

Name: _____

SSN (last 4 digits): _____

UNIVERSITY OF HOUSTON

FALL SEMESTER, 2004

BIOLOGY

BIOL4397 — Evolution of Development

NOTE: The maximum score is **100 points**. Answer all true/false questions by ticking boxes; other kinds of answers will be ignored. An incorrect, non-blank answer to a true/false question will incur a deduction of 25% of its score. Time allowed: **50 minutes**.

1. Evaluate the following statements about Fisher's model of adaptation (including the extensions introduced by Kimura and Orr): **[3 points each]**

- (a) Mutations of small effect are more likely to be deleterious than mutations of large effect. True [] False [x]
- (b) The model assumes that mutations do not have pleiotropic effects. True [] False [x]
- (c) Mutations of large effect are more likely to form the genetic basis of adaptation because they occur more frequently than mutations of small effect. True [] False [x]
- (d) The magnitudes of the effects of mutations fixed during an adaptive walk tend to decrease as a population approaches the optimum. True [x] False []

2. Evaluate the following statements on the genetic and evolutionary implications of the modular architecture of *cis*-regulatory regions: **[3 points each]**

- (a) Mutations may alter only a subset of the functions of a gene. True [x] False []
- (b) Mutations of large effect are more likely to occur than mutations of small effect. True [] False [x]
- (c) The probability of preservation of both copies of a gene that has undergone duplication is low. True [] False [x]
- (d) The coding sequences of genes can evolve faster. True [] False [x]

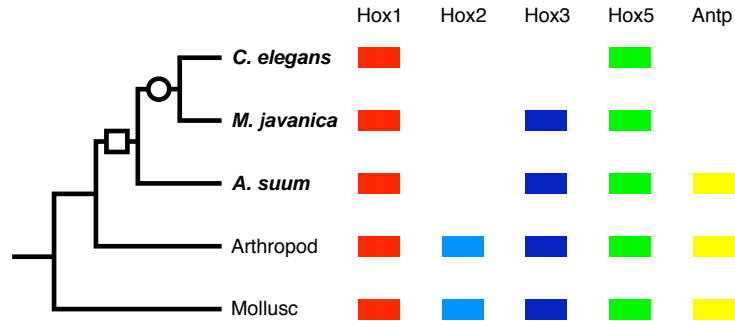


Figure 1: Presence/absence of five groups of Hox genes in 3 species of nematodes (bold: *Caenorhabditis elegans*, *Meloidogyne javanica* and *Ascaris suum*). Boxes of the same color indicate orthologs. The phylogeny is based on SSU rDNA sequences.

3. The nematode *C. elegans* stands out as having a greatly reduced Hox cluster. Recently, orthologs of several Hox genes have been identified in other nematodes (Fig. 1). Consider the most parsimonious scenario for the evolution of these genes. Evaluate the following statements: **[3 points each]**

- (a) At least six Hox gene losses are required to explain the observed pattern. True [] False [x]
- (b) No more than two Hox gene losses and one Hox gene duplication are required to explain the observed pattern. True [] False [x]
- (c) A deletion of Hox2 occurred in the branch represented by a square. True [x] False []
- (d) A duplication of Hox1 occurred in the branch represented by a circle. True [] False [x]
- (e) The *C. elegans* Hox gene cluster must resemble that of the ancestor of all bilaterian animals because it is the simplest. True [] False [x]

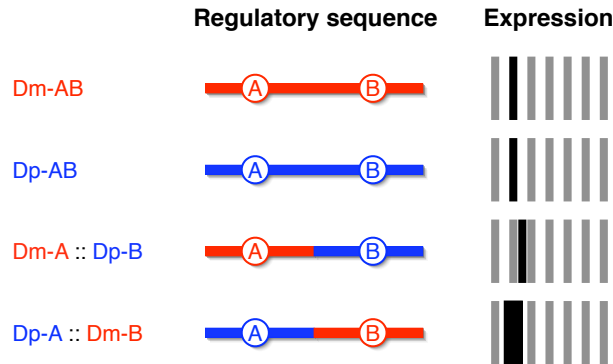


Figure 2: Natural and chimaeric *eve* stripe 2 elements were used to drive expression of *lacZ* in *D. melanogaster*. Sequences from *D. melanogaster* (Dm) are displayed in red and sequences from *D. pseudoobscura* (Dp) are shown in blue. The expression pattern cartoons show the seven stripes of *eve* mRNA in grey and the *lacZ* mRNA in black. The expression pattern of *eve* mRNA was the same in all experiments. The chimaeric regulatory sequence constructs are complementary.

4. *Even-skipped* (*eve*) is a pair-rule gene that encodes a homeobox transcription factor. The *eve* stripe 2 element controls the expression of the second transverse stripe of *eve* mRNA in *Drosophila melanogaster* embryos, and is one of the best characterized eukaryotic enhancers. Fig. 2 shows the expression patterns of *lacZ* mRNA under natural and chimaeric *eve* stripe 2 elements from *D. melanogaster* and *D. pseudoobscura*. Evaluate the following statements: [3 points each]

- (a) The *eve* stripe 2 elements from both species are capable of driving expression of *lacZ* mRNA to the location of the second *eve* mRNA stripe. True [x] False []
- (b) The expression pattern of the second stripe of EVE protein is probably not conserved in the two species. True [] False [x]
- (c) The function of EVE protein is probably not conserved in the two species because their *eve* stripe 2 elements are identical in sequence. True [] False [x]
- (d) The function of EVE protein is probably conserved in the two species because their *eve* stripe 2 elements cause *lacZ* mRNA to be expressed in a similar pattern. True [] False [x]
- (e) The posterior shift in *lacZ* mRNA expression under the Dm-A::Dp-B regulatory sequence suggests that the Dp-B region might contain one or more regulatory elements required for correct expression of the second stripe of *eve* in *D. pseudoobscura*. True [x] False []

- (f) The expansion of the domain of *lacZ* mRNA expression under the Dp-A::Dm-B regulatory sequence suggests that the Dm-B region does not contain any regulatory elements required for correct expression of the second stripe of *eve* in *D. melanogaster*. True [] False [x]
- (g) The *lacZ* mRNA expression patterns generated by the chimaeric regulatory sequences suggest that the *eve* stripe 2 elements of *D. melanogaster* and *D. pseudoobscura* must differ in at least two regulatory elements. True [x] False []

5. Describe how you might obtain a more accurate estimate of the number of regulatory element differences between the *eve* stripe 2 elements of the two species. [20 points]

Will be discussed in class.

6. One function of the EVE protein is the regulation of segment polarity through an indirect regulation of *engrailed* (*en*). In odd parasegments, graded expression of *eve* establishes the *en* stripes by setting the boundaries of the activator *paired* and the repressors *runt* and *sloppy paired*. Imagine that the expression patterns of all the genes mentioned above are conserved in *D. melanogaster* and *D. pseudoobscura*. Explain how you might test whether the EVE protein is functionally conserved in the two species. [20 points]

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