

● KATHRYN M. FLINN

ABSTRACT

In this classroom activity, students build a phylogeny for woody plant species based on the morphology of their twigs. Using any available twigs, students can practice the process of cladistics to test evolutionary hypotheses for real organisms. They identify homologous characters, determine polarity through outgroup comparison, and construct a parsimonious tree based on synapomorphies (shared derived characters). This activity efficiently demonstrates many systematics concepts, including homology, homoplasy (convergence and reversal), polarity, synapomorphy, symplesiomorphy, autapomorphy, polytomy, and parsimony. It also engages students in inquiry, promotes student collaboration, raises awareness of plant structure, and exposes students to the diversity of common local trees.

Key Words: Phylogeny; systematics; cladistics; morphology; homology; homoplasy; polarity; synapomorphy; polytomy; parsimony.

Understanding how biologists learn about the pattern and process of evolution is a fundamental component of biology curricula. Unfortunately, the new concepts, the wealth of terminology, and the specialized methods of systematics can prove difficult. This activity provides an effective way to develop an understanding of systematics, by giving students the experience of building a phylogeny. It can follow a reading and/or lecture that briefly introduces systematics concepts (e.g., Freeman & Herron, 2007, pp. 111–119; Freeman et al., 2014, pp. 506–510). Primed with these ideas, students can then go through the entire process of testing evolutionary hypotheses based on organismal morphology. This generates an informed discussion of the implications of character choice, the basis of cladistics, and the principle of parsimony. With somewhat different emphasis, such a plan has proved useful in both introductions to evolutionary biology and more advanced systematics courses – in the context of comparisons between phenetics and cladistics, for example. The activity could also be simplified for the high school level by focusing on the concepts of

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analogous characters, shared derived characters, and, perhaps, convergence and reversal. Because it requires only whatever twigs are at hand and one 50- or 80-minute classroom session, this activity offers a very efficient method for involving students in the science of systematics.

○ Preparation

Collect twigs of five woody plant species, enough for each group of two to four students to have one of each species. Any available species will work. Many field guides have simple winter keys for identifying twigs (e.g., Cope et al., 2002; it is not actually necessary to identify the twigs to complete the activity, but students may be curious). Clip terminal twigs to ~30 cm to allow use of terminal bud characters. One species should appear different enough to serve as an outgroup; in eastern North America, *Rhus typhina* (staghorn sumac) works well. The activity also works well when two of the species are closely related, such as *Acer negundo* (box elder) and *A. saccharum* (sugar maple). Twigs can be collected during the dormant season and stored for use at any time of year. Fresh twigs work best for characters like the wintergreen odor of *Betula lenta* (sweet birch) and the bitter almond odor of *Prunus serotina* (black cherry), but twigs refrigerated in plastic bags will keep for years. Use a different color of lab tape to mark the twigs of each species, leaving the outgroup unmarked. Revealing the identity of the twigs at the end of the activity helps students use only observable characters to build the phylogeny and allows them to try identifying the twigs themselves.

Provide students a reference on twig anatomy, showing features such as arrangement (alternate or opposite), lenticels, leaf scars, pith, and bud scales. Many references have relevant definitions and figures (e.g., Core & Ammons, 1958; Harlow, 1959); I especially recommend the diagrams freely available online from Kessler and Schoenike (1998).

You may wish to prepare a handout or slides to guide students through steps 3–4 below. A handout with a worked example such as in Tables 1–5 and Figure 1 is probably most time-efficient and affords student groups more independence, but showing each step on slides or on the chalkboard would allow more teacher–student interaction. Especially for high school students, you may want to provide a handout with a worked example and go through each step of the example together before students begin to work on their own.

○ Activity

1. Have students form groups of two to four, present them with the twigs (Figure 2) and the twig anatomy reference, and explain that they will build a phylogeny by identifying homologous characters, determining polarity through outgroup comparison, and constructing a parsimonious tree based on synapomorphies. Designate the outgroup.

Table 1. Example matrix of twig character states for five woody plants native to eastern North America.

Species	Arrangement	Lenticels	Leaf Scar Wraps around Bud Sides?	Twig Surface	Strong Nonwoody Odor?	Buds White–Pubescent?	Pith	Bud Scales >2?
<i>Acer negundo</i>	Opposite	Prominent	Yes	Smooth	No	Yes	Light	No
<i>A. saccharum</i>	Opposite	Prominent	Yes	Smooth	No	No	Light	Yes
<i>Betula lenta</i>	Alternate	Prominent	No	Smooth	Yes	No	Light	Yes
<i>Prunus serotina</i>	Alternate	Prominent	No	Smooth	Yes	No	Light	Yes
<i>Rhus typhina</i>	Alternate	Prominent	Yes	Hairy	No	No	Dark	Yes

Table 2. Matrix with character states coded as 0 = ancestral or 1 = derived, based on comparison with the outgroup, *Rhus typhina*.

Species	Arrangement	Lenticels	Leaf Scar Wraps around Bud Sides?	Twig Surface	Strong Nonwoody Odor?	Buds White–Pubescent?	Pith	Bud Scales >2?
<i>Acer negundo</i>	1	0	0	1	0	1	1	1
<i>A. saccharum</i>	1	0	0	1	0	0	1	0
<i>Betula lenta</i>	0	0	1	1	1	0	1	0
<i>Prunus serotina</i>	0	0	1	1	1	0	1	0
<i>Rhus typhina</i>	0	0	0	0	0	0	0	0

Table 3. Matrix showing the numbers of derived characters shared by each pair of species.

	<i>A. negundo</i>	<i>A. saccharum</i>	<i>B. lenta</i>	<i>P. serotina</i>	<i>R. typhina</i>
<i>Acer negundo</i>		3	2	2	0
<i>A. saccharum</i>			2	2	0
<i>Betula lenta</i>				4	0
<i>Prunus serotina</i>					0
<i>Rhus typhina</i>					

Table 4. Matrix showing the numbers of derived characters shared by each pair of taxa, after combining the species with the highest numbers of shared derived characters into a single taxon.

	<i>A. negundo</i>	<i>A. saccharum</i>	<i>B. lenta–P. serotina</i>	<i>R. typhina</i>
<i>Acer negundo</i>		3	2	0
<i>A. saccharum</i>			2	0
<i>Betula lenta–Prunus serotina</i>				0
<i>Rhus typhina</i>				

Table 5. Matrix showing the numbers of derived characters shared by each pair of taxa, after again combining the taxa with the highest numbers of shared derived characters into a single taxon.

	<i>A. negundo</i> – <i>A. saccharum</i>	<i>B. lenta</i> – <i>P. serotina</i>	<i>R. typhina</i>
<i>Acer negundo</i> – <i>A. saccharum</i>		2	0
<i>Betula lenta</i> – <i>Prunus serotina</i>			0
<i>Rhus typhina</i>			

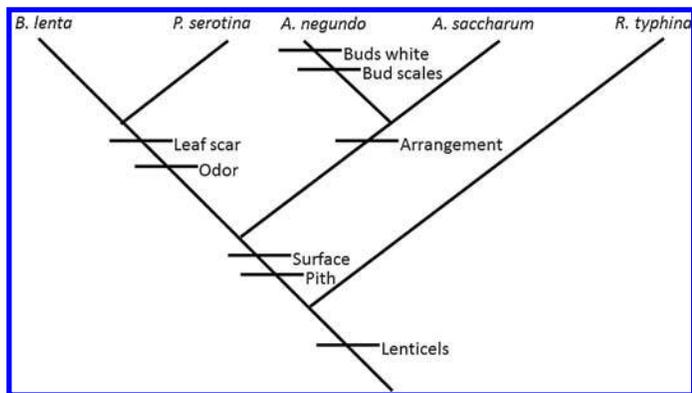


Figure 1. Phylogeny of five woody plants native to eastern North America, resulting from the analysis in Tables 1–5, with character-state changes mapped onto the tree. Characters are as in Table 1.

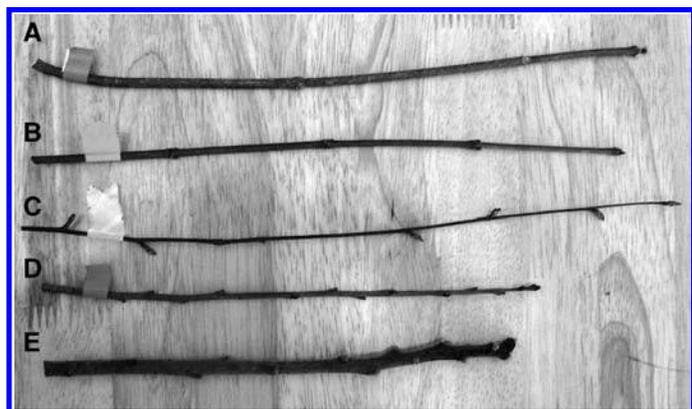


Figure 2. Twigs used in this activity. From top to bottom: (A) *Acer negundo*, (B) *A. saccharum*, (C) *Betula lenta*, (D) *Prunus serotina*, and (E) *Rhus typhina*.

character-state changes. Make sure the class reaches a consensus on the character states. Students may need help polarizing characters and recognizing synapomorphies. Once species are combined into taxa (Tables 4 and 5), it is possible that one member of a taxon may have a synapomorphy with another species when the other member of the taxon does not; this can be counted as half a synapomorphy. Ties in the numbers of derived characters a taxon shares with two other taxa will create polytomies.

- Once students have built a phylogeny, they can work in their groups to analyze it by listing the synapomorphies, symplesiomorphies, and autapomorphies in the form: “[Odor] is a [synapomorphy] for species [red and yellow].” They should also be able to identify all of the clades and any examples of homoplasy. Or, to simplify and provide more guidance, you may wish to lead the class in identifying the shared derived characters and clades.

○ Discussion

After having students offer their examples of synapomorphies, symplesiomorphies, autapomorphies, clades, and homoplasies, questions like these could take the discussion in a number of directions.

- What is the evidence that the character states you chose were homologous?
- How might choosing a different outgroup affect the phylogeny?
- Which characters were informative and which were not informative? Why and why not?
- How might symplesiomorphies and autapomorphies be useful in other contexts?
- Why were only synapomorphies used to build the tree?
- Were any species indistinguishable, based on the characters you used? How could this be remedied?
- If polytomies occurred, how could they be resolved?
- If homoplasy occurred, can you know whether it involved convergence or reversal?
- Is your phylogeny the most parsimonious? How do you know?
- Are any other phylogenies equally parsimonious? Students could map character-state changes onto alternative phylogenies to compare.

○ Acknowledgments

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References

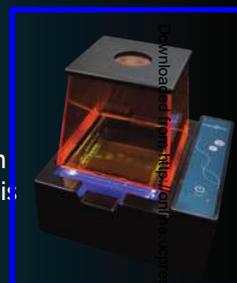
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