

Surprise! A New Hominin Fossil Changes ... Almost Nothing!

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Overview: This lesson combines the basic principles of constructing and understanding phylogenetic trees and applies these skills to interpreting the impact of new fossil discoveries.

Lesson Concepts: Evolutionary trees are based on the *characters* of the organisms that we are studying.

Branches of the tree are drawn based on changes in those characters in groups of related organisms.

Each branch must include all the descendants of a common ancestor defined as the first to incorporate changes in the characters that define the branch.

Discoveries of new fossils add data to these trees.

Background: Whenever a new fossil is discovered — especially a hominin fossil — headlines often trumpet that the new species completely changes our understanding of human evolution. In reality, such a monumental change in our understanding is quite rare. This activity focuses on a discovery of a hominin fossil that had a few surprising characteristics that did not fit easily into existing models of human evolution. Its name, *Australopithecus garhi*, is derived from the word meaning “surprise” in the native language spoken in the region where it was found. This activity demonstrates that, even with its unexpected combination of traits, *A garhi*, did not change our basic understanding of the history of the hominin lineage, though it did enrich our models.

Grade Range: This document is intended to provide background information and examples for teachers preparing to teach about human evolution, evolutionary modeling, or evolutionary relationships (also called “Classification”) in the middle and high school grades.

Advance Preparation: Review section on evolutionary trees at [Understanding Evolution](#) and [Tree-thinking.org](#).

Time: About 1 hour for each of the analyses; about 4–6 hours for the entire set.

Grouping: Recommended, 2–3 students in a group; maximum 4. There should be no solos.

Materials: Use the information from Table 1 below for the two main analyses.

Use supplemental information for additional analyses.

Use example cladograms for practice or demonstrations.

Table 1: Brief Comparison of *Australopithecus* with early *Homo* fossils

Species	Apes (outgroup)	<i>Australo- pithecus afarensis</i>	<i>Australo- pithecus africanus</i>	<i>Australo- pithecus garhi</i>	Early <i>Homo</i>
Time Range	15–7 MYA	4.4–3.3 MYA	3–2.5 MYA	2.7–2.5 MYA	1.8–0.6 MYA
Feature	Appearance				

Species	Apes (outgroup)	<i>Australo- pithecus afarensis</i>	<i>Australo- pithecus africanus</i>	<i>Australo- pithecus garhi</i>	Early <i>Homo</i>
Molar & premolar size	large	moderate	moderate to large	very large	moderate
Anterior upper premolar	asymmetrical	asymmetrical	more oval	more oval	more oval
Tooth enamel thickness	thin	fairly thick	thick	thick	thick
Dental arcade shape	rectangular	rectangular	rectangular	rectangular	parabolic
Dental arcade shape	parallel	converges backward	diverges posteriorly	diverges	diverges
Anterior depth of palate	shallow	shallow	varies	shallow	deep
Diastema in upper jaw	common	common	absent	present	rare
Anterior pillars on face	yes	no	yes	no	no
Prognathism	strong	strong	usually strong	strong	reduced
Supraorbital structure	Heavy bar	thin bar	thin bar	thin bar	torus
Cranial capacity	400cc	343-500cc	428-ca 515cc	450cc	510-752cc

The outgroup “apes” is used in a general way; these are features of the skull generally associated with the African species of great apes that are considered to have a more recent common ancestor with hominins than other populations. It is possible to include data from fossil apes from Africa, such a *Proconsul* or *Kenyapithecus*.

Features for A garhi based on Asfaw and others, 1999

Asfaw B, White T, Lovejoy O, Latimer B, Simpson S, Suwa G. *Australopithecus garhi*: a new species of early hominid from Ethiopia. *Science* 1999; 284:629-5.

Source: Groves C. 1999. *Australopithecus garhi*: A New-Found Link? *Reports of the National Center for Science Education* 19(3): 10–13. <http://ncse.com/rncse/19/3/australopithecus-garhi-new-found-link>

Some Images of these specimens can be found here:

Fossil Evidence in 3D: <http://www.anth.ucsb.edu/projects/human/>

Smithsonian Institutions 3D Fossil and Artifact Collection: <http://humanorigins.si.edu/evidence/3d-collection>

Bone Clones catalog: <http://www.boneclones.com/catalog-fossil-hominids.htm>

Teacher Background:

Teacher Resources: [Understanding Phylogenies](#)

[Reading, Constructing, and Using Phylogenetic Trees](#)

[A Brief Introduction to Cladistics](#)

[Life On Earth](#)

David Koch Hall of Human Origins at the Smithsonian Institution:

[Main Education Resources Page](#)
[Mystery Skull Interactive Program](#)
[Lesson Plans for Teachers](#)

Teaching Tips:

Students tend to approach biological classification as a “sorting” problem — looking for global similarities in a “like goes with like” approach. The goal here is to introduce students to phylogenetic models that construct tree diagrams based on evolutionary relationships.

The first step in this process is to identify characters (traits) that differ systematically from one set of related organisms to another. The first step is for students to learn to “see” these characters and then to describe the “states” of these characters as ancestral or derived. As a starting point, we choose an *outgroup* — a taxon that is a more distant relative to the specimens we are analyzing than any of these organisms are to each other.

Vocabulary:

apomorphic: a derived state of a character that differs from that of the common ancestor (or outgroup)

cladogram: a phylogenetic tree based on a sequence of changes in character states; all members of a single branch share the same apomorphic states traced to changes that occurred in an ancestral lineage

character: a biologic feature of an organism that appears in (at least) two discernible states in the history of a taxon.

common ancestor: the biologic population that is defined by a specific combination of character states and that passes down this combination to other populations that inherit them from this ancestral population.

hominin: a member of an evolutionary branch that includes bipedal primate descendants of ape ancestors; members are in genera *Homo*, *Australopithecus*, *Parathropus*, *Ardipithecus*, *Sahelanthropus*, *Kenyapithecus*, and *Orrorin*.

monophyletic: describes a branch of a cladogram that is defined by the characters of the common ancestor and includes *all* the taxa that are descended from that ancestral population.

outgroup: a taxon that shares a distant common ancestor with the specimens in any analysis; the outgroup is used to identify the ancestral states for the organisms in the analysis

paraphyletic: describes a branch of a cladogram that mixes organisms from different common ancestors; this arrangement is to be avoided.

parsimony: describes a cladogram that has the fewest number of independently derived characters (those appearing in more than one branch, but *not* inherited from a common ancestor)

pleisomorphic: an ancestral state of a character that is the same as that of the common ancestor (or outgroup)

polarity: describes the character state (usually into “polar” opposites: ancestral and derived)

robusticity: describes a cladogram in which the branches remain unchanged when new characters or new data are added to the analysis

state: refers to the condition (polarity) of a character as being ancestral or derived.

taxon (pl. taxa): a general term for a group of related organisms; a taxon may be a species, a genus or any other level of biologic relationships.

Procedure:

If you or your students are experienced in constructing cladograms, then skip to the analysis of hominin fossil data [here](#).

Analysis 1 — Optional Pre-Analysis Practice

1. Create a new table or open a spreadsheet and make 4 columns with the following headers: Outgroup, Species 1, Species 2, Species 3.
2. Use the data in the table below to create a practice cladogram.
3. The character states of the outgroup will be considered ancestral, and their polarities are indicated with a 0.
4. For each column of characters for the remaining species in the chart, we use the number 0 when it matches the state of the character found in the outgroup, and insert the number 1 when it is different from the outgroup.
5. Now, reshuffle the rows and columns so that you create a step-wise pattern of 0 and 1s.

For example, if your original matrix looks like this:

Character	Outgroup	Species 1	Species 2	Species 3
1	0	0	1	0
2	0	0	1	1
3	0	1	1	1
4	0	0	0	0
5	0	0	1	1

Then your “step-wise” matrix will look like this:

Character	Outgroup	Species 1	Species 3	Species 2
4	0	0	0	0
1	0	0	0	1
2	0	0	1	1
5	0	0	1	1
3	0	1	1	1

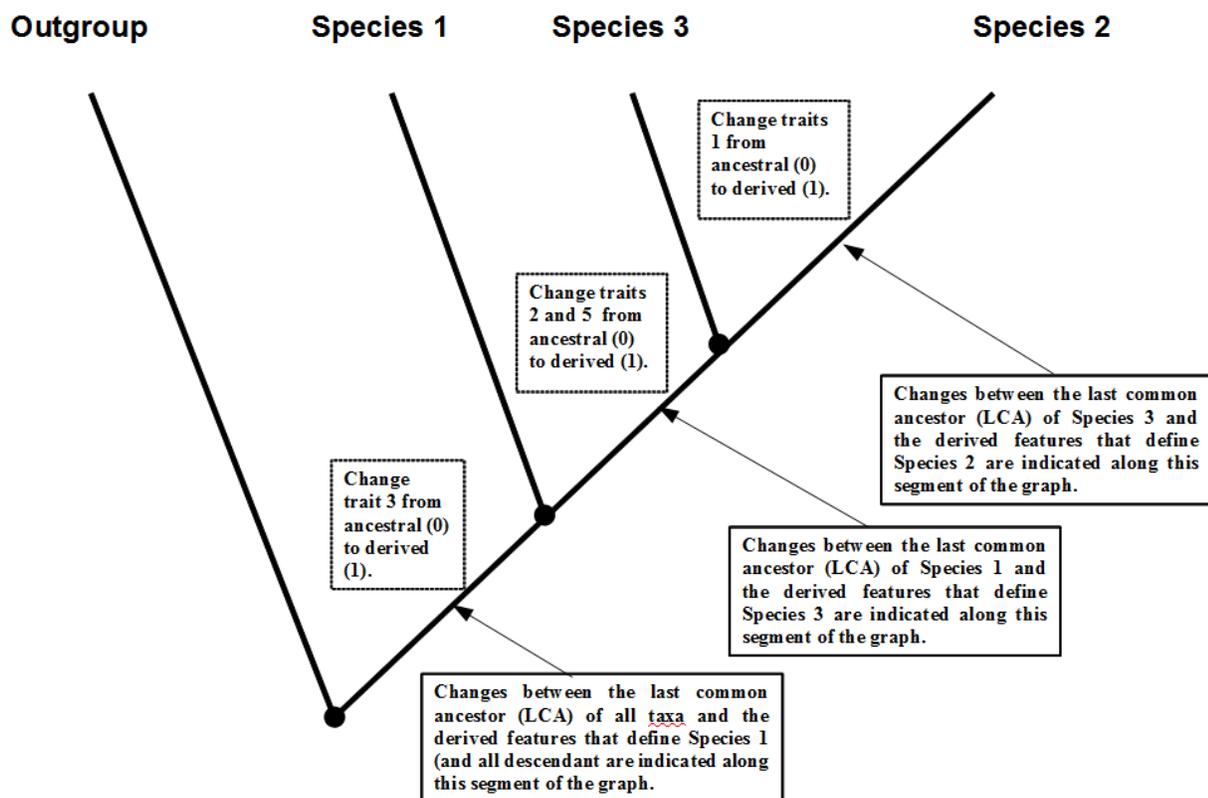
In this case, we have re-ordered the traits so that we can see that Species 1 shows the ancestral state in characters 1, 2, 4, and 5. The species with the next most derived states is Species 3 with ancestral states

only in characters 4 and 1. And finally, Species 2 retains an ancestral state only in character 4.

When we construct the cladogram for these data, each of these “steps” represents a branching off of a new lineage, and these branches form the family tree of the group of species. When we succeed in making a “stairway” pattern like this one, we have identified a sequence of anatomical changes that change once in the sequence and then remain changed for all the taxa that follow in the chart. These are the changes that represent the features of the last common ancestor for every species to the left of the shaded area in the chart.

In a cladogram, this pattern appears as nodes and branches. The nodes indicate changes in at least one character from the ancestral state. The branch should include the taxa that exhibit those changed states.

Each new node describes *additional* changes that define new branches that share the derived state with the prior branches, but add changes in more characters.



If we were to make new discoveries to add to our data, we would add these new specimens to our exiting cladogram. For example,

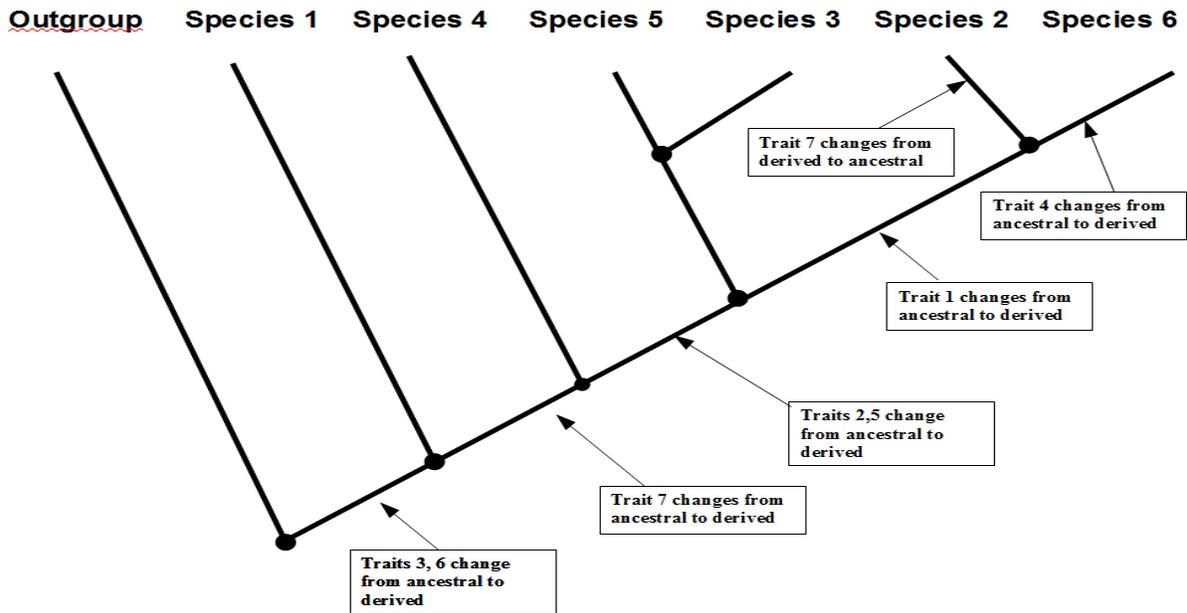
Character	Outgroup	Species 1	Species 2	Species 3	Species 4	Species 5	Species 6
1	0	0	1	0	0	0	1
2	0	0	1	1	0	1	1
3	0	1	1	1	1	1	1
4	0	0	0	0	0	0	1
5	0	0	1	1	0	1	1
6	0	1	1	1	1	1	1
7	0	0	0	1	1	1	1

These additional data need to be moved into the “staircase” pattern.

Character	Outgroup	Species 1	Species 4	Species 5	Species 3	Species 2	Species 6
4	0	0	0	0	0	0	1
1	0	0	0	0	0	1	1
2	0	0	0	1	1	1	1
5	0	0	0	1	1	1	1
7	0	0	1	1	1	0	1
3	0	1	1	1	1	1	1
6	0	1	1	1	1	1	1

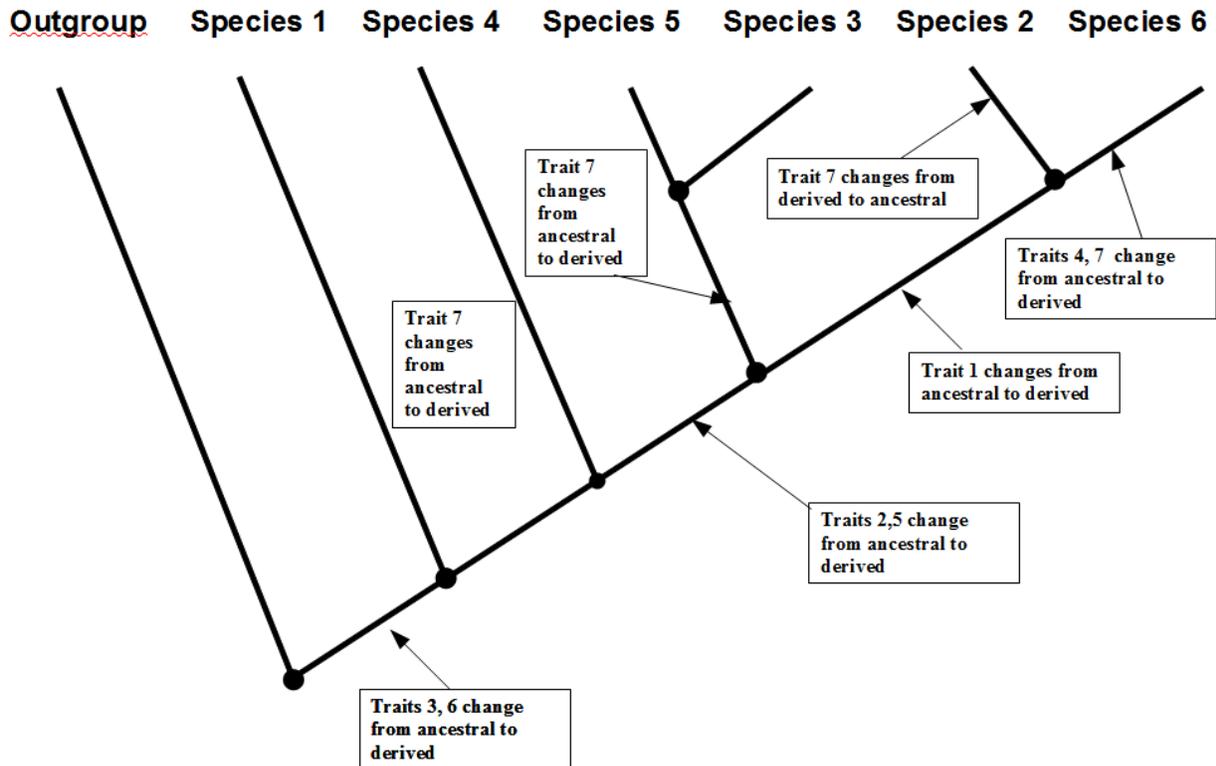
When we add these new data and re-arrange the taxa into our “staircase” pattern, we can make several observations. First, our original cladogram was robust: the additional information does not change the relationships among the taxa that we saw in the original data.

Second, we learned more about the features of species 2: character 7 appears in the ancestral state. In the absence of any additional data, it is more parsimonious to infer that the common ancestor of species 4, 5, 3, 2, and 1 possessed a derived state for character 7, and then it was reversed in species 2. This is because there are only 6 changes in state required for this solution, compared to 7 changes in state if we infer that species 4, 5, 3, and 6 each derived this state individually.



The **cladogram** based on this new table would look like this:

For the purposes of comparison, here is an alternative cladogram that relies on independent derivation of character 7 in separate branches:



We can also calculate a ratio of the number of repeated state changes compared to the total number of state changes; a smaller number is better. In this case, we had 1 reversal to the ancestral condition out of 6 state changes for a ratio of 0.167. In the alternative, we would have had 3 repeats (independent derivations) in character 7 out of 7 total changes, for a ratio of 0.43.

This is a robust cladogram, however, because none of the branches had to be repositioned relative to each other when we added the new data or when we altered the sequence of state changes.

We are free to make these inferences in this case, in part because we have no information on the temporal relationship of these species. In the analysis of hominin fossils that follows, we must take into account the fact that we know that some species — with their unique combinations of character states — appeared either before or after others. In these cases, our shuffling of species is limited because more recently emerged species cannot be ancestral to more remotely emerged species.

Note: This sort of analysis cannot tell us who is ancestral to whom — that is, which of these species is “the ancestor” of which other(s). The arrangement on the cladogram only tells us which species share a more recent common ancestor with each other than they do with others. The most distant (and most inclusive) common ancestor is at the left side of the diagram.

Analysis 2 — Hominin Phylogeny Before Discovery of Australopithecus garhi

1. Create a new table or open a spreadsheet and make 4 columns with the following headers: Apes, *Australopithecus afarensis*, *Australopithecus africanus*, early *Homo*.
 - (a) Use the “Apes” column for outgroup data.
 - (b) Note: the species' data must be arranged in chronological order.
2. Create a table with a polarity of 0 for each of the characters in the outgroup column.
3. For each column of characters for the fossil taxa listed in the chart, insert the number 0 when it matches the state of the character found in the apes, and insert the number 1 when it is different from the outgroup.
4. Now, reshuffle the rows and columns so that you create a step-wise pattern of 0 and 1s.
5. Now draw the cladogram.
6. Finally, save the graphic and proceed to part 2:

Analysis 3 — Hominin Phylogeny After Discovery of Australopithecus garhi

1. Create a new table or open a spreadsheet and make 5 columns with the following headers: Apes, *Australopithecus afarensis*, *Australopithecus garhi*, *Australopithecus africanus*, early *Homo*.
 - (a) Use the “Apes” column for outgroup data.
 - (b) Note: the species' data must be arranged in chronological order.
2. Create a table with a polarity of 0 for each of the characters in this column
3. For each column of characters for the fossil taxa listed in the chart, insert the number 0 when it matches the state of the character found in the apes, and insert the number 1 when it is different from the outgroup.
4. Now, reshuffle the rows and columns so that you create a step-wise pattern of 0 and 1s.
5. Now draw the cladogram, and save the graphic.

Compare the result of the two analyses.

- A. Did your graphic of the evolutionary relationships among the hominins change when you added this new species?
 - (i) If so, what part of the graphic was altered.?
- C. Compare your final cladogram with that of some others who have worked with these data. In what ways do they differ?
- D. Which cladogram is most parsimonious (fewest instances of repeatedly derived traits)?
 - (i) You can calculate a rough measure of parsimony by dividing the number of repeatedly derived character states in the cladogram by the total number of state changes.
- E. Were the original cladograms robust (the relative positions of the branches changes least when adding new data)?

- (i) You can calculate a rough measure of robusticity by dividing the number of branches changed between the data sets by the total number of branches.

Analysis 3: Extensions of this Activity

- A. Search the literature or associated websites for newer hominin fossil finds and add their data to the chart.
- B. Compare the cladograms that you create with the new data against the original one from the data in this activity.
- C. Does the addition of new data change the branches of the original cladogram? How?
- D. If so, use the character state table that you created to identify the characters that were responsible for re-drawing the tree.

Assessment

Item Nr	Item	Rubric	Score
1	Vocabulary & definitions	4. Student correctly uses terms and concepts in all cases. 3. Student correctly uses terms and concepts in most cases (1-2 errors). 2. Student correctly uses terms and concepts in many cases (1-2 items appear to be used incorrectly consistently in assignment). 1. Student correctly uses terms and concepts inconsistently. 0. Student correctly uses terms and concepts rarely.	
2	State Assignment	4. Student correctly assigns all characteristic states as ancestral or derived. 3. Student correctly assigns most characteristic states as ancestral or derived. 2. Student correctly assigns many characteristic states as ancestral or derived. 1. Student correctly assigns only some characteristic states as ancestral or derived. 0. Student correctly assigns no characteristic states as ancestral or derived.	
3	Tree Construction	4. Student correctly constructs all nodes and branches of cladogram based on the transitions in character states in the data table. 3. Student correctly constructs most nodes and branches of cladogram based on the transitions in character states in the data table. 2. Student correctly constructs many nodes and branches of cladogram based on the transitions in character states in the data table. 1. Student correctly constructs some nodes and branches of cladogram based on the transitions in character states in the data table. 0. Student correctly constructs none of the nodes and branches of cladogram based on the transitions in character states in the data table.	

Item Nr	Item	Rubric	Score
4	Tree Comparisons	4. Student correctly applies measures of robusticity and parsimony to evaluate all solutions. 3. Student correctly applies measures of robusticity and parsimony to evaluate most solutions. 2. Student correctly applies measures of robusticity and parsimony to evaluate many solutions. 1. Student correctly applies measures of robusticity and parsimony to evaluate a few solutions. 0. Student does not correctly apply measures of robusticity and parsimony to evaluate solutions.	
	Rubrics for general goals for writing, content knowledge, curriculum objectives, etc., may be added here.		