

Fossils Everywhere

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Abstract: History is omnipresent in the natural world, from inside rocks on the continents to the genes, cells, and organs of each creature on the planet. Linking the historical records of rocks, fossils, and genes has been a boon to understanding the major events in evolution. We use these seemingly different lines of evidence as tools for discovery: analyses of genes can predict likely places to find fossils, and new fossils can provide the means to interpret insights from genetics. Viewed in this way, every living thing on Earth is the extreme tip of a deeply branched tree of life that extends three billion years into the past. Genes and fossils reveal how deeply connected our species is to the rest of the living world and the planet itself.

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More than a century of discovery has led us to the realization that the descendants of fish now walk on land, those of dinosaurs fly in the air, and the evolutionary offspring of arboreal primates fly in space and have left footprints on the moon. One hundred years ago these evolutionary transitions would have seemed utterly impossible, or worse, unthinkable. For example, most fish reproduce, feed, and breed in water; for their relatives to invade land, almost every system of their bodies would apparently need to change. If the same conceptual challenges hold for every major step in the history of life, how could we ever come to terms with ancient events, let alone understand their relevance to our lives today? We must look to the genes, cells, and organs of every creature alive today to understand the more than 3.5 billion years of the history of life. Each new piece of evidence that emerges helps reveal how the past has shaped us and our world.

We live in an age of invention; new technology changes what we can do, how we live, and what kinds of questions we can ask about our world. The doubling time of computer chip speeds is surpassed by the rate at which we can sequence whole genomes at ever-decreasing cost. The genome of any species can now be identified and compared among crea-

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tures as different as yeast and humans.¹ Genes can even be swapped between species, moving basic bits of DNA between flies, worms, and mice. The exponential rate of technological change in biology once prompted a colleague of mine to admit that he could have collected all the data for his Ph.D. thesis – written in the early 1990s – in a single week. My colleague made that comment about five years ago; he could now execute the dissertation in an afternoon.

In the face of this technological revolution, fossil bones seem almost quaint. Most of us encounter these relics in museums, where the dinosaurs, ground sloths, and mammoths stand motionless in neo-classical buildings of marble and granite. Both the subject and the field appear frozen in time; paleontologists digging in rocks to find remnants of long-lost life is a far cry from a roomful of humming computers and gene sequencers. But these are special times; profound insights into the great transformations of life have come from linking new genetic, developmental, and computational tools with approaches that date from the days of Leonardo da Vinci.

Fossils are a kind of window into our perceptions of life, the planet, and our historical connection to them.² Most of us take their meaning entirely for granted, so much so that it is hard to envision how strange these objects seemed when first encountered by philosophers centuries ago. Our own conception of them – as evidence of creatures that inhabited long-lost worlds – arose in parallel with an entirely novel way of thinking about the natural world.

In 1541, Conrad Gessner, then twenty-five years old, landed in Zurich as a lecturer in physics. His path to his new post was anything but easy: having lost his father in battle at a young age, he found himself

in an unfortunate marriage. Friends bailed him out of the union, ultimately helping him travel to France to study medicine. Returning to Zurich, Gessner had many loves, not least of which were the mountains of Switzerland. His passions were the beauty of nature and the physical exercise of climbing. Lured by the majesty of the snow line, he declared a goal of reaching the summit of a different challenging Swiss mountain each year.

Gessner developed an ardor for describing nature – first the plants, then the animals. His four-volume opus *Historiae Animalium*, published between 1551 and 1558, was remarkable for its richly detailed descriptions and illustrations of the world's living things. In this tome, Gessner did something that relatively few had done before him: he specifically compared entities inside rocks to bones and shells of contemporary organisms. He illustrated crabs, clamshells, and urchins, revealing that a number of rocks contained similar entities.

How could rocks look like living creatures? In the 1500s, answers to this question took several forms.³ One common explanation was that the rocks held monstrosities that were destroyed in the great flood during Noah's time. Another theory, common in Gessner's day, was that life-like objects were produced by the same forces that made the rocks: some stones contained things that only coincidentally looked like wood, bones, and teeth. These objects were not associated with creatures alive or dead because they were considered natural outgrowths of the rock itself. The other explanation was that fossils reflected a kind of Loch Ness phenomenon: perhaps they were mysterious animals that could be found alive in remote or unexplored regions of the planet.

All these conceptions changed in 1666, when fishermen working on the coast of Italy caught a giant shark. This monster

from the deep drew the attention of the Grand Duke of Tuscany, who was a great patron of science. He ordered it sent to Niels Stensen, one of the young scientists he was supporting at the time. Stensen (known in his publications by the latinized *Steno*) studied medicine and had originally earned the Duke's favor for his extraordinary knowledge of anatomy and his clever use of experimentation to understand how bodies function. Steno described the bones, muscles, and nerves of the shark head, but his most memorable observation came from studying teeth.

A long-standing puzzle, dating from before Steno's time, was the presence of oddly shaped objects, known as "tongue stones," commonly found in clumps on the ground or still embedded in rocks. These stones had an uncanny resemblance to shark teeth. The Roman natural historian Pliny the Elder declared that they either fell out of the sky or dropped from the moon. Others followed the standard interpretation, viewing them as natural outgrowths of rocks. Steno changed everything. He looked not only at the stones, comparing them to teeth, but also at the rocks in which they were found. He noted that the stones were recovered from cliffs made up of layer after layer of rock, one on top of another. To Steno, tongue stones were actually shark teeth, and not just any shark teeth – they were ancient shark teeth, buried under layers of sediment. Steno developed a theory about what the stones were and how they were preserved. The completion of his shark monograph in 1667 was an important moment in the birth of paleontology as a discipline.⁴

Viewing fossils as the remnants of past life, and layers of rock as reflecting a succession of ages, is a relatively new way of understanding the planet and life on it. The rocks of the world are a library of sorts, whose pages and chapters record

eons of time. Layer after layer reflect changes in the atmosphere, climate, and geography of the planet, and the fossils inside provide a window into the succession of living things.

This approach is not just a new way of thinking; it also is a means of discovering. Since the days of Steno and his contemporaries, paleontologists have used a growing knowledge of the world to identify places likely to yield fossil discoveries. While paleontological discovery is often accidental – for example, by construction or road crews hitting fossil bones as they unearth rock – most discoveries are planned. That is, to examine a question or problem, such as determining links between fish and amphibians, we begin by narrowing down the mapped regions of Earth to small sites where fossils might be found. The approach is straightforward: find places where rocks of the right age and the right type to preserve fossils of interest are exposed at the surface. Economic incentive fuels part of this search: geological surveys spurred by the potential of oil, gas, and mineral development often prompt states and private industries to map the rocks within their purview. Geological maps, commonly made at a very fine scale, are often easy to come by, as are aerial photographs that reveal the exposures in any given area.

Knowing a few relatively simple features about the geological landscape greatly enhances the odds of finding new fossils. The first is rock type. Sedimentary rocks are best: unlike igneous or metamorphic rocks, they have not been superheated or transformed by the tremendous pressures that exist within the Earth. They may have been laid down in ancient oceans, streams, soils, or even sand dunes.

Understanding how grains sort inside a rock, as well as how different layers of rock change relative to one another, can give clues to the kind of environment in which

Neil H. Shubin

the rock was deposited. Stream beds, for example, can have a lenticular shape, almost like the cross section of a channel bed. Within ancient channels are often grains that range from rounded cobbles to fine particles. The size of these sediments and the way they are sorted within the deposit reveal not only if the rock was deposited in a stream, but also whether the channel was big or small and if the water was running fast or slowly. By studying these features, fossil hunters can predict where they might find fossils in the field. The likelihood of finding a complete articulated skeleton in the middle of an ancient channel bed is vanishingly small: moving water may have scattered and broken bones, particularly smaller and fragile ones. When looking for high-quality bones in freshwater settings, we tend to focus on the margins of streams, in the eddies and banks where matter would settle out at different times of the year. Field paleontologists develop a catalog of rock occurrences like these and, when on the rocks, will typically make a beeline for their favorites.

Finding new places to look also means predicting the right age of rock to investigate. Here, the full suite of biological information comes into play. To appreciate this approach, we must look back to a time in biology when the study of DNA and the study of fossils were utterly separate approaches to science.

Biology is a vast field encompassing multiple levels of organization, from molecules, to genes and cells, to entire ecosystems. Work on each of these levels has its own empirical approach: different tools of microscopy, spectroscopy, and field analysis underlie disciplines as varied as structural biology and ecology. In the 1970s, biology became increasingly fragmented according to level and approach, with a number of prominent, comprehensive

biology departments splitting into the more narrowly focused departments of molecular biology, cell biology, organismal biology, and so on. But at the same time that the biological disciplines were becoming more divided, the questions and conceptual tools to unite them began to emerge with increasing rapidity.

One of the greatest boons to paleontology originally appeared to be the most significant threat to its existence as a productive field of inquiry. The approach began with a simple notion of Darwin's: descent with modification.⁵ If there is a common history to life on Earth, then descendants should be modified versions of their ancestors. Just as each individual is a modified descendant of its parents, so, too, should species be descendants of their ancestors. This pattern of descent with modification should yield a pattern in the history of life: that is, the features that creatures share with one another should reflect their history. For example, if we wanted to know how clams, fish, mice, and people are all related, we would compare their characteristics and discover that these creatures share DNA, cells, and other features, but that fish, mice, and people share characteristics absent in clams – such as a backbone, skull, and centralized brain. Mice and people are even more similar; unlike fish, they share hair, warm bloodedness, and mammary glands. We could even look at the genes and proteins of each of these animals and come to the same conclusion: fish, mice, and people are more closely related to one another than any are to clams. Moreover, mice and people have more in common with each other than they do with fish.⁶ By adding species and features to this analysis, we could ultimately develop a hypothesis of a complete tree of life.

The important point to draw from this exercise is that we do not need a single fossil to infer the relationships among living

things. By applying the “descent with modification” approach to the relationships discussed above, we can infer that mice and people share a more recent common ancestor with each other than they do with fish. Armed with a knowledge of genes, tissues, and organs of living creatures, we can infer the hierarchy of life – a tree of relatedness that shows the relative recency of common ancestry.

Far from removing fossils from the picture, however, this approach defines their importance. Plotting the relationships between living vertebrates helps us construct the family tree, for example, by demonstrating that turtles and lizards are more closely related to mammals than birds are. But this method alone cannot tell us what the ancestors of mammals looked like. When we explore the fossil record from rocks 230 million years old, we find a number of creatures with reptilian jaws and skulls, but with a dog-like posture. These creatures have features of the ear, teeth, and skull that reveal intermediate conditions between so-called reptilian bodies and those of mammals. Fossils bring to light transitional features, ancient environments, and ecosystems that have been lost in time.⁷

Together, genes and fossils provide information that each alone cannot. If you take a tree of relatedness developed from genes, or from any kind of data (Figure 1a), and map known fossil occurrences onto it (Figure 1b), the end result is a clear picture of what is unknown (Figure 1c). By looking for these so-called ghost taxa⁸ – extinct species we infer should be present but are absent – we can concentrate our field efforts to fill huge gaps in the fossil record with transitional forms. There is a deep beauty to the idea that comparisons of DNA in different species can give us clues about where to discover new fossils inside rocks.

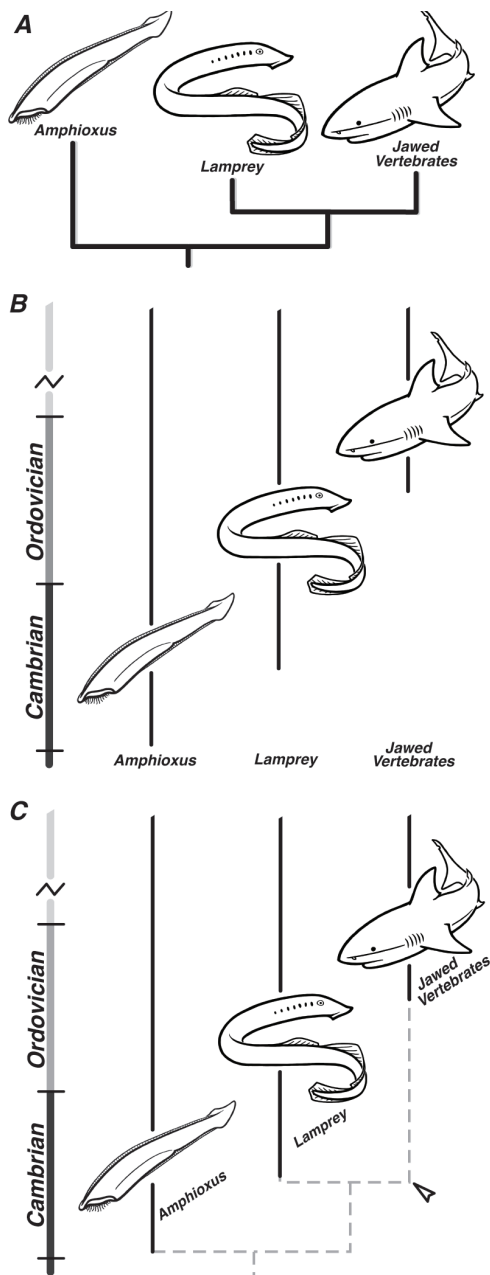
In the 1940s, no approach helped paleontologists understand the origin of whales. With nostrils modified to become blowholes, no hind limbs, and extreme modifications of the brain case, whales were a complete enigma. They were so odd that they could not easily be compared to any creature – living or extinct. The problem was so great that the paleontologist George Gaylord Simpson inserted the group arbitrarily into his classic 1945 classification of mammals, saying that cetaceans are “the most peculiar and aberrant of mammals,” and adding that “there is no proper place for them in a *scale naturae*.”⁹

A few years later, in the late 1940s, two scientists used a crude test to look at the similarity of proteins in the blood of different mammals.¹⁰ Using an assay that criminologists employed to discern human from animal blood at a crime scene, they tested the plasma of different species by looking at how they interacted with antibodies. Closely related species should have more similar antibody reactions than more distantly related ones. The scientists found that the proteins in the blood of whales were more similar to those of even-toed ungulates – including deer, hippos, and goats – than to anything else. But this was a puzzling discovery. These creatures, artiodactyls, have a very distinctive ankle bone, consisting of a double pulley joint that helps them with their running and bounding gaits. Extant whales not only had no ankle bones with a pulley joint, but they had no hind limbs whatsoever. So how could there be a connection? Simpson’s problem remained.

As new techniques to compare genes and proteins emerged in the ensuing decades, scientists gained a bonanza of new data to compare whales with other mammals. By the mid-1990s, mitochondrial genes,¹¹ milk casein genes,¹² and others not only strengthened the artiodactyl idea

Neil H. Shubin

Fossils Everywhere
Filling Gaps



Using genes to explore for fossils, (a) an evolutionary tree can be constructed for living creatures, such as sharks, jawless fish, and their closest invertebrate relatives; (b) the fossil representatives of each form can be mapped in time; and (c) merging the tree and the fossil occurrences reveals places in the geological record where fossils are likely missing (indicated by the dotted line and arrow). Source: Figure created by John Westlund, University of Chicago; used here with permission from Westlund.

but led to the proposition that one group, hippos, are the closest living relative of whales. Yet fossil data spoke to a different theory of whale relationships, although not conclusively. Comparison of the teeth and skulls of whales to other mammals suggested a relationship to an extinct group of terrestrial, four-legged creatures known as mesonychids. In fact, everything known of the anatomy suggested that artiodactyls are only distantly related to whales. As the authors of one of the genetic studies noted, “paleontological information is grossly inconsistent with [the artiodactyl] hypothesis.”¹³

About ten years before this flurry of molecular work, Philip Gingerich and his colleagues were investigating fossil exposures in Pakistan. Gingerich had followed the paleontological rulebook: the rocks, at about forty-seven million years old, were the right age (they reflected the interval when the diverse orders of mammals came about); were the right type (they were mapped as ancient stream deposits); and were well exposed. Gingerich, however, was working from an inaccurate map, and once on-site, he realized that instead of stream beds, he was standing on an ancient ocean. That setback did not stop him from looking for fossils anyway. He and his team found a number of new fossils, including pelvic bones that the team jokingly called “walking whales.” A few years later, the rocks yielded whale fossils in the form of some isolated skulls.¹⁴ But those pelvic bones remained enigmatic.

With whale origins now on his mind, Gingerich shifted his focus to Egypt, the home of well-exposed marine rocks from a slightly younger age. Sure enough, the team discovered whales. In addition, and fittingly for the Darwinian theory, these whales had hind limbs. This was a gratifying and important discovery, but not entirely unexpected under Darwinian thinking. Because whales share a com-

mon ancestor with other mammals, their close relatives must have been quadrupeds.

Neil H. Shubin

Then, as one of Gingerich’s graduate students was cleaning a fossil whale skeleton in preparation for its extraction back to the lab, a small, pulley-shaped bone appeared to poke out of the rock. Once removed and cleaned, the bone was clearly identifiable as an ankle bone. And this was not just any ankle bone, but one from the double-pulleyed ankle of an artiodactyl. Armed with the new fossils showing the transformational character of evolution, we are now in a position to understand how the whale’s unique body plan arose and what the ecosystems it lived in looked like during the change. A prediction, born of blood samples and extended to proteins and genes, was confirmed inside ancient rocks.¹⁵

We are accustomed to thinking of a revolution in gene sequencing and molecular technology, but we are also experiencing one in the field of paleontology. Whales with legs are one of a number of creatures that tell us of the great transformations in the history of life. Using the paleontological playbook, expeditions have discovered worms with heads,¹⁶ fishes with elbows, wrists, and necks,¹⁷ feathered dinosaurs,¹⁸ and human precursors,¹⁹ to name only a few. Indeed, in the last twenty years, we have discovered more creatures informative of evolutionary transitions than in the previous millennium.

Exploratory paleontologists such as Phil Gingerich use knowledge of evolutionary history and the geological record to find evidence of ancient transitions. Another record altogether can provide clues. In the late 1990s, David Kingsley and Katie Peichel began a hunt for the ideal species to study the way traits and genes evolve in natural populations.²⁰ Ever since the days of T. H. Morgan, biologists have used so-called model organisms, such as fruit flies,

house mice, and African clawed frogs, to provide insights into basic questions of genetics, cell biology, and development. Laboratory species have features that make studying their basic biology accessible: they typically breed rapidly and easily, have anatomical or behavioral features that might provide general insights, and are tractable to study using molecular, microscopic, and cellular methods. Kingsley and Peichel had an additional goal: they wanted to find a creature that would allow them to trace the genes involved in the origin of new organs, physiological processes, and behaviors. Their search revealed the potential of a fish, ranging from one to four inches long, called the threespine stickleback.

The threespine stickleback is an ordinary-looking fish with a long history of study. The famed Dutch ethologist Niko Tinbergen won a Nobel Prize in part for his work on them. Ecologists and paleontologists have had their turn at the species, too, producing a vast literature that contains thousands of scientific papers and analyses. To Kingsley and Peichel, the stickleback had all the characteristics of an excellent genetic system: the creatures breed easily and develop relatively rapidly. But most interesting was the tremendous variety of subspecies of threespine sticklebacks that have evolved since the glaciers retreated fifteen thousand years ago. As the ice gave way, new lakes and streams emerged. From their ancestral marine range, migratory ocean sticklebacks invaded or became restricted to different streams and lakes, often becoming isolated and evolving a number of important characteristics. The ecological and physiological environment of freshwater forms is so different from the denizens of the oceans that the freshwater sticklebacks evolved a number of new features – losing their protective armor, changing their feeding structures, and sometimes reduc-

ing or losing hind limbs, among a host of other new traits.

The key point is that the differences between freshwater and marine sticklebacks are so large that, for all intents and purposes, they could be characterized as different species. However, although they are often reproductively isolated in the wild, these very different kinds of sticklebacks can still be coaxed to interbreed under the right conditions in the laboratory. Thus, the team could interbreed the animals and identify the chromosomal regions responsible for the differences among natural populations. By breeding the different kinds of fish and analyzing their genetic structure, Kingsley, Peichel, and their colleagues could trace how changes at the genetic level were associated with dramatic changes in the body and physiology of the new kinds of stickleback.

One of the novelties that distinguishes many freshwater from marine sticklebacks is a reduction in the pelvis and the pelvic spines that attach to it. Marine sticklebacks live with a number of predators, and the presence of big pelvic spines is one defense to avoid being eaten. Freshwater sticklebacks, on the other hand, frequently evolve in environments that lack the soft-mouthed predators found in the ocean. Moreover, because fin skeletons are metabolically expensive to develop, the freshwater fish often have smaller pelvises and spines, or they lose these features altogether. With this information as their inspiration, Kingsley, Peichel, and colleagues set off to collect sticklebacks for breeding experiments that would identify the genetic region responsible for the loss of the pelvis and spines in different populations. Much like Gingerich homing in on sites to find fossil whales, Kingsley and colleagues chose the right places on Earth to obtain the sticklebacks.

The resulting genetic analysis revealed a number of chromosomes involved in the

reduction of the pelvic appendage. But in terms of relevant data, one site reigned supreme: the region responsible for most of the limb loss²¹ contained the famous *Pitx1* gene. *Pitx1* was known in mammals and fish to be involved in the development of tissues across the body, from heads to appendages.

When the team looked at the differences in the gene itself, they found that the DNA sequence of *Pitx1* was largely unchanged between marine and freshwater fish.²² At first glance this finding seems utterly strange: how can *Pitx1* be involved with a major anatomical change like loss of the pelvis if the gene itself does not have any recognizable differences among the different fish? If the structure for the gene is not the culprit, perhaps the loss of pelvic fins relates to a change in the elements that control the activity of the gene. Genes often have one or more outside elements that serve as a kind of switch determining when and where the gene is active. Some of these regions, known as regulatory elements, are highly specific to one organ or tissue. Changes to the regulatory elements can bring about a modular change specific to one region. By contrast, a change in the sequence in the gene itself could have an effect everywhere the gene is active. Imagine a house with one furnace but different thermostats in each room. A change to the furnace would affect the entire house, a change to a thermostat only a single room. The same is true with the genes and their regulatory elements.

Detecting regulatory elements is difficult and involves fusing DNA sequences with visible labels in order to determine where particular sequences are active, manipulating the DNA to see what happens when a region is deleted or changed, and sometimes swapping DNA between species and individuals. With this tool kit, Kingsley's group identified a relatively

short stretch of DNA that serves as a regulatory switch controlling *Pitx1*'s expression only in hind fins.²³ A mutation in this region – the “thermostat” for a single location in the body – leads to loss of fin development in the hind fin while preserving other functions of *Pitx1*. The difference between freshwater fish that lack pelvic fins and their marine cousins that retain them lies largely in the stretches of DNA that control gene activity. This makes sense: a change in the structure or sequence of the gene would affect every tissue in which the gene is active. Given that *Pitx1* has global effects, a change is likely to be harmful, if not lethal. The tissue-specific changes in gene activity mean that fins can change independently of the rest of the body.

Not only can this area of regulatory DNA be identified and its function mapped, but it can be swapped between different kinds of stickleback.²⁴ When the Kingsley group took the *Pitx1* regulatory element from a stickleback with a complete pelvis and inserted it into an individual from a population that had lost the pelvis, something remarkable happened: like a ghost from the past, the pelvis appeared.²⁵ Kingsley and his colleagues swapped genes to make a fossil of sorts.

Little sticklebacks may open a window to great transformations, perhaps even to the hind-limb loss we see in fossils like those discovered by Gingerich. The more we look, the more we find similarities in the regulatory genes that underlie the development of tissues, organs, and the architecture of the bodies of diverse animals. *Pitx1* is no different; it is seen in mammals, fish, lizards, and birds. And the gene leaves a signature of its activity in the limb, showing a preference for one side of the body over the other. Given this clue, Kingsley and his coauthors suppose that modifications of the regulation of this gene may underlie limb reduction in

Neil H.
Shubin

many other creatures, including aquatic mammals such as manatees.²⁶ Indeed, mutations in *Pitx1* activity cause a range of limb malformations in mammals, such as clubfoot in human infants.²⁷

This story is more general than *Pitx1*, manatees, whale fossils, or even human skeletons. By leveraging the genetic and geological record to discover fossils, and moreover, by using molecular biology to isolate genes underlying evolutionary change and test their effects in the laboratory, the study of great transformations in the history of life can look forward to a future as a predictive science. In the coming years, it is not unlikely that we will be able to study evolution in the distant past both by finding fossils with increasing

precision and by reconstructing evolution's effects, either in part or in full, in the laboratory.

The layers of crust on Earth, like the genes, cells, and DNA of every living thing, are chronicles of history. But rocks, bodies, and genes are not independent records of time; they are linked by billions of years of planetary and biological evolution. Every living thing is the most extreme tip of a branch of an almost boundless tree of life; and all living creatures contain artifacts of a history nearly as ancient as the planet. There is something almost poetic to the notion that 3.5 billion years of change has brought one of these species to a moment when it can see its own past and grasp the deep interconnections embedded in the world around it.

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