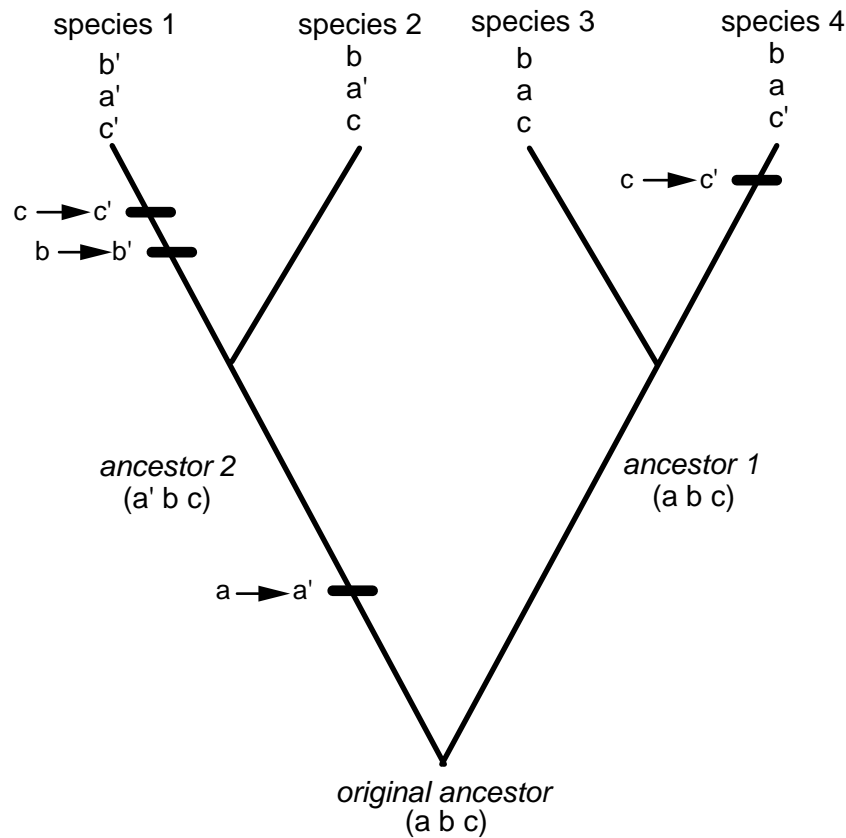


How characters define evolutionary groups for classification

The following tree depicts an imaginary group of four species whose evolutionary history is known to us. In this example, we know that a single species 'original ancestor' split into two species: 'ancestor 1' and 'ancestor 2'. Each of these species, in turn, split into two more daughter species, resulting in the four species on the top of the tree. We have examined three characters: *a*, *b*, and *c* in our four extant species, and we label the derived state of each character with a ' sign (e.g. *a'* is the derived state of *a*). We could theoretically classify the species on the basis of any of these three characters. However, we only obtain a classification that reflects the evolutionary process that created these four species if we use character *a*.



*Character evolution*- The original ancestor had the ancestral form of all three characters. With respect to these characters, ancestor 1 was identical to the original ancestor. However, *a* changed to the derived state *a'* in ancestor 2. Character *b* changed to the derived state *b'* in Species 1. Character *c* evolved the derived state twice: in Species 1 and in Species 4.

*Defining the characters*- To define the characters, you need to specify the groups you are examining. Species 1 and Species 2 share the derived character state *a'*, which they inherited from their most recent common ancestor (ancestor 2). This character is a derived homology

because it is shared by the common ancestor and *all* descendants. Species 2, 3 & 4 share the ancestral state of *b*, which they inherited from their most recent common ancestor (original ancestor). This character is a homology. However, not all descendants of the original ancestor possess this character state (Species 1 possesses the derived state *b'*), and we define *b* as an ancestral homology for Species 2, 3 & 4. Finally, Species 1 and Species 4 share the derived state of *c* (i.e. *c'*). Their most recent common ancestor is the original ancestor, which possesses the ancestral form of *c*. Species 1 and Species 4 *convergently* evolved *c'*.

*Making groups based on these characters*-Now imagine that we did not know the evolutionary history of the characters, and that we wished to classify the four species using one of them. If we used character *c'*, we would group Species 1 and Species 4 together. This would be a *polyphyletic* group, in which we would not be grouping based on recent common ancestry but rather on overall similarity of appearance. If we used character *b* to group Species 2, 3 and 4, we would form a *paraphyletic* group. A paraphyletic group includes the most recent common ancestor, but it excludes some of its descendants. If we used character *a'* to group Species 1 and Species 2, then we would form a *monophyletic* group.

*Systematic methods*- The phenetic school of systematics does not distinguish between types of characters. A pheneticist may use analogies, ancestral homologies, or derived homologies to classify organisms. The cladistic school of systematics proposes to use only derived homologies to classify organisms. Only monophyletic groups are created from groups based on derived homologies. The evolutionary systematics school uses derived or ancestral homologies to classify organisms. This allows for paraphyletic groups, which does not reconstruct the evolutionary tree. Evolutionary systematists try to avoid polyphyletic groups. Many of the major insect groups that we will study were classified based on evolutionary systematic principles. They are often paraphyletic, but systematists are presently reclassifying them based on cladistic principles.