Evidence for evolution from fossils

For a much more detailed discussion of evidence for evolution, see
http://www.talkorigins.org/faqs/comdesc/

We will now discuss evidence for evolution, beginning with fossils. In general, gradual transitions can be seen along many lines, but not all. In addition, the evidence does depend on us being able to assign dates to the fossils. We will therefore begin our discussion by talking about ways to determine the age of fossils, then by exploring some of the conditions needed for fossilization.

Dating fossils

The fundamental problem we face is that for life on Earth, the fossils that trace it are vastly older than humanity. Therefore, we don't have the luxury of looking at historical writings to establish age. This is important, because evolutionary expectations are that there should be a fairly clear sequence of changes with time. How can we go about figuring out ages?

The most reliable method turns out to be a technique known as radiometric dating. It relies on the decays of atomic nuclei, so let's discuss that for a bit.

Some atomic nuclei are completely stable in isolation as far as we know. If you let a carbon-12 nucleus alone, it will apparently sit there unaltered until the end of time. In contrast, other nuclei change spontaneously with time. For example, carbon-14 (with six protons and eight neutrons) reaches a lower energy state via the decay

$$ {}^{14}_{6}\mathrm{C} \rightarrow {}^{14}_{7}\mathrm{N} + e^- + \bar{\nu}_e \; . \tag{1}$$

That is, carbon-14 decays into nitrogen-14, an electron, and an electron antineutrino. Laboratory experiments demonstrate that it is not possible to predict when any given nucleus will decay. In addition, the probability of decay in the next time interval dt is *completely independent* of how long the nucleus has lasted up to that point, be it an attosecond or a billion years. What this means is that the probability that a nucleus will decay at a time between t and $t + dt$ after its formation is

$$P(t)dt = e^{-t/t_0}dt \tag{2}$$

where t_0 depends on the particular nucleus. This is often phrased in terms of the *half-life* $t_{1/2}$, which is the time by which half the nuclei would have decayed: $t_{1/2} = \ln(2)t_0 \approx 0.7t_0$. Because nuclei are very compact compared to the distance between atoms, external effects have negligible impact on the spontaneous decay rates.

A point worth stressing here is that the nature of this process allows half-lives to be measured even if they are extremely long compared to a laboratory timescale. For example, suppose that you have 10^{20} atoms of uranium-238. After one hour, you determine that there have been approximately 1.8 million decays. From the equation $P(t) = e^{-t/t_0}$ you know that in a time $t \ll t_0$ a fraction $\approx t/t_0$ of the nuclei will decay. Therefore, in this case $t_0 \approx 6.43 \times 10^9$ yr and $t_{1/2} \approx 4.46 \times 10^9$ yr.

This is all very well, but how does it help us determine ages? The simplest case would be one in which we know the initial amount of the radioactive substance. For later purposes, we will call the initial amount P, which will stand for "parent nucleus." Similarly, D will be the initial amount of "daughter nucleus." For example, ${}^{14}_{6}\mathrm{C}$ is a parent nucleus, and ${}^{14}_{7}\mathrm{N}$ is a daughter nucleus. Suppose that P_t is the amount of the parent nucleus at time t. The time is then simply

$$t = t_0 \ln(P/P_t) \; . \tag{3}$$

Fine, except that we *don't* know the initial quantity of the parent nucleus. Luckily there is a circumstance in which we can know something almost as valuable: the *ratio* of the initial quantity of a radioactive *isotope* of a nucleus to a nonradioactive isotope of the same element. I'm talking, of course, about radiocarbon dating, which since its discovery in 1949 by Willard Libby and colleagues has been the workhorse for dates within historical times. We'll discuss this in a little detail (although it is restricted to timescales within about 50,000 years). For longer timescales, different nuclei can be used, but (with a couple of twists) it's the same process.

Carbon, with six protons, has a very common stable isotope (carbon-12), an uncommon stable isotope (carbon-13), and a moderately common unstable isotope (carbon-14). Neutrons in cosmic rays entering the Earth's atmosphere can interact with nitrogen to form this isotope:

$$n +^{14}_{7} \mathrm{N} \rightarrow^{14}_{6} \mathrm{C} + p \; . \tag{4}$$

The cosmic rays do most of their work at high altitudes, 9–15 km, but the carbon gets taken up in carbon dioxide and spreads around all altitudes and latitudes. Plants acquire it during photosynthesis, and animals acquire it by eating plants. The net result is that for living things there is an approximately constant ratio

$$n_{{}^{14}_{6}\mathrm{C}}/n_{{}^{12}_{6}\mathrm{C}} \approx 10^{-12} \; . \tag{5}$$

After the animal or plant dies, however, there is no additional intake of ${}^{14}_{6}\mathrm{C}$, so the ratio decreases steadily on the carbon-14 half-life $t_{1/2} = 5730$ years. As a result, measurement of the isotopic ratio (most sensitively using mass spectrometry) tells us the age of a given sample. In practice, ages beyond about 10 half-lives are inaccurate because there are so few carbon-14 nuclei left. However, within historical times this method is outstanding, and as I indicated before one can use other isotopes for longer times.

But what did paleontologists do before radiocarbon dating? They had another method available to them that gives good *relative* dates, but not such good *absolute* dates. This is the method of *stratigraphy.* Basically, one can look all around the world and see similar layers of rock in similar orders. Occasionally one sees other things as well: for example, around 66 million years ago, one finds a layer of iridium all over the Earth that is thought to have been deposited when the dino-killer asteroid hit. By comparing these layers, one gets a relative ordering of when the rocks were layed down.

Even if we can get the ages of fossils, though, what should we expect? For example, if nearly every animal is fossilized, then we would anticipate a clean, continuous record of life on Earth (and we'd have one heck of a lot of fossils!). To explore this, we need a little understanding for the conditions for fossilization.

Conditions for fossilization

In fact, it turns out to be extremely rare for life to become fossilized. In most cases, the animal/plant/bacterium/archean simply decays away. Even bones weather into dust pretty rapidly if they are exposed.

In most cases, it is necessary for the individual to be covered up with sediment as rapidly as possible (e.g., in a river bed). There are occasions, though, when conditions that prevent decay (dessication, low temperatures, or oxygen-free environments such as peat bogs) can preserve a fossil in pretty good shape for a while. Even in these circumstances, though, it is much easier to fossilize something with hard parts (e.g., bones or exoskeleton) than something that is purely soft (e.g., bacteria). These requirements tell us that fossilization is actually quite rare, and biased to boot: finding things that have skeletons is much easier than finding leaves, jellyfish, or whatever.

In detail, there are many different ways in which fossils can be formed. For example, empty spaces in an organism can fill with groundwater that then leaves behind minerals. This can lead to fossils with lots of fine detail. Something like a leaf can be compressed, which can change the leaf chemically. Sometimes trails or footprints are even fossilized. However, the takeaway message here is that fossilization is a lucky event that happens much more to some organisms than to others. The fossil record therefore needs to be examined with understanding of incompleteness and bias.

Fossils tell the story of life on Earth

The story told by fossils is a remarkably consistent one. Before about 550 million years ago, almost all organisms on Earth were single-celled. Some evidence of life can be traced back to about 3.8 billion years ago, but it tends to be indirect (e.g., based on chemical evidence rather than fossils).

About 550 million years ago, however, there was a burst of diversification of life. Now, when we say “burst”, what we really mean is that over some tens of millions of years most of the basic body plans now used by life emerged, so “burst” may sound like we’re overdoing it. However, when you compare it with the three billion years of single-celled life that preceded it, that’s pretty fast! The most famous deposit of fossils around this time is in the Burgess Shale, a region in the Canadian Rockies. This stage in life’s history is known as the Cambrian explosion, based on the geological era of the rocks in the Burgess Shale and elsewhere. From that point on, fossils of large animals and plants become more common, telling the story of the development of sea creatures first, then plants on land followed by insects, then early amphibians, reptiles and mammals, and birds. Anatomically modern humans appeared around a hundred thousand years ago.

Stated dryly like that, it is difficult to conceive of the vast stretches of time that are involved. We will therefore use a standard analogy. Suppose that we compress the entire 4.6 billion year history of the Earth into a single day, starting at midnight. The first life, which we assume to be 3.8 billion years ago, appeared at 4:10 AM. This may well have been basically as soon as it could have, given that the Earth was being pounded by large planetesimals prior to that. Then, however, there was a very long stretch in which, no doubt, the single-celled life was changing in many important biochemical ways. From our standpoint, however, nothing much occurred until the appearance of the first multicellular life, about 800 million years ago. That would put it at 7:50 PM(!!), most of the way through the day! The Cambrian explosion occurred at 9:08 PM. About 230 million years ago (10:48 PM), the dinosaurs appeared, and about 66 million years ago (11:39 PM), they checked out when a large asteroid hit. Anatomically modern humans appeared around 100,000 years ago (11:59:58), and all of our recorded history of about 6,000 years fits in the last 0.1 seconds!!!

Phrased this way, we really seem like an afterthought in life. Therefore, we can ask whether the fossil record accords with the expectations of evolution. Indeed it does: simple things appear first, for example, and you never get fossils of complex modern animals in rocks that are, say, a billion years old. For lineages with many fossils (e.g., our own ancestors), there are very well recorded transitions between types. In the late 1800s and through the first half of the 1900s, there was an interesting puzzle that kept cropping up, which is that very similar fossils were found very far apart on the globe. For example, fossils were quite similar in South America and Africa, or in Antarctica (of all places!) and Australia. To make a long and pretty interesting story short, it turns out that continents move around a lot in hundreds of millions of years, and indeed those pairs were part of one continent in the good old days. The theory of plate tectonics, which explains such movements, also explains the distribution of earthquakes and volcanoes, and is the organizing theory of geology.

In addition, there are endless specific predictions that evolution makes. For example, according to the story laid out by fossils, birds split off from the dinosaur line long after mammals had split from reptiles. Therefore, one does not expect any transitional fossils between mammals and birds.

In contrast, one *does* expect transitional forms between (for example) fish and amphibians, and between amphibians and reptiles. However, as we noted earlier, most organisms never fossilize and therefore there will always be gaps. This is something often pounced on by opponents of evolution, who like to point to existing gaps and announce that they are impossible to bridge. As we noted earlier, though, this is a dangerous policy, because future discoveries can fill those gaps. We now discuss some of those "missing links" and how they were filled.

The issue of missing links

In a given lineage, it is possible that the fossil record contains only one individual in a stretch of millions or tens of millions of years (this is more and more likely for progressively more ancient fossils). This inevitably leads to gaps in the fossil record. We will examine two such cases: the evolution of whales, and the transition between fish and amphibians. Both, as it happens, are gaps that have been filled in fairly recently.

Whales, of course, are mammals that live their entire lives at sea. Although they don't get their oxygen from the water as fish do, they are otherwise superbly adapted for aquatic living. They are streamlined for swimming, their air holes are on the tops of their heads, they echolocate, and so on.

At the same time, however, there are features of whales that seem to point to a terrestrial origin. For example, some species have vestigial pelvises, occasionally one sees greatly reduced and nonfunctional hind limbs, and so on. Based on these and other features, in 1883 Flower suggested that whales might have descended from extinct ungulates (hoofed animals, with current examples being horses, pigs, sheep, etc.). Later, the hypothesis sharpened: whale ancestors were thought to be part of a specific group called artiodactyls (pigs, camels, cattle, hippopotami, etc.). However, this seemed to pose a problem: how would one get from carnivorous cows (or whatever!) to whales? At that time, transitional species were unknown. Indeed, by the mid-1980s there were still no transitional fossils along this line, leading to various bits of name-calling from anti-evolutionists.

However, in the past 20–30 years, there have been excavations (largely in Pakistan) that have revealed a wonderfully mapped out set of intermediate organisms, from *Pakicetus* 53 million years ago (which has an ear structure found only in modern whales) to *Ambulocetus* 50 million years ago (an amphibious creature much better suited for swimming than Pakicetus, and it could swallow underwater), to *Rhodocetus* 47 million years ago (with some transitional bone structure, e.g., a large pelvis fused to vertebrae), to *Basilosaurus* 40 million years ago (60 feet long, with vestigial hind limbs), to *Squaladon* 33 million years ago (the first fossil with a melon-shaped forehead, typical of creatures that echolocate). Many other examples exist as well. Basically, in the last few decades this lineage has gone from having no transitional forms to one with a huge abundance. In every case, the evidence is consistent with gradual changes. For instance, starting with *Pakicetus*, the nasal openings go from the front of the nose, to the middle, to the top of the skull. Pretty impressive!

Another famous recent example is the transition between fishes and four-legged animals (also called tetrapods). Enormous numbers of fossil fish, amphibians, and reptiles had already been discovered. However, there were various gaps in the limb structure and ear regions between fish of about 380 million years ago, and the first clear tetrapods of about 365 million years ago.

Knowing that evolutionary theory predicted that intermediate forms should be found in rocks of intermediate age, Neil Shubin of the University of Chicago and his colleagues decided to do excavations in rocks on Ellesmere Island, Canada, that were of the right age. The team worked for five years, and were at the end of their funding, when they finally saw a remarkable skull poking out of a cliff. This was named *Tiktaalik* after the Inuktitut language for a particular fish. Indeed, the group found several such fish, and these were precisely the intermediate forms that they had expected.

These are, of course, not the only such examples! Every year brings new discoveries of fossils that fit well into the evolutionary picture. Note, also, that paleontologists don't just dig randomly and hope to find something. Like Shubin and colleagues, they go to places that are expected based on evolutionary and geological theory to have the greatest likelihood of containing the fossils that interest them. No authentic fossil has been found to conflict with the basic principles of evolution, which is really saying something given the tens of thousands of fossils that have been discovered!

Evidence for evolution from experiments and genetics

A successful theory must be able to accommodate new data, and evolutionary theory has had to deal with a breadth of data that may well be unmatched in the history of science. Specifically, in the more than one and a half centuries since Darwin presented his ideas, the mechanism for heredity has become clear and the information that is now available allows a host of detailed and profound tests of the basic ideas. In this class we will examine the genetic evidence and then talk about evolutionary experiments in the lab as well as observations of evolution in the field. We will start by giving an overview of how genetic information is stored in life on Earth.

DNA

DNA (deoxyribonucleic acid) is an extremely long molecule shaped in a double helix (i.e., two spirals connected by rungs). It is the carrier of genetic information in all known non-viral organisms and some viruses. Each rung connects a “base pair”; the bases are molecules that are abbreviated A, C, G, and T, and the only possible pairings are A-T and C-G. If you pick one of the two strands, therefore, you can have a sequence like AATGTACT and the opposite strand has to be TTACATGA. Different species have different numbers of these pairs; humans, for example, have about three billion(!), which means that if you stretched out the molecule fully it would extend to about one meter(!!!). Given that every cell contains a copy of our DNA in its nucleus, you can therefore see that the molecule is coiled very tightly.

The sequence of base pairs codes for amino acids that are used in the synthesis of proteins. It has been determined that each triplet of base pairs codes for a given amino acid. However, since there are 4x4x4=64 possible triplets and only 20 amino acids are used in nature, there is some overlap. For example, GGT, GGC, GGA, and GGG all code for glycine, and TGT and TGC both code for cysteine. There are also triplets that code for the start or stop of a gene (genes can be thought of as units of inheritance). The redundancy is important to note for later, because we see that, e.g., changing GGT into GGC has *no effect whatsoever* on the organism (well, except that it might change the speed of production a bit). This means that, except for evolution and common descent, there is no reason at all to expect different organisms to have the same sequence of base pairs. We’ll get to that later.

For now, let’s step back a bit. This is a course on life in the universe, not just life on Earth. We can certainly argue that evolution as a process is likely to be universal to life. But is DNA going to arise on other planets? It is not nearly as clear. In fact, DNA in its current form is far too complex to have arisen in the very first life. It does turn out that some viruses use much shorter strands of another molecule called RNA (ribonucleic acid, which also plays an important role in helping transcribe the instructions in DNA) as the carrier of genetic information. People have speculated that very early life could have been an “RNA world”. Note that in the very early days, without any robust DNA organisms around, even a much less effective system would have had a competitive advantage, and that’s all evolution needs to proceed.

Now let’s see how the details of proteins and DNA compare with expectations from evolution.

Case study: the cytochrome c protein

We will focus on one particular protein, cytochrome c, which plays an essential role in the transport of oxygen. As a result, it is found in plants, animals, and many single-celled organisms. This protein typically consists of a sequence of 104 amino acids, with the exact number varying somewhat between species. Cytochrome c is an example of a "ubiquitous protein", which means that it is basically found everywhere. To draw from Douglas Theobald's webpage http://www.talkorigins.org/faqs/comdesc/, the importance of ubiquitous proteins in a test of evolutionary principles is:

- Ubiquitous proteins perform the same basic function in all organisms; the needed function does not depend on whether the organism is a plant or animal, for example.
- For a given function, there are an astronomically large number of different amino acid sequences that will do the same job. In the case of cytochrome c, we can see differences in the sequences between different organisms, but substitutions lead to no problems. As an example, yeast cytochrome c differs from the human version in about half of the protein, but human cytochrome c can be substituted into yeast and the yeast functions perfectly. It has been estimated that there are more than 10^{93} functional variants of cytochrome c, which is vastly more than all the particles in the observable universe, not to mention the number of organisms that have ever lived on Earth!
- As a result, for the purposes of functionality, there is no reason at all for a given sequence to exist in a given organism, and no reason that even closely related organisms *must* have the same sequence.
- However, heredity *demands* that there be such relations. We said earlier that there could be more that 10^{93} functional variants of cytochrome c. However, the total number of possible 104 amino acid sequences is $20^{104} \approx 2 \times 10^{135}$, a vastly larger number. Since the role of cytochrome c is so critical, this means that most variations will kill the organism. In an evolutionary model, one therefore expects that transcription of this sequence will be really, really robust, so that closely related organisms will have amino acid sequences in cytochrome c that are close to each other. However, more distantly related organisms would be expected to have ever-decreasing similarity. The key question is then: is the tree of relations of life derived in this way consistent with what has been derived independently by the fossil record?

The answer is a resounding yes! Humans and chimpanzees have exactly the same cytochrome sequence. Their sequences differ by at most 10 amino acids from any other mammal. In contrast, a particular species of yeast differs in 51 amino acids. We also note that the sequence for bats is much more similar to that of other mammals than it is to birds (who might be thought to have closer to the same specific requirements), and similarly the sequence for dolphins is much closer to ours than to sharks. Similar correspondence exists for other proteins. This is a great success for the theory.

Similarity of DNA sequences

There is another prediction that can be applied, given our understanding of how DNA codes for amino acids. Remember that we said there are 64 possible triplets, but only 20 amino acids? This means that for a given amino acid there are on average about 3 triplets that code for it. For cytochrome c, with 104 amino acids, this means that there are about $3^{104} \approx 4 \times 10^{49}$ base pair sequences that give *exactly* the same protein, with zero functional change. To drive home that point, from the functional standpoint there is nothing at all to demand any given sequence out of the possible 4×10^{49}.

Heredity, however, implies similarity between the sequences, and in this case we can be specific. The background mutation rate per base pair per generation in mammals has been measured to be $1-5\times10^{-8}$. An average primate generation is about 20 years, and the fossil record indicates that we diverged from chimpanzees less than 10 million years ago, so around 500,000 generations. We therefore expect a less than 3% difference in the sequence of base pairs in the gene that codes for cytochrome c. The actual difference is 4 base pairs out of the 3x104=312, or a 1.3% difference. Overall, in fact, human and chimpanzee DNA differ by only about 2%, which is expected if there is common descent but is not even remotely required by functionality.

Using evolutionary principles: the AIDS cocktail

Our understanding of evolution is not merely academic. It has played an extremely important role in our treatment of disease. Bacteria and viruses have very short generational times, meaning that they can evolve rapidly in response to external pressures. One of those pressures involves the medicines and treatments that we apply to get rid of them. If we apply a treatment that does not get rid of all the invaders, and that they can adjust to without multiple simultaneous (and thus highly improbable) mutations, then we are just helping them get stronger. Overuse of antibiotics has had this effect, leading to multiple drug-resistant strains of many maladies we thought we'd conquered (e.g., tuberculosis).

A happier story, at least at the present, has to do with treatment of patients with HIV (human immunodeficiency virus, the cause of AIDS). There is still no cure for AIDS, and millions of people die from it every year. There is, nonetheless, a ray of hope for those who can afford somewhat expensive therapy. If you look at a plot of AIDS deaths in the United States, you see that it rose rapidly to a peak of more than 40,000 in 1995. It then dropped quickly to 15,000-19,000 per year; still a horrifying number, but far less than before. What happened?

From studies of the virus it became clear that its spectacular replication rate in human hosts meant that it is poised to adapt quickly to medicines. The key, though, is that there is a limit to what evolution can do. If a simple flip of a gene is needed, sure, no problem. However, if multiple mutations are required *all at once*, and there is no selective advantage for any of the mutations individually, then it is highly improbable that the mutations will happen as needed. Without understanding of evolution, there would be no particular reason to think that a virus couldn't make the large leap.

With this background, scientists developed a three-drug regimen that is applied all at once. These hold back critical enzymes at the beginning and the end of the HIV replication, and so far HIV appears not to have breached the defenses. We are still a long way from a vaccine, and there is still no substitute for safety, but this is a clear case in which evolutionary knowledge has saved tens of thousands of lives per year.

Evolution in the lab: the Lenski experiments

An elegant experiment in evolution has been carried out by Richard Lenski and colleagues at Michigan State University and elsewhere. For more details on this I strongly recommend that you go to his home page: http://myxo.css.msu.edu/index.html, and look at the links to his long-term evolution experiment.

The basic idea is simple. Bacteria reproduce rapidly, so they are ideal for evolutionary experiments. They can also be cloned easily, so in 1988 Lenski set up 12 flasks that contained cloned members of an original E. coli bacterium (this is a bacterium we have in our intestines). Into each flask he put a small amount of glucose (a type of sugar). Since then, daily, he has let the bacteria run through the sugar, then the next morning he would transfer some of the survivors in each flask to a new flask. He and his lab have now run through more than 60,000 generations of bacteria (i.e., several per day). This is the equivalent of about a million years of human evolution!

The point, of course, is to determine how mutation and other variational mechanisms would change the properties of the bacteria. The answer: a lot! He has frozen samples every now and then, so that direct comparison is possible. The current bacteria average twice the size of their ancestors, and are 70% more efficient at metabolizing the glucose. Most of the improvement occurred early on, but the changes are not identical in each of the flasks. In fact, now that gene sequencing is fast and efficient, the scientists can follow the precise changes that occur.

Since the original experiments, others have tried different environments. Julian Adams at the University of Michigan also started with genetically identical E. coli, and grew them in a device called a chemostat that made sure that all the lines had identical conditions. However, commonly, he found that in a given flask more than one strain of E. coli would develop. He found that initially the E. coli evolved to metabolize glucose more efficiently. After a while, however, the amount of glucose was too much to metabolize, so the E. coli added another pathway that generated acetate as a waste product. Enough acetate was produced that a mutant emerged that used the acetate as fuel. Pretty impressive adaptation!

Similarly, Lenski's lab found that somewhere around generation 30,000 there were some strains that had evolved to be able to metabolize citrate in the presence of oxygen, which is impossible for E. coli in the wild. They were able to trace the origin of this capability to three separate mutations that happened thousands of generations apart. Each independently didn't do much, but in a great example of neutral drift there were some of the organisms that had those mutations and eventually, when the third happened, it gave an important new metabolic path to the E. coli.

Evolution of fruit flies in the laboratory

Being human, of course, we tend to focus on things closer to ourselves. Bacteria are pretty far away; has evolution ever been seen in animals? Again, of course, we need to look at things that have short generational times.

For this purpose, fruit flies are ideal subjects. They breed like mad and are easy to care for, so they have been the workhorses of genetics laboratories since the early 1900s. Tons of changes have been seen to arise spontaneously, such as eye color, but what we're really interested in is whether a new species has emerged at any point.

To determine this, we need a definition of species. As we discuss in more detail in our fourth supplement, biologists classify living things based on a taxonomic scale, in which the broadest category is the domain (bacteria, archaea, and eukarya, which constitute plants, animals, fungi, etc.; yes, all those really are more related than we are to bacteria!), followed by kingdom, phylum, class, order, family, genus, and species. The boundaries are often a little fuzzy, but for animals and plants species can be defined fairly specifically, if you'll pardon the pun. Individuals of a species can produce viable offspring (i.e., offspring that can produce offspring). Individuals of different species can't. Therefore, all horses are part of the same species, but horses and donkeys aren't because although they can reproduce the result (a mule) is sterile.

With this in mind, the laboratory of Dobzhansky saw speciation that occurred some time between 1958 and 1963. The strain in question started from a single inseminated female that was captured in Columbia, and as of 1958 it produced fertile hybrids when crossed with its original strain. As of 1963, however, crosses produced only sterile males. This satisfies the definition of the emergence of a new species.

Observed speciation in nature

You may wonder, though, whether new species have ever been seen to emerge in nature, as opposed to a lab (although the principles are of course identical). Yes, using our previous definition, speciation has been seen in various plants (e.g., the evening primrose, fireweed, maize, and several others); by "seen" here I mean that people have actually observed different species produced over the course of years of observation.

Over longer times, of course, the changes can mount up, so that even larger organisms with longer generational times can speciate. A good example is the greenish warbler, a bird of central Asia that is the poster child of the "ring species" phenomenon. These birds live in trees in a wide portion of Asia that fully rings the Tibetan plateau, which does not have trees. Along the ring one can do tests of various aspects of the birds, such as their coloration, songs, and genetic makeup. There are continuous changes going from the north boundary of the region (Siberia), westward, southward, and back again north. However, in Siberia itself there are two varieties that appear to be different species! They don't mate, the males ignore each other's songs, and so on. It has been suggested that the original species started in the south, then as time went on some moved gradually west and north, whereas others moved gradually east and north.

There are also a number of cases of speciation that could be happening right now. On the Hawaiian island of Kauai, for example, the crickets have to deal with a rather vile fly parasite, which lays its eggs in the cricket and the young then eat the cricket. Not pleasant. Even worse is that the fly uses the sounds the male cricket makes to hone in on them. The cricket population responded, in fewer than 20 generations, by having more than 90% of the males mutate into a silent form. You have to feel sorry for the poor crickets, because this is how they signal to potential mates, but it is a great example of evolutionary adaptation!

Summary

The evidence of fossils, molecular genetics, and laboratory and field observations is unanimous that there is not a single aspect of the development of life that is inconsistent with evolutionary theory. More specifically, every aspect of life that we know about seems completely accessible via a series of minor changes, rather than large leaps. People experiment all the time and given the pace at which science advances we can expect more tests in the next decade than in all of previous human history. For now, though, evolution as a fact is as solidly established as any scientific principle, and the basic principles of evolution are established beyond any reasonable doubt (although many details are being explored, of course).

This is the reason that I have taken you through these two lectures. Evolution is such a simple mechanism that it seems that once life gets going anywhere in the universe, evolution will cause adaptation. How far it would go in any environment, we don't know. As a result, we will now go into classes that discuss questions that are important for life in many environments. (1) What exactly is life, and how did it arise? (2) What are the environments in which life on Earth can exist? (3) How fragile is life; could it be snuffed out by a cataclysmic event?