCATAGCGA 3'

f) After sequencing the TOU gene obtained from your genomic library you find a 32 base pair insert in the middle of it that does not correspond to the mRNA for TOU. What is it?

*The insert is an intron – the sequence that will be edited out of the final mRNA product before translation.*

g) You want to express the TOU gene in *E. coli*.

i. Given the result in part f, would you want to use genomic or cDNA library for this experiment? Why?

*We would want to use cDNA library because the fragments in that library would correspond to final mRNA product, i.e. there will be no introns. If introns are present, bacteria could not edit them out of the mRNA, and so it would not be able to produce functional protein.*

ii. What organism must the promoter be from? Why?

*The promoter would have to come from *E. coli*. Promoters are not universal, and *E. coli* transcription machinery would only recognize *E. coli* promoters.*