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CHAPTER 5

The Value of the Tree of Life

"Nothing makes sense except in light of evolution"

Dobzhansky, 2013 [1973]

To this insightful phrase, numerous biologists studying biodiversity have added the corollary:

Everything in biology makes more sense in light of phylogeny.

As portions of the Tree of Life (e.g., vertebrates, butterflies) have been better resolved, together with the recent publication of the first rough draft tree of all named life (see Chapter 3), the scientific community, as well as the general public, have increasingly come to appreciate its value. Through yielding powerful insights into the past, the Tree of Life provides a means to interpret the patterns and processes of evolution, as well as the ability to predict the responses of life in the face of rapid environmental change. Broad knowledge of species relationships is fundamental, providing crucial new information regarding the discovery of medicines, combatting diseases, and crop improvement. This information has also had major impacts in the diverse fields of genomics, evolution, and development, while providing insights into the study of adaptation, speciation, community assembly, and ecosystem functioning. Given the many benefits, it is therefore hard to summarize, in a few words, the immense implications and applications of the Tree of Life to biology and human well-being.

All of these benefits of a better knowledge of phylogeny and the Tree of Life are made possible for the same reason that a clear understanding of your own family tree is important—knowledge of relationships matters. We all seem to have a fascination with family trees—who were my ancestors? How am I related to others? In addition, we all understand clearly that if a close relative has a disease that is inherited, say a certain cancer, then there is a good probability that we may have inherited the genes for that trait (Fig. 5.1).

In much the same way as understanding your family tree is enlightening, the Tree of Life similarly has informative and predictive value. We

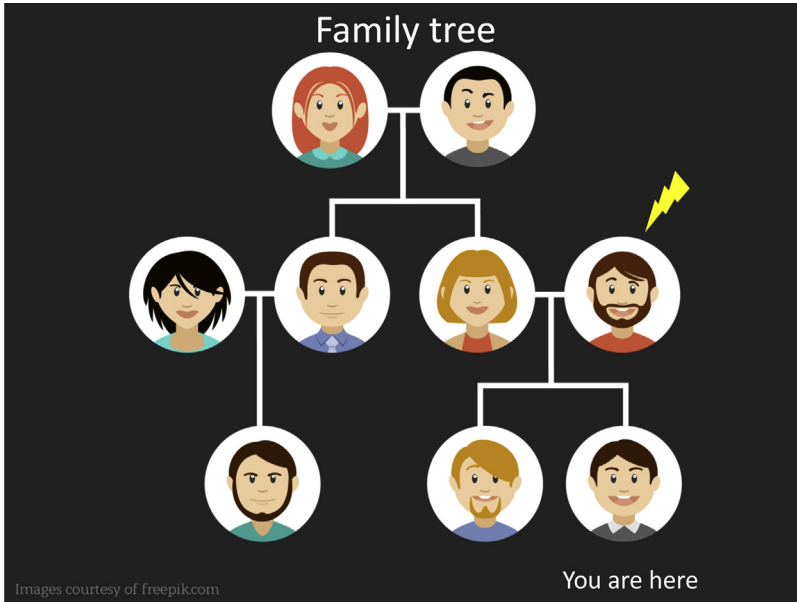


Figure 5.1 An imaginary family tree in humans showing that relationships matter for you as an individual. We all realize that if a relative or ancestor (lightning bolt) has a disease that is inherited genetically, there is a good likelihood that we inherited that trait. *Wikipedia Free Commons.*

can use the Tree of Life to inform, discover, and solve major problems that affect our own species. Closely related organisms may produce similar chemical compounds of medicinal value to our species. Close relatives of crops are the best source of genes for disease and drought resistance. Closely related strains of disease (e.g., the flu) will likely respond similarly to similar vaccines. And because closely related species will likely respond in similar ways to increases in temperature or drought stress, the Tree of Life can even be used to predict how organisms may respond to a rapidly changing climate. All of these examples and the predictive power of relationships depend on a firm knowledge of the Tree of Life.

Another way to look at the huge potential impact of the Tree of Life is that it represents the biodiversity equivalent of the human genome project. When the human genome project was initiated, there was considerable debate as to its actual value and whether it was worth the immense expense. To some skeptics, the human genome project represented a costly, lengthy, and basic research project with few practical outcomes. And while the cost of the first human genome was ~ 2.7 billion dollars and the project took over 10 years to complete ([International Human](#)

Genome Sequencing Consortium, 2004), the human genome project is now considered one of the great accomplishments of modern science. The human genome sequence has spurred on the discovery of the functions of numerous genes and the genetic underpinning of many diseases, transforming medical research. It has also impacted the study of human population genetics, revealing patterns of human migration through time. Furthermore, the human genome project also generated advances in DNA sequencing, making it now so routine that you can obtain your own genome sequence for less than \$100. As sequencing costs decrease, your own genome sequence will soon be a fundamental part of your medical record. Efforts, in fact, are underway in China to sequence the genome of every person on Earth, and scientists have set goals of sequencing 10,000 plant species (the 10KP project; <http://www.sciencemag.org/news/2017/07/plant-scientists-plan-massive-effort-sequence-10000-genomes>), 10,000 vertebrate species (the G10K project; <https://genome10k.soe.ucsc.edu/>), and even all of life (the Earth BioGenome Project; <https://www.earthbiogenome.org/>).

Just as the sequencing of the entire human genome provided numerous and largely unanticipated new biological discoveries, reconstructing the entire Tree of Life has already fueled and will continue to fuel fundamental research and the development of practical tools to sustain biological diversity and enhance the quality of human life, whether through combatting disease, improving crops, or discovering new medicines. The multifaceted value of biodiversity to human well-being in this broad sense is crucial (see Grifo and Rosenthal, 1997; Chivian and Bernstein, 2008; Sala et al., 2012).

MEDICINES

There are multiple considerations regarding the importance of the Tree of Life and drug discovery. In fact, most of our medicines trace originally to chemical compounds from plants—humans did not invent these compounds, nature did. Species in nature have evolved numerous chemicals with diverse purposes and roles—the benefits range from defense to capturing prey. Those same chemicals may also be of value to our own species. Many of these useful compounds are discovered by chance through the basic research of an observant/inquisitive biologist, or traced to a long history of use in traditional medicines. On the one hand, it is therefore important to preserve the Tree of Life simply because there is so much

hidden, as-of-yet untapped medical value in the species that compose the Tree of Life. Numerous chemical compounds of direct medical value to our own species await discovery.

Plants, fungi, and animals have been used for medicinal purposes for thousands of years. Indeed, modern research sometimes entails the detailed study of traditionally used medicinal plants (e.g., [Zhang, 2002](#); [Patwardhan and Mashelkar, 2009](#)). However, as species are lost to extinction, that potential utility is also lost forever—hence, the importance of protecting the species that constitute the Tree of Life, simply for utilitarian reasons. Imagine the loss of a species that held the cure to a disease that might have saved your life, or the lives of your friends, relatives, or children. But imagine that this same species was driven to extinction before that knowledge was realized. How many potential medicines have already been lost due to species loss in the Anthropocene, and how many more will soon follow? If half of all plants (the major source of medicines) go extinct by the end of the century as predicted (see Chapter 6), imagine the human impact on medical loss alone!

As noted, new medicines often come from unexpected sources, and these make interesting stories in natural history and for the importance of protecting biodiversity. Consider a few examples provided below... and then contemplate what would have happened had these organisms gone extinct before this medicinal potential was even understood.

Hundreds of potential new compounds are discovered each year ([Proksch et al., 2002](#)), and excellent examples of the discovery of unanticipated new medicines trace to pitcher plants in the genera *Nepenthes* ([Fig. 5.2A](#)) ([Eilenberg et al., 2006](#)) and *Sarracenia* ([Harris et al. 2012](#)). Pitcher plants are carnivorous, widely known for trapping insects and other prey items and digesting them as a source of nitrogen. Prey items fall into a pool of fluid located inside the modified leaf (pitcher) ([Fig. 5.2B](#)) that contains digestive enzymes. Basic research has revealed that the pitchers of these plants have also evolved compounds that are antifungal—special enzymes that dissolve the cell walls of fungi. By producing these enzymes, the plants are able to inhibit fungal growth and by so doing the plants do not lose the resources in the prey trapped in the pitcher to fungi ([Eilenberg et al., 2006](#)). Significantly, these enzymes have shown great promise as new antifungal drugs in treating infections in our own species. Drugs derived from pitcher plants have been used to treat sciatic pain, symptoms of the herpes simplex virus ([Mishra et al., 2013](#)), diabetes ([Muhammad et al., 2012](#)), and tumors.

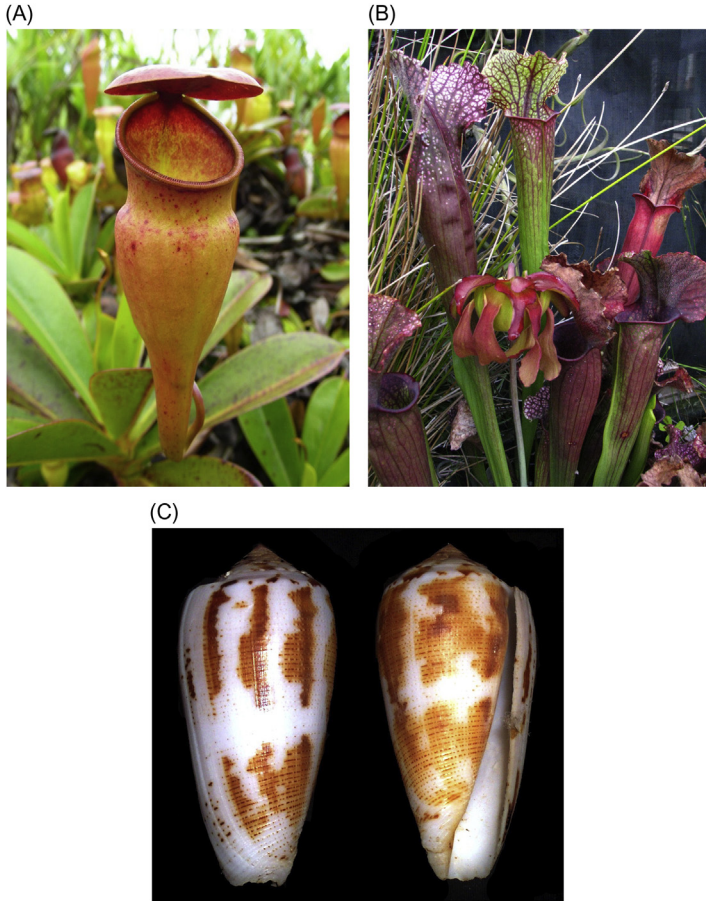


Figure 5.2 (A) Photograph of a species of *Nepenthes*, one of the pitcher plants, a plant with antifungal properties and medicinal value that were recently ascertained by scientists. (B) Photograph of a species of *Sarracenia*, another pitcher plant (distantly related to the *Nepenthes* in (A)); this is the source of sarapin, a compound of medicinal value. The close relatives of this species produce similar active compounds. (C) Photograph of *Conus magus*, the cone snail; neurotoxins that are naturally produced by this snail for paralyzing and capturing prey have been found to have uses in medicine as pain killers. *Wikipedia Free Commons*.

But the chemical constituents in these plants had until recently not been studied in great detail across all species of another group of pitcher plants, *Sarracenia* and related genera. A recent in-depth survey of numerous species and multiple genera of Sarraceniaceae pitcher plants not only provided a detailed survey of the chemical composition of numerous

species, but also showed that chemical composition was highly correlated with phylogeny—that relationships are predictive (Hotti et al., 2017). This study represents a focused example of how phylogenetic trees are already forming the underpinning for more and more investigations of plants and medicinal compounds.

Another wonderful example of the value of unanticipated new medicines, as well as the importance of the basic research that yields these discoveries, traces to marine sea snails. Who would think that the venom of a poisonous sea snail, *Conus magus* (Fig. 5.2C) (McIntosh et al., 1982; Skov et al., 2007), could yield a new drug? A young scientist (B. Olivera) was fascinated by the ability of these organisms to produce a venom that can paralyze and kill prey. Years of research on the toxic compounds in these venoms resulted in the discovery of ziconotide, a nonaddictive drug, more powerful than morphine, that is used as a treatment for the chronic pain associated with cancer and AIDS.

There are similar examples of drug discovery in other marine organisms—for example, a bacterium that lives in close association with the bryozoan (*Bugula*) and secretes a substance that covers the larvae of the bryozoan and makes them distasteful to predators (Proksch et al., 2002) is the source of a potential Alzheimer's disease and cancer drug (Singh et al., 2008; Ruan and Zhu, 2012). As with many newly discovered chemical compounds useful to humans, the substance was discovered by basic, discovery-driven research as part of a survey of marine organisms for potentially beneficial chemical compounds (see <https://pubs.acs.org/cen/coverstory/89/8943cover.html>). Use of the Tree of Life and careful examination of close relatives of this bryozoan (or more specifically, close relatives of the bacterium) may be a useful way to find additional effective drugs.

Because closely related species often produce similar chemicals, the Tree of Life can be a road map to the discovery of new medicines. There are many such examples, but a classic case involves the Pacific yew (*Taxus brevifolia*; Fig. 5.3A) from western North America. This relative of pine trees is the original source of the drug paclitaxel (PTX0, sold using the brand name Taxol), a medicine that has been used to treat several types of cancer (Jordan and Wilson, 2004). From 1967 to 1993, nearly all paclitaxel was derived from bark obtained from the Pacific yew. But because the Pacific yew is uncommon and the process of obtaining the bark for medicine is a destructive process that kills the tree, the species is a problematic long-term source of the drug. Consequently, another source of

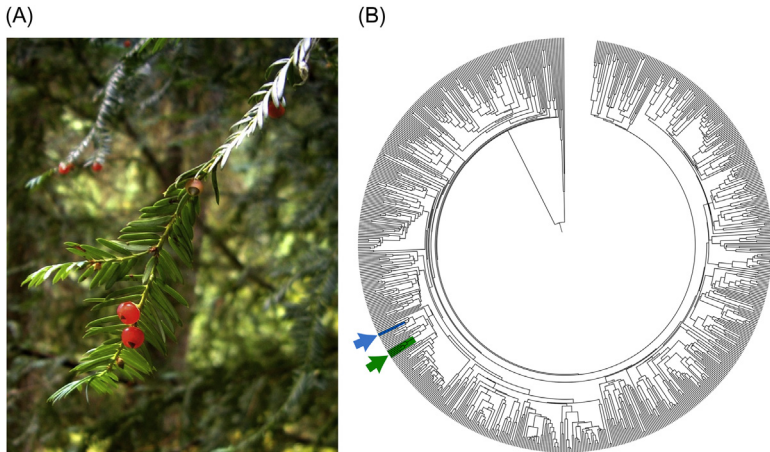


Figure 5.3 (A) The Pacific Yew, *Taxus brevifolia*, the original source of the cancer-treating drug Taxol. This species is rare, however. Using a tree of relationships, a close relative of this species from Europe (a species that is common) became the commercial source of Taxol until the drug was ultimately produced synthetically. (B) Chemical compounds of possible medical use to humans are often localized or clustered on the plant Tree of Life—these are “medicinal hotspots.” Two such hotspots are shown here (in blue and green) in this circle tree of relationships of the flowering plants. Tree modified here to show useful chemistry of Solanaceae (tomato family) and Apocynaceae (dogbane or milkweed family). (A) *Wikipedia Free Commons*. (B) *Tree from Magallon, S., Gomez, S., Sánchez Reyes L.L., Hernández-Hernández, T., 2015. A metacalibrated time-tree documents the early rise of flowering plant phylogenetic diversity. New Phytol. 207. doi:10.1111/nph.13264. The tree is from Dryad and has no use restrictions. Tree modified here to show useful chemistry of Solanaceae (tomato family) and Apocynaceae (dogbane or milkweed family).*

the drug was needed. To find chemicals similar to what the Pacific yew produces, where do we look? Rather than randomly examining all 350,000 species of seed plants, the best approach is to use the Tree of Life to focus on the closest relatives of this species—and that is what was done. A commonly grown related species, the European yew, *Taxus baccata*, was then instead widely used in medicine until Taxol ultimately was made synthetically.

We also know that there are hotspots in the Tree of Life in which similar pharmacologically active compounds are produced by closely related species. These are excellent examples of how relationships matter. Consider the flowering plant families Solanaceae and Apocynaceae (indicated with blue and green in Fig. 5.3B); both are characterized by the production of diverse alkaloids that serve a defensive (antiherbivory) role.

In Solanaceae, the nightshade family (also the potato and tomato family), approximately 20 of the 90 genera have at least one or more species with medicinal properties. There are many well-known medicinal plants in the family including the nightshades (*Solanum*), belladonna (*Atropa*), pepper (*Capsicum*), jimsonweed (*Datura*), tobacco (*Nicotiana*), and mandrake (*Mandragora*); there is much medicinal potential remaining in the family with many species and genera still requiring detailed chemical characterization (Shah et al., 2013).

Just as is the case with the nightshade family (Solanaceae), the flowering plant family Apocynaceae (milkweed family) also has numerous plants with chemically active compounds. One common name for the family is “dogbane,” referring to the fact that species in the family are poisonous for dogs. In fact, many members of Apocynaceae are poisonous, and again many have useful medicinal properties (Anderson, 1967). The family is a hotspot for chemical compounds, including cardiac glycosides used in heart ailments (e.g., the genera *Acokanthera*, *Apocynum*, *Cerbera*, *Nerium*, *Thevetia*, and *Strophanthus*). Other genera contain active alkaloids that have applications in the treatment of cancer (*Catharanthus*), and still others have uses in relieving high blood pressure (*Rauwolfia*) or produce alkaloids with potentially beneficial psychoactive properties (*Tabernanthe*).

Despite the wealth of chemically active compounds in both Solanaceae and Apocynaceae, more medicinal discoveries are likely. For example, the applications in traditional medicine remain greatly underappreciated and understudied in species of both of these families, as well as in most families of plants in general. Just recently, in the Rajshahi district of Bangladesh, 14 species in 12 genera of Apocynaceae were identified with local medicinal uses (Rahman and Akter, 2015).

Fungi represent one of the great untapped parts of the Tree of Life for compounds of medicinal and other value to humans. Certain fungi have been major sources of useful medicinal compounds for human well-being (e.g., antibiotics) and offer enormous opportunity for discovering new compounds with diverse applications for human health (Katz and Baltz, 2016). To quote Tan et al. (2006), “Far from being mutually exclusive, biodiversity and genomics should be the driving force of drug discovery in the 21st century.” We include the use of trees of relationship as another important component of the pathway to medicine discovery.

Rather than randomly surveying thousands of plants (there are roughly half a million green plants) or fungi (more than 120,000 species have been named, but there may be over 5 million species of fungi) for

chemicals—the traditional approach—one can target hotspot areas or species closely related to known species of medical value. Such focused studies of known hotspots, coupled with the rapid evaluation of poorly known (dark areas) of the Tree of Life known to house useful compounds, may be the best path forward to the discovery of useful medical compounds (e.g., [Cragg and Newman, 2013](#); [Katz and Baltz, 2016](#)).

But the practical value of the Tree of Life in terms of materials that may benefit our species includes far more than chemicals that provide medicines. The silk of spiders is incredibly strong and therefore has long been the source of interest for human needs in everything from lightweight shoes to support structures. Recent efforts that seek to combine knowledge of the structure of spider silk obtained from basic research with molecular genetic methods to produce these silk compounds in bacteria show signs of promise ([Pennisi, 2017](#); [Service, 2017](#)).

DISEASE

Trees of relationships are now part of the first line of defense in combatting diseases. For example, when a new flu strain is detected, one of the first steps performed by researchers is to sequence the DNA of that strain and then gene sequences from that strain are compared using a phylogeny to other known viruses—in this way, a better understanding of the relationships of that strain can be quickly understood (see specific example below). That information allows more rapid vaccine development, based on knowledge of what has been employed as successful vaccines in what are determined to be closely related strains.

The appearance of new pathogens in humans following transfer to our species from other species poses special problems for vaccine development because the source of the new pathogen is not always clear. By sequencing these pathogens and using phylogenetic methods (tree building), the pathogen can be placed in the Tree of Life and its likely original host species determined. Consider SARS (severe acute respiratory syndrome), one of the classic examples of the use of phylogeny in tracing the origin of an infectious disease in humans. The presence of SARS in humans was first noted in China in November, 2002, and the disease ultimately spread around the globe to 30 countries and infected thousands of people worldwide. SARS resulted in hundreds of human deaths, as well as a worldwide health scare. It was clear that the original source was an animal species with transfer to humans, but the animal species that was the source of the

Phylogeny of SARS virus strains

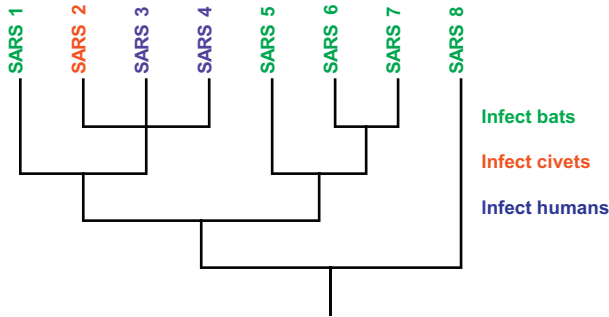


Figure 5.4 Use of a phylogeny to determine the origin of SARS in humans. Based on this simple tree, the closest relative of the strain in humans traces to two other mammals—civets or possibly bats. *Redrawn based on Eickmann, M., Becker, S., Klenk, H.D., Doerr, H.W., Stadler, K., Censini, S., Guidotti, S., et al., 2003. Phylogeny of the SARS coronavirus. Science 302, 1504–1505.*

virus that caused SARS in humans was initially unknown. However, phylogenetic analyses of DNA taken from viral strains occurring in various animals showed that human SARS traced its origin to civets and bats (Fig. 5.4; http://evolution.berkeley.edu/evolibrary/news/060101_batsars) (Eickmann et al., 2003; Guan et al., 2003).

Another classic example of the use of tree building in the study of disease is a case of HIV contracted in 1990 by a woman who had no real risk of obtaining HIV. This example is another “whodunit”, solved using a phylogeny. The HIV virus evolves rapidly, and it is often possible to match the HIV in a patient to the original source, or human donor. It was determined using DNA sequence data and a phylogeny that the woman obtained the disease from her dentist, who was HIV positive. In fact, several other patients also obtained HIV from the same dentist, as clearly seen in a phylogenetic tree (Ou et al., 1992) (Fig. 5.5).

Phylogenetic analysis and the Tree of Life can also be used to combat influenza, a rapidly evolving virus. Because many strains of the flu virus have been stored over many years, DNA phylogenies can be produced to represent these known strains. As new flu strains emerge, they can be sequenced and then added to that phylogeny. In fact, via phylogenetic analyses, it has been possible to predict the likely dominant flu strain that will emerge the following year. This process of phylogenetic analysis is helpful in producing new flu vaccines and serves as critical information

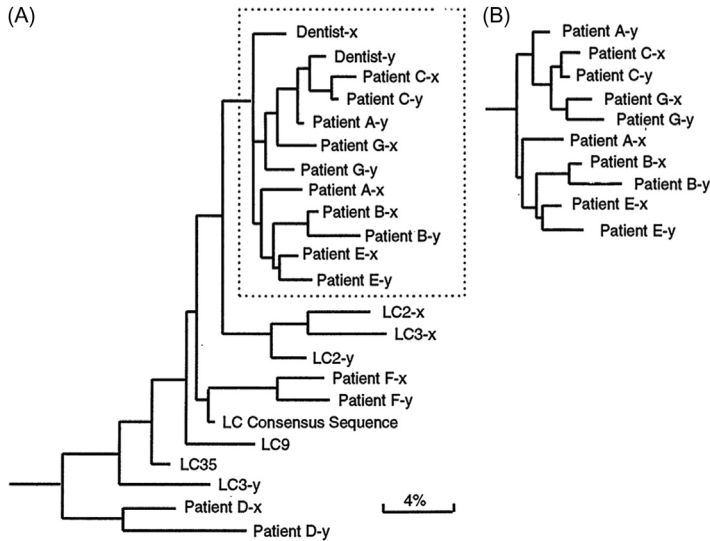


Figure 5.5 Use of DNA sequence data and a tree of relationships to track the transmission of HIV in a dental practice from dentist to some of the patients of that dentist. This is an example of the use of trees of relationship in detective work—to assess whether the dentist transmitted HIV to his patients. The tree indicates that he did. *Figure redrawn from Fig. 1 (A and B) of Ou, C.-Y., Ciesielski, C.A., Myers, G., Banda, C.I., Luo, C.-C., Korber, B., Mullins, J.I., et al., 1992. Molecular epidemiology of HIV transmission in a dental practice. Science 256, 1165–1171.*

for designing the vaccine from one year to the next (Fig. 5.6; Fitch et al., 1997; Bush et al., 1999; Cui et al., 2016, www.cdc.gov/flu/professionals/laboratory/genetic-characterization.htm).

CONSERVATION

Phylogenetically Distinct Species

There are also multiple applications of the Tree of Life for conservation. The importance of phylogeny as a tool for conservation has been well reviewed elsewhere, including in other books devoted solely to that topic (e.g., Purvis et al., 2005, and the chapters therein). Given the large number of possible applications of the Tree of Life to conservation efforts, we will only focus on a few topics here.

Probably the most straightforward instances of the use of phylogeny in conservation are those examples involving the preservation of individual species. Take the white-winged warbler (*Xenoligea montana*), for example.

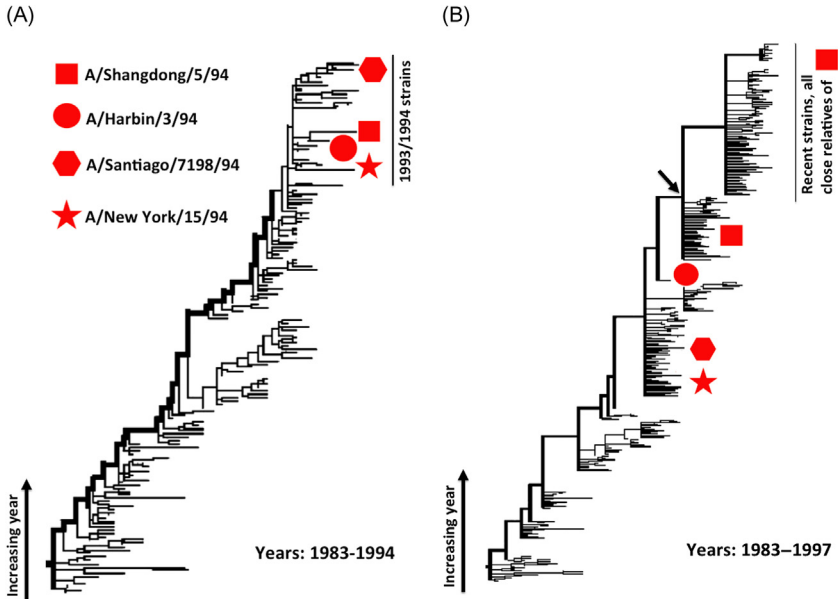


Figure 5.6 Predicting the evolution of human flu (influenza). [Bush et al. \(1999\)](#) examined the evolution of one domain of the human influenza or flu virus (domain HA1 of the H3 hemagglutinin gene). By building a phylogenetic tree, they found that a single dominant lineage persisted through time. Red symbols indicate several important recent strains. The tree in (A) shows the evolution of the HA1 domain from 1983 through 1994. Part (B) contains isolates from 1983 through 1997. In (B), the authors collapsed many branches of the tree for which they lacked strong support. Note that strain A/Shangdong/5/94 (indicated by a red square) descends from the node indicated by an arrow in tree B—this represents an uppermost node on (A) (A/Shangdong/5/94 is shown on both trees). This strain is further up the trunk of the tree in (B) than any of the other isolates from 1A—and it is also the isolate most closely related to future lineages (indicated by a vertical line). Thus, a tree can be used to predict future evolution of the virus. The authors also found evidence that 18 codons had been under selection in the past to change the amino acid they encoded. *Redrawn and modified from Bush, R.M., Bender, C.A., Subbarao, K., Cox, N.J., Fitch, W.M., 1999. Science 03 Dec 1999: 1921–1925 (see also Fitch, W.M., Bush, R.M., Bender, C.A., Cox, N.J., 1997. Long term trends in the evolution of H (3) HA1 human influenza type A. Proc. Natl. Acad. Sci. U.S.A. 94, 7712–7718).*

The white-winged warbler was long considered just one of many species of warbler . . . however, use of DNA data and the Tree of Life showed it was not a true warbler ([Fig. 5.7](#)) ([Klein et al., 2004](#)). In a phylogeny of birds, the white-winged warbler occurred on its own branch, outside of the group or clade of true warblers. Based on these data, the bird was placed in its very own family. And because it only occurs on Hispaniola,

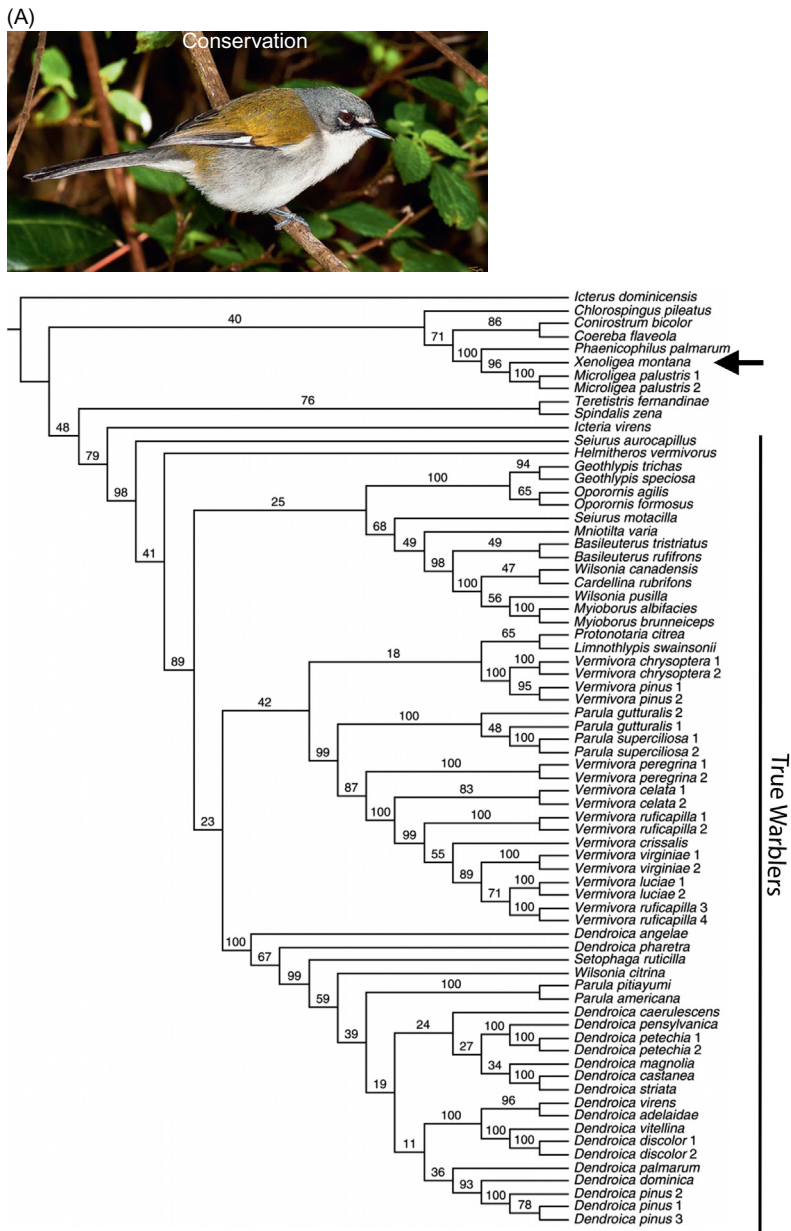


Figure 5.7 (A) The white-winged warbler, a bird that DNA data and the Tree of Life showed was not a true warbler. (B) Phylogenetic tree showing that the white-winged warbler (indicated by arrow) is not in the group (clade) with other warblers (true warblers indicated with vertical line). (A) From Dave Steadman. (B) From Fig. 1 of Klein, N.K., Burns, K.J., Hackett, S.J., Griffiths, C.S., 2004. Molecular phylogenetic relationships among the wood warblers (Parulidae) and historical biogeography in the Caribbean Basin. *J. Caribbean Ornithol.* 17, 3–17.

this distinct line of birds now merits extra conservation concern (Fig. 5.7).

A comparable example involving plants is *Amborella trichopoda*, a flowering plant that, until recently, was so poorly known that it does not even have a common name (consequently, we will refer to it simply as *Amborella* here). *Amborella* is a shrub or small tree and comprises perhaps only 12 populations, all restricted to the island of New Caledonia, which is over 1000 km off the east coast of Australia (reviewed in Soltis et al., 2008, 2017; *Amborella* Genome Project, 2013). *Amborella* remained largely unstudied and poorly understood until just a few decades ago, so its relationships to other flowering plants were unclear. Some researchers thought it was a member of the avocado or laurel family (Lauraceae), while other plant experts placed it in its own family (Amborellaceae), but still close to Lauraceae (reviewed in Soltis et al., 2008, 2017).

For decades, *Amborella* remained a poorly understood plant of very little broad interest to other scientists or to the public. But when DNA studies in the 1990s finally showed the placement of *Amborella* in the plant Tree of Life, that all changed. *Amborella* has the distinctive position as sister to all other living flowering plants (Fig. 5.8). That is, *Amborella* is to flowering plants what the duckbilled platypus is to mammals (Warren et al., 2008). This unique position in the flowering plant Tree of Life (Fig. 5.8) heightened conservation concern of *Amborella*, as this single surviving lineage of early angiosperms can provide critical insights into flowering plants.

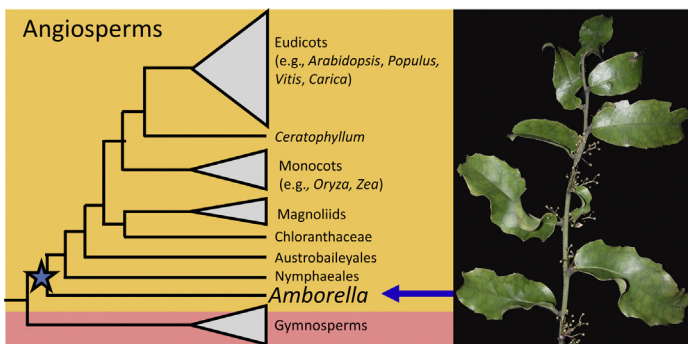


Figure 5.8 The flowering plant *Amborella trichopoda* and its pivotal position in the flowering plant Tree of Life as sister to all other living flowering plants. *Plant photograph* courtesy of S. Kim, Sungshin University.

Amborella has now been studied intensively because of its pivotal phylogenetic position. The complete genome of *Amborella* has been sequenced to provide an evolutionary reference for other flowering plant genomes and for applications in crop science (*Amborella Genome Project, 2013*). *Amborella* provides a baseline for comparison to help interpret gene and genome evolution in more derived flowering plants. Modern crops have highly complex and modified genomes—think of them as sophisticated fighter planes. If you know nothing about flight, these genomes are hard to interpret. *Amborella* is the genome equivalent of a biplane, providing the context needed to interpret the genomes of more complex, derived angiosperms (e.g., our crops) (*Amborella Genome Project, 2013*). All of this importance was only attached to *Amborella* once its position in the Tree of Life was ultimately realized.

Conservation Genetics—Breeding Programs

The Tree of Life can also play an essential role in designing breeding programs for the last survivors of a species. This lesson was learned too late for the dusky seaside sparrow, once native to the Atlantic Coast of Florida. When the numbers of this bird dwindled to a few males, a captive breeding program was designed using females from a geographically close subspecies of seaside sparrow, a program that failed (*Avise and Nelson, 1989*). Unfortunately, once a tree of relationships was later constructed for these birds, it revealed that the dusky seaside sparrow was most closely related to a seaside sparrow on the Gulf Coast of Florida rather than to geographically closer seaside sparrows as had been assumed. The captive breeding program should have involved this more closely related Gulf Coast subspecies instead, but insights from phylogeny came too late to save the dusky (*Fig. 5.9*).

There are other examples of how poor knowledge of organismal relationships can be deadly to those species. Conversely, other studies employing DNA markers and phylogeny have been useful in conservation, showing, as just one example, in freshwater mussels in Europe that populations actually remain of a rare species some had thought extinct; DNA data also revealed that those remaining populations are clearly genetically distinct from another closely related, more geographically widespread species. The two species had been confused because of their similar appearance (*Prie et al., 2012*).



Figure 5.9 Dusky seaside sparrow, an example of an organism that is now extinct where conservation efforts were not guided by a tree of relationships. Breeding programs to save the sparrow unfortunately did not pick the closest living relative of the dusky. *Free image online.*

Discovering Cryptic Species

For centuries, humans have identified and distinguished species based on physical appearance (morphology). But, two distinct species can appear so similar that biologists may have mistakenly considered them a single species. This topic was covered in Chapter 4. But to review, there are frog species that look nearly identical, but differ in their vocalizations, or calls; although difficult for us to distinguish by appearance, the frogs have no problem distinguishing each other. Similarly, there are plant populations that are very much alike in appearance and differ only in chromosome number—they cannot interbreed and have different environmental ranges. Distinct butterfly species may differ only slightly in spot pattern, or species that appear similar may have different behavior patterns. There are many other examples of cryptic species in other lineages, and they abound in nature, as reviewed in Chapter 4. As a result, we have grossly underestimated the number of species on our planet, even in those parts of the Tree of Life where we think we know a great deal (see Chapter 4). By using DNA sequence data and the Tree of Life, it is possible to more rapidly identify cryptic species. DNA sequence data and tree building (often

referred to as phylogenetic reconstruction) have been applied to address this question of cryptic species. This approach may reveal that two entities that look similar differ in DNA sequence and have different placements in the Tree of Life. This type of investigation has been applied to several geographic regions thought to harbor large amounts of still undetected biodiversity; using DNA data and comparisons with species already in the Tree of Life can identify such cryptic biological entities quickly (e.g., [Lahaye et al., 2008](#)). Such DNA approaches and use of the Tree of Life are becoming more commonly applied by specialists in the continuing search for as yet undiscovered and unnamed species.

Protecting Areas Rich in Biodiversity

Another use of the Tree of Life is in assessing biodiversity and determining which areas of the Earth are most important to protect. Biologists already have a general understanding of where many biodiversity hotspots are located, although new ones are often discovered and proposed (e.g., the North American Coastal Plain). Compilations of massive amounts of natural history specimen data can help with these assessments of where there are major concentrations of biodiversity (e.g., [Ulloa et al., 2017](#); [Givnish, 2017](#)). Phylogeny is also critical in determining which regions are home to the biggest part of the Tree of Life (e.g., [Vázquez and Gittleman, 1998](#); [Allen et al., in press](#); [Lu et al., 2018](#)).

An essential new conservation goal is to determine how much of the Tree of Life is present in any given area. This can be calculated using a phylogenetic tree and a measure called phylogenetic diversity (PD) ([Faith, 1992](#); [Mishler et al., 2014](#)). Exploring PD is now a major research theme in biodiversity studies. An estimate of PD is not the same as an assessment of either the total number of species or the number of rare species in an area, both commonly used metrics when discussing conservation. While all three measures are incredibly important, they reveal very different things. Imagine two areas in a very simple example ([Fig. 5.10](#)). Which do you protect? The most species, the rare species, or the largest swathes of the Tree of Life (i.e., protecting PD)? While protecting as many species as possible, especially rare species, is inarguably important, it may be more effective to spend resources to protect PD.

[Forest et al. \(2007\)](#) provide an early example of the use of PD and the Tree of Life for conservation. This study showed important implications for conservation in the Cape Region of South Africa, a floristically rich

Area 1: Oaks



Area 2: More Phylogenetic Diversity



Figure 5.10 Explaining phylogenetic diversity (PD). Consider two hypothetical geographic areas of the same size with the same number of species, all depicted here. The area at the top has many species of oaks, some of them very rare. The area shown on the bottom has a wide diversity of species. Although the area on the top may have more rare species, the area on the bottom has much higher coverage of the Tree of Life, and much higher PD.

area that is a well-known for its biodiversity. Using a phylogeny for the plants of the region, [Forest et al. \(2007\)](#) revealed that the area with the highest PD did not correspond to the area with the greatest number of rare species, further illustrating that while these measures of biodiversity are not correlated, they are both critical for conservation.

To provide additional examples of the study of PD, we use recent studies from Florida and China to illustrate use of the Tree of Life to assess where PD is distributed. China is amazing in its extent of plant diversity—the country is home to nearly 10% of the $\sim 350,000$ species of flowering plants in the world. Using a large phylogenetic tree for all the genera of China, as well as a second tree for the 26,978 named flowering plant species there, it was possible to assess how the major components of the present-day vegetation came together and what areas are home to the highest PD. In their study, [Lu et al. \(2018\)](#) discovered that the flora of eastern China harbors many of the older lineages in China; distant relatives often co-occur in this part of China, and it has higher PD than does western China. In contrast, western China shows the co-occurrence of closely related plants that appear to be the result of recent mountain uplift, the formation of the Qinghai-Tibetan Plateau, and a resulting rapid radiation in that area; as a result, it has lower PD than observed in eastern China ([Fig. 5.11](#)). These results are important because they

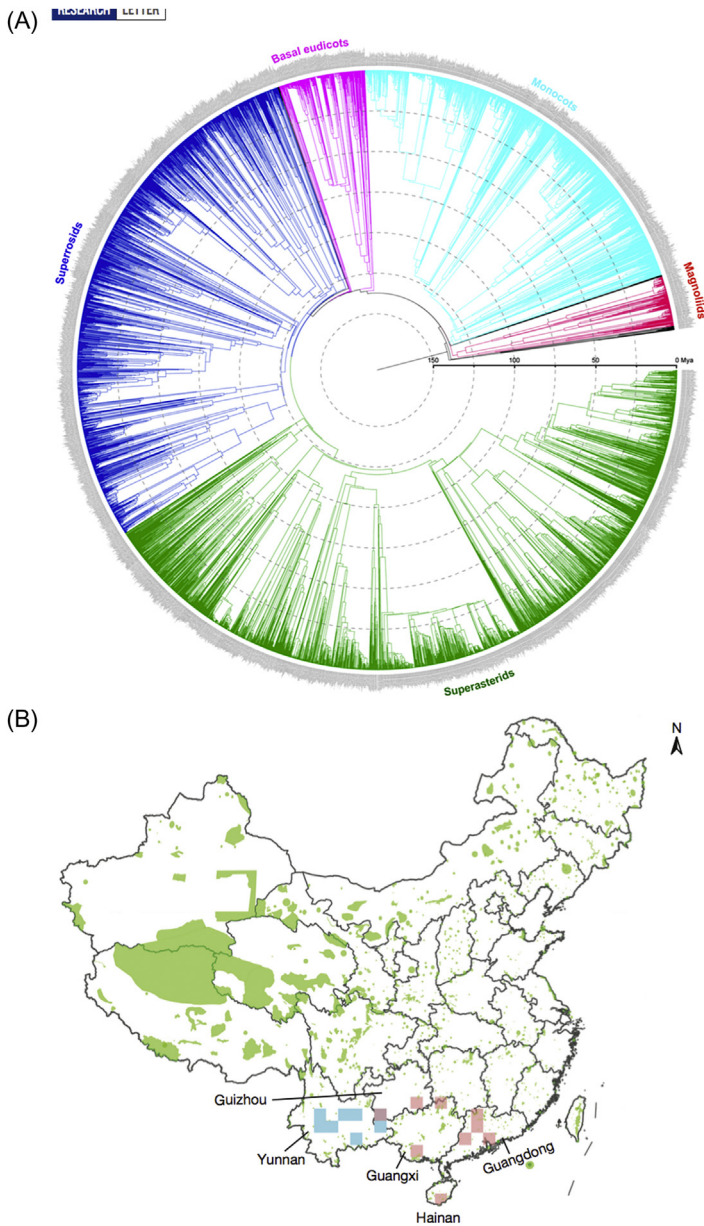


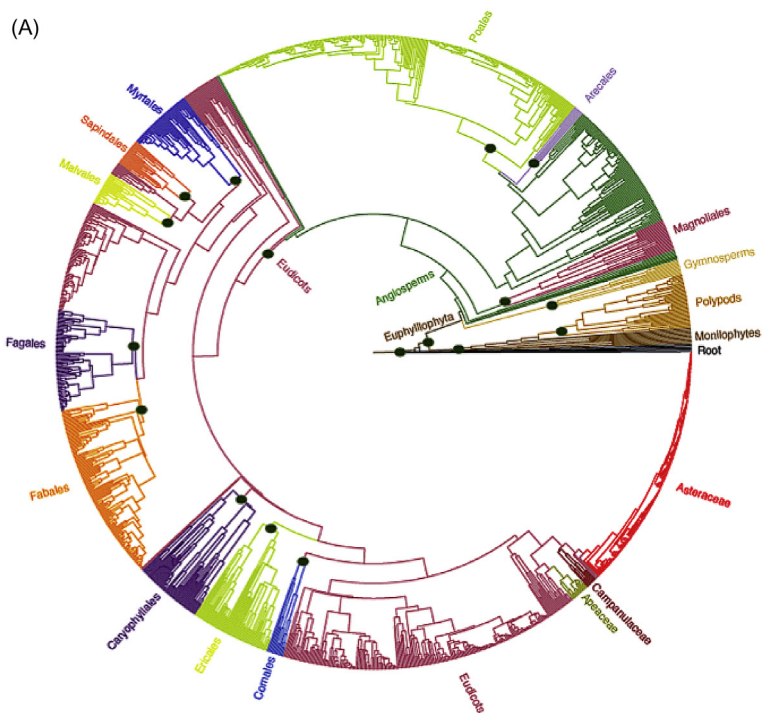
Figure 5.11 (A) Tree of relationships for the flowering plants of China. Major groups (clades), including magnoliids, monocots, superrosoids, and superasterids, as well as the basal eudicot grade, are indicated with different colors. (B) The distribution of plant phylogenetic diversity (PD) in China. Grid cells with the top 5% highest phylogenetic diversity at the genus (pink) and species (blue) levels. Protected areas are highlighted in green, showing that areas of highest PD in China are not protected. (A and B) From Lu, L.M., Mao, L., Yang, T., Ye, J.F., Liu, B., Li, H.L., et al., 2018. *Evolutionary history of the angiosperm flora of China*. *Nature* 554, 234–238. doi:10.1038/nature25485. (B) Maps adapted from National Administration of Surveying, Mapping and Geoinformation of China (<http://www.sbsm.gov.cn>; review drawing numbers: GS(2016)1576, GS(2016)1549).

identify areas of high PD and provide important data for conservation efforts. For example, the areas of high PD in western China are largely protected, but the same is not the case for areas of high PD in eastern China (Fig. 5.11). This lack of preservation of land in eastern China is often due to urbanization and the division of areas into different administrative units. Because the PD data indicate such high biodiversity in eastern China, an effective and supportive argument can be made for the necessity of more connectivity between national parks and nature reserves in that area (Lu et al., 2018).

Florida represents another good example of estimating PD for conservation purposes and future planning. With its many diverse habitats, Florida is also home to a highly diverse flora, including over 4300 species of vascular plants. Various locations in Florida are considered hotspots of biodiversity, including a portion of coastal Florida that is part of the North American Coastal Plain biodiversity hot spot (Noss et al., 2015) and the panhandle of Florida (Stein et al., 2000). This illustrates a problem with biodiversity hotspots—although important for conservation, there is no standard measure of assessment or calculation. This is why a measure such as PD is so valuable—it can be clearly defined, measured, and compared.

Importantly, Allen et al. (in press) found that PD was actually higher in the northern peninsula of Florida than in the coastal plain or peninsular hotspots (Fig. 5.12B). This can be explained in terms of the diverse habitats that come together in northern peninsular Florida (Allen et al., in press). In contrast, the Lake Wales Ridge, the high-elevation backbone of central Florida, is an area of low PD (see arrow on map of Florida in Fig. 5.12B). This ridge is an area well known for sand-scrub endemics—it is home to numerous closely related species, so the low PD is expected. Similarly, the Everglades at the southern tip of Florida also have low PD, reflecting its rather uniform habitat and species composition. The presence of a large number of closely related species in a region results in low PD, even if some of these species are rare (Fig. 5.12).

It is important to stress that no single biodiversity measure alone is right or wrong, whether it be the total number of species, the number of rare species, biodiversity hotspot designation, or estimate of PD; all are important ways to measure biodiversity. However, because PD is clearly defined, relies on the Tree of Life, and serves as a way to discover and hopefully preserve areas that are home to big pieces of the Tree of Life, it is important to measure PD and use it in making conservation decisions.



(B) Phylogenetic Diversity (PD) in Florida

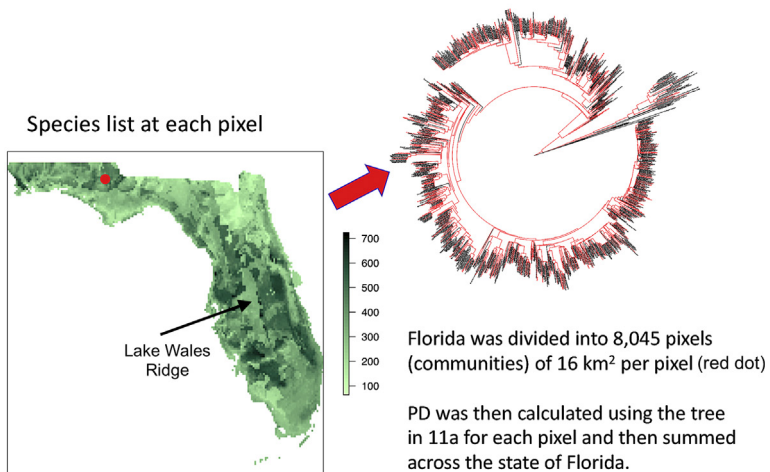


Figure 5.12 (A) Phylogeny of vascular plants in Florida—the Florida vascular plant Tree of Life. This tree was constructed based on gene sequence data. It contains 1498 species (38% of the species of vascular plants in Florida); 685 genera (44% of the total); and 185 families (78% of total). Major groups of plants are labeled and color-coded. (B) Using the tree in 12A to show where plant phylogenetic diversity (PD) is located in Florida. Florida was divided into 8045 pixel (communities) of 16 km² (the red dot in northwest Florida shows one such pixel). A species list for each pixel was then generated, and using the Florida Plant Tree of Life, the phylogenetic diversity of each pixel (community) was calculated and then summed across the state of Florida. If a species on the tree is in the pixel, it is colored red on the tree. Darker green on the map represents higher PD. The arrow on the map indicates Lake Wales Ridge, an area with low PD (light green). (A and B) From *Allen et al. (in press)*.

At a time in which the leaves (species) of the Tree of Life are quickly disappearing or under threat (see Chapter 6), measuring PD across large regions of the globe is the best way to assess which regions to protect to save as much of the Tree of Life as possible.

RESPONSE TO CLIMATE CHANGE

Phylogenetic trees are now also essential tools in ecology. As closely related species often respond in similar ways to changes in the environment, scientists can employ phylogenetic relationships to predict how species may respond to such events as higher temperatures or less water. In a rapidly changing world, this important implementation of the Tree of Life cannot be understated.

A group of flowering plants called Saxifragales—or saxifrages, sometimes amusingly referred to as sexy-frages, due to the plants' attractiveness—serves as a prime example of how phylogenetic relationships in the Tree of Life can be useful in projections of response to climate change (Fig. 5.13). This small group of about 2500 flowering plant species contains some well-known woody plants, including sweet gum, currants, and witch hazel, as well as ornamentals including peonies, piggyback plant, coral bells, *Sedum* (stonecrops), and mother of thousands (Fig. 5.13). Despite the small number of species in this group, the saxifrages have enormous habitat variation; some are temperate forest trees, others are desert succulents, another group arctic alpines, and still others aquatic.

Using a phylogenetic tree for Saxifragales, it is clear that habitat shifts are very rare in these plants (Fig. 5.14). This habitat constancy is obvious just looking at the colors that correspond to habitat types in Fig. 5.14. The colors correspond closely to lineages within the saxifrages. Once a habitat shift was made over evolutionary time, for example, to a desert or aquatic or alpine habitat, lineages do not switch (or only rarely switch) out of that habitat—changes in habitat are canalizing events, and those habitats are the ones in which that lineage remains for millions of years.

We can illustrate the rarity of major niche shifts or changes in organisms by mapping the temperature preferences of species in the saxifrages on a phylogenetic tree that encompasses the ~110–120-million-year history of the group. This exercise is valuable because it shows that the group originated from a temperate ancestor with multiple changes or adaptations to cold temperatures and to warm temperatures (Fig. 5.15). But, once a change was made to cold temperatures, the plants do not



Figure 5.13 The flowering plant group Saxifragales; photographs of plants showing the tremendous diversity in a small group of approximately 2500 species. (A) *Heuchera* sp. (“*Heuchera* × *bryzoides*”), (B) *Tolmiea menziesii* Torr. and A. Gray, (C) *Kalanchoe blossfeldiana* Poelln., (D) *Sedum middendorffianum* Maxim., (E) *Liquidambar formosana* Hance, (F) *Ribes rubrum* L., (G) *Paeonia* “Red_Charm” (*Paeonia lactiflora* Pall. × *P. officinalis* L.), (H) *Hamamelis* × *intermedia* Rehder, (I) *Saxifraga caesia* L. Photographs from *Wikipedia Free Commons*. Compiled by D. Soltis and E. Mavrodiev, Florida Museum of Natural History, University of Florida.

quickly switch to growing in warm temperatures. This is also the case when a few lineages adapted to warm temperatures millions of years ago—they do not then switch to cold.

This work illustrates what biologists refer to as *phylogenetic constraints*. This seems at first glance an intimidating term, but it simply means that features that have already evolved in these organisms will play a major role in what those lineages can do in the future. That is, the evolutionary history of a group (or phylogeny), indeed the entire Tree of Life, may constrain future evolutionary options. In the case of saxifrages, once a lineage is cold-adapted, it is hard to switch—that is a phylogenetic constraint. These are the additional major features that a phylogeny can reveal. Similar findings have been reported for diverse geographic areas as well as other very different lineages of life, including rattlesnakes (e.g.,

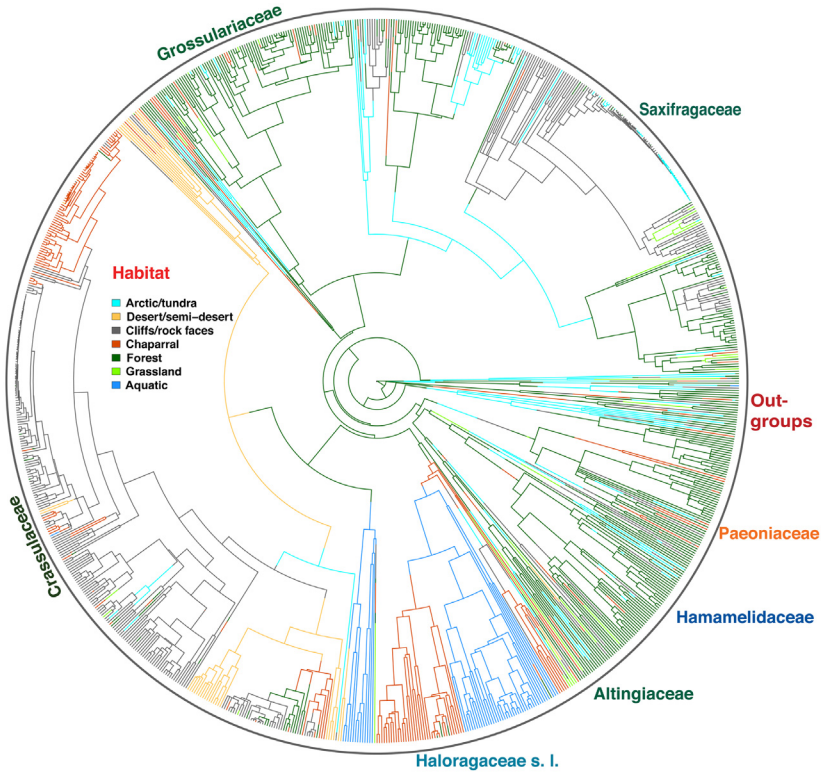


Figure 5.14 A tree of relationships for the flowering plant group Saxifragales, with habitat type mapped onto the tree using different colors. The group is highly diverse in habitat, with some species in desert, forest, arctic, and even aquatic habitats. Note that the colors correspond very closely to groups or clades (an ancestor and its descendants) in the tree. This shows that changes in habitat are rare, and when they do occur, they are often canalizing events. *For background see Soltis, D.E., Mort, M.E., Latvis, M., Mavrodiev, E.V., O'Meara, B.C., Soltis, P.S., Burleigh, J.G., and Rubio de Casas, R.R., 2013. Phylogenetic relationships and character evolution analysis of Saxifragales using a supermatrix approach. Am. J. Bot. 100, 916–929 and Rubio de Casas, R. R., M. E. Mort, and D. E. Soltis. 2016. The influence of habitat on the evolution of plants: a case study across Saxifragales. Annals of Botany 18(7):1317–1328.*

Kuntner et al., 2014; Lawing and Polly, 2011; Willis et al., 2008). These other studies, in addition to the case study of Saxifragales, indicate that it will be very difficult, and likely improbable, for many lineages of life to adapt to rapid climate change. The future of many lineages of life is indeed bleak—and using the Tree of Life, scientists can actually predict which lineages are most likely to have the greatest difficulty adapting to

Saxifragales: Ancestral Niche

- Temperature variables (e.g., **mean annual temperature**) suggest a temperate origin
- Shifts out of a state are rare

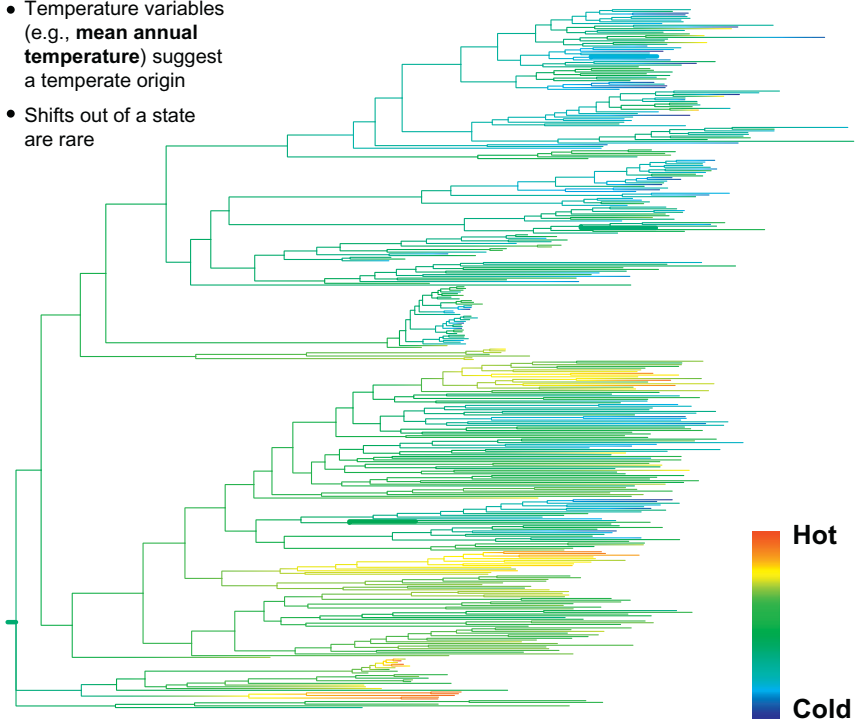


Figure 5.15 The response of members of Saxifragales to temperature using a tree of relationships (see above) and plotting the average mean temperature of species occurrence on the tree (the tree is now horizontal in orientation, not circular as in Fig. 5.14). By using a tree of relationships, it is clear that the group originally evolved over 100 million years ago in cool temperatures (probably as forest trees). As the clade evolved and new species emerged, some lineages became adapted to very cool temperatures (blue) and others to warmer temperatures (yellow/red). But these evolutionary changes are canalizing events (as seen also in Fig. 5.14). Cool-adapted lineages have remained so for millions of years and do not spawn new species that are warm-adapted. The future for such lineages under scenarios of rapid climate change is bleak. *From Ryan Folk, Florida Museum of Natural History, University of Florida.*

any dramatic change in climatic factors, whether it be temperature or moisture.

CROP IMPROVEMENT

The Tree of Life is also important for crop improvement. If crop scientists want to find a way to make a crop more water-efficient—an important

consideration today—or introduce disease resistance genes, where does one look for a source of genes (germplasm) for these goals? A common approach is to use knowledge of the Tree of Life to determine the crop's closest relatives to see if a closely related species has the trait of interest.

The critical importance of knowledge of phylogeny, the Tree of Life, to agriculture and crop improvement is vastly underappreciated. Some of our crops would not have survived without the introduction of genes from wild relatives. Consider sugarcane. “If no germplasm from wild relatives had been used there would probably not be a viable sugarcane industry in any place in the world” (J.D. Miller, USDA).

Also consider cultivated squash. Cultivated squash species require a considerable amount of water, but phylogeny reveals a group of close relatives of the cultivars that are drought-tolerant. These related, drought-tolerant species could provide a source of germplasm for crop improvement to help make the cultivated squashes more water-efficient (Fig. 5.16).



Figure 5.16 Cultivated species of squash and pumpkin (*Cucurbita*) require a great deal of water. Using a phylogeny for all species of *Cucurbita*, the cultivars were found to all be part of a mesic or wet-adapted clade. However, a tree of relationships reveals close relatives of the cultivars that are dry-adapted—these species are from the arid Southwest of the United States, as shown here. These closely related dry-adapted species are possible sources of germplasm for breeding purposes and ultimately the production of cultivars with greater water-use efficiency. This represents one example of how the Tree of Life can be used in agriculture. From Heather Rose Kates, Florida Museum of Natural History, University of Florida.

Legumes (Fabaceae; the bean family) represent the second most economically important family of plants after the grasses. Traditional efforts in crop breeding involved assessing genetic diversity among lines of domesticated species. Recently, however, the importance of phylogeny has increasingly emerged in legume breeding efforts (Smykal et al., 2015). Knowledge of the legume Tree of Life is crucial for understanding the origin, evolution, and ecology of legume crops. Many legume crops still have wild relatives in nature (unlike some of our cereal and mustard crops), so identifying these relatives can provide crucial information to improve disease resistance, water-use efficiency, and yield.

An excellent example of how the impact of knowledge of phylogeny can influence applied research can be seen in efforts to move the process of nitrogen fixation from legumes to other crops. Farmers and nonfarmers alike remain aware of the traditional process of crop rotation, in which a legume crop (e.g., alfalfa) is grown after a grain crop, such as corn, to enrich the soil with nitrogen. This is made possible because many legumes have special structures on their roots called nodules, which house special bacteria that can convert nitrogen from the air into nitrates that the plant can use. This adaptation enables legumes to thrive in poor soils. In many regions, crop rotation has largely been replaced by the application of large amounts of nitrogen-containing fertilizers.

Although these fertilizers have vastly increased the ease of growing the same crop annually, they also have shortcomings. The runoff containing these fertilizers, for instance, can prove immensely damaging to aquatic ecosystems. Another drawback of these fertilizers is their high cost in terms of both energy and finances. These issues have helped heighten a decades-long interest in understanding the mechanism used by legumes to produce nodules, moving this capability to crops that lack it, and then growing these plants without the use of fertilizers. Imagine the positive possibilities of growing numerous crops in poor or marginal soils at a potentially lower cost without the negative environmental effects of fertilizers.

It is also important to note that legumes are not the only plant family with species that have the ability to house nitrogen-fixing bacteria in root nodules. Nine other flowering plant families—including *Ceanothus* (wild lilac), members of the rose family, and a relative of cannabis—have similar capabilities. Because these plants look very different, they were long considered distantly related, implying that nodule production evolved over and over again. However, phylogenetic studies revealed—to the surprise of most botanists—that all of the plants that house nitrogen-fixing

bacteria in root nodules are very closely related, meaning that the ability to produce root modules may have evolved just once. There is a single underlying mechanism that must be elucidated to move a cassette of genes from plants that can fix nitrogen via their bacterial partners to non-nitrogen fixers. In the past, research focused just on legumes to increase our understanding of nodulation. Now, however, research is focusing on these other members of the nitrogen fixing group to find the commonalities among species representing all ten families of plants with this ability. Importantly, this research strategy was made possible by improved understanding of the Tree of Life.

Trees of relationships are similarly used to determine the close relatives of plants of horticultural importance, and that information can then be used to select wild species and traits of interest for improvement of ornamental species (Handa et al., 2006; Takashi et al., 2006). For example, Japanese azaleas (*Rhododendron*; family Ericaceae) are widely cultivated and prized for their flowers. By using DNA data and building a tree of relationships, the closest relatives of the cultivated species were determined. These close wild relatives have desirable traits for breeding, including flowering time, different flower shapes and colors, and traits of cold and shade tolerance that could be used for improvement of Japanese azaleas.

PHYLOGENETIC DETECTIVE: FORENSICS AND THE TREE OF LIFE

The Tree of Life now plays a major role in detective work. In a manner similar to that of your favorite TV show involving forensics, DNA markers and the Tree of Life can be used to solve crimes. In what is essentially biodiversity forensics, a tool called DNA barcoding can be used to identify a species from a small amount of material or tissue. In this process, a genetic marker (a DNA sequence from one or more regions of the genome) is used to determine which species in the Tree of Life matches the DNA of the organism of interest (Fig. 5.17). Examples of the application of DNA and the Tree of Life in detective work range from the sale of mislabeled fish, to the smuggling of drugs, to the illegal harvesting of protected species. These approaches can also be used for conservation and the nondestructive assessment of the frequency of rare/endangered species. Several examples are reviewed below.

When you buy fish at the market or order it at a restaurant, how do you know it is cod, tuna, mackerel, or whatever species you think you

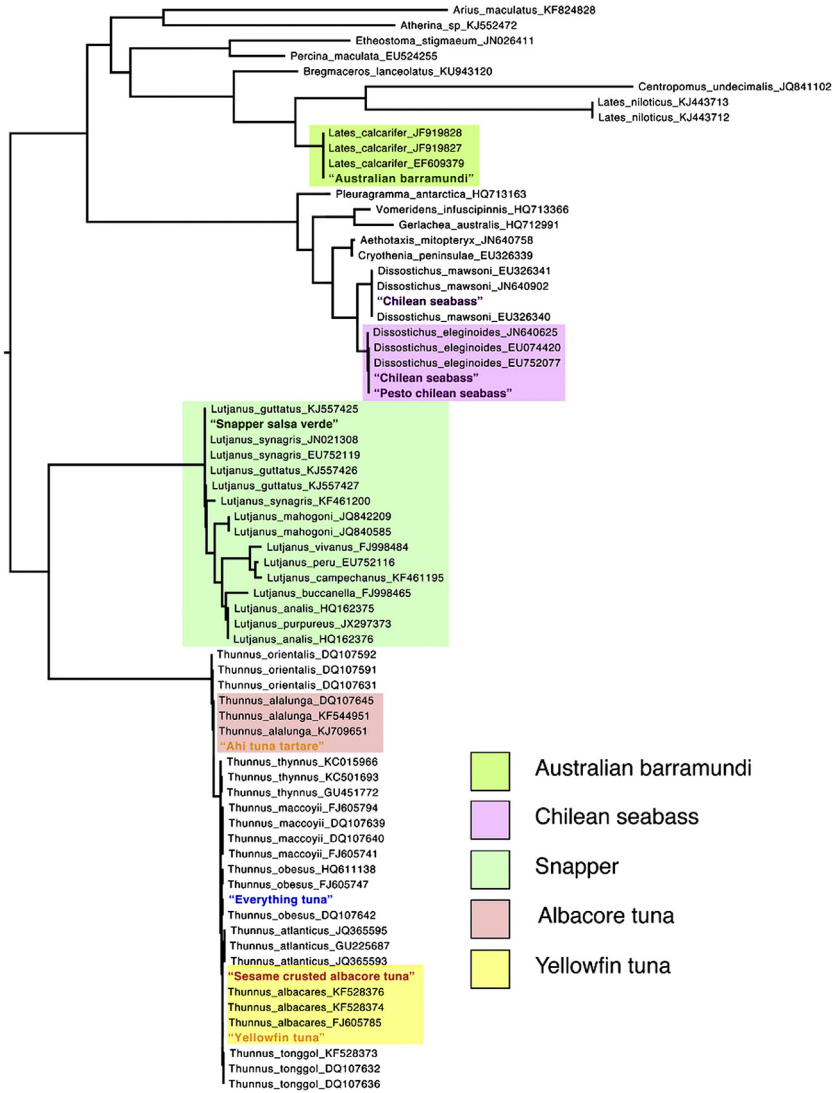


Figure 5.18 Tree of relationships based on DNA sequence data showing how the true identity of fish used in restaurants can be determined. DNA from a fish labeled “Snapper” in the market should appear in the tree shown here with other snapper samples. If that DNA appears with another species, the buyer has been misled—in fact, many of the fish on restaurant menus were found to be incorrectly named. Open access: Stern, D.B., Nallar, E.C., Rathod, J., Crandall, K.A., 2017. DNA barcoding analysis of seafood accuracy in Washington, D.C. restaurants. *Peer J.* 5, e3234. <https://doi.org/10.7717/peerj.3234>.

and the Tree of Life can also be used to detect the smuggling of other drugs, such as cocaine and fragments of marijuana (*Cannabis sativa*) (Coyle et al., 2003; Linacre and Thorpe, 1998; Staginnus et al., 2014).

Illegal logging and trading of timber are now major problems worldwide, resulting in threats or loss of rare plant species and threatened populations (UNOC Best Practice Guide for Forensic Timber Identification, 2016). The logging of dipterocarp forests in southeastern Asia serves as a prime example. Dipterocarps were once the dominant forest trees in much of southeast Asia, but the highly prized wood of these species resulted in their decimation. Some dipterocarp species are rare and endemic to certain small areas and are therefore protected. Consequently, poachers attempt to transport logs of these rare species, which resemble common species, once cut. Using DNA barcodes, however, it is possible to differentiate among dipterocarp species and detect logs of rare species that have been illegally harvested (Finkeldey et al., 2010; Dormontt et al., 2015). Various other endangered plants and animals can also be smuggled across borders, and DNA sequences and use of the Tree of Life for comparison can similarly be used to identify species listed in the Convention on International Trade of Endangered Species (CITES) appendices (Lahaye et al., 2008).

Another use of the Tree of Life illustrates the enormous power of “tree knowledge” in a way that would have been hard to imagine or anticipate even a few decades ago. In aquatic ecosystems, assessment of the fauna living there (e.g., fish and amphibians) has typically required netting or electrical shock methods that temporarily stunned organisms so they could be counted and inventoried. Both processes, however, are harmful methods of census for many organisms and perhaps not the best way to assess the population sizes of rare species.

Enter environmental DNA as an important diagnostic tool to probe aquatic ecosystems and determine the fish and amphibian species that are present in a nonintrusive manner. As aquatic organisms swim, they naturally slough off cells into the environment. DNA detection methods are very sensitive—so sensitive that it is possible to sample water from an aquatic habitat and examine the DNA fragments in that sample of water via amplification and DNA sequencing and then match those DNA sequences against data for living aquatic organisms, allowing one to assess which species in the Tree of Life are present in a particular aquatic location. In this way, the presence or absence of rare species can be assessed without disturbing them, and the existence of introduced species can also

be determined without harm to the native species (e.g., Valentini et al., 2016; Olds et al., 2016; Evans et al., 2016).

ECOSYSTEM SERVICES

It is clear that healthy ecosystems rich in biodiversity play a major role in our own survival. In other words, the Tree of Life and biodiversity are also fundamental to what are termed “ecosystem services” (Naeem et al., 2009; Costanza et al., 2014). These are broadly defined as the numerous benefits *Homo sapiens* naturally obtains from properly functioning ecosystems. Some of these ecosystem functions seem obvious once we consider them and include things such as clean water, fertile soils, and pollination of plants (including our crops). Healthy ecosystems also reduce flooding, moderate climate, provide clean air, and reduce disease. There are additional recreational and spiritual (mental health) benefits to healthy ecosystems.

Four broad categories of ecosystem services are recognized (Table 5.1): *provisioning*, including providing water and food; *regulating*, such as the control of climate and even disease; *supporting*, such as various nutrient cycles and natural pollination; and *cultural*, which includes recreational opportunities and mental health (Holzman, 2012).

Areas that represent healthy ecosystems are each home to a broad swathe of the Tree of Life. However, during the Anthropocene, rapid changes have occurred in the structure and function of ecosystems, and the pace of ecosystem degradation continues to accelerate (see Chapter 6). As leaves (species) and even entire branches of the Tree of Life are lost from ecosystems, the ability of those ecosystems to function and provide these diverse ecosystem services we humans take for granted is compromised or destroyed (e.g., Palmer et al., 2004; Kremen, 2005).

Ecosystem services have largely been unappreciated and typically are not accounted for in terms of economic impact or cost of the benefits they provide. Such underappreciation of the importance of biodiversity and healthy ecosystems, however, has begun to change over the last few decades. Costanza et al. (2014) first provided an estimate for ecosystem services (based on data for 1997), suggesting that on a worldwide basis they could be valued at ~\$33 trillion annually (>\$44 trillion today). Although any such numbers are hard to evaluate and can be controversial, they are a step in the right direction. Without a healthy Tree of Life on a worldwide basis, humanity will suffer greatly—a price tag that is too high

Table 5.1 Summary of ecosystem services

Provisioning services. These species maintain the supply of natural products that are required for human survival. These include food, timber, fuel, various fibers used for clothing, water, soil, medicinal plants, and animals.

Regulatory services. These species facilitate the smooth operation or running of our natural world. As examples, these elements filter pollutants to maintain clean air and water; they also help moderate the climate, work to sequester and store carbon. The recycling of waste and dead organic matter is also included here as are the natural controls of organisms considered agricultural pests and vectors of disease.

Supporting services. These are the services that maintain the provisioning and regulatory services noted above. Include here is the formation of soil, the vital process of photosynthesis by which plants convert sunlight into food by using carbon dioxide and releasing oxygen; these services provide for a healthy habitat. Healthy habitats maintain species diversity as well as genetic diversity; both are the crucial framework of all provisioning and regulatory services noted.

Cultural services. These include the diverse benefits to human well-being that come from contact with nature, including positive psychological and spiritual impacts. These benefits all result from diverse aspects of human culture (e.g., hiking, boating, visits to wild and scenic areas, bird watching, fishing, hunting, gardening). These services have clear health benefits (e.g., stress reduction).

Modified from Holzman, D.C., 2012. Accounting for nature's benefits: the dollar value of ecosystem services. *Environ. Health Perspect.* 120, A152–A157.

to fathom. Therefore, guarding or protecting the Tree of Life is important so as to ensure a healthy environment for the survival of our own species.

MORAL RESPONSIBILITY AND MENTAL HEALING

In the sections above, we have argued for the importance of knowledge of the Tree of Life, largely from a utilitarian standpoint. However, several authors, including [Gorke \(2003\)](#), have argued that a perspective centered on the benefit to our own species is “not only shortsighted but morally bankrupt” (<https://www.kobo.com/us/en/ebook/the-death-of-our-planet-species>). There is intrinsic value to nature and the many species on our planet. In a way, this relates to what some might refer to as the spiritual benefits of the Tree of Life.

The value of biodiversity extends beyond the dollars and cents of the economic value of medicines, crop relatives, and ecological services of clean air and water ([Naem et al., 2009](#); [Costanza et al., 2014](#)). Nature

and biodiversity should be protected for the simple reason of their intrinsic beauty and value; even this aspect of biodiversity provides highly significant benefits to our species. Biodiversity provides the inner peace and tranquility that comes from a walk in the woods, a trip to the mountains, or a day spent on a river or lake. Make no mistake, there is an economic benefit to *H. sapiens* for the tranquility that biodiversity provides. Studies have shown the benefits of biodiversity (and the Tree of Life that connects it) to relieving stress and enhancing the quality of life in humans. Nature is our home—we are not originally creatures of enormous concrete cities, but of woodlands and savanna, and when green spaces are provided, residents of large cities often flock to even these seminatural areas.

Several authors have discussed the physical and emotional impacts on humans that result from the loss of biodiversity (see chapters in [Chivian and Bernstein, 2008](#)). Although many recent papers and books now espouse the value of the Tree of Life for mental health, the importance of biodiversity from the standpoint of mental health and spiritual well-being has long been recognized and has a rich history tied to some of the major writers, poets, and philosophers in the United States. Early important figures include Ralph Waldo Emerson, who had a large impact on Henry David Thoreau. Thoreau was deeply influenced by nature and the spiritual healing it afforded. His writings of living in nature in the northeastern United States (“Walden”; [Thoreau, 2004 \[1854\]](#)) represent a classic example of the spiritual value of biodiversity. “I went to the woods because I wished to live deliberately, to front only the essential facts of life, and see if I could not learn what it had to teach, and not, when I came to die, discover that I had not lived. I did not wish to live what was not life . . .”

In the western United States, John Muir’s travels and experiences in nature shaped a conservation movement; he cofounded the Sierra Club and influenced generations of people worldwide (http://vault.sierraclub.org/john_muir_exhibit/life/). Muir, who was greatly influenced by Thoreau, similarly espoused the spiritual value of nature, of biodiversity, of the Tree of Life . . . “Keep close to Nature’s heart . . . and break clear away, once in a while, and climb a mountain or spend a week in the woods. Wash your spirit clean.” ([Muir, 1918](#), first printed in 1890; reprinted in 1918).

DEVELOPING COUNTRIES—THE MOST TO LOSE

The areas that have the most to gain from the Tree of Life are often in the biggest jeopardy of species loss and thus have so much more to lose. The tropics are home to the greatest proportion of terrestrial biodiversity, and yet many countries in these same areas are often jeopardizing their own future for short-term gain. In these same areas, poor people living outside of large cities in rural areas or remaining areas of rainforest actually depend on biodiversity (a functional Tree of Life) for their well-being and very survival (e.g., [Byg et al., 2007](#); [Mertz et al., 2007](#); [Peters et al., 1989](#)). The long-term goals of conservation efforts and those of native or indigenous peoples are similar—protect the Tree of Life; but the interactions have sometimes been problematic ([Dowie, 2009](#)). Native peoples should not have to choose between survival and conservation. As noted by [Dowie \(2009\)](#) and paraphrased here, when conservation efforts and indigenous peoples work together and acknowledge the interplay and interdependence of biodiversity conservation and cultural survival, they can produce a novel and more effective conservation paradigm—this is a crucial realization.

There are many examples of thoughtful conservation efforts that take this approach of protecting native peoples and their cultural heritage while preserving the Tree of Life; those involving ecotourism are a typical case in point. But other examples get less attention, but may be more effective. For example, we consider here the people in the Amazonian area of Guyana. The arapaima, native to the Amazon basin, is the world's largest scaled freshwater fish—they can reach up to 200 kg (400 lb) in weight. Four or five species may currently exist (one or more may be extinct), but they are not well studied so experts are not really sure how many species there are—another great example of our poor understanding of the Tree of Life. Arapaima have long been hunted for food by indigenous peoples of the Amazon. But, with the incursion of Europeans, the arapaima was harvested in large numbers. As a result of this recent overfishing, they are now considered vulnerable to extinction. The species is an unusual, distinctive lineage in the Tree of Life with no close living relatives. However, these fish are also prized for sportsfishing. Recently, catch and release fly fishing was introduced as a means to protect not only this species but also the land of the native peoples where these fish are found—the income and protection of the land also protects the native peoples' way of life. Sports fisherman will pay large amounts to

fish for this species. In addition, members of the village serve as fishing guides and cooks. Fishing has made it far more worthwhile to protect the fish than to hunt and eat them (Purnell, 2018).

The loss of biodiversity in developing countries has many sources—destruction of forest for oil palm (Byg et al., 2007) or for soybeans in Brazil (much of which ultimately feeds pigs and chickens for fast food restaurants worldwide) or cattle ranching (Kirby et al., 2006) or timber resources (Fernside, 2005)—most of which then end up in wealthy countries. These activities provide only short-term gain for the people who make those areas home. The longer-term consequences of that damage to the Tree of Life are significant for the peoples in those areas, but the overall global impact is also enormous.

Solutions to the biodiversity (Tree of Life) crisis in developing countries are varied and highly complex and well beyond the scope of this short book. Obvious solutions (but not necessarily easy to implement) include sustainability, ecotourism, and even local recreational fishing and hunting. Without biodiversity, these pastimes or hobbies are not possible.

The world's wealthiest countries already make a considerable investment in protecting biodiversity in developing countries as well as in training scientists from those countries. But, while developed countries now pledge large amounts to help protect biodiversity in developing countries (~\$10 billion annually as of 2015), these amounts are low when one considers the estimated amount needed to curb the loss of biodiversity (~\$80–200 billion) ([//india.blogs.nytimes.com/2012/10/23/developing-countries-turn-to-each-other-for-conservation/](http://india.blogs.nytimes.com/2012/10/23/developing-countries-turn-to-each-other-for-conservation/)). While funds to protect biodiversity in developing countries, as well as the important investment in training scientists from those countries to go back to help their home countries do make an enormous difference, ultimately more people in the developing countries have to have ownership—more self-directed and owned initiatives that will promote saving the Tree of Life from within rather than primarily from without.

CONCLUSION

As discussed in Chapter 6, what we don't know can hurt us! There are numerous reasons to be concerned about a sixth mass extinction and the rapid loss of species over a relatively short time frame—the loss of organisms that directly or indirectly hold the key to cure a human disease or improve the human condition. Many organisms have a hidden value as

components to ecosystems—often underappreciated. As aptly stated by [May \(2011\)](#), “We are astonishingly ignorant about . . . how many [species] we can lose yet still maintain ecosystem services that humanity ultimately depends upon.” Ecologists have long evoked a rivet hypothesis ([Ehrlich and Ehrlich, 1981](#)) to explain the crucial impact of species loss. Imagine an ecosystem as a large complex airplane, held together with many rivets. As more and more rivets are lost from the airplane (ecosystem), eventually there is a crucial point of malfunction, or collapse—the plane crashes; or in our metaphor, the ecosystem collapses. Furthermore, as species in the ecosystem are lost, the rate of extinction itself increases. As wonderfully stated by [E.O. Wilson \(2016, p. 14\)](#), “As more and more species vanish or drop to near extinction, the rate of extinction of the survivors accelerates.” “As extinction mounts, biodiversity reaches a tipping point at which the ecosystem collapses.” This is a possibility that should concern all of us today (e.g., [Diamond, 2011](#)).

Even if one struggles with these biological concepts or ideas, the fact is that we are the dominant organism on our planet—as [Wilson \(2016\)](#), [Gorke \(2003\)](#), and others have argued, do we not have the moral responsibility to care about the fate of other species—and the Tree of Life—to feel the importance of that connectivity to all life . . . a connectivity that our ancient ancestors and indigenous peoples today certainly cherish? In addition, although we often stress the direct economic benefits to humans to protect and preserve the Tree of Life—medicines, crop improvement, ecosystem services (fresh water, clean air)—there is more than that at stake. There is the preservation of the intrinsic value of nature itself—that all species matter and have value ([Gorke, 2003](#)).

Numerous authors have made a moral argument for conservation and saving the Tree of Life. Great quotes are found in the many pages written on the topic, for example: “no species is more valuable or meaningful than another except in the minds of humans” ([Klinkenborg, 2014](#)). The moral argument for shaping our view of biodiversity and the Tree of Life has been made by such legends as Rachel Carson, Aldo Leopold, and E.O. Wilson, with numerous recent thoughtful contributions on the topic (e.g., [Kolbert, 2014](#)).

Is there hope? Without a sustained effort, maybe not ([Cafaro, 2015](#)). [Wilson \(2016\)](#) argues for setting aside half the world as wild or natural. With the current estimate of only 17% of the Earth protected, we have a long way to go. Humans appear to show little interest in limiting growth to save our own grandchildren, let alone other species ([Dowie, 2009](#)).

But humans also show enormous capacity to work together to solve complex problems and effect change. Every person can make a difference; by working together, the enormous challenges to protecting the Tree of Life can be solved. There is hope.

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