



Invertebrate Evolution: Making a Phylogenetic Tree

Designed by

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Background

This activity is a webquest that guides students through various bioinformatics tools on the internet including the protein database at NCBI, Cn3D protein viewer, and ClustalW. Students will focus on cytochrome b protein sequences. They will compare protein sequences from different marine organisms and use this to investigate evolutionary relationships.

Description of Audience:

This biotechnology/bioinformatics activity is designed for use in a high school Biology, AP Biology, Biotechnology, Marine Biology, or equivalent course.

State Standards:

This biotechnology/bioinformatics activity fulfills the following State of California Science Standards:

Biology: Grades 9-12: 1b, 1d, 1h, 4b, 4e, 4f, 5a, 7c, 8f

Chemistry: Grades 9-12 10a, 10c

Investigation and Experimentation: Grades 9-12: 1d, 1g, 1i

National Science Standards:

This biotechnology/bioinformatics activity fulfills the following National Science Standards:

Content Standard A: Science as Inquiry

- Identify questions and concepts that guide scientific investigations
- Design and conduct scientific investigations
- Use technology and mathematics to improve investigations and communications
- Formulate and revise scientific explanations and models using logic and evidence
- Recognize and analyze alternative explanations and models

Content Standard C: Life Science

- Biological evolution
- Energy and organization in living systems

Content Standard E: Science and Technology

- Abilities of Technical Design (Propose design and choose between alternative solutions)
- Understanding about science and technology.

STEM Connection:

Bioinformatics is being used increasingly in many aspects of research science. Tools such as the ones here can be used in research fields as varied as pharmaceuticals, medicine, marine science, agricultural science, molecular biology, epidemiology, and taxonomy.

Technology Integration:

Students will use computers to access three websites online: NCBI, ClustalW and Cn3dProtein viewer.

- NCBI: Students will use this database to locate protein sequences for organisms.
- ClustalW: Students will use this site to align and compare the relatedness of multiple organisms. They will use this site to create phylogenetic trees.
- Cn3d Protein viewer: Students will be able to visualize and manipulate a three dimensional image of the polypeptide chains from their sequence results.

Goals:

The goals of this lesson are to:

- Expose students to bioinformatics tools and technology on the web.
- Allow students to visualize and manipulate the 3D structure of a protein.
- Show students how phylogenetic trees can be used as a model of evolutionary relationships.
- Show students how differences at the molecular level can be used to infer evolutionary relationships.

Learning Objective(s)

Upon completion of this lesson, students will be able to:

- Use NCBI to find protein structure files and protein sequences.
- Use Cn3D to visualize and manipulate protein files.
- Acquire protein sequences from various invertebrates and align them using ClustalW.
- Explain how organisms with dissimilar protein sequences are more distantly related than organisms with more similar protein sequences.
- Recognize that there are multiple interpretations of scientific data.

Purpose/Rationale

The purpose of this lesson is to provide a process for students to follow in which they generate data and interpret that data. They will be using modern bioinformatics as a research tool. This process allows them to become familiar with modern research techniques and exposes them to extensive online databases. They will compare their results to other taxonomic trees and recognize that many interpretations of data are possible.

Materials/Resources

In order to complete this lesson, the following materials are needed:

- Student access to computers with Internet (1 computer per student)
- The following websites:
<http://www.ncbi.nlm.nih.gov/>
<http://align.genome.jp/>
- The protein viewer software may be downloaded from:
<http://www.ncbi.nlm.nih.gov/Structure/CN3D/cn3d.shtml>

- A list of the binomial names of the 17 reference species (1 per student)
- Invertebrate Evolution Process Sheet (lesson worksheet)
- Other invertebrate cladograms (for comparisons) are available at:
<http://www.palaeos.com/Invertebrates/Lists/Cladogram.html>
<http://www.biology.ualberta.ca/courses.hp/zool250/Z250.html>
 and their textbook.

Teacher Preparation

Students should already be familiar with the concepts of taxonomy including cladograms and common ancestry. They should understand the relationship of DNA sequences to amino acid sequences and protein structure. They should know the role of cytochrome b in electron transport.

3-Step Procedure

#1 Introduction

- Review the role of cytochrome b in cellular respiration, protein structure and the relationship of structure and function.
- Assess student's prior knowledge of taxonomic trees, and taxonomy nomenclature.
- Demonstrate the use of the computer to access the relevant websites. Choose one species to walk through the process of protein sequence acquisition (NCBI) and use a group sequences to demonstrate the use of the alignment website (ClustalW)
- Remind students of the procedure for saving files on the school computers.
- Prior to lab, have students research the organisms on the species list and find their phylum.

#2 Exploration

- Students will be working individually following the directions on the Process sheet and answering the two worksheets that accompany the directions.

#3 Application

- Students will compare their taxonomic trees to those published by other authors. They will identify similarities and differences and judge what they think makes a taxonomic tree reliable.

Assessment

Students will complete worksheets as they do the activity. They will produce a copy of their taxonomic tree.

- *Lesson variations:* students needing more support should be given a modified assignment with fewer species. They may be given a prewritten list of sequences to which they add one or more that they have acquired and then they can make a tree from the combined data.

This lesson will require the teacher to be checking for understanding with individual students throughout the activity.

- *Lesson extension:* Students who quickly complete the lesson can be given protein sequences that they use to predict the phylum of unknown organisms. Alternatively, they can be challenged to find additional organisms and compare the tree they produce with the class set.

Teachers' Self Evaluation

[in progress]

Note: Reflect on strengths and weaknesses of the lesson based on how it was taught.

- *Describe individual student responses to techniques used. How did they react?*
- *Discuss student "thinking" and ideas.*
- *Include samples of students answers on lab sheet or journal entry (photocopy is fine).*
- *Ask students for a brief evaluation of lesson. Include their responses.*
- *Discuss fulfilled and unfulfilled expectations. Any surprises?*
- *In retrospect, how would you modify this lesson?*

Included in accompanying file:

- Student directions page (Parts 1 and 2)
- Student answer sheets (Parts 1 and 2)
- List of invertebrate species
- Sample completed taxonomic tree
- Reference amino acid sequences