## **APPENDIX D: TERM PROJECT**

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Due in lab November 23 - 25, 2015

## **Background**

For your Term Project you will learn elementary cladistics and basic phylogenetic tree construction. You will complete this project independently, but you are welcome to discuss your research and ideas with other students. You are also highly encouraged to explore the web and other out-of-class resources to better understand these topics. This project aims not only to guide you in learning about the evolution of plants, but it will also demand that you master a new topic largely on your own.

In Unit 12 you learned how to group organisms by taxonomic categories that were based on morphological characters. The discovery of evolution and modern genomics has revealed that the classification of organisms is more complex than early taxonomists recognized. The evolutionary relationships between organisms (i.e., taxa) are depicted using phylogenetic trees, and most modern trees are constructed using molecular data (e.g., DNA and proteins).

For this project you will select 18 organisms, use two methods to hypothesize the evolutionary relationships between the taxa, and then write a report of your findings. The first evolutionary tree that you will construct will be based upon the principle of *parsimony*—that the simplest explanation to fit the evidence is likely true. For this type of tree you will arrange the taxa (i.e., branches) based upon the minimum number of character changes (i.e., synapomorphies). You will also construct a second tree using sequenced genomic information. To get you started, you will be provided some background information into the evolution of plants and phylogenetic methods. You can also begin your exploration at this website: http://evolution.berkeley.edu/evolibrary/article/phylogenetics\_01

#### **Procedure**

- 1. First, read the background literature you provided, and the following website: http://www.ncbi.nlm.nih.gov/books/NBK21122/ Don't worry if you don't understand *everything*. The purpose of this project if for you to compare and contrast your trees and to interpret their evolutionary connotations.
- 2. From the list of organisms, select <u>two</u> organisms—one with a shaded cell, and one plain—from <u>each</u> of the nine groups.
- 3. Locate the picture for each of your organisms on Blackboard.
- 4. From the provided pictures *alone*, delineate morphological characters by which to match your taxa into closely related pairs.
- 5. Based on the characters you've designated, construct a tree using the principle of parsimony. Draw your hypothesized tree with a computer program (e.g., Word, Powerpoint, Paint, etc.) to be used as a figure in your report. Label the tree with the character changes you used to group the organisms.
- 6. Next, you will construct a tree based on the organisms' molecular data, specifically protein sequences. Go to the phyloT website (http://phylot.biobyte.de); this site will generate a simple tree based upon the NCBI taxonomy and GenBank protein sequences. In the "Tree elements" box list the names of your taxa, separated by commas. Then click "Visualize in iTOL"; this will take you to a new page that tell you that the tree was generated, how many nodes and branches there are.
- 7. Under "What now?" click the link "the main display page." This will take you to your interactive tree. In "Basic controls" click the link next to "Mode" and choose "Normal mode". Then click "Update tree".

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8. You should see all your organisms' names organized on the tree. Next you want to save the tree so you can include it as a figure in your report. Do this by clicking "Export tree" and saving the tree in the portable network graphics (png) format. When you are shown the link "Your file is ready for download." click it and then save the image.

## Report

You will format your paper the same as a lab report (Appendix B), but you must also compare and contrast your parsimony tree with your sequenced tree in the discussion. You are required to use primary literature for this assignment; *at least* five peer-reviewed papers (in addition to the resources we provide you). You may also use library books or textbooks. These sources will be dependent upon the organisms you choose, and the conclusions you draw from your trees. Below are some questions to help guide your assessment:

- a) What traits of the organisms did you consider when constructing your parsimony tree, and why?
- b) What information would have helped you construct a better parsimony tree?
- c) What does it signify when branches are not bifurcating (i.e., there are polytomies)?
- d) Why might distantly related organisms have very similar traits?
- e) Why might closely related organisms have very dissimilar traits?
- f) Which tree do you believe to be a *better* hypothesis of the evolutionary relationships between your taxa, and why?

#### **List of Organisms**

GROUP	ORGANISM
1 (outgroup)	Euglena gracilis
	Karenia brevis
	Chondrus crispus
	Ahnfeltia plicata
	Laminaria digitata
	Fucus vesiculosus
2	Volvox aureus
	Spirogyra
	Ulva lactuca
	Chara vulgaris
3	Ceratophyllum demersum
	Dendroceros
	Marchantia polymorpha
	Plagiochila asplenioides
	Sphagnum angustifolium
	Polytrichum commune

4	Lycopodiella inundata
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	Selaginella moellendorffii
	Botrychium lunaria
	Dicksonia antarctica
	Adiantum tenerum
	Polystichum acrostichoides
5	Ginkgo biloba
	Cycas circinalis
	Gnetum africanum
	Welwitschia mirabilis
	Taxus baccata
	Abies koreana
6	Amborella trichopoda
	Nymphaea alba
	Magnolia virginiana
	Tillandsia usneoides
	Asparagus aethiopicus
7	Vanilla planifolia
	Ficus microcarpa
	Rafflesia arnoldii
	Cuscuta campestris
	Darlingtonia californica
	Utricularia aurea
8	Carnegiea gigantea
	Pereskia grandifolia
	Aloe vera
	Agave tequilana
	Cocos nucifera
	Zea mays
	Coffea arabica
	Solidago canadensis
9	Mimosa pudica
	Fragaria vesca
	Carica papaya
	Salix alba