# FRQ Friday – 4/9

AP Biology Insta-Review @apbiopenguins

## 2016 #1

## 2015 #3

# FRQ 2016 #1

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TABLE 1. PERCENT OF INDIVIDUALS POSSESSING *lap*$^{94}$ ALLELE

| | Long Island Sound | | | | | Atlantic Ocean | | |
|---|---|---|---|---|---|---|---|---|
| Site | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
| *lap*$^{94}$ frequency (%) | 13 | 16 | 25 | 37 | 55 | 59 | 59 | 59 |
| Salinity | Low → | | | | High | High | | |

Leucine aminopeptidases (LAPs) are found in all living organisms and have been associated with the response of the marine mussel, *Mytilus edulis*, to changes in salinity. LAPs are enzymes that remove N-terminal amino acids from proteins and release the free amino acids into the cytosol. To investigate the evolution of LAPs in wild populations of *M. edulis*, researchers sampled adult mussels from several different locations along a part of the northeast coast of the United States, as shown in Figure 1. The researchers then determined the percent of individuals possessing a particular *lap* allele, *lap*$^{94}$, in mussels from each sample site (table 1).

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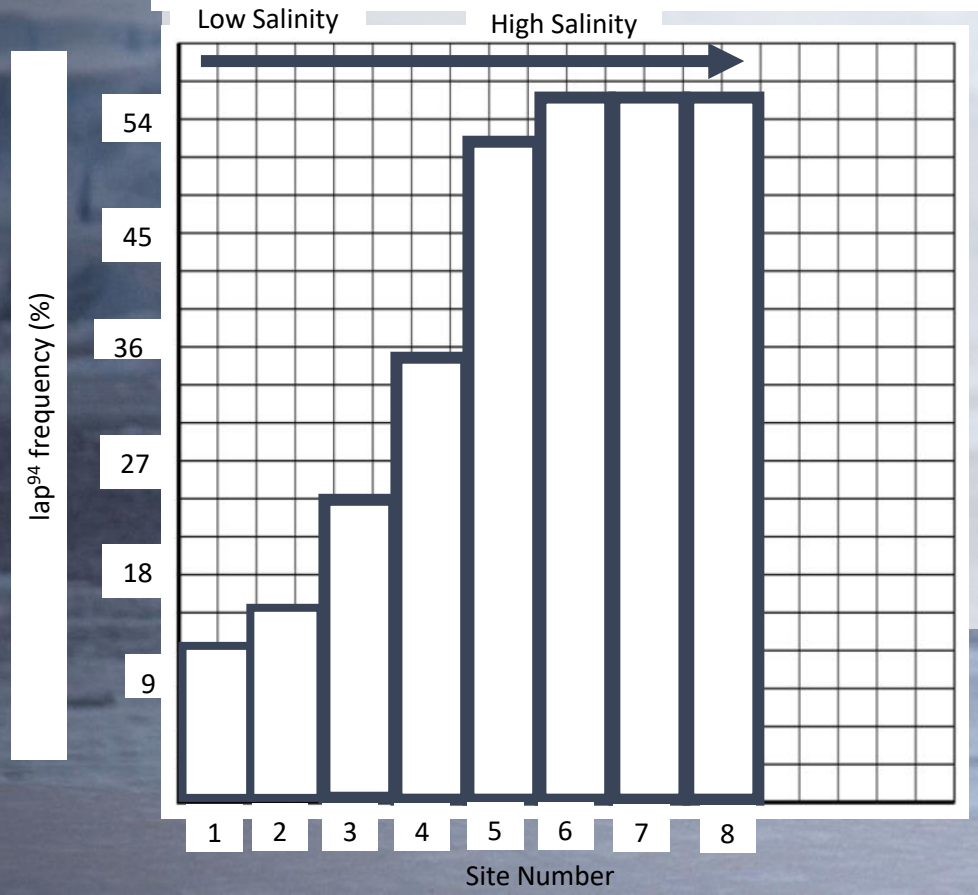
(a) On the axes provided, **construct** an appropriately labeled bar graph to illustrate the observed frequencies of the *lap*$^{94}$ allele in the study populations.

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**Construct graph (3 points)**

- Correctly plotted bar graph that accurately represents the trend
- Correct axis labeling
- Correct scale and units

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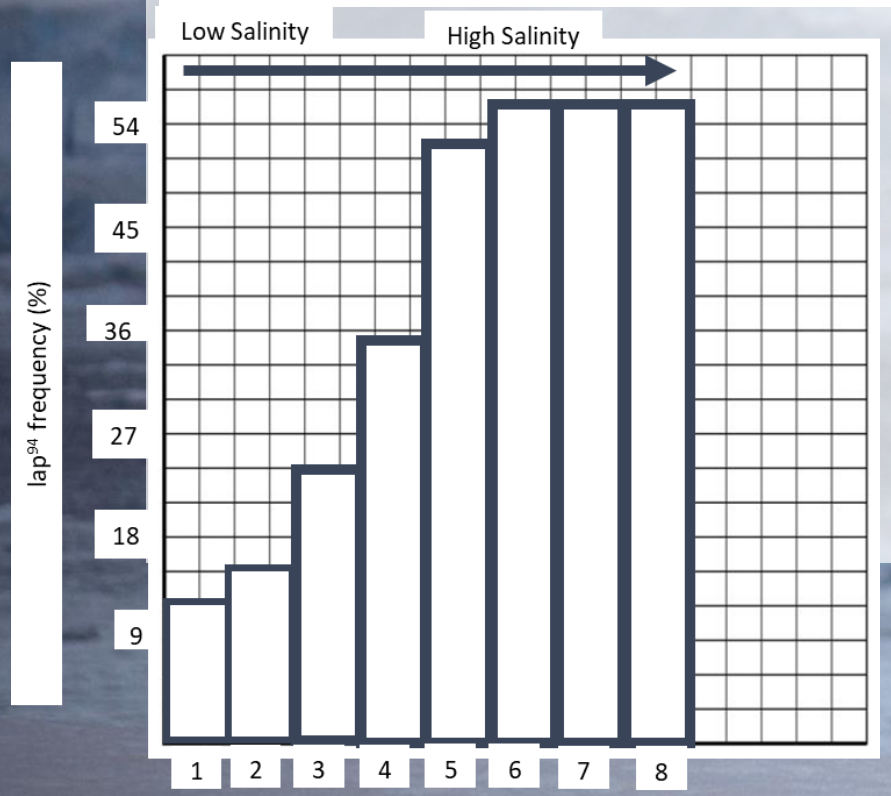
(b) Based on the data, **describe** the most likely effect of salinity on the frequency of the *lap*$^{94}$ allele in the marine mussel populations in Long Island Sound. **Predict** the likely *lap*$^{94}$ allele frequency at a sampling site between site 1 and site 2 in Long Island Sound.

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**Description (1 point)**

- As salinity increases *lap*$^{94}$ frequency increases
- As salinity decreases *lap*$^{94}$ frequency decreases

**Prediction (1 point)**

Between 13 and 16 percent (or a selected value between 13 and 16 percent)

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(c) **Describe** the most likely effect of $LAP^{94}$ activity on the osmolarity of the cytosol. **Describe** the function of $LAP^{94}$ in maintaining water balance in the mussels living in the Atlantic Ocean.

| **Describe effect of $LAP^{94}$ activity (1 point)** | **Describe function of $LAP^{94}$ in maintaining water balance (1 point)** |
|---|---|
| • $LAP^{94}$ increases osmolarity/solute concentration of the cytosol<br>• $LAP^{94}$ decreases water potential of the cytosol | Prevents water loss to the environment |

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(d) Marine mussel larvae are evenly dispersed throughout the study area by water movement. As larvae mature, they attach to the rocks in the water. **Explain** the differences in *lap*$^{94}$ allele frequency among adult mussel populations at the sample sites despite the dispersal of larvae throughout the entire study area. **Predict** the likely effect on distribution of mussels in Long Island Sound if the *lap*$^{94}$ allele was found in all of the mussels in the population. **Justify** your prediction.

| Explanation (1 point) | Prediction (1 point) | Justification (1 point) |
|---|---|---|
| • Mussels with *lap*$^{94}$ allele are more likely to survive in high salinity/less likely to survive in low salinity.<br>• Mussels without *lap*$^{94}$ allele are less likely to survive in high salinity/more likely to survive in low salinity. | • Mussel population will increase in high salinity.<br>• Mussel population will decline in low salinity. | • Mussels in high salinity with *lap*$^{94}$ allele will osmoregulate.<br>• Mussels in low salinity with *lap*$^{94}$ allele will not osmoregulate. |

# FRQ 2015 #3

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The amino acid sequence of cytochrome *c* was determined for five different species of vertebrates. The table below shows the number of differences in the sequences between each pair of species.

THE NUMBER OF AMINO ACID DIFFERENCES IN CYTOCHROME *c* AMONG FIVE SPECIES

| | *E. ferus* | *D. polylepis* | *G. gallus* | *A. forsteri* | *E. africanus* |
|---|---|---|---|---|---|
| *E. ferus* | 0 | 21 | 11 | 13 | 1 |
| *D. polylepis* | | 0 | 18 | 17 | 20 |
| *G. gallus* | | | 0 | 3 | 10 |
| *A. forsteri* | | | | 0 | 12 |
| *E. africanus* | | | | | 0 |

# FRQ 2015 #3

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(a) Using the data in the table, **create** a phylogenetic tree on the template provided to reflect the evolutionary relationships of the organisms. **Provide reasoning** for the placement on the tree of the species that is least related to the others.

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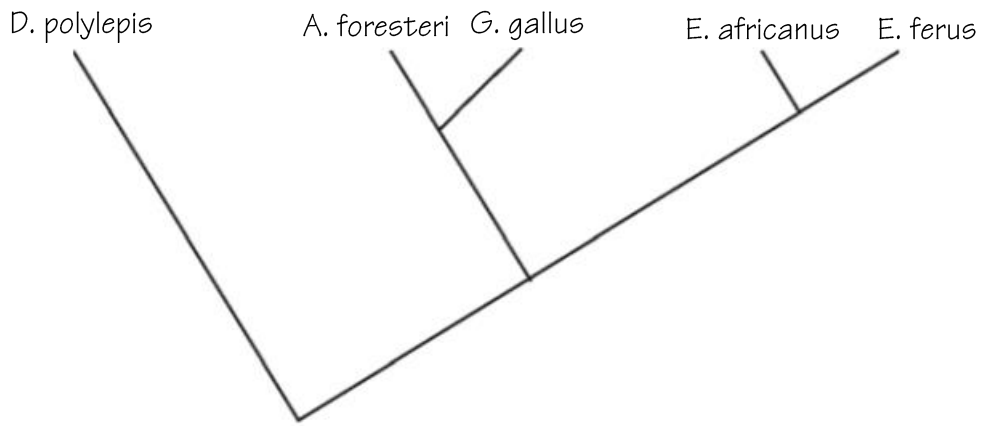


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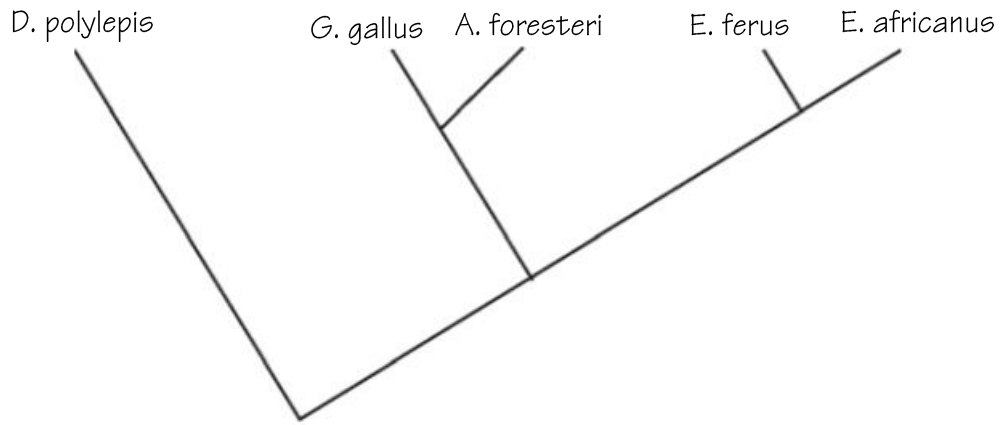


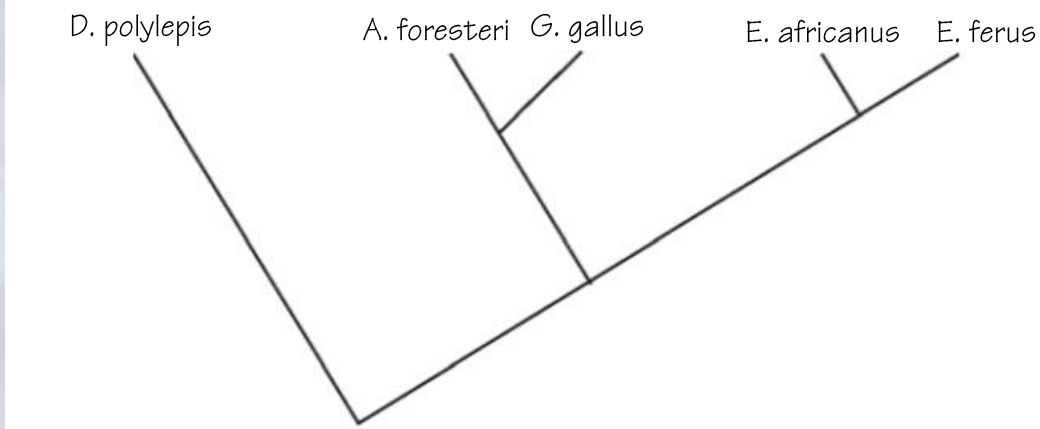


Based on the rotating points, this is also acceptable

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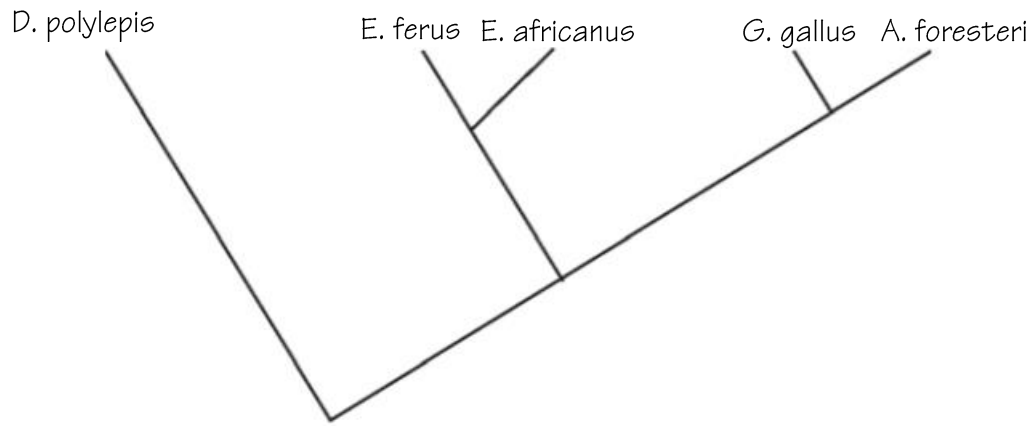


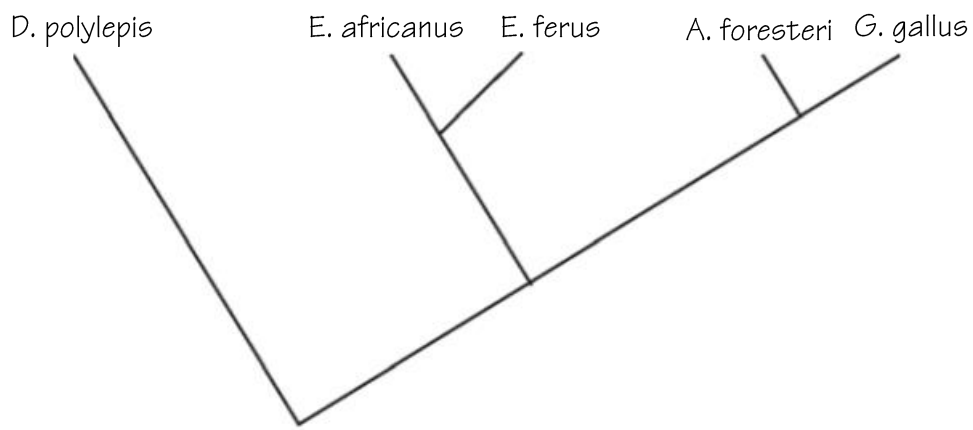


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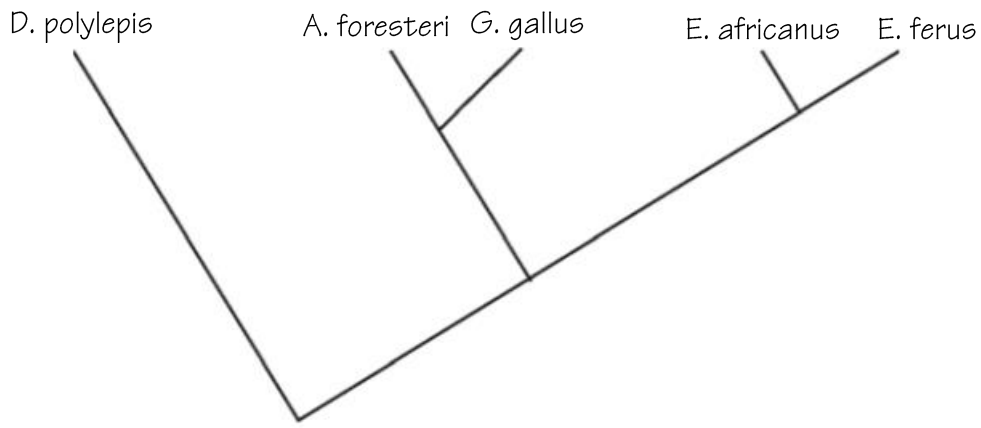


**Reasoning (1 point)**

- D. polylepis has the most differences in amino acids (or changes in DNA or proteins as they relate to amino acids).

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(b) **Identify** whether morphological data or amino acid sequence data are more likely to accurately represent the true evolutionary relationships among the species, and **provide reasoning** for your answer.

**Identification (1 point)**

- Amino acid/molecular data

**Reasoning (1 point)**

- Morphology may be similar (due to convergent evolution/analogous structures) even if there are differences in amino acid/DNA sequences.
- Molecular data (e.g. amino acid changes, DNA changes) directly show genetic make-up/ reveal evolution.

**Identification (1 point)**

- Morphological data

**Reasoning (1 point)**

- Similar molecular sequences may result in different morphologies.
- An example of species with similar proteins but different morphology (e.g., chimps and humans).

# Next FRQ Friday (4/16)

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2013 #3

2015 #2