EVOLUTION OF THE CHOCOLATE BAR:
A Creative Approach to Teaching
PHYLOGENETIC RELATIONSHIPS Within Evolutionary Biology

ROMI L. BURKS   LARRY C. BOLES

Chocolate calms the mind, yet excites the senses. Chocolate also unites cultures. *Chocolat* (2000), a movie about a small town French chocolate shop, made millions internationally. Starring actors contributed partly to the film's success but the film also drew salivating viewers worldwide to the multiple applications of chocolate. With its stimulant properties, chocolate generally makes people feel good. Chocolate may also inspire creativity. For example, every day biologists can use chocolate's fortunate property of appearing in different shapes, sizes, and compositions to help students understand basic principles of evolution. Few students have visited the Galapagos to see Darwin's finches, but nearly all have sampled a variety of chocolate bars. Using chocolate as a "model organism" can make understanding key elements of evolution more palatable to the student. Chocolate represents an ideal model for exploration because it comes in many variations, some of which make good choices for describing evolutionary history and some of which change too much to be useful. In addition, a little Web research produces a timeline for the debut of different candies (Figure 1) that can lend insight into the construction of evolutionary trees.

Teaching Evolution

The theory of **evolution** (for **bold** words, see Figure 2, Glossary) is unfortunately and undeservingly fraught with controversy (Scott & Branch, 2003; Langen, 2004); most of it political (Weis, 2001). Despite its acceptance by the scientific community as the theory that explains how organisms change through time, innumerable debates flourish about when, where, or even why to teach evolution (NAS, 1998; Bybee, 2002). Still, even after one is undeniably convinced of the merits of teaching evolution, the practicality of such a task can be daunting and pose its own unique challenges (Bybee, 2001). Communicating such a monumentally critical theory as evolution may take on its own sense of arduous-

> **Figure 1.** Abridged history of the chocolate bar and candies.
>
> - **1890** George A. Bayle Jr., of St. Louis, Missouri, packages peanut butter in barrels and sells it for six cents a pound.
> - **1900** Milton S. Hershey of Lancaster, Pennsylvania, introduces the first HERSHEY'S® Milk Chocolate bar.
> - **1903** George Washington Carver researches uses for peanuts. Peanut butter introduction to the world occurs a year later at the Universal Exposition in St. Louis.
> - **1920** Baby Ruth® candy bar is first sold, named for President Grover Cleveland's daughter.
> - **1928** Hershey introduced peanut butter cups later named after Harry Burnett (H.B.) Reese, a former dairy employee.
> - **1930** M & M/Mars introduces the SNICKERS® Bar, named for a favorite horse owned by the Mars family. One candy bar costs a nickel.
> - **1941** M & M'S® Plain Chocolate Candies (later M & M'S® Milk Chocolate Candies) introduced.
> - **1954** M & M'S® Peanut Candies introduced.
> - **1978** REESE'S PIECES candy is introduced.
> - **1982** REESE'S PIECES candy makes its big screen debut as "E.T.'s" favorite candy in the movie *E.T., The Extra Terrestrial*.
> - **1981** A European favorite since 1974, SKITTLES® Bite Size Candies are introduced in the U.S. by M & M/Mars.
> - **2001** SNICKERS® Cruncher premiers.
> - **2002** SNICKERS® with Almond Bars replace Mars Bar.
> - **2004** M & M'S® and chocolate bar merge into M-Azing® Crunchy and Peanut Butter versions.
>
> Sources: National Confectioners Association (http://www.candyusa.org/Classroom/timeline.asp), http://www.peanutbutterlovers.com/history/, M&M Mars Corporation (http://www.mmmars.com/cai/snickers/faq.html#top, http://www.snickers.com/history.asp, and http://us.mms.com/us/about/history/story/)), and Hershey Foods Corporation (http://www.hersheys.com/consumer/history.shtml;. All candies are registered trademarks.

ROMI L. BURKS, Ph.D. (burksr@southwestern.edu), is Assistant Professor of Biology, and LARRY C. BOLES was Visiting Assistant Professor of Biology, both at Southwestern University, Georgetown, TX 78626.

ness, especially when sharing such ideas with newly-minted undergraduates or high school students who may or may not have experienced a progressive biology curriculum (Bybee, 2001; Langen, 2004).

Figure 2. Glossary.

- **Adaptation** – any morphological, physiological, or behavioral change that enhances survival, growth, and the reproductive success.
- **Character** – a feature or attribute that has been selected for classification purposes, is capable of being measured, and will have character states.
- **Character states** – any of the possible distinct conditions or forms that a character may exhibit.
- **Clade** – a group of taxa that all share an immediate common ancestor and therefore are more closely related to each other than any other taxa.
- **Cladistics** – a classification method in which the members of taxa have been grouped together on the basis of phylogenetics, i.e., the members of the taxa share a more recent common ancestor with each other than with the other members of any other group.
- **Cladogram** – a branching, treelike diagram in which the endpoints of the branches represent specific taxa of organisms. With a common bifurcating pattern, it is used to illustrate phylogenetic relationships and show points at which various taxa have diverged from common ancestral forms; *cladogenesis* = the evolutionary change and diversification resulting from the branching off of new taxa from common ancestral lineages.
- **Classification** – the systematic process of forming and ordering groups based on similarity.
- **Convergence** – similarity, especially of function, appearing in taxa that do not share an immediate common ancestor, due primarily to similar selective pressures.
- **Derived** – a character state that is a modified version of the ancestral state.
- **Evolution** – change in allele frequencies in a population over time.
- **Evolutionary step** – acquisition or loss of a character that changes the resulting lineage.
- **Extant** – living today.
- **Fitness** – measure of one's genetic contribution to the next generation relative to other individuals.
- **Homoplasy** – similarity due to independent evolutionary change. Homoplasy is either parallelism (= independent gain) or reversal (= loss).
- **Natural selection** – different survival and reproduction of individuals carrying alternate inherited characteristics.
- **Monophyletic** – a set of taxa containing a common ancestor and all its descendants.
- **Node** – a branch-point on a tree/cladogram.
- **Outgroup** – a taxon used to help resolve the polarity of characters, and that is hypothesized to be less closely related to each of the taxa under consideration than any are to each other.
- **Paraphyletic** – set of species containing an ancestral species together with some, but not all, of its descendants.
- **Parsimony** – one of several criteria that may be optimized in building phylogenetic trees. The central idea of cladistic parsimony analysis is that some trees will fit the character-state data better than other trees. Fit is measured by the number of evolutionary character-state changes implied by the tree.
- **Phenetics** – a method of classification by which similarity is determined by considering phenetic characters (characters responsible for an entity's appearance). Characters are selected without regard to an entity's evolutionary history.
- **Phenotypic plasticity** – non-genetic variation in organisms in response to environmental factors.
- **Phylogenetic tree** – a diagram representing the evolutionary development of related species.
- **Rooted tree** – a cladogram with a hypothetical ancestor, which that to the root, that is the node at the base of the tree. When outgroups are used, this is the node that connects the outgroups to the ingroup, and thus specifies the direction of evolutionary change among the character-states (cf. unrooted tree).
- **Sister group** – a clade that is believed to be the closest genealogical relative of a given taxon exclusive of the ancestral species of both taxa. Or the descendant branches from a node on a cladogram.
- **Synapomorphy** – a derived or specialized character shared by two or more groups that originated in their last common ancestor.
- **Topology** – the branching sequence of a tree.

Nevertheless, we know that "[n]othing in biology makes sense except in the light of evolution" (Dobzhansky, 1973). Thus, the need for biology educators across multiple educational levels to tackle the subject of evolution will only increase over time. A newly-renewed interest by scientists in the way that evolution is taught (Alters & Nelson, 2002) has spawned a number of helpful Web sites and technological resources (AIBS, 2004). In addition, Darwinian excerpts from *The Origin of Species* (1859) may help elucidate the foundational concepts of evolution (i.e., **natural selection, fitness,** and **adaptation**) (Costa, 2003). However, only a few of these resources delve further into "descent with modification" (Darwin, 1859) and investigate the process of determining the evolutionary relationships between organisms. Yet, without such understanding, an introductory exploration of the "Tree of Life" (Maddison, 2004) with high school students or undergraduates can be a rough journey.

Phylogeny, Classification, Cladograms & Trees

We commonly hear that "a picture is worth a thousand words." Darwin may have thought this when writing his *Origin of Species* (1859) where he chose to include only one diagram (Freeman & Herron, 2001). Darwin's "hypothetical tree" illustrated his view of how species change through time. Today, **phylogenetic trees** serve as visual representations of the possible historical relationships between species (i.e., **phylogeny**) where species at the tips or ends of trees represent species, genera, or other taxa living today (i.e., **extant**) or that might have gone extinct. Branches of trees then represent ancestral populations of species through time, and **nodes** designate points where one species splits into two more descendent populations (Freeman & Herron, 2001). **Rooted trees** identify the origin of
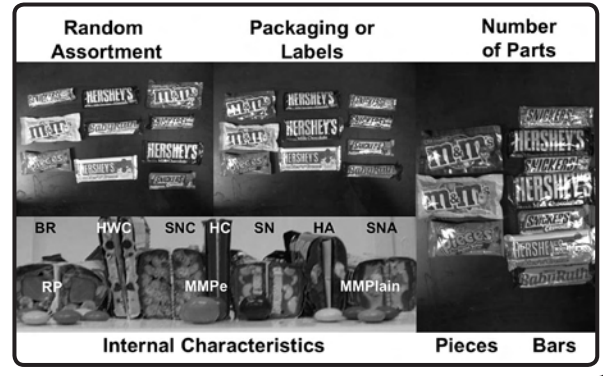
the lineage and the combination of tips, branches, and nodes illustrate Darwin's concept of "descent with modification" and the plausible relationships between organisms.

The mode of discovering phylogenetic relationships by creating bifurcating tree diagrams (i.e., **cladograms**) and testing them against what is known about organisms often proves frustrating. However, these diagrams help to illustrate the key principle that species are not independent and that a group of **characters** connects them with other species. Humans also have a natural instinct to classify or arrange things in groups. However, the multiple ways in which **classification** of species occurs lends little direct insight into how they are related to each other evolutionarily (i.e., phylogeny). For example, one could classify a group of candies based on their packaging, number of parts, shape, or internal characteristics (Figure 3). From our own observations of seasonal changes, we know that candy bars often come in different wrappers and we can subsequently deduce that outward appearance is likely too plastic a character for reliable phylogenetic analysis. **Phenetic** characters comprise those responsible for appearance and are selected without regard to evolutionary history. We can speculate that internal content may remain more consistent. However, it can still be quite difficult for both scientists and students to know what characters will yield the most acceptable phylogenetic tree. Historically, organisms have been placed in taxonomic groupings based on physical characteristics. More recently, data from molecular biology have been used as characters in biological classification schemes. Because there are a tremendous number of possible characters that could be used to classify taxa, researchers must carefully consider on which traits they will rely.

Cladistics (or phylogenetic systematics after Hennig, 1966) is a method of phylogenetic classification that attempts to limit comparisons within groups to those characters thought to have evolved within a given group, also known as **derived characters**. The process of cladistics works by analyzing different taxa to find objective similarities and differences between them. One then uses those similarities and differences to create a tree structure illustrating the most similar taxa. The assumption is that similar taxa are similar because they are evolutionarily related. Therefore, trees produced by cladistic analysis can be considered approximations to the phylogeny of the group being studied. Cladists attempt to create **monophyletic** groupings, ones that include ancestral taxa and all of the descendants. Some traditional taxonomic groupings however, are considered **paraphyletic** because they do not include all descendants. The traditional Class Reptilia, for instance, is considered paraphyletic because it does not contain the birds (Class Aves), which are clearly descended from reptilian ancestors. Taxonomists must also be scientists and use multiple characters to generate tree diagrams. Each of these cladograms represents a hypothesis about the evolutionary relationships of the taxa in the tree. Scientists subscribe to the logic of **parsimony,** i.e., that the most likely tree is the simplest, or the one that takes the least number of **evolutionary steps** to create. Characters that are shared because they were modified in a common ancestor are called **synapomorphies**. In cladistics analysis, no living taxon can by definition be an ancestor of another living taxon. This leads to the concept of

Figure 3. Different ways to classify sets of candies. In the cut-away view:

BR = Baby Ruth®
RP = REESE'S PIECES
HWC = HERSHEY'S® White Chocolate
SNC = SNICKERS® Cruncher
MMPE = M & M'S® Peanut
HC = HERSHEY'S® chocolate bar
SN = SNICKERS®
HA = HERSHEY'S® with Almonds
MMPL = M & M'S® Plain
SNA = SNICKERS® Almond Bar.

Figure 4. Sample phylogenies for sister groups of candy pieces (A) and candy bars (B). Perpendicular lines on branches represent evolutionary steps.
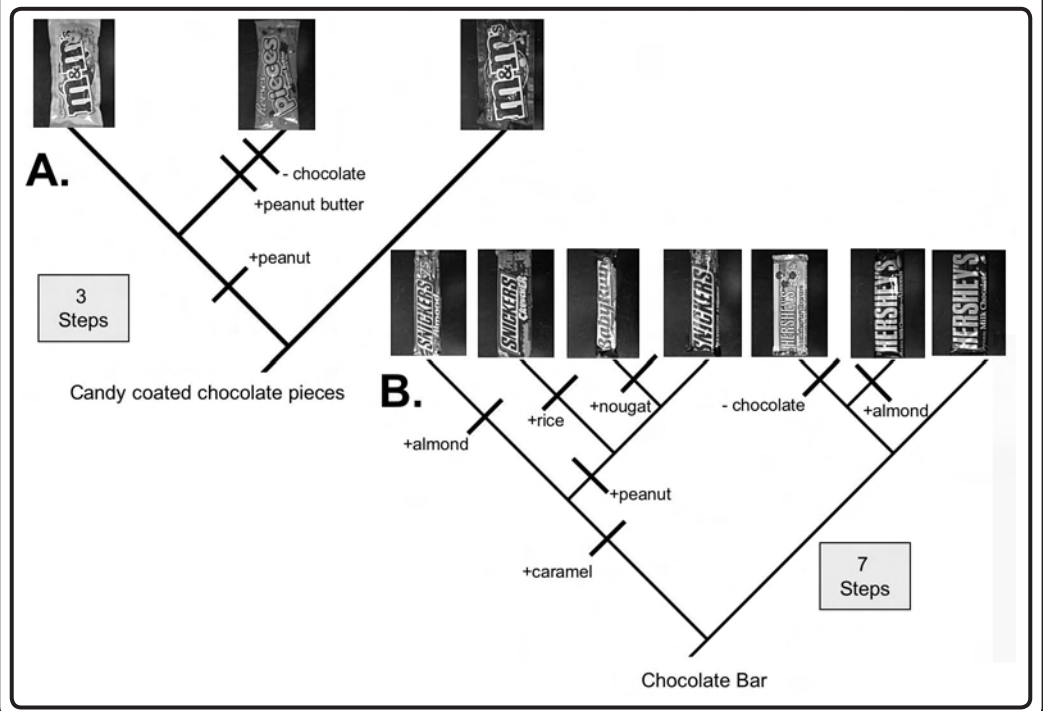
sister taxa, such as all varieties of candy with pieces (Figure 4A), which are all derived from an unknown common ancestor.

Darwin's finches serve as the model for asking evolutionary questions (Grant & Grant, 2003), but life on the Galapagos may be too far removed from students to make an impact. Students and teachers generally react quite favorably to chocolate and may even know something about its history (Figure 1), which is fascinating although beyond the scope of this publication. In the age of alternative teaching strategies (for excellent resources, see Bean, 1996; McKeachie, 2002; Michel, 2003), the lecture approach for complex ideas such as phylogenetics often leaves students pining for practical application. In the following exercise, students use a group of candy bars to learn about phylogenetic principles and how scientists work to understand the relationships that exist between organisms. Framing a discussion about evolution by using chocolate simply provides a boundary for students to frame their conceptions about a topic that is often difficult to approach and teach. The exercise described below is easily assembled, works as a class demonstration, spawns small group projects, fits a variety of class timeframes including labs, and provides for substantial discussion.

Figure 5. Example of MacClade windows and output. Four possible cladograms shown on the left with the most parsimonious tree (13 steps, shown in Tree Window) appearing below the data matrix (seen in Data Editor window). Larger box shows tool palette from MacClade where the arrow is used to move branches to arrive at the tree with the fewest steps. Common ancestor assumed to be a chocolate bar.

Methods

This exercise requires little more than a bit of creativeness, $10, and a trip to the grocery store. For a classroom demonstration, we suggest that you conduct this exercise in a setting that allows access to a large writing surface (whiteboard, blackboard, or posters). For a more time-consuming and intensive investigation (such as a lab period), trial versions of phylogenetic analysis programs, such as MacClade (http://macclade.org/macclade.html), can also prove useful for generating cladograms based on the characters chosen by your class (Figure 5). The basic idea of this exercise could be executed with any number of examples, which enables it to be adapted to suit one's own interest.

1. To follow our example, purchase the following candies:

   Baby Ruth® (BR)

   HERSHEY'S® chocolate bar (HC)

   HERSHEY'S® with Almonds (HA)

   HERSHEY'S® White Chocolate (HWC, which sometimes comes with Cookies n' Cream)
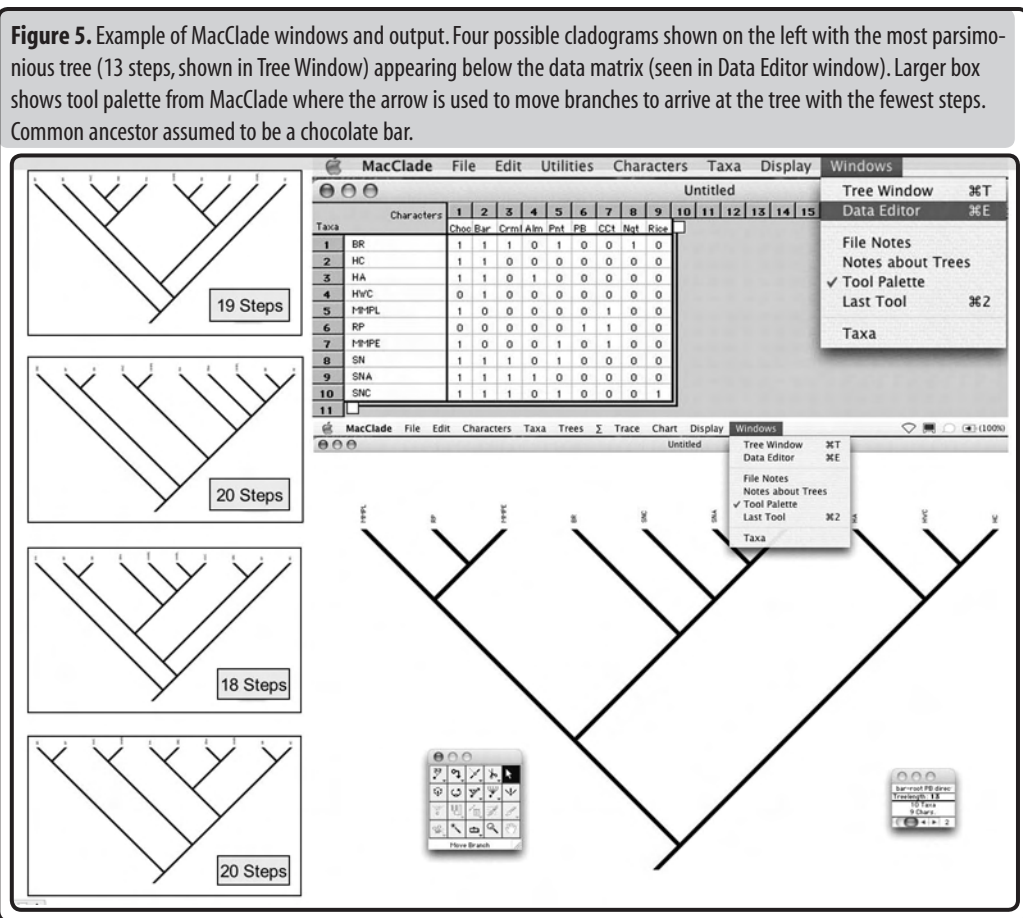
   M & M'S® Plain (MMPL)

   M & M'S® Peanut (MMPE)

   REESE'S PIECES (RP)

   SNICKERS® (SN)

   SNICKERS® Almond Bar (SNA)

   SNICKERS® Cruncher (SNC).

   The advanced critical thinking exercises also require REESE'S peanut butter cups (RPBC) and SKITTLES® (SK). The abbreviations for these candies appear on the data matrix and some cladograms. Note, for group exercises, that multiple sets of the candies will be needed.

2. First introduce students to the goal of phylogenetic analysis, i.e., determining the most parsimonious tree. Preface the exercise with an introductory discussion of how scientists try to determine the phylogenetic relationships between organisms and the implications this has for the study of evolution. Several quality Web sites (Unda, 2005; NCBI, 2005; Tree of Life Project, 2005) can provide the instructor with background information. Distinguish between **phylogeny, cladistics,** and **classification** as described above. Remind the students that all cladograms are types of phylogenetic trees, but not all phylogenetic trees need be cladograms. Emphasize to the students that they are not classifying taxa but instead generating hypotheses (i.e., cladograms) about phylogenetic relationships.

3. Next, give the students the two packages of M & M'S® (Plain and Peanut) and the package of REESE'S PIECES and allow them to build a sample phylogeny (Figure

4A). Ask them to identify what **characters** they would use to propose relationships between these species. Then ask the students to list the **character states** for each character. For example, if shape was the character, then bar and pieces could be the character states. Allow the students to sample a few candies if necessary. They should arrive at chocolate, peanuts, and peanut butter as the characters, and the presence or absence of these characters as the character states. They may suggest using other characters such as wrappers or candy color. Take this moment to further discuss **phenotypic plasticity** and the notion that quality characters are reliable in their nature and usually not **phenetic**. You could suggest that colors may be uninformative by using the example that yellow and orange M & M'S® Peanut Butter look similar to REESE'S PIECES in valid characters (candy coating, peanut butter), but only the M & M'S® retain chocolate. Then, after they have successfully constructed one possible cladogram, request that the students identify the **synapomorphies**, or shared characteristics (i.e., individual pieces, candy coating) and speculate about the common ancestor at each branch of the tree.

- Depending on how quickly the students grasp the ideas, you may also suggest that they build a separate cladogram for those candies that come in bar form (Figure 4B) before including all the candies.

4. Having constructed a sample phylogeny in the form of a simple cladogram (Figure 4A or B), the students are now ready to broaden the exercise. Give them the remaining seven candies (HC, HA, HWC, SN, SNA, SNC, BR) and ask them to again identify which characters best describe all of the chocolates independently (10 taxa). Independent characters do not include other characters. For example, just having nuts is not a good choice because nuts involve both peanuts and almonds. Instead, choose peanuts and almonds because as different kinds of nuts they meet

the criteria of independence. After identifying the characters, have the students score each of the candies. The goal is to create a data matrix. Again reject characters that appear plastic in nature (i.e., color, size). You can make a comparison to breeds of dogs. All dogs are the same species (*Canis familiaris*), although Great Danes and Bichon Frise breeds look very different.

5. Create a data matrix of the best characters. A data matrix shows the relationship between taxa and characters. If you have access to MacClade, then you can enter this information into a data matrix by dragging a box that defines both the characters (in columns) and the chocolate taxa (in rows). For only two character states, a "0" denotes absence and a "1" presence (Figure 5). For ease of review, MacClade will also color code your characters. Please note: if you are using a trial version of MacClade, be careful not to close the windows because you cannot save your data matrix. You will want to use Shift+Command+3 to screen capture the image.

6. The first step to creating trees for students will be to arrange the candy bars by hand on a large surface. Then, the students should discuss what similarities or differences exist within the groups to identify the **evolutionary steps**. Either on paper or using MacClade, have your students document the cladogram that represents their visual arrangement. Repeat two to four times or get one cladogram from multiple groups. Explain to the students that hundreds, even thousands, of trees can be created but that you are only interested in the ones that make logical sense and require the fewest steps.

- For MacClade, choose the "Tree Window" to view a randomly generated tree (Figure 5). The Σ box on each chart shows the number of steps it took to construct the tree. MacClade will not automatically generate the most parsimonious tree but will give you clues to the number of steps required. By choosing "Trees" and then "Create Trees," MacClade can generate multiple possibilities of trees (i.e., 1000) and then provide a chart that shows the number of trees of each length. By examining the chart, you can determine the fewest number of

steps required. Remember the trial version requires that you screen capture to save the clado-grams.

7. From the clado-grams created, insert steps (represented by small lines per-pendicular to the branch) that identify the characters com-mon to the resulting lineage. Recognize each "step" as an addition or loss of a character (for exam-ple, Baby Ruth® contains unique nougat where the other members of that **clade** do not). Next, identify the most parsimonious tree by counting the number of steps on each cladogram. You want the one with the least number of steps.

Figure 6. Two most parsimonious cladograms, each with 13 steps. A) Common ancestor assumed to be the chocolate bar B) Common ancestor assumed to be candy coated chocolate pieces. Perpendicular lines on branches represent evolution-ary steps and text defines addition or loss of a character.

- In MacClade, this process of arriving at the most parsimonious tree is done by moving the branches of a default cladogram (using the arrow tool, Figure 5) until you have minimized the tree length (basing this number from the chart you produced earlier). Just as you would do on paper, you should move the branches to positions that make sense in light of any historical records that you may have (Figure 1). In the full version, it is possible to use PAUP 4.0 (Phylogenetic Analysis Using Parsimony; http://paup. csit.fsu.edu/about.html) to help identify the most par-simonious tree.

Results & Discussion

For our example, we discuss two parsimonious cladograms, each with 13 steps (Figure 6A, B) that we rooted in different **out-groups**. Regardless of where we root the tree, either with a classic HERSHEY'S® bar or with candy in pieces, the most parsimonious branching (i.e., **topology**) remains the same. The two trees illus-trate that the difference comes with the inference to the direction of change, i.e., loss or gain of a given character. In Figure 6A, candy coating is added and the bar form lost to arrive at the candies with pieces. If you start with pieces in the bottom cladogram (Figure 6B), then the candy coating is lost and the bar form gained to create the HERSHEY'S® clade. Students can further explore the directionality of change by examining any assumptions that they made in constructing their cladograms. In our example, we assumed that peanut butter came from peanuts based on our research (Figure 1) and early school lessons about George Washington Carver. However, in building phylogenetic trees, it is just as parsimonious for the change to go in the other direction,
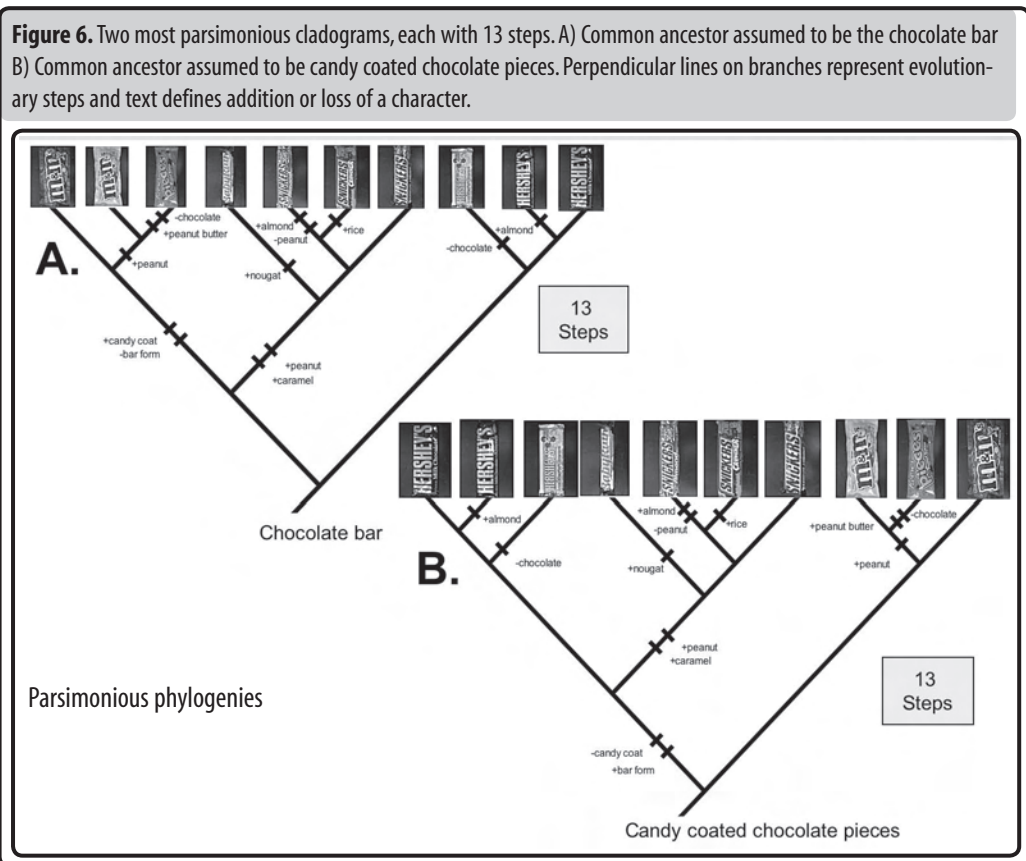
where peanuts coalesce out of a soft amalgam of "peanutty" mate-rial. Knowing the ancestral condition *a priori* allows us to make better educated guesses as to the most plausible phylogeny.

Figure 6A uses HERSHEY'S® chocolate bar as the **outgroup**. Based on the history of chocolate (Figure 1), we know that HC appeared before any of the other candies and is the logical choice for the outgroup. The evolutionary conclusion from this is that the outgroup branched from the parent group before the other groups (or clades) branched from each other. However, without this knowledge, students could make convincing arguments for the reverse scenario that begins with candy coated pieces. Instructors could ask students to defend their choices and then introduce the "historical evidence" (Figure 1) and illustrate how that information confirms one hypothesis over another. Therefore, even though both of these trees contain the same number of steps, one could then advocate for the chocolate bar as the ancestral taxon.
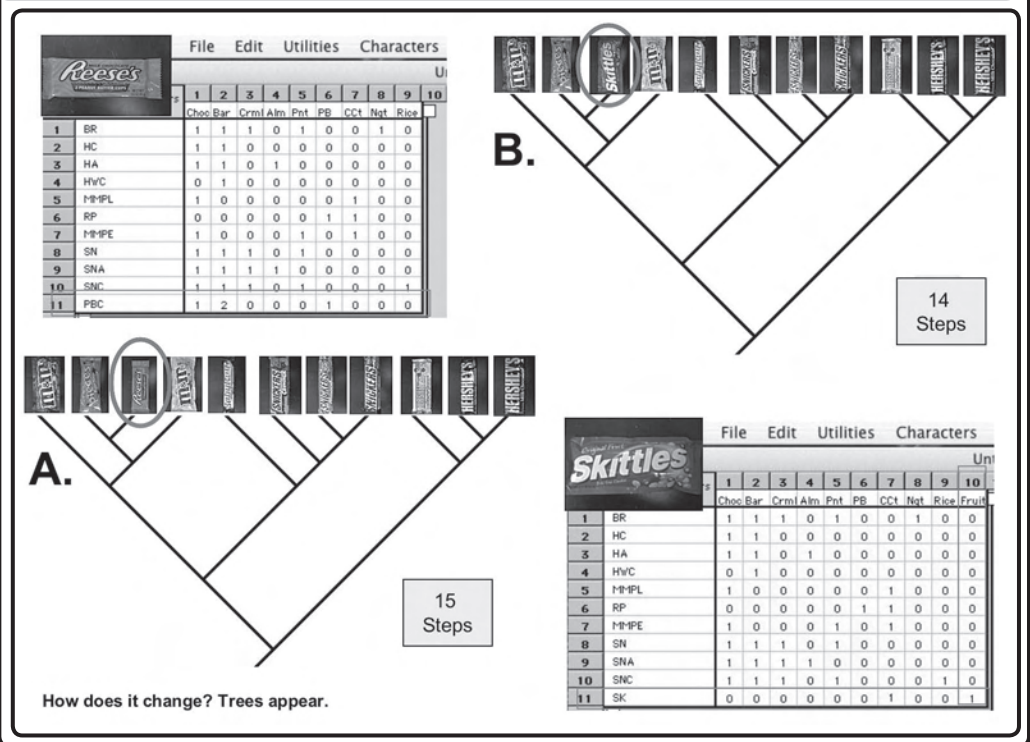
We can use the cladograms generated to show both **conver-gence** as well as **homoplasy**. If you look at the tips (i.e., external nodes) of the cladograms, 7 out of 10 of the **extant** taxa have some version of nut. Peanuts and almonds appear multiple times on different clades. In real evolutionary scenarios, conver-gence may arise due primarily to the independent species lines experiencing the same kinds of natural selection pressures (i.e., competition, predation, parasitism, etc.). Although this borders on the "limits" of this exercise, one could include a discussion of artificial selection, i.e., the selective breeding of domesticated plants and animals to encourage the occurrence of desirable traits. Of course, candy bars do not naturally reproduce but the point is that humans, by their buying habits, select these traits artificially as we have done with our crops, livestock, and pets. In our cladograms, we also see examples of **homoplasy** where simi-

larity occurs independently of evolutionary change. Loss of chocolate to have either REESE'S PIECES or HERSHEY'S® White Chocolate would be one example. In addition, the arrangement of the illustrations into clades emphasizes the sister groups that occur, including M & M'S®, SNICKERS® varieties, and HERSHEY'S® bars. Therefore, this exercise provides opportunities to discuss the intricacies that Darwin observed when he first described descent with modification.

Incorporating a New "Taxon"

The exercise described above is comprehensive enough in nature to easily occupy an entire class period (50-75 minutes). However, we wanted to provide instructors with a couple ways to extend the discussion. It is important to remind the students that each cladogram represents one hypothesis and that hypotheses need to be modified as discoveries happen. With another $1.50 for two more candies (RPBC and SKITTLES®), instructors can test students' ability to revise their cladograms. Adding REESE'S peanut butter cups to our previous group adds two evolutionary steps (Figure 7A). In the data matrix, we did not add any new characters but instead modified the character state of "bar" to include three possible types (bar, pieces, or cup), with the new designation receiving a "2" in the matrix (Figure 7A). The most parsimonious cladogram shows RPBC as a sister group to REESE'S PIECES with the new steps as loss of candy coating and formation into a cup shape. Interestingly, both RPBC and SKITTLES® occupy similar positions on our cladograms. However, adding SKITTLES® to our previous group only required one more step (Figure 7B), addition of fruit flavor, because loss of chocolate already occurred on the branch with REESE'S PIECES. Using fruit flavor did constitute a new character in our data matrix as it did not fit as a state to our existing characters (Figure 7B). Although we chose these two candies to add, any number of manipulations could occur that help test students' understanding of how to determine good **characters**, recognize different **character states**, and count **evolutionary steps**.

Figure 7. Change in data matrices and cladograms with additions of new taxa. A) REESE'S peanut butter cups B) SKITTLES®. A non-shaded rectangular box shows score of new taxon in the data matrix and a circle shows the location in the cladogram. See text for discussion of evolutionary steps.

File Edit Utilities Characters

Reese's

		1	2	3	4	5	6	7	8	9	10
		Choc	Bar	Crml	Alm	Pnt	PB	CCt	Ngt	Rice	
1	BR	1	1	1	0	1	0	0	1	0	
2	HC	1	1	0	0	0	0	0	0	0	
3	HA	1	1	0	1	0	0	0	0	0	
4	HWC	0	1	0	0	0	0	0	0	0	
5	MMPL	1	0	0	0	0	0	1	0	0	
6	RP	0	0	0	0	0	1	1	0	0	
7	MMPE	1	0	0	0	1	0	1	0	0	
8	SN	1	1	1	0	1	0	0	0	0	
9	SNA	1	1	1	1	0	0	0	0	0	
10	SNC	1	1	1	0	1	0	0	0	1	
11	PBC	1	2	0	0	0	1	0	0	0	

B. 14 Steps

A. 15 Steps

How does it change? Trees appear.

File Edit Utilities Characters

Skittles

		1	2	3	4	5	6	7	8	9	10
		Choc	Bar	Crml	Alm	Pnt	PB	CCt	Ngt	Rice	Fruit
1	BR	1	1	1	0	1	0	0	1	0	0
2	HC	1	1	0	0	0	0	0	0	0	0
3	HA	1	1	0	1	0	0	0	0	0	0
4	HWC	0	1	0	0	0	0	0	0	0	0
5	MMPL	1	0	0	0	0	0	1	0	0	0
6	RP	0	0	0	0	0	1	1	0	0	0
7	MMPE	1	0	0	0	1	0	1	0	0	0
8	SN	1	1	1	0	1	0	0	0	0	0
9	SNA	1	1	1	1	0	0	0	0	0	0
10	SNC	1	1	1	0	1	0	0	0	1	0
11	SK	0	0	0	0	0	0	1	0	0	1

Scientific Limitations & Pedagogical Value of This Exercise

Evolution is difficult to teach and educators need to strategize about the most effective ways to communicate complex, often distant, concepts. Some may think use of candies in this exercise trivializes the process of biological evolution. This exercise does lack a realistic connection to changes in the genetic makeup of

a population, the real basis for evolution. Chocolate bars do not have genes. Of course, it is impossible to examine any changes at a molecular level, which is an increasing area of emphasis in biology. We never see the "mutant" candies that remain in the factory. Although we provided some suggestions for discussion, candy bars as a model for living organisms only go so far. In addition, cladistics analysis emphasizes **monophyletic** groups and thus gives a limited picture of evolution. Each monophyletic group is a clade, comprising an ancestral form and all of its descendants, and so forming one (and only one) evolutionary group. Our analysis presents evolution of all the candies from a common ancestor. Alternatively, inclusion of other candies might suggest a **paraphyletic** group, which is similar but excludes some of the descendants that have undergone significant changes. To extend

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Appendix

Challenge Questions

Below we describe three challenges that could be used as homework, an additional lab, or a research project (Figure 8).

1. Many companies that produce chocolate candies release a number of different versions that differ only slightly in their nature. Expand the cladogram already constructed (Figure 7A) to include the entire clade of REESE'S peanut butter cups as shown below in A.

   a. How many more evolutionary steps did it take?

   b. What new characters or states did you have to include?

   c. How did these characters differ from the ones in the original cladogram?

   d. What is the common ancestor to this clade?

2. Recently, M & M/Mars came out with a new product (Figure 1) that adds a twist to our discussion of pieces versus bars as the ancestral trait for American chocolate candies. It's new product, M-Azing® (see B below), is a fusion of M & M'S® (Plain or Peanut Butter varieties) with the plain chocolate bar.

   a. Knowing that this only recently appeared, how does this change your cladogram?

   b. If you just "found" this taxa without having any indication of its history, how would that knowledge change your cladogram?

   c. To include this new taxa, would you need to have additional character states from the example given? If yes, what would they be?

   d. For fun, devise a "biological" story that hypothesizes how these two taxa came together. In your story, identify what basic biological principles you include. Speculate as to the benefit or cost that each taxa incurs in this arrangement.

3. Our exercise uses common American chocolate candies (i.e., HERSHEY'S®, SNICKERS®, M & M'S®). To add an international flavor, do some Web research and create a phylogeny for some European chocolate bars (see C below). This challenge is probably best done using MacClade as the cladograms may get large quickly. Start with each "historical population" within European countries famous for chocolate. These include England (Cadbury in 1824), Belgium (Cote d'Or in 1883; Leonides pralines in 1935), and Switzerland (Lindt in 1845). Choose a limited number of candies per country (~10). Several Web sites exist that cater to global chocolate lovers and can help in your selections. After discovering the most parsimonious cladogram for each historic population, try and combine them into one large analysis. Consider the following questions:

   a. Do you see any convergence in the historic populations? Do you see similar trends in European as American candies?

   b. Could you determine an appropriate outgroup? If so, what information provided the basis for that decision?

   c. Did you choose different characters for your individual country analysis versus the synthetic one? If so, what prompted the change?

Visual illustrations for "challenge" exercises that can be used for homework, special projects, or group labs. A) Recent varieties seen in REESE'S peanut butter cups B) Appearance of a new hybrid candy (M-Azing®) with the different kinds of candy coated pieces (chocolate or peanut butter) melded within a chocolate bar C) Examples of European chocolatiers.
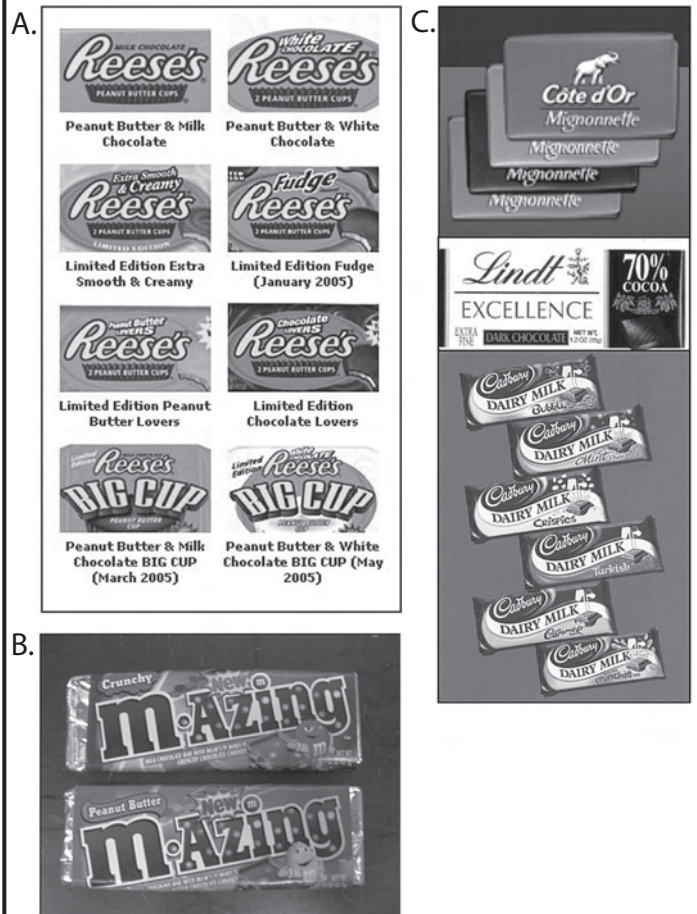
this idea to our example, all candies that now incorporate white chocolate may be better hypothesized as a paraphyletic group. Therefore, using cladistics analysis does limit some intrepretations and alternate hypotheses should be considered.

For the purposes of pedagogy, however, a little pretending can go a long way. We argue that this exercise provides a first step for students to get their heads around the basic ideas that Darwin first proclaimed in *The Origin of Species*. As instructors delve into discussing phylogenetic relationships between real living organisms, this exercise serves as a reference point or analogy to remind students of the principles that go into constructing evolutionary history. Teaching evolution should not inspire anxiety or dread in those lacking a specific Ph.D. in evolutionary theory. Framing the discussion of the principles of evolution by using candy bars simply provides a boundary for students to frame their conceptions and questions. The time scale of this exercise is also limited as we look only at "evolution" occurring over the last hundred years. However, this allows the instructor to point out that evolutionary processes occur at different rates for different taxa (i.e., much faster in bacteria than plants). Lastly, some could argue that students might not take the analogy seriously and subsequently dismiss the idea that evolution is occurring all the time in all living things. Yet students often respond with a seriousness equal to that of the teacher and appreciate attempts to introduce creative ideas into the classroom. Overall, the key to a successful exercise is to encourage students to think critically, propose, defend, and reject hypotheses, and acknowledge assumptions. In conclusion, we believe that a serious, critical exploration of evolution may have an increased likelihood of staying with students who fall under the mysterious spell of chocolate, and end up relaxed within a sugar-rushed, caffeine-dosed classroom climate. Particularly at 8 am or late afternoons.

Acknowledgments

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