# **Species Identification and Systematics**

## Linda T. Collins and Charles H. Nelson

Department of Biological and Environmental Sciences University of Tennessee at Chattanooga Chattanooga, Tennessee 37403 (423) 755-4797 lcollins@utcvm.utc.edu

An important objective for biologists is to determine the phylogenetic relationships among species. This exercise is designed to introduce introductory biology students to the study of systematics. First, students learn how to use a dichotomous key to identify tree cones and fruits. The key to 30 cones and fruits is written so students can easily identify at least 10 specimens in less than one hour. The cones and fruits were chosen to be sufficiently sturdy to endure use by students for many years, and they are substantially different from each other to allow easy use of alternative choices in the key. The language in the key does not require a background in botany.

Second, students use characteristics of the cones and fruits to design a phylogram. A phylogram reveals which species descended from other species or, alternatively, which species share immediate common ancestors. The construction of a phylogram is based on a fundamental assumption: when two species share similar characteristics, the characteristics are acquired from a similar characteristic in a common ancestor. If the assumption is correct, then it is possible to state that there is a phylogenetic relationship between the two species. Similar characteristics in two species that are inherited from a common ancestor are homologous. Students determine the numbers of homologous characteristics in common in five tree species and construct a phylogram to organize the species on the basis of their evolutionary relationships.

#### Species Identification. Using a Dichotomous Key to Identify Tree Species

Use the dichotomous key to identify ten cones and fruits.

#### KEY TO TREE CONES AND FRUITS

| 1. | Cone with overlapping scales                                |  |
|----|---|--|
| 1. | Fruit, not a cone. If cone-like lacking overlapping scales. |  |
|    | 2. Cone scales more or less thickened (pines)               |  |
|    | 2. Cone scales almost paper thin (spruces and hemlocks      |  |
| 3. | Cones at least 4" long                                      |  |
| 3. | Cones less than 4" long                                     | 4  |
|    | 4. Cones unsymmetrical (lopsided), with stout prickles      |  |
|    | 4. Cones with slender prickles                              | Virginia or scrub pine Pinus virginiana  |
| 5. | Cones less than 1" long                                     | Eastern hemlock <i>Tsuga canadensis</i>  |
| 5. | Cones 1" long or more                                       | Red spruce <i>Picea rubens</i>           |
|    | 6. Fruit shaped like a bean pod                             | 7  |
|    | 6. Fruit not shaped like a bean pod                         |  |
| 7. | Pod about 2" to 3" in length, very straight                 | Eastern redbud Cersis canadensis         |
| 7. | Pod 8" or more in length                                    | Honeylocust <i>Gleditsia triacanthos</i> |
|    | 8. Fruit with a thin wing                                   | 9  |
|    | 8. Fruit not winged   | 15                                       |

| 9.<br>9. | <ul> <li>Fruit paired (double), the two parts united at the base (maples</li> <li>Fruit single, not in pairs</li></ul>  |   |
|----------|---|---|
|          | Fruit wings forming an angle greater than 90 <sup>o</sup> , nearly straight from end to end   |   |
| 11.      | Fruit wings forming an angle less than 90 <sup>o</sup><br>12. Fruit V-shaped  | Boxelder Acer negundo                         |
| 13       | 12. Fruit U-shaped<br>Wing encircling the seed cavity   | American elm <i>Ulmus americana</i>           |
|          | Wing terminal (at end of seed cavity)<br>14. Seed cavity 4-angled in cross section  |   |
|          | 14. Seed cavity flat in cross section   | Green ash Fraxinus pennsylvanica              |
|          | Fruit made of many small units packed tightly together or bo<br>Fruit solitary  |   |
|          | <ul><li>16. Fruit cone-shaped</li><li>16. Fruit not cone-shaped</li></ul>   | Magnolia <i>Magnolia grandiflora</i><br>17    |
| 17.      | Fruits borne in a cluster, bright red when fresh or dark red or   | black when dry                                |
| 17       |   | Dogwood Cornus florida                        |
| 17.      | <ul> <li>Fruit round, golf ball size or smaller</li> <li>18. Fruit round and hard with sharp projections</li> <li>18. Fruit round, lacking sharp projections</li></ul>  | Sweetgum <i>Liquidambar styraciflua</i>       |
|          | Fruit an acorn (oaks)   |   |
| 19.      | Fruit not an acorn  | Willow oak <i>Quercus phellos</i>             |
|          | Cup conspicuously fringed at its edge<br>Cup not fringed  | Bur oak Quercus macrocarpa                    |
| 21,      | <ul><li>22. Cup deep, almost covering nut</li><li>22. Cup shallow</li></ul>   | Overcup oak <i>Quercus lyrata</i>             |
| 23.      | Nut tawny, cup usually elongate at base, cup scales long and  | relatively thin                               |
| 23       | Nut brown, cup usually round at the base, scales warty in app   |   |
| _0.      | 24. Nut narrow and oblong, thin spike at the tip  |   |
|          | 24. Nut wide, thick spike at the tip  |   |
| 25.      | Nut shiny dark brown with one light spot  | Buckeye Aeculus glabra                        |
| 25.      | <ul> <li>Nut not shiny dark brown with one light spot</li> <li>26. Husk covering nut without seams</li> <li>26. Husk covering nut splits along definite seams</li></ul> | Black walnut <i>Juglans nigra</i><br>27<br>28 |
| 28.      | Nut rounded in cross section, more than 2" in diameter, spine   | e of husk branched, needle sharp              |
| 28.      | Nut triangular in cross section, less than 1" long, spines of hu  | isk weak, not branched                        |
| 29       | Husk winged at seams  |   |
|          | Husk not winged at seams the smooth or slightly ridged along seam   |   |
| -        |   |   |

#### Systematics. Construction of a Phylogram

To construct a phylogram the systematist first observes the structural differences and similarities that exist among organisms. It should be noted that such an analysis is based on a fundamental assumption: when two species are found to share similar characteristics it is assumed that these similar characteristics were acquired from a similar characteristic in a common ancestor. If this assumption is correct, then it is possible to state that there is a phylogenetic relationship between these two species. Similar characteristics in two species that are inherited from a common ancestor are spoken of as being homologous. A systematist determines the organisms with the largest number of homologous characteristics in common and then constructs a phylogram to organize the species into larger groupings. Suppose you have to construct a phylogram to represent the ancestor descendent relationships of five vertebrate animals found in the surrounding area. First, you list characteristics that indicate structural similarities and differences that exist for these organisms. Next, you indicate with a '+' if the organism possesses the characteristic and a '0' if it does not possess the characteristic.

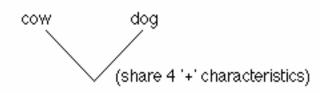
| Characteristic              | Bass | Lizard | Duck | Cow | Dog |
|-----------------------------|------|--------|------|-----|-----|
| Gives birth to living young | 0    | 0      | 0    | +   | +   |
| Walking legs present        | 0    | +      | +    | +   | +   |
| Body with hair              | 0    | 0      | 0    | +   | +   |
| Warm-blooded                | 0    | 0      | +    | +   | +   |

Vertebrate Animals

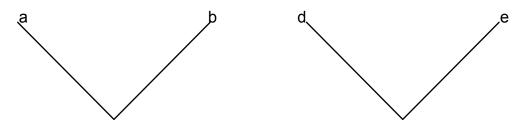
Compare each organism to one another and indicate the number of shared '+' characteristics between each pair.

| Total number of shared '+' characteristics |     |              |     |           |     |            |  |
|--|-----|--------------|-----|-----------|-----|------------|--|
| bass, lizard                               | = 0 | lizard, duck | = 1 | duck, cow | = 2 | cow, dog=4 |  |
| bass, duck                                 | =0  | lizard, cow  | = 1 | duck, dog | = 2 |            |  |
| bass, cow                                  | =0  | lizard, dog  | = 1 |           |     |            |  |
| bass, duck                                 | =0  |              |     |           |     |            |  |

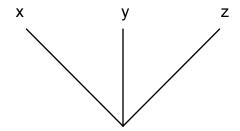
A phylogram is constructed by joining first the most similar pair(s) which, in our example turns out to be the cow and the dog because they share 4 '+' characteristics. This pair is connected by a bifurcating branch:



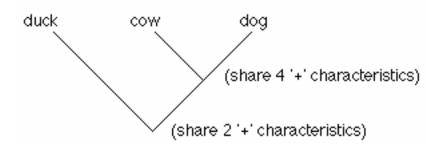
Note that if two pairs of organisms shared the same number of characteristics, for example, hypothetical organisms a, b sharing 4 '+' characteristics and hypothetical organisms d, e sharing 4 '+' characteristics, they would have been simultaneously joined as follows:



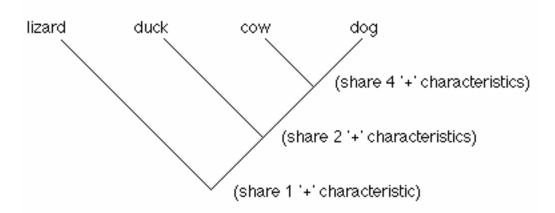
If three organisms x, y, and z are equally similar among themselves, for example, if x, y share 3 '+' characteristics and x, z share 3 '+' characteristics and y, z share 3'+' characteristics, then the three are joined by a trifurcating branch:



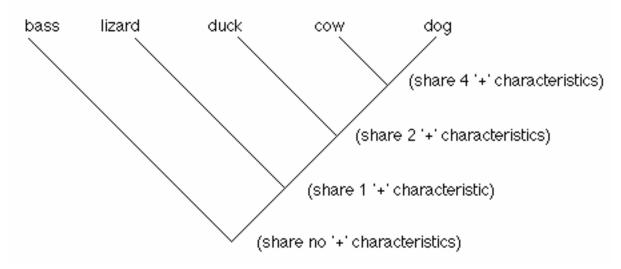
In the next step you <u>compare the unconnected organisms to each other and to the (cow, dog)</u> <u>branch</u>. You measure the number of shared '+' characteristics between an unconnected organism to an established branch such as the (cow, dog) by finding the largest number of shared '+' characteristics between the unconnected organisms and either the cow or the dog. In this step you find that the most similar pair(s) is the duck, (cow, dog) sharing 2 '+' characteristics. You now connect the duck to the (cow, dog) branch by a new bifurcating branch.



Repeat the above step until all organisms are connected by branches. Thus, in the next step you find that the most similar pair is the lizard (duck (cow, dog)) branch sharing 1 '+' characteristic. The lizard is then connected to the (duck (cow, dog)) branch by a new bifurcating branch.



The final step connects the last remaining unconnected organism, the bass, to the (lizard (duck (cow, dog))) branch to form the completed phylogram.



Constructing a phylogram with a large number of organisms or a large number of characters can be quite laborious. Systematists, therefore, rely on computers whenever they can to shorten the effort involved in computation. In the remaining part of this exercise you will construct a phylogram of five tree cones and fruits.

- 1. Examine five fruits and cones carefully. Enter distinguishing traits in the box under "Characteristic".
- 2. Fill in the box by putting a "+" showing that the characteristic is present or a "0" showing that the characteristic is absent.

### 320 Mini Workshops

Tree species

| Characteristic | Species 1 | Species 2 | Species 3 | Species 4 | Species 5 |
|----------------|-----------|-----------|-----------|-----------|-----------|
|                |           |           |           |           |           |
|                |           |           |           |           |           |
|                |           |           |           |           |           |
|                |           |           |           |           |           |
|                |           |           |           |           |           |
|                |           |           |           |           |           |
|                |           |           |           |           |           |

3. Compare the five tree species to one another and indicate the number of '+' characteristics between each pair.

|        | Total number of shared '+' characteristics |        |        |  |  |  |  |  |
|--------|--|--------|--------|--|--|--|--|--|
| 1, 2 = | 2, 3, =                                    | 3, 4 = | 4, 5 = |  |  |  |  |  |
| 1, 3 = | 2, 4 =                                     | 3, 5 = |        |  |  |  |  |  |
| 1,4=   | 2, 5 =                                     |        |        |  |  |  |  |  |
| 1, 5 = |  |        |        |  |  |  |  |  |

4. Using the procedure described above, construct a phylogram for the five tree species.