Write your name and student ID# on EVERY PAGE of your exam

MCB 141 Midterm I  Feb. 15, 2011

Question #1  _____________ / 32 pts
Question #2  _____________ / 27 pts
Question #3  _____________ / 24 pts
Question #4  _____________ / 17 pts

TOTAL  _____________ / 100 pts

Exam is closed book, closed notebook
NO CELL PHONES or other electronic devices
Exams must be turned in by 12:30 PM
All answers must be written in ink.
If you need extra space, write on the back of the page, but clearly indicate this on the front page of the question
Regrade policy: Turn in your entire exam to your TA and include a written explanation as to why you think you deserve additional credit.
Question #1
We have discussed the pathway that establishes the initial dorsal/ventral polarity of the fly embryo (see below).

Predicted the phenotype (dorsalized, ventralized, or normal) of embryos produced by females of the following genotypes (assume all “–” alleles are complete lack of function alleles.). No explanation is needed for 1a-f, but do provide a brief explanation of your answers for 1g-i.

1a) snake− / snake− [1 point; no explanation needed]

1b) cactus− / cactus− [1 point; no explanation needed]
1c) torpedo− / torpedo− [1 point; no explanation needed]

1d) snake− / snake−; cactus−, / cactus− [2 points; no explanation needed]

1e) snake− / snake−; torpedo− / torpedo− [2 points; no explanation needed]

1f) snake− / snake−; cactus− / cactus−; torpedo− / torpedo− [4 points; no explanation needed]
You discover a new, "magic" technique that allows you to create female flies in which you can have follicle cells that differ in their genotypes within a single female. You are able to watch oocytes developing inside a female, and as soon as you see the oocyte nucleus moving to one side (before gurken secretion begins), you can make the genotype of what should be the future dorsal follicle cells different from the genotype of what should be the ventral follicle cells. Combining this with pole cell transplants, you can thus generate females in which there are three distinct genotypes (see diagram on left).

1g) [7 points]
Assume the female has:

germline:    dorsal− / dorsal−; torpedo− / torpedo−; cactus+ / cactus+
dorsal follicle cells: dorsal+ / dorsal+; torpedo+ / torpedo+; cactus+ / cactus+
ventral follicle cells: dorsal+ / dorsal+; torpedo− / torpedo−; cactus− / cactus−

Predict the phenotype of the resulting embryos:

Briefly explain your answer.
**1h) [7 points]**
Assume the female has:
- germline: $\text{dorsal}^+ / \text{dorsal}^+; \text{torpedo}^- / \text{torpedo}^-; \text{cactus}^+ / \text{cactus}^+$
- dorsal follicle cells: $\text{dorsal}^+ / \text{dorsal}^+; \text{torpedo}^+ / \text{torpedo}^+; \text{cactus}^+ / \text{cactus}^+$
- ventral follicle cells: $\text{dorsal}^+ / \text{dorsal}^+; \text{torpedo}^- / \text{torpedo}^-; \text{cactus}^- / \text{cactus}^-$

Predict the phenotype of the resulting embryos:

Briefly explain your answer.
1i) [7 points]
Assume the female has:
germline:  \( \text{dorsal}^{+} / \text{dorsal}^{+}; \text{torpedo}^{+} / \text{torpedo}^{+}; \text{cactus}^{+} / \text{cactus}^{+} \)
dorsal follicle cells:  \( \text{dorsal}^{+} / \text{dorsal}^{+}; \text{torpedo}^{-} / \text{torpedo}^{-}; \text{cactus}^{+} / \text{cactus}^{+} \)
ventral follicle cells:  \( \text{dorsal}^{-} / \text{dorsal}^{-}; \text{torpedo}^{+} / \text{torpedo}^{+}; \text{cactus}^{-} / \text{cactus}^{-} \)

Predict the phenotype of the resulting embryos:

Briefly explain your answer.
Question #2

You are studying the function of three gap genes, X, Y, and Z. The corresponding gap gene protein products are expressed as shown below:

![Gene Expression Diagram](Image)

You also investigate the regulation of stripe 5 of the primary pair-rule gene, runt. You isolate the enhancer for runt stripe 5, and observe that runt stripe 5 (indicated by grey bar below) is expressed in between the expression domains of gap genes X and Z as shown below:

![Runt Gene Expression Diagram](Image)
You sequence the enhancer for runt stripe 5 and notice that three different nucleotide sequences are repeated several times within the enhancer. [Note: Do not worry about the reverse strand DNA sequence – this is not meant to be a trick question.]

The three sequences that are repeated are:

CGCGATAT
TTTTTCGCG
ATATCCCCC

You create a series of synthetic enhancers (see below) and place each one in front of a lacZ reporter gene and introduce each into flies via P-element transposition. You then observe the pattern of lacZ expression in embryos of the transgenic lines that you establish.

Synthetic enhancer A (SynR5A) – all the CGCGATAT repeats are specifically eliminated from the normal enhancer. Instead of a normal runt stripe 5 pattern, you see no expression of the lacZ reporter in an otherwise wild-type embryo.

Synthetic enhancer B (SynR5B) – all the TTTTTTCGCG repeats are specifically eliminated from the enhancer. Instead of a normal runt stripe 5 pattern, you see a broadened stripe of lacZ expression (broadened in the anterior direction) in an otherwise wild-type embryo.

Synthetic enhancer C (SynR5C) – all the ATATCCCCC repeats are specifically eliminated. Instead of a normal runt stripe 5 pattern, you see a broadened stripe of lacZ expression (broadened in the posterior direction) in an otherwise wild-type embryo.
2a) Based on these data, predict the sequence that is bound by protein Y (circle the correct answer below). Give a brief explanation for your answer. [6 points]

CGCGATAT
TTTTTCGCG
ATATCCCCC

2b) Based on these data, predict the sequence that is bound by protein Z (circle the correct answer below). Give a brief explanation for your answer. [6 points]

CGCGATAT
TTTTTCGCG
ATATCCCCC
2c) [15 points]
You create a synthetic enhancer SynR5D with the sequence:

TTTTTCGCGCGATATATATATCCCCC

You put SynR5D in front of a lacZ reporter gene and introduce it into flies via P-element transposition. You expect the lacZ pattern to mimic runt stripe 5, but instead you get a stripe that is much broader (spread both anteriorly and posteriorly from the normal boundaries for runt stripe 5).

You create a second synthetic enhancer called SynR5E with the sequence:

TTTTTCGCGATATCCCCC

You put SynR5E in front of a lacZ reporter gene and introduce it into flies via P-element transposition. You find that the lacZ pattern now perfectly mimics the pattern of runt stripe 5.

Give an explanation for your results. What does this tell you about how protein X, Y, and Z function? Why the difference in results for SynR5D and SynR5E?
Question #3

Ubx in Artemia (brine shrimp) is expressed from T1 on back, while Ubx in Homarus (lobster) is expressed from T3 on back (see panel A below). Recall the cis versus trans test that we designed in lecture to test why Ubx showed different expression patterns in the two species. In that case we used the Artemia and Homarus enhancers to control the expression of lacZ. Imagine instead that we replace the endogenous Ubx gene (that includes the coding region plus enhancers) with the Ubx enhancer plus Ubx coding region from the opposite species (see panel B below). Draw the expected results if the different expression patterns are from trans changes, and the expected results if the different expression patterns are due to cis changes. In your drawings show the expected expression domain of Ubx as well as the expected morphology of the appendage on each segment (see panel C below), and provide a brief explanation for your answers. (Note: Assume that there are no amino acid differences between the Ubx proteins of Artemia and Homarus, thus the two proteins function identically).

A

Artemia

Ubx expressed T1 on back

Homarus

Ubx expressed T3 on back

B

Art-enh

Ubx protein coding region

place into Homarus

Hom-enh

Ubx protein coding region

place into Artemia

C

Artemia feeding appendages of the head

Artemia swimming appendages of the thorax

Homarus feeding appendages of the head and thorax

Homarus swimming appendages of the thorax
3a) [12 points]
ASSUME TRANS CHANGES BETWEEN ARTEMIA AND HOMARUS
(draw expected Ubx expression domains and draw the appendage morphology you expect to see)

**Artemia** now containing [Hom-enh]-Ubx

**Homarus** now containing [Art-enh]-Ubx

Explain your answer:
3b) [12 points]
ASSUME CIS CHANGES BETWEEN ARTEMIA AND HOMARUS
(draw expected Ubx expression domains and draw the appendage morphology you expect to see)

Artemia now containing [Hom-enh]-Ubx  Homarus now containing [Art-enh]-Ubx

Explain your answer:
Question #4 [17 points]

In the crab, Cleves, one claw is always larger than the other claw. Crabs with larger right claws are known as "Righties", and those with larger left claws are known as "Lefties". This difference is controlled by a single maternal effect gene, called Claw. Gene Claw has two alleles, called Claw(R) and Claw(L).

On the island of Moorea, all Cleves are Righties and all have the genotype Claw(R)/Claw(R). On the Island of Bora Bora, all Cleves are Lefties and all have the genotype Claw(L)/Claw(L).

You are told by a colleague that Claw(L) is dominant to Claw(R). You cross a Cleves from Moorea with a Cleves from Bora Bora to obtain animals that have the genotype of Claw(R)/Claw(L).

You then set up a cross between a female Cleves with the genotype Claw(R)/Claw(L) to a male Cleves with the genotype Claw(R)/Claw(L). Write out the different genotypes seen in the progeny of this cross, and the phenotype (Rightie or Leftie) for each of the genotypes. Provide an explanation for your answer.