Biology 13 Summer 2008 Final Exam

This exam has 11 numbered pages
including this cover page and a blank page that you may use for scratch paper.

Please make sure you have **11** different pages.
Be sure to write your name at the top of each page.

If you need additional scratch paper, just ask. I have additional blank sheets that you may use.

Confine your answers to the pages on which the questions appear;
if you need more space to write, use the back of the page on which the question appears.

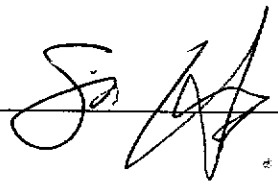
If you wish to use a diagram as part of an answer, you may do so,
but make sure that you label all appropriate items in the figure.

There are 100 points total. Good luck.

You have three hours to complete this exam. Please pace yourselves accordingly.

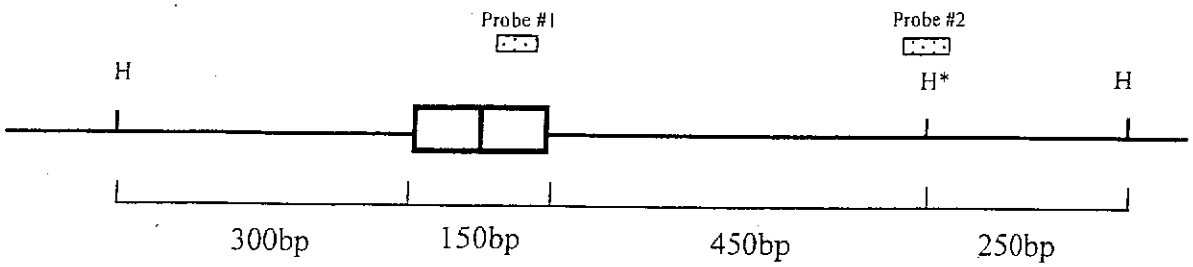
Students taking this exam are expected to abide by the Dartmouth honor principle.
Please read the following statement and sign in the indicated place.

In accordance with the Dartmouth honor principle, my signature below indicates that I submit this examination paper as totally my own.

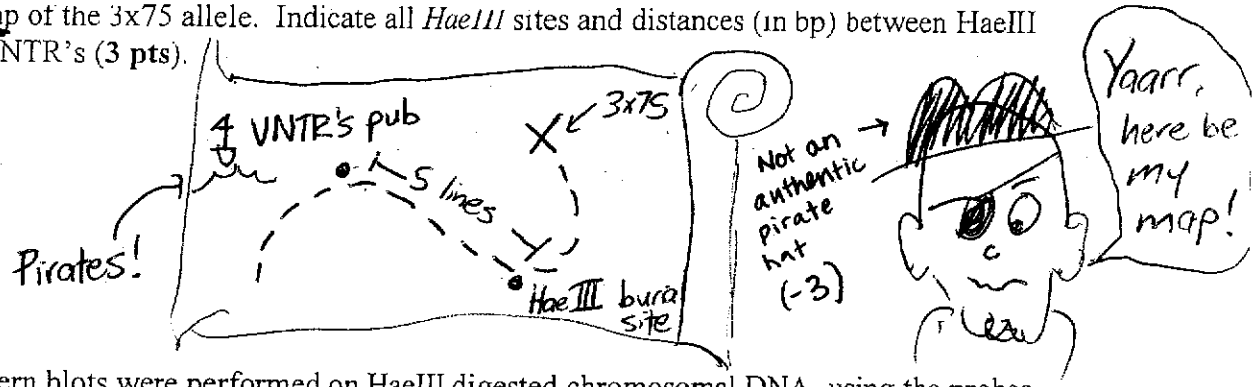
Signature: 

(I really like you guys, and this is meant in humor.)

1. An autosomal VNTR has two alleles: one with two 75bp repeats (2x75), the other with three 75bp repeats (3x75). The diagram below shows a chromosome with the 2x75 allele (boxes) and the flanking *HaeIII* restriction sites. The *HaeIII* site with the asterick (*) is polymorphic in the population where it is always present in the chromosome containing the 2x75 allele and is never present in the chromosome containing the 3x75 allele.

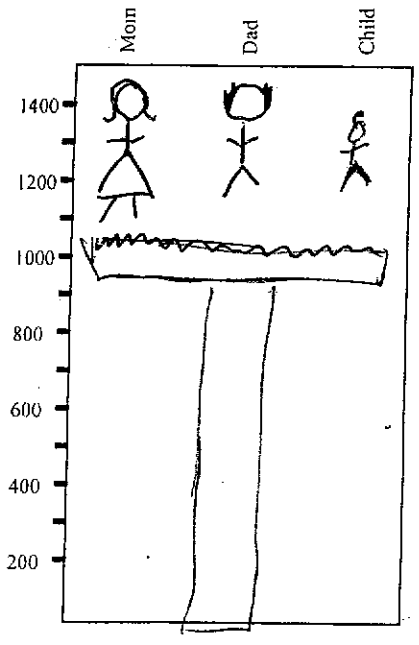


a) Draw a map of the 3x75 allele. Indicate all *HaeIII* sites and distances (in bp) between HaeIII sites and VNTR's (**3 pts**).

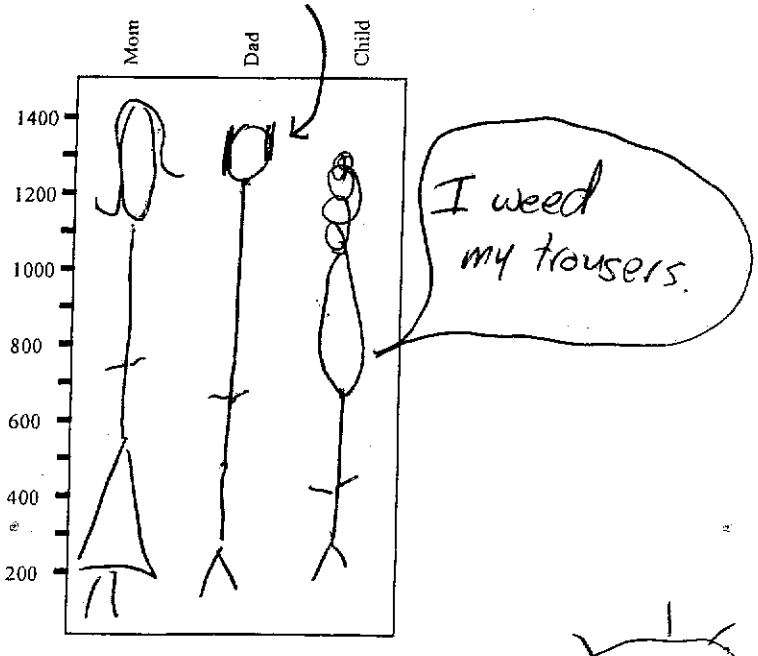


b) Two Southern blots were performed on HaeIII digested chromosomal DNA, using the probes shown in the diagram. On the Southern blots below, draw the hybridization pattern for (**6 pts**):
- a mom homozygous for the 2x75 allele
- a dad homozygous for the 3x75 allele
- their child.

Dad's head is not stretched (-3)



Probe #1



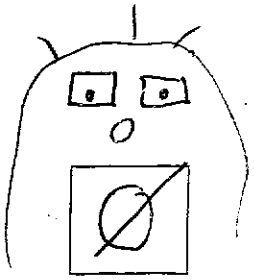
Probe #2

Before

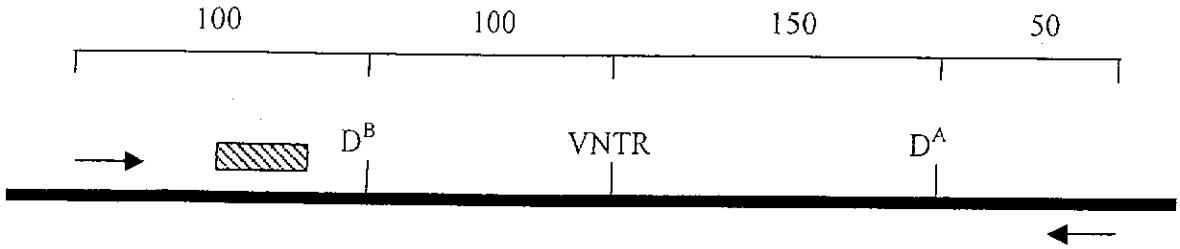
1-800-Stretch-Me

too many #'s for a real phone # (-3)

After!



2. The thick line is a piece of genomic DNA. The thin line above the DNA shows the distance between the elements in base pairs. The arrows indicate the position of primers used for PCR. The D indicates the position of DraI restriction sites. Inserted at the VNTR position can be 1, 2, or 3 repeats of 50bp.

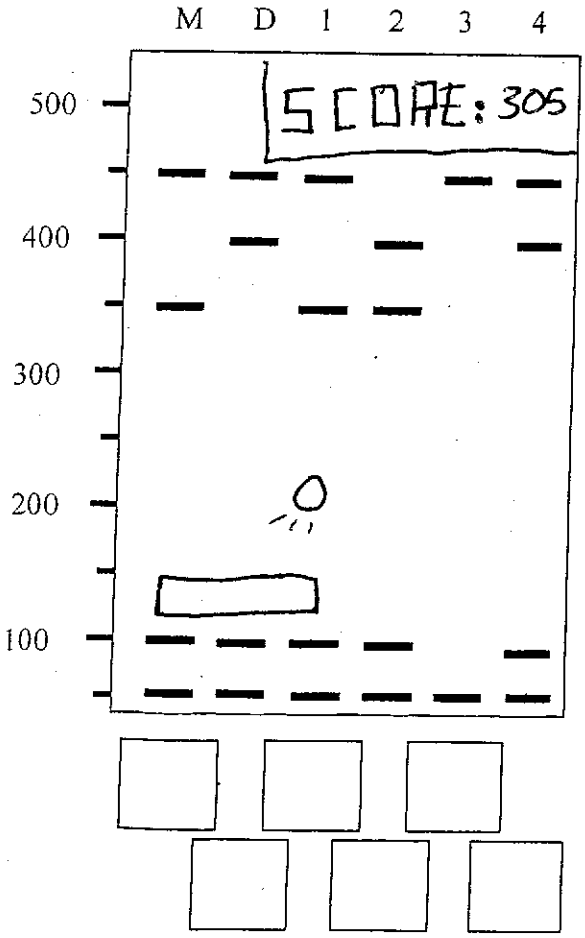


There are three alleles in the human population:
- Allele #1 - One 50bp repeat and the D^A site is missing
- Allele #2 – Two 50bp repeats and the D^B site is missing
- Allele #3 – Three 50bp repeats and both DraI sites are present

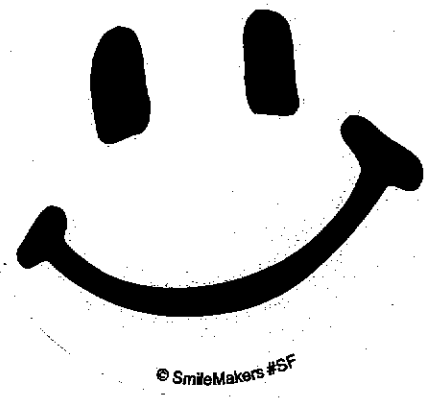
For all six individuals, a DNA fragment is generated by PCR using the primers shown above, the fragment is digested with DraI and the resulting fragments are visualized using agarose gel electrophoresis (shown below). The mother is indicated by M, the father by D and the children are numbered 1-4. **(14 pts)**

+10

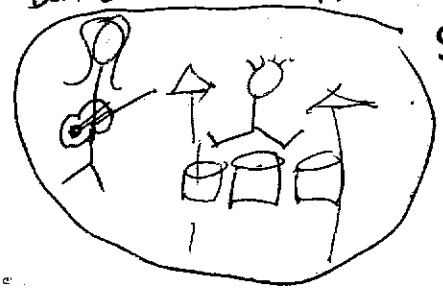
a) Given the pattern below, indicate the allelic combination for each individual in the boxes given below.
b) If the hatched box indicated were used as probe in a Southern blot, circle the bands that would be detected.
c) If there are any conclusions you can draw from this data, please explain them in the space to the side.



a.



b. Bands detected: Nirvana



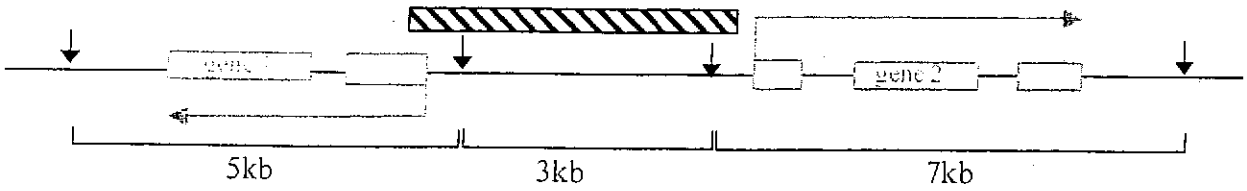
smells like teen spirit

c. The hi-score to the left indicates talent and fertility.

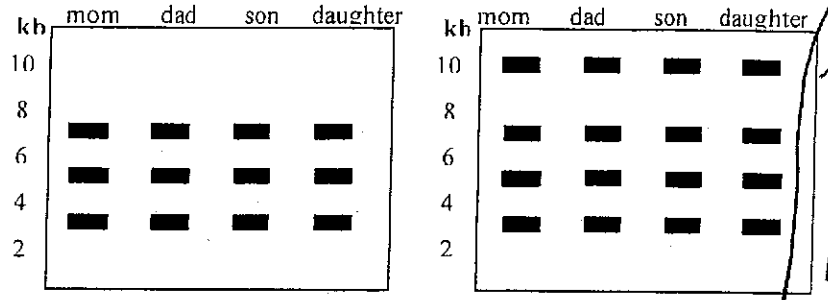
Pay to the order of Sam Haynor

in the amount of $ 1 0 0 ∅

3. You are studying a disease that exhibits interesting inheritance characteristics and decide to investigate whether genomic imprinting is involved. You have narrowed down the genomic interval responsible for the disease to two closely linked genes. A map of the region is shown with exons depicted as white boxes.



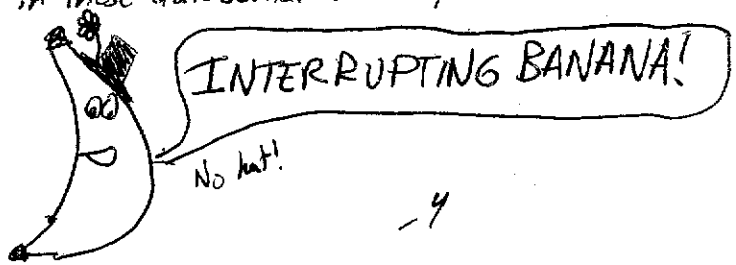
You digest genomic DNA with either MspI or HpaII both of which recognize the site 5'CCGG. Unlike MspI, HpaII does not cut its target site if cytosine is methylated. Enzyme sites are indicated with vertical arrows on the map and fragment sizes are given. The probe you use for Southern blotting is indicated as a hatched box.



a) On the map above, circle the site that is affected by methylation. (1 pt)

b) Based on the data above, you conclude that genomic imprinting in this region is likely. Briefly explain your reasoning and what specific data allowed you to reach this conclusion. Be sure to include a discussion of both homologous chromosomes in your answer. (4 pts)

I believe genomic printing in these autosomal homologs on account of.....



-4

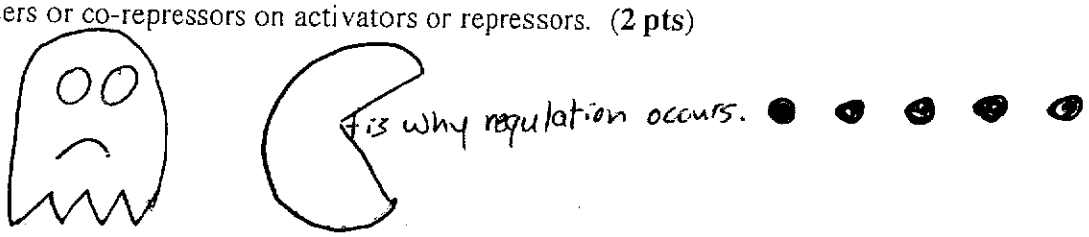
4. You are studying a gene (*YFG45*), and you have found that *YFG45* mRNA accumulates in the heart but not in the kidney. If the regulation of *YFG45* were transcriptional, would you expect the promoter of *YFG45* to be sensitive to DNAse I in the heart? Would you expect this in the kidney? Explain. (4 pts)

5. In bacteria, MerT is an enzyme that makes cells resistant to the toxic effects of mercury. It is regulated by the protein, MerR. In the presence of mercury, merT is highly expressed. Bacteria that contain mutations in the merR gene do not express merT and are sensitive to mercury.

a) Is merT controlled by positive or negative regulation? Is the system inducible or repressible? (2 pts)

0 Mert is her own woman, and controlled by nobody. You can't repress her.

b) Briefly explain how this regulation is occurring based on what you know about the effects of inducers or co-repressors on activators or repressors. (2 pts)

0 

6. Describe ~~the role(s) of sequences 1, 2, 3 and 4 in the mRNA of the leader peptide-coding region of the trp operon.~~ (8 pts) pandas.

0 They are furry and like lollipops.

7. Although attenuation is a relatively common mechanism to regulate the expression of amino acid biosynthetic pathways in bacteria, it is not used in eukaryotes. Why is this? (2 pts)

0 Because Destiny's child broke up.

I know, it hurts me, too.

Check out my donut in a box! ↳ 0

8. When analyzing a cell line you find that the transcription of a copper transporter (CUT1) is induced under conditions of low intracellular copper. You also isolate a DNA binding protein (Cu-BP) that binds to both the enhancer of the CUT1 gene and to copper. (**10 pts**)

a. Would you predict that Cu-BP operates in *trans* or in *cis*?

(-1) Cu-Bp mostly operates downtown.

b. Would you predict that the CUT1 enhancer operates in *trans* or in cis?

CUT1 is often all up in Cu-Bp's turf.

Describe models for both positive and negative control of the CUT1 gene. In your model, be certain to include a role of the Cu-BP protein, as well as an explanation for low levels of CUT1 transcription in the presence of Cu and high levels of CUT1 transcription in the absence of Cu.

c. Positive control model

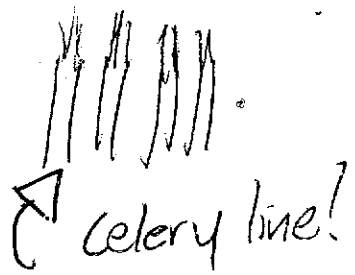
(-3) Madonna

d. Negative control model

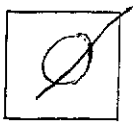
(-3) Britney Spears

e. You isolate a cell line with loss-of-function mutation in the Cu-BP protein. How could you use this cell line to distinguish between these two models?

(-3) I would ask the cell line politely to check for a shaved head. ← or a bad weave.



I call it, "Cheerio in a square bowl"



8. Describe two different mechanisms by which chromatin can be remodeled for transcription. (4 pts)

a) I think a great remodel would be to add a nice kitchenette suite in mahogany.

+Ø

bee!

9. Three different versions of the gene that encodes IRE-BP were constructed.

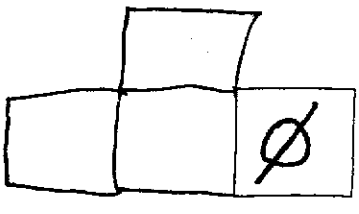
+Ø

IRE-BP$^+$:	wild-type copy of the protein
IRE-BP-nobind:	the nucleic acid binding domain is eliminated
IRE-BP-noFe:	the protein can bind nucleic acids but cannot bind iron
IRE-BP-superFe:	the protein can bind nucleic acids but binds iron under conditions of low iron concentrations

Reverse genetic methods were used to introduce the versions of IRE-BP in place of the normal genomic copies of the IRE-BP gene. Crosses were then done to establish the genotypes listed below. In each case, indicate whether the levels of transferrin receptor protein and ferritin protein would be expected to be either high or low under the indicated iron concentrations. Assume that the IRE-BP is generated in vast excess of transferin and ferritin mRNA's (**8 points**)

	Low iron		High iron	
	Ferritin Protein	Transferin Protein	Ferritin Protein	Transferin Protein
IRE-BP$^+$ / IRE-BP$^+$				
IRE-BP-nobind/ IRE-BP-nobind				
IRE-BP- noFe / IRE-BP- noFe				
IRE-BP- noFe / IRE-BP- nobind				
IRE-BP- noFe / IRE-BP$^+$				
IRE-BPsuperFe/ IRE-BPsuperFe				
IRE-BPsuperFe/ IRE-BPnobind				
IRE-BPsuperFe/ IRE-BP$^+$				

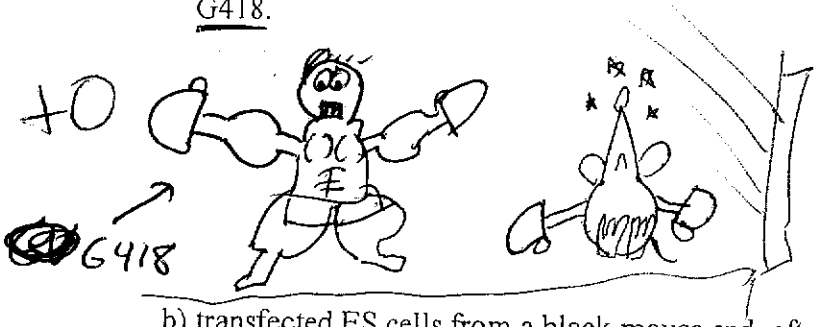
NEXT PIECE:



10. You are trying to study the gene, *YFG1*. In order to examine the function of this gene in mice, you decide to construct a knockout mouse. Unfortunately, you run into some trouble along the way. For each of the following scenarios, explain why the mistake you made would be a problem. Assume that you did everything correctly up until the step mentioned and in subsequent steps. (12 pts)

a) forgot to add gancyclovir when you were generating a knockout mouse but you still added G418.

+0



-3. ambiguous perspective,

b) transfected ES cells from a black mouse and, after selection, injected the desired cells into the blastocyst of a brown mouse.

the mouse is KO but appears to be standing. An inherent contradiction!

+0 Answer written in invisible ink →

-3. I heated the page over a candle and nothing appeared...

c) implanted the blastocyst into a surrogate mother mouse with a chimeric coat.

+0 Answer written in white pen →

-3. I looked at the page under many angles of light and UV, but nothing appeared...

d) swapped the locations of the neomycin cassette and thymidine kinase (i.e. you inserted your gene of interest adjacent to the neomycin cassette and then inserted thymidine kinase into your gene)

+0.1 Answer not written →

-2.9. 0.1 for honesty. (yes, this is how much we value honesty...)

Ha! Beat you to it!

Aha! Not so fast...

0

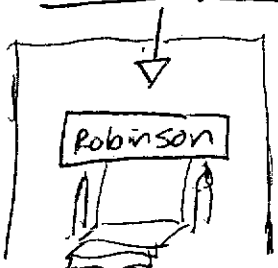
0.1

11. Two STR loci were determined to have the follwing allele frequencies in the general population:

STR A	STR B
1A: 0.1	1B: 0.4
2A: 0.55	2B: 0.4
3A: 0.25	3B: 0.2
4A: 0.1	You sunk my battleship!

A suspect in a criminal trial was genetically tested for these loci and found to have the genotype (1A/1A) for STR A and (2B/3B) for STR B. What is the probability that a randomly sampled person from the population would have this genotype? Please show your work. **(4 pts)**

I work here. →



12. In her lecture, Dr. Dinulos presented a number of case studies; for most of these, what was the first test she proposed doing? **(2 pts)**

Probably the first mid-term

13. Dr. Dinulos explained how genetic testing was different from medical testing and talked about some of the issues geneticists have to consider when doing genetic testing. Please briefly discuss any two issues she mentioned. **(4 pts)**

The War on Poverty and the conflict in Georgia.

This is going to have a big fat zero.

40

0

14. In the table below, the ß-Gal activity for different strains is given. Based on what you know about the lac operon, fill in the blank spaces with the potential growth conditions. Use + to indicate that it was included in the growth medium, - to indicate its omission and +/- to indicate that either would give the same results. (5 pts)

	Glucose	Lactose	ß-Gal activity
I+, P+, O+, Z+, Y+	+	+/-	50
I+, P+, O+, Z+, Y+	x -	+	500
I+, P-, O+, Z+, Y+	$\int x^2 dx$ +/-	% +/-	0
I+, P+, O^c, Z+, Y+/ F' O+	+ -	Σ lactose +/-	500
I+, P+, O+, Z+, Y+/ F' I^s	A +/- +	Desired grade +/-	50
I^d, P+, O+, Z+, Y+/ F' I+	F - +	Actual grade +/-	50

+0

15. Briefly describe the pathway for female development in Drosophila. (5 pts)

+0 a. Drosoph13 says: omg, my mom totally doesn't understand me.

Genquy2000 says: rofl, y u say that?

Drosoph13 says: I'm a changing fly, you know?

Genquy2000 says: How R U dvlping?

Drosoph13 says: Well, I

(Connection to Drosoph13 lost)

Genquy2000: U there?

b. cobblestoned.

0