

## MORPHOLOGICAL AND MOLECULAR ANALYSIS OF PLANT PHYLOGENY AND DIVERSITY

### LEARNING OBJECTIVES

Upon completing this exercise, students will be able to:

- Apply knowledge of plant anatomy and morphology to the study of plant diversity.
- Name the major taxonomic groupings of plants and describe their features.
- Describe major innovations and patterns of trait evolution in plants.
- Understand phylogenetic relationships among different plant taxa.
- Identify important characters, assign character states, and code characters for phylogenetic analysis.
- Construct, compare, and interpret phylogenetic trees using morphological and molecular data.

Develop a consensus phylogeny based on different data.

### SUMMARY

Evolutionary biologists use morphological, anatomical, ecological, genetic, and other forms of data in phylogenetic analyses to test hypotheses that investigate different biological questions. Because each type of data has its own, assumptions, strengths, and limitations, it is important to recognize these features of the data and take them into consideration when interpreting results.

This laboratory module explores plant diversity and evolution through phylogenetic analyses using 1) plant morphological and anatomical data and 2) molecular data. The combination of analyses using different forms of data will promote deeper understanding of important evolutionary innovations, patterns of diversity, and major trends in plant evolution. In this exercise, you will collect morphological data to construct an initial phylogeny of the study organisms that describes broad patterns of trait evolution among taxa. Next, you will compare your data with four molecular phylogenies for a more fine-grained analysis of relationships among taxa. You will then use the data from the different data sets to develop a consensus phylogeny to describe relationships among taxa and patterns of trait evolution. Comparisons of phylogenies also provides an opportunity for critical analysis of phylogenetic data interpretation

## PROCEDURE

1. Prior to lab, review the characteristics of different plant groups (bryophytes, seedless vascular plants, gymnosperms, and angiosperms) described in your lab manual and textbook.
2. Working in small groups, rotate among the stations on the different tables and observe the fresh material, living plants, preserved specimens, and microscope slides. Using the list of characters and character states provided in Table 1, identify the characters and score the character states for what best represents the specimens at each station.
3. Make note of the traits that are 1) similar among the plant specimens at the different stations and 2) different among the plant specimens at the different stations.
4. Record the character states in Table 2. Make note of some of the genera and species names on the specimens at the different stations.
5. After recording the character states for the different stations, make a prediction about what the phylogenetic relationships will be among the taxa at the different stations. Draw your predicted phylogeny in the space below for Figure 1.
6. Next, use your data matrix to generate a phylogenetic tree using Mesquite that has each station as a separate taxon in your analysis. Indicate the character state changes on your phylogeny. This is your **morphological tree**. After looking at your data matrix, can you identify the plant groups represented at the different stations?
7. Once you have drawn the morphological tree, you will be provided data to conduct a molecular analysis using either Mesquite or the MABL website. Generate a the most parsimonious phylogeny or phylogenies using these data.
8. Indicate which species on the molecular trees are from the different plant taxa represented at the stations (i.e., bryophytes, seedless vascular plants, gymnosperms, monocots, and dicots). You may need to look this up online or in your text.
9. Next, map your morphological trait character changes would occur on the appropriate clades. (This can be done by hand or on a computer.)
10. How do the morphological and molecular trees compare? Do they show the same patterns of relationships among taxa? Do they show the same patterns of character evolution? Explain. Do the molecular trees all show the same patterns of relationships among taxa? What is similar? Different? What do you think this means?
11. How should you resolve the differences among phylogenies? How should

you come to consensus?

12. Are the different plant groups (bryophytes, seedless vascular plants, gymnosperms, angiosperms) monophyletic? How can you tell? What does this indicate?

**Table 1.** Characters and character states for plant phylogenetic analysis.

Character	Character states (Coding)
Body	0: unicellular and multicellular 1: multicellular adults only
Leaves with veins	0: absent 1: present
Pollen production	0: absent 1: present
Woody tissues	0: absent 1: present
Xylem present in stem	0: no 1: yes
Xylem present in root	0: no 1: yes
Seed production	0: no 1: yes
Fruit production	0: no 1: yes
Flower	0: no flowers 1: yes, flower parts in multiples of 4 or 5 2: yes, flower parts in multiples of 3
Woody female cones produced	0: no 1: yes
Stem	0: small or non existent in some species 1: present, obvious, may or may not branch

**Table 2.** Data matrix of character states for outgroup and five ingroup taxa.

Character	Algae (outgroup)	Station A	Station B	Station C	Station D	Station E
Body						
Leaves with veins						
Pollen production						
Woody tissues						
Xylem present in stem						
Xylem present in root						
Seed production						
Fruit production						
Flower						
Woody female cones produced						
Stem						

**Figure 1.** Predicted phylogeny of plant groups at different stations based on morphological traits.

*(Draw your tree in the space below.)*