SYSTEMATICS, TAXONOMY, AND PHYLOGENY

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INTRODUCTION

Students of zoology (including ornithology) are often frustrated as the classification of organisms changes. They often encounter major classification differences between texts, between checklists, or have difficulty researching organisms that have undergone name changes (lumping of genera, etc.). These changes are generally based on a change in the understanding of the evolutionary relationships among individuals. New information and new methods of reconstructing evolutionary histories often yield different taxonomic groups or perhaps the same taxonomic groups with different members. This exercise examines how these changes come about, and why.

LEARNING OBJECTIVES

The student will:

- differentiate between systematics, taxonomy, and phylogeny
- demonstrate an understanding of the hierarchical system of nomenclature (and basic conventions of taxonomy)
- develop a basic understanding of cladistics, including the importance of synapomorphies, monophyletic groups, and character mapping

MATERIALS

4 screws (or other pieces of hardware) as taxa of interest
2 different screws (or other pieces of hardware) as outgroups

PROCEDURE

Exercise 1. Determination of characters and character states.

To investigate the relationships of organisms, we begin by looking at characters (often these are morphological traits, internal or external; protein bands on electrophoresis gels; chromosome banding patterns; DNA base pair sequences; or protein amino acid sequences). Often traits are investigated by their presence or absence (e.g., birds have feathers, mammals don't).

You will begin with 4 screws obtained from your instructor. Looking at these screws for differences in morphology (shape), create a list of potential characters. Then go back to each screw and code it for the presence of that character (+) or the absence of that character (-).

"Species"											

Exercise 2. Traditional systematics.

Systematics refers to the organizing of organisms (classification). While some classification schemes are based on shared behavior or ecology, generally zoologists attempt to have classification systems reflect the *phylogeny* (evolutionary history) of organisms. After biologists have examined a number of characters, they attempt to classify organisms based on their similarities and/or differences of many different characters. The traditional method of classification looks at the overall similarities between organisms. You may decide that some similarities are more important and others are less important.

Based on the similarities you have found, you should create a system of *taxonomy* (naming of organisms) to describe the relationships you have found. You should group the things that appear to be the most similar together, perhaps in the same genus. Then if there is another organism that seems closer to those than the others, you should put all three in a single family. Continue to work your way up through the classification scheme.

Your classification system should include all of the levels of classification we have studied in this class (Kingdom, Phylum, Class, Order, Family, Genus, and Species). Each species should be assigned to each of these levels. Note: you will have 4 species, but may only have 2 or 3 genera. As you move up in classification you will have the same or fewer taxa at each level (i.e., 2-3 genera, 2-3 families, 1-2 orders, etc.).

Don't forget to capitalize and underline (*italicize*) as appropriate.

Sample

Species: Blackpoll Warbler

Kingdom: Animalia

Phylum: Chordata

Class(es):   Aves

Order(s):   Passeriformes

Families: Emberizidae

Genera: <u>Dendroica</u>

Species: <u>D.</u> <u>striata</u>

Notes:
   Orders end in -iformes
   Families end in -idae
   Generally genus and species names are of the same gender (either masculine or feminine)
   e.g., *Geothlypis trichas* or *Certhia americana*

Exercise 3. Cladistic classification.

When trying to determine the evolutionary history of organisms, all characters are not equal. Cladistics is a relatively new method of determining evolutionary relationships (phylogenies) based on derived characters (*apomorphies*). To examine apomorphies, we must know the ancestral or primitive character state (known as a *plesiomorphy*). This is generally done by using an *outgroup*, an organism that is closely related to the taxa of interest, but is more primitive than they are.

At this point you should come get your first outgroup. It is a fossil form that existed before your taxa appear to have evolved. You should code the character states of the outgroup on the chart on the previous page. You may also need to add characters.

Now we can look at derived characters. Shared derived characters are known as *synapomorphies* and should be used to join taxa within a group. Shared ancestral or primitive characters are *symplesiomorphies* and are not of interest in this system. (Hint: go through the chart on the previous page and circle the apomorphies).

Based on the synapomorphies you have determined,

(1) you should create a tree (diagram) of the relationships among the organisms being studied (the screws)—grouping those that share derived characters together. You should give me the shortest possible tree (the one that is most *parsimonious*–contains the fewest steps).

In addition, you should map the characters onto your tree. Where do they arrive? Are there any reversals (places where you revert back to the ancestral condition)?

To aid in this process, I have provided the 15 possible cladograms for 4 organisms. After mapping the characters onto each of these cladograms, you can count the number of steps it takes for the relationship in each cladogram and determine which tree is most parsimonious.

(2) you should use this diagram to create a classification system to describe the relationships you have found (as above). Also write the synapomorphy(s) that combines the members of a group beside the name you give to that group. *Compare this classification system to the one determined in exercise two. Is it the same? Are there any differences?*

Exercise 4. Choice of Outgroup.

Instead of the outgroup in exercise 3, you decide to use a newly discovered fossil taxa as your outgroup for this analysis. You will now investigate how the choice of outgroup affects your classification system.

Using a different outgroup may change some of your designations of primitive and derived character states. First, you will need to obtain your new organism from your instructor (and get rid of outgroup 1, you won't need it again). Now, you should code the character states of this new outgroup on the chart on page 1. You may also need to add characters. Then you can look at

derived characters. (Hint: go through the chart on the previous page and either make the apomorphies bold or shade in cells containing the apomorphies).

Based on the synapomorphies you have identified using outgroup 2,

(1) you should create a tree of the relationships among the organisms being studied (the screws)— grouping those that share derived characters together. You should draw the shortest possible tree (the one that is most *parsimonious*). Remember to map the characters onto your tree.

(2) you should use this diagram to create a classification system to describe the relationships you have found (as above).

How did the use of your new outgroup affect your tree and your classification system? Did any of the relationships change?

Note: At the end of the exercise, you will need to have 3 classification systems, two cladograms that include the characters you used, and answers to the italicized questions.
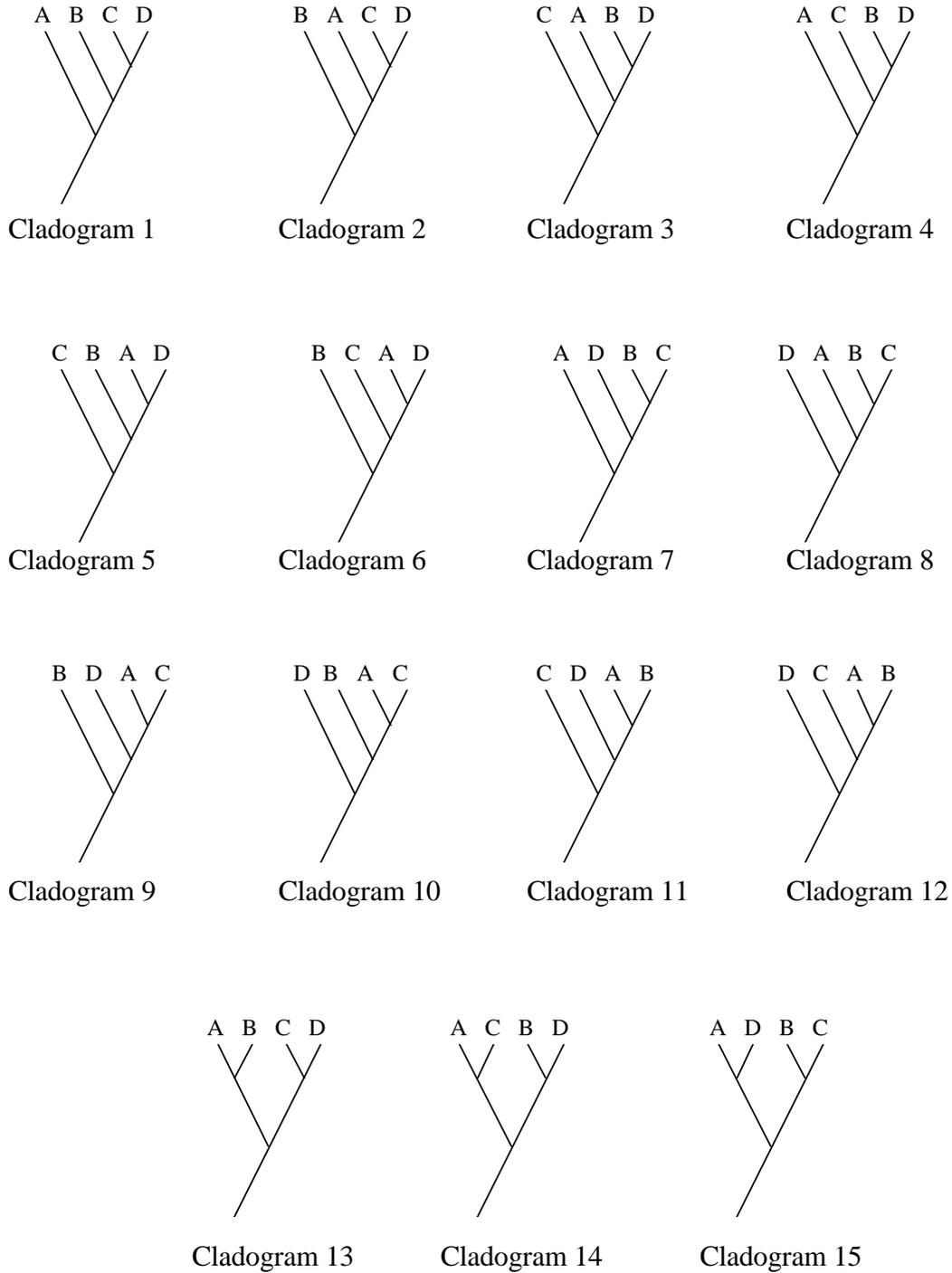
A B C D

Cladogram 1

B A C D

Cladogram 2

C A B D

Cladogram 3

A C B D

Cladogram 4

C B A D

Cladogram 5

B C A D

Cladogram 6

A D B C

Cladogram 7

D A B C

Cladogram 8

B D A C

Cladogram 9

D B A C

Cladogram 10

C D A B

Cladogram 11

D C A B

Cladogram 12

A B C D

Cladogram 13

A C B D

Cladogram 14

A D B C

Cladogram 15

Figure 1. Possible cladograms of four organisms.

CLADISTICS OVERHEADS

The following pages are intended to be used as overhead masters. These may be used when introducing students to cladistics and explaining how the lab will be run. I generally begin with a group of 3 organisms and an outgroup that are different from what we are studying (for example a baseball, tennis ball and football might be good).
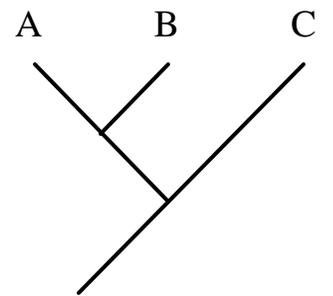
"Species"

A   B   C

Cladogram X

B   C   A

Cladogram Y

A   B   C
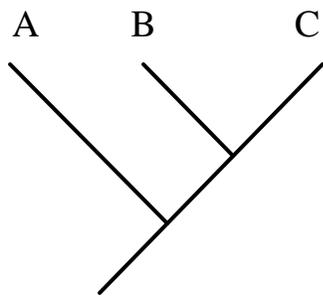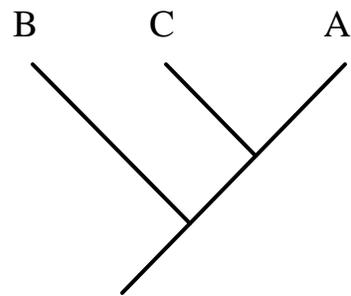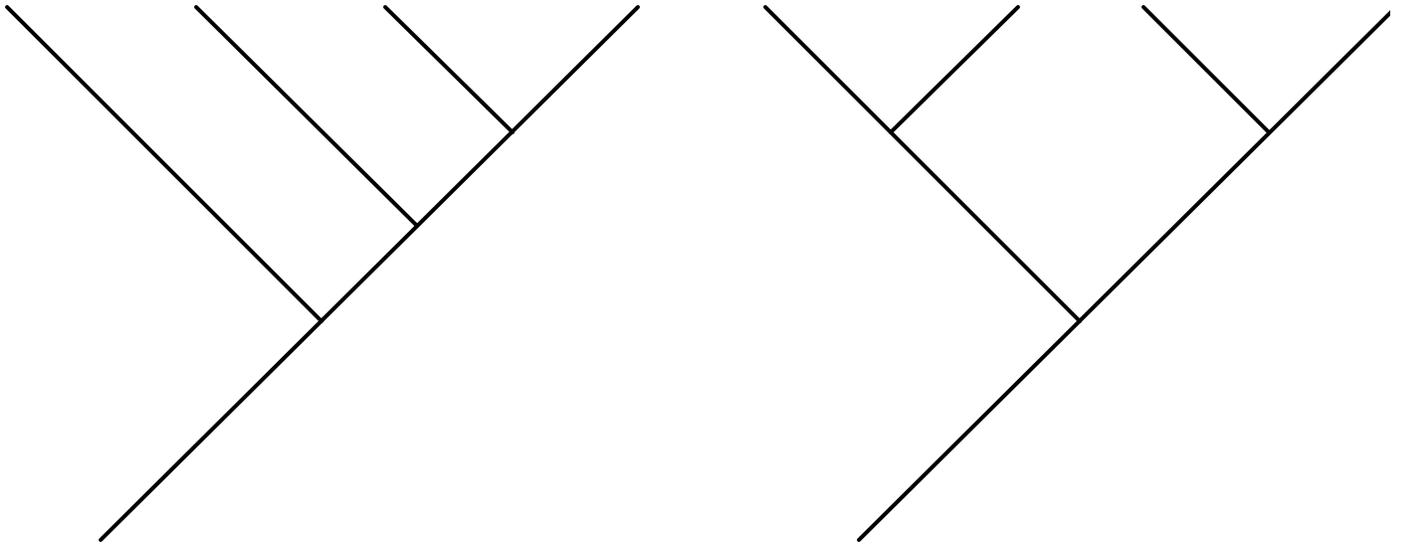
Cladogram Z

"Organism:"

Kingdom:

Phylum:

Class:

Order(s):

Families:

Genera:

Species:

Potential cladograms for the classification of 4 organisms