Instructor's 5 Step Resource:

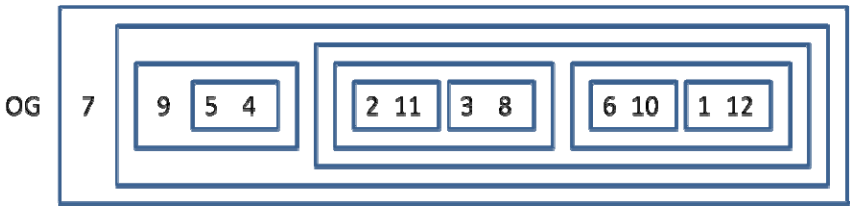
Step 1: Data Matrix

	A	B	C	D	E	F	G	H	I	J	K	L	M
Species 1	1	1	0	1	0	0	1	0	1	0	1	0	0
Species 2	1	0	0	0	0	1	1	0	1	0	0	0	2
Species 3	1	0	2	0	1	0	1	0	1	0	1	0	2
Species 4	1	0	0	0	0	0	1	1	1	0	0	0	1
Species 5	1	0	0	0	0	0	0	1	1	0	0	0	1
Species 6	1	2	0	0	0	0	1	0	1	0	1	1	0
Species 7	0	0	0	0	0	0	0	0	1	0	0	0	0
Species 8	1	0	1	0	1	0	1	0	1	0	1	0	2
Species 9	1	0	0	0	0	0	0	0	1	0	0	0	1
Species 10	1	2	1	0	0	0	1	0	1	0	1	1	0
Species 11	1	0	0	0	0	1	1	0	1	1	0	0	2
Species 12	1	1	0	0	0	0	1	0	1	0	1	0	0
Out Group	0	0	0	0	0	0	0	0	0	0	0	0	0

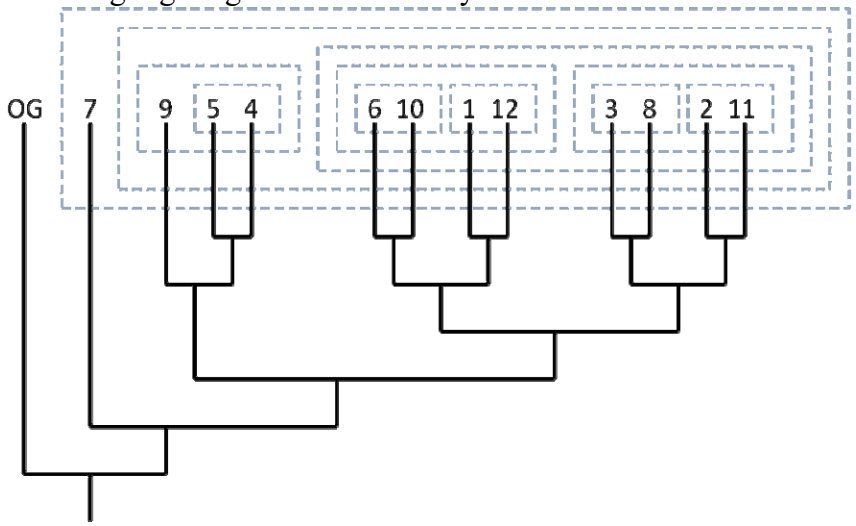
Step 2: Reorganize Data Matrix

	I	A	G	K	H	F	E	L	J	D	M	C	B
Species 12	1	1	1	1	0	0	0	0	0	0	0	0	1
Species 1	1	1	1	1	0	0	0	0	0	1	0	0	1
Species 10	1	1	1	1	0	0	0	1	0	0	0	1	2
Species 6	1	1	1	1	0	0	0	1	0	0	0	0	2
Species 8	1	1	1	1	0	0	1	0	0	0	2	1	0
Species 3	1	1	1	1	0	0	1	0	0	0	2	2	0
Species 11	1	1	1	0	0	1	0	0	1	0	2	0	0
Species 2	1	1	1	0	0	1	0	0	0	0	2	0	0
Species 4	1	1	1	0	1	0	0	0	0	0	1	0	0
Species 5	1	1	0	0	1	0	0	0	0	0	1	0	0
Species 9	1	1	0	0	0	0	0	0	0	0	1	0	0
Species 7	1	0	0	0	0	0	0	0	0	0	0	0	0
Out Group	0	0	0	0	0	0	0	0	0	0	0	0	0

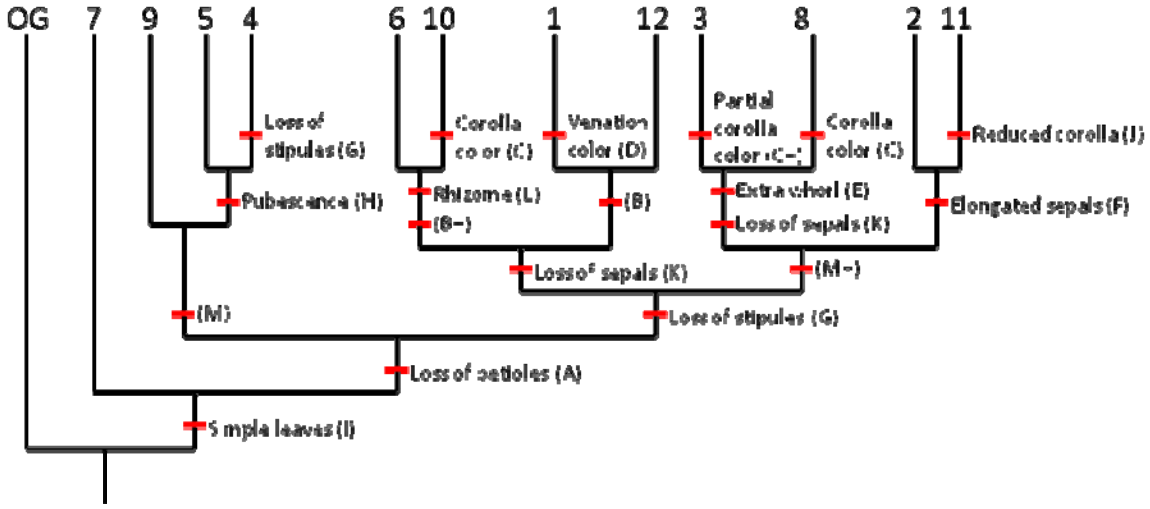
Step 3: Assist students with splitting the species into monophyletic groups by focusing on apomorphies. Isolate each species (or sister group) into its own circle with the most related nested in the most circles.



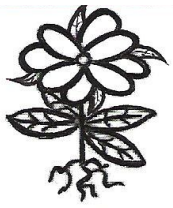
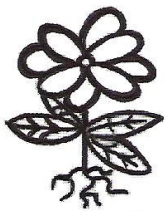
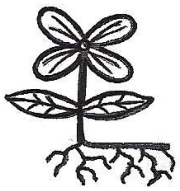
Step 4: Once the clades have been identified from the evidence provided, students can begin drawing branches and highlighting common ancestry.

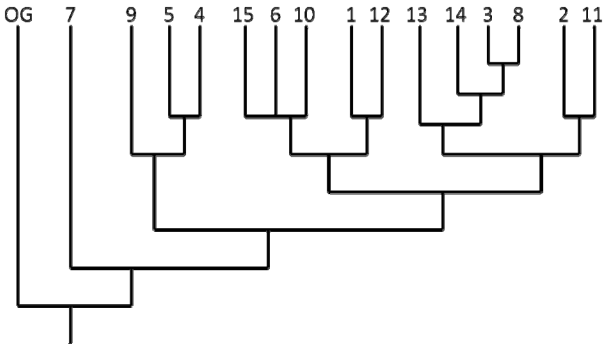


Step 5: By adding character states and rooting the tree, students will have built a phylogeny from the data they used.

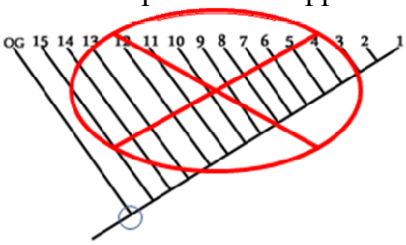


**Note: This activity has some character states (e.g., loss of stipules and corolla color) that evolved more than once. Also, it's perfectly fine if the species are in a different order as long as the groupings are the same. For more information about this – see a tree-reading lesson.
*(Optional adaptation: Include these extinct Pseudocot species from the fossil record when constructing the Pseudocot phylogeny ***Note: if you are using fossils in your phylogeny, then they will not have DNA data. This is a good discussion point for class – why we don't or have difficulties obtaining DNA evidence from extinct species. You can have students add in morphological evidence to help these species fit in very easily.):*

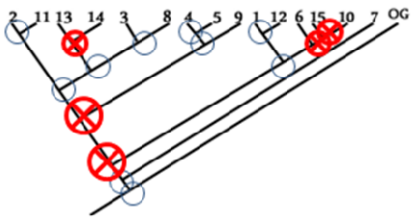
Extinct	Extinct	Extinct
		
Species 13	Species 14	Species 15



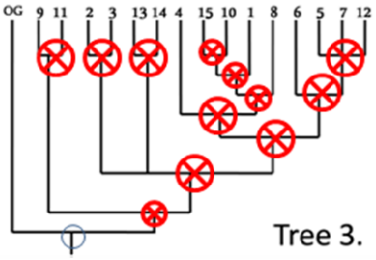
Here are examples comparing 3 different phylogenies to the tree generated *including fossils*. These examples show supported nodes circled and non-supported nodes crossed out.



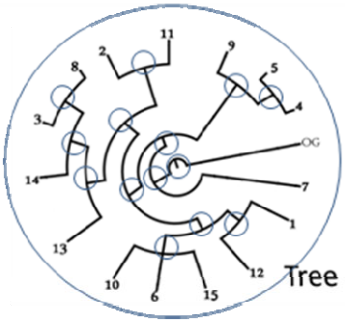
Tree 1.



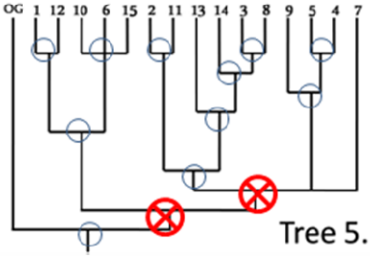
Tree 2.



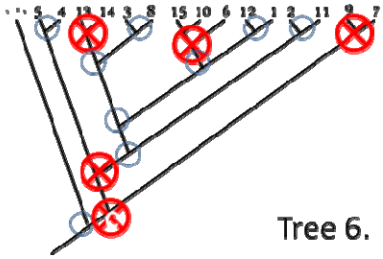
Tree 3.



Tree 4.



Tree 5.



Tree 6.