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Evidence Supporting Biological Evolution

Along path leads from the origins of primitive "life," which existed at least 3.5 billion years ago, to the profusion and diversity of life that exists today. This path is best understood as a product of evolution.

Contrary to popular opinion, neither the term nor the idea of biological evolution began with Charles Darwin and his foremost work, *On the Origin of Species by Means of Natural Selection* (1859). Many scholars from the ancient Greek philosophers on had inferred that similar species were descended from a common ancestor. The word "evolution" first appeared in the English language in 1647 in a nonbiological connection, and it became widely used in English for all sorts of progressions from simpler beginnings. The term Darwin most often used to refer to biological evolution was "descent with modification," which remains a good brief definition of the process today.

Darwin proposed that evolution could be explained by the differential survival of organisms following their naturally occurring variation—a process he termed "natural selection." According to this view, the offspring of organisms differ from one another and from their parents in ways that are heritable—that is, they can pass on the differences genetically to their own offspring. Furthermore, organisms in nature typically produce more offspring than can survive and reproduce given the constraints of food, space, and other environmental resources. If a particular off-

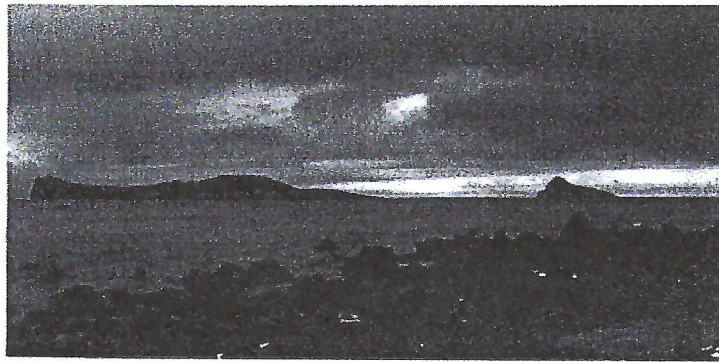
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Charles Darwin arrived at many of his insights into evolution by studying the variations among species on the Galápagos Islands off the coast of Ecuador.

Remember:
Darwin didn't come up with the term Evolution
Remember those before him who influenced him -
Aristotle
Lyle
Hutton
Malthus
Lamarck -

Darwin put it all together -
"Descent with modification" means Evolution



Remember the "Peppered Moth" during the Industrial Revolution

spring has traits that give it an advantage in a particular environment, that organism will be more likely to survive and pass on those traits. As differences accumulate over generations, populations of organisms diverge from their ancestors.

Darwin's original hypothesis has undergone extensive modification and expansion, but the central concepts stand firm. Studies in genetics and molecular biology—fields unknown in Darwin's time—have explained the occurrence of the hereditary variations that are essential to natural selection. Genetic variations result from changes, or mutations, in the nucleotide sequence of DNA, the molecule that genes are made from. Such changes in DNA now can be detected and described with great precision.

Genetic mutations arise by chance. They may or may not equip the organism with better means for surviving in its environment. But if a gene variant improves adaptation to the environment (for example, by allowing an organism to make better use of an available nutrient, or to escape predators more effectively—such as through stronger legs or disguising coloration), the organisms carrying that gene are more likely to survive and reproduce than those without it. Over time, their descendants will tend to increase, changing the average characteristics of the population. Although the genetic variation on which natural selection works is based on random or chance elements, natural selection itself produces "adaptive" change—the very opposite of chance.

Scientists also have gained an understanding of the processes by which new species originate. A new species is one in which the individuals cannot mate and produce viable descendants with individuals of a preexisting species. The split of one species into two often starts because a group of individuals becomes geographically separated from the rest. This is particularly apparent in distant remote islands, such as the Galápagos and the Hawaiian archipelago, whose great distance from the Americas and Asia means that arriving colonizers will have little or no opportunity to mate with individuals remaining on those continents. Mountains, rivers, lakes, and other natural barriers also account for geographic separation between populations that once belonged to the same species.

Once isolated, geographically separated groups of individuals become genetically differentiated as a consequence of mutation and other processes, including natural selection. The origin of a species is often a gradual process, so that at first the reproductive isolation between separated groups of organisms is only partial, but it eventually becomes complete. Scientists pay special attention to these intermediate situations, because they help to reconstruct the details of the process and to identify particular genes or sets of genes that account for the reproductive isolation between species.

A particularly compelling example of speciation involves the 13 species of of finches studied by Darwin on the Galápagos Islands, known as Darwins

Individuals drive Natural selection but populations drive Evolution

How new species form:

Geographic Isolation eventually creates new species.

Genetic Variation results from changes (mutations) in the nucleotide sequences.

Life Form	Millions of Years Since First Known Appearance (Approximate)
Microbial (procaryotic cells)	3,500
Complex (eucaryotic cells)	2,000
First multicellular animals	670
Shell-bearing animals	540
Vertebrates (simple fishes)	490
Amphibians	350
Reptiles	310
Mammals	200
Nonhuman primates	60
Earliest apes	25
Australopithecine ancestors of humans	5
Modern humans	0.15 (150,000 years)

Fossil Record:

Nearly All fossils are intermediates as are all life forms - something came before them, which led to them, and they led to the species that came after them!

So many intermediate forms have been discovered between fish and amphibians, between amphibians and reptiles, between reptiles and mammals, and along the primate lines of descent that it often is difficult to identify categorically when the transition occurs from one to another particular species. Actually, nearly all fossils can be regarded as intermediates in some sense; they are life forms that come between the forms that preceded them and those that followed.

The fossil record thus provides consistent evidence of systematic change through time—of descent with modification. From this huge body of evidence, it can be predicted that no reversals will be found in future paleontological studies. That is, amphibians will not appear before fishes, nor mammals before reptiles, and no complex life will occur in the geological record before the oldest eucaryotic cells. This prediction has been upheld by the evidence that has accumulated until now: no reversals have been found.

Common Structures

Homologous Structures

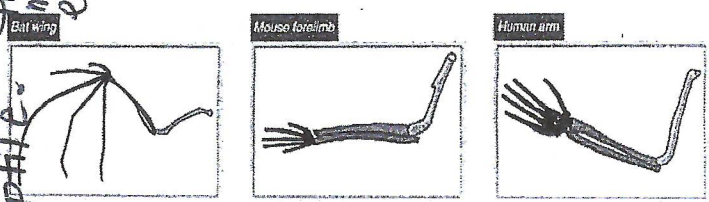
Inferences about common descent derived from paleontology are reinforced by comparative anatomy. For example, the skeletons of humans, mice, and bats are strikingly similar, despite the different ways of life of these animals and the diversity of environments in which they flourish. The correspondence of these animals, bone by bone, can be observed in every part of the body, including the limbs; yet a person writes, a mouse runs, and a bat flies with structures built of bones that are different in detail but similar in general structure and relation to each other.

Scientists call such structures homologies and have concluded that they are best explained by common descent. Comparative anatomists investigate such homologies, not only in bone structure but also in other parts of the body, working out relationships from degrees of similarity. Their conclusions provide important inferences about the details of evolutionary history, inferences that can be tested by comparisons with the sequence of ancestral forms in the paleontological record.

Homologous Structures are structures in different species that are structurally similar, but have a different function.

Homologous Structures indicate "Descent from ancestral forms" or relatedness of species

Mammal-like reptile w/ double jaw bone
 → the 1 bone in the jaw becomes the ear of the mammal that evolves from this reptile.
 Mammal-like reptile w/ double jaw bone → the 1 bone in the jaw becomes the ear of the mammal that evolves from this reptile.



A bat wing, a mouse forelimb, and a human arm serve very different purposes, but they have the same basic components. The similarities arise because all three species share a common four-limbed vertebrate ancestor.

Reptile with many bones in jaw



The mammalian ear and jaw are instances in which paleontology and comparative anatomy combine to show common ancestry through transitional stages. The lower jaws of mammals contain only one bone, whereas those of reptiles have several. The other bones in the reptile jaw are homologous with bones now found in the mammalian ear. Paleontologists have discovered intermediate forms of mammal-like reptiles (Therapsida) with a double jaw joint—one composed of the bones that persist in mammalian jaws, the other consisting of bones that eventually became the hammer and anvil of the mammalian ear.

Common Ancestry through Transitional Stages!

The Distribution of Species

(Evolution)

Biogeography also has contributed evidence for descent from common ancestors. The diversity of life is stupendous. Approximately 250,000 species of living plants, 100,000 species of fungi, and one million species of animals have been described and named, each occupying its own peculiar ecological setting or niche; and the census is far from complete. Some species, such as human beings and our companion the dog, can live under a wide range of environments. Others are amazingly specialized. One species of a fungus (*Laboulbenia*) grows exclusively on the rear portion of the covering wings of a single species of beetle (*Aphaenops croneti*) found only in some caves of southern France. The larvae of the fly *Drosophila carcinophila* can develop only in specialized grooves beneath the flaps of the third pair of oral appendages of a land crab that is found only on certain Caribbean islands.

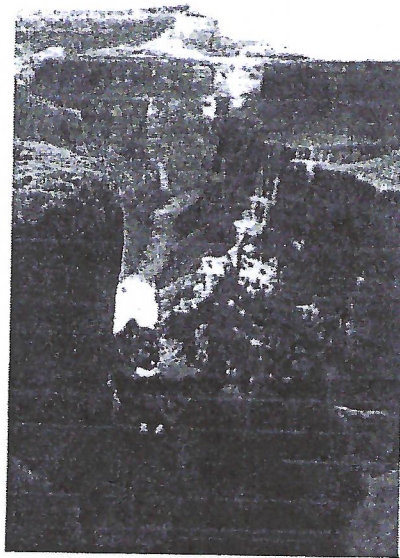
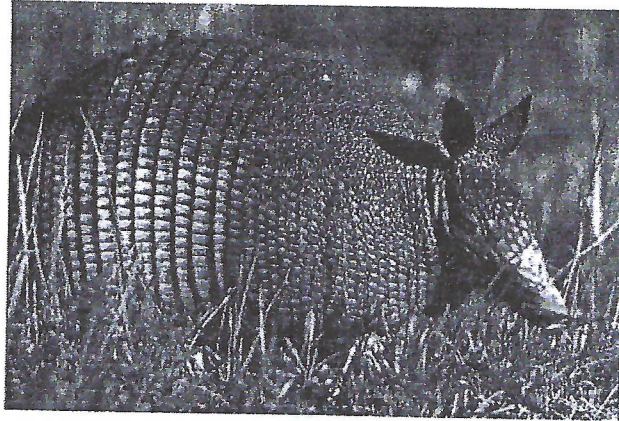
How can we make intelligible the colossal diversity of living beings and the existence of such extraordinary, seemingly whimsical creatures as the fungus, beetle, and fly described above? And why are island groups like the Galápagos so often inhabited by forms similar to those on the nearest mainland but belonging to different species? Evolutionary theory explains that biological diversity results from the descendants of local or migrant predecessors becoming adapted to their diverse environments. This explanation can be tested by examining present species and local fossils to see whether they have similar structures, which would indicate how one is derived from the other. Also, there should be evidence that species without an established local ancestry had migrated into the locality.

Wherever such tests have been carried out, these conditions have been confirmed. A good example is provided by the mammalian populations of North and South America, where strikingly different native organisms evolved in isolation until the emergence of the isthmus of Panama approximately 3 million years ago. Thereafter, the armadillo, porcupine, and opossum—mammals of South American origin—migrated north, along with many

When migrant predecessors become adapted to the new environment—over time, you get a new species

other species of plants and animals, while the mountain lion and other North American species made their way across the isthmus to the south.

The evidence that Darwin found for the influence of geographical distribution on the evolution of organisms has become stronger with advancing knowledge. For example, approximately 2,000 species of flies belonging to the genus *Drosophila* are now found throughout the world. About one-quarter of them live only in Hawaii.



Until about 3 million years ago, North and South America were separated by a wide expanse of water, so mammals on the two continents evolved separately. After the isthmus of Panama formed, armadillos and opossums migrated north, and mountain lions migrated south. These movements are documented in the fossil record.

Example of
geographic
isolation
eventually
leading to
new species!

More than a thousand species of snails and other land mollusks also are found only in Hawaii. The biological explanation for the multiplicity of related species in remote localities is that such great diversity is a consequence of their evolution from a few common ancestors that colonized an isolated

environment. The Hawaiian Islands are far from any mainland or other islands, and on the basis of geological evidence they never have been attached to other lands. Thus, the few colonizers that reached the Hawaiian Islands found many available ecological niches, where they could, over numerous generations, undergo evolutionary change and diversification. No mammals other than one bat species lived in the Hawaiian Islands when the first human settlers arrived; similarly, many other kinds of plants and animals were absent.

The Hawaiian Islands are not less hospitable than other parts of the world for the absent species. For example, pigs and goats have multiplied in the wild in Hawaii, and other domestic animals also thrive there. The scientific explanation for the absence of many kinds of organisms, and the great multiplication of a few kinds, is that many sorts of organisms never reached the islands, because of their geographic isolation. Those that did reach the islands diversified over time because of the absence of related organisms that would compete for resources.

* In the absence of competitors, species can thrive and diversify.

Similarities During Development

Embryology, the study of biological development from the time of conception, is another source of independent evidence for common descent. Barnacles, for instance, are sedentary crustaceans with little apparent similarity to such other crustaceans as lobsters, shrimps, or copepods. Yet barnacles pass through a free-swimming larval stage in which they look like other crustacean larvae. The similarity of larval stages supports the conclusion that all crustaceans have homologous parts and a common ancestry.

(Evolution)

Similarly, a wide variety of organisms from fruit flies to worms to mice to humans have very similar sequences of genes that are active early in development. These genes influence body segmentation or orientation in all these diverse groups. The presence of such similar genes doing similar things across such a wide range of organisms is best explained by their having been present in a very early common ancestor of all of these groups.

* fruit flies, worms, mice, human's all have early common ancestor (similar sequence of genes that are active early in development)

(5) Similar Nucleotide and Amino Acid Sequences. New Evidence from Molecular Biology

(Evolution)

The unifying principle of common descent that emerges from all the foregoing lines of evidence is being reinforced by the discoveries of modern biochemistry and molecular biology.

The code used to translate nucleotide sequences into amino acid sequences is essentially the same in all organisms. Moreover, proteins in all organisms are invariably composed of the same set of 20 amino acids. This unity of composition

and function is a powerful argument in favor of the common descent of the most diverse organisms.

In 1959, scientists at Cambridge University in the United Kingdom determined the three-dimensional structures of two proteins that are found in almost every multicelled animal: hemoglobin and myoglobin. Hemoglobin is the protein that carries oxygen in the blood. Myoglobin receives oxygen from hemoglobin and stores it in the tissues until needed. These were the first three-dimensional protein structures to be solved, and they yielded some key insights. Myoglobin has a single chain of 153 amino acids wrapped around a group of iron and other atoms (called "heme") to which oxygen binds. Hemoglobin, in contrast, is made of up four chains: two identical

(Evolution)

2 proteins Found in almost EVERY MULTI-CELLED animal.

Barnacles cannot move like other crustaceans yet their early larval stage is very similar to the other crustacean larval stages -

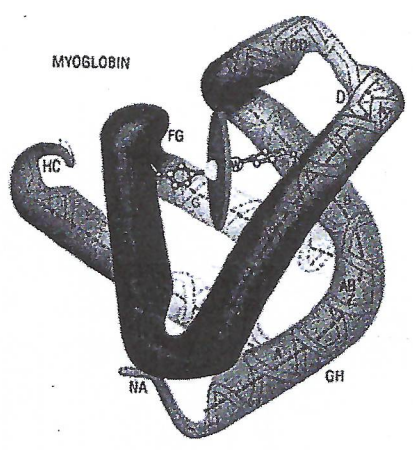
Similar Embryonic Structures, But different functions = Common ancestor - they are related.

Proteins in all organisms are composed of the same 20 amino acids.

It is obvious that the (2) molecules (proteins) are very closely related.

chains consisting of 141 amino acids, and two other identical chains consisting of 146 amino acids. However, each chain has a heme exactly like that of myoglobin, and each of the four chains in the hemoglobin molecule is folded exactly like myoglobin. It was immediately obvious in 1959 that the two molecules are very closely related.

During the next two decades, myoglobin and hemoglobin sequences were determined for dozens of mammals, birds, reptiles, amphibians, fish, worms, and molluscs. All of these sequences were so obviously related that they could be compared with confidence with the three-dimensional structures of two selected standards—whale myoglobin and horse hemoglobin. Even more significantly, the differences between sequences from different organisms could be used to construct a family tree of hemoglobin and myoglobin variation among organisms. This tree agreed completely with observations derived from paleontology and anatomy about the common descent of the corresponding organisms.



Myoglobin, which stores oxygen in muscles, consists of a chain of 153 amino acids wrapped around an oxygen-binding molecule. The sequence of amino acids in myoglobin varies from species to species, revealing the evolutionary relationships among organisms.

Similar family histories have been obtained from the three-dimensional structures and amino acid sequences of other proteins, such as cytochrome c (a protein engaged in energy transfer) and the digestive proteins trypsin and chymotrypsin. The examination of molecular structure offers a new and extremely powerful tool for studying evolutionary relationships. The quantity of information is potentially huge—as large as the thousands of different proteins contained in living organisms, and limited only by the time and resources of molecular biologists.

As the ability to sequence the nucleotides making up DNA has improved, it also has become possible to use genes to reconstruct the evolutionary history of organisms. Because of mutations, the sequence of nucleotides in a gene gradually changes over time. The more closely related two organisms are, the less different their DNA will be. Because there are tens of thousands of genes in humans and other organisms, DNA contains a tremendous amount of information about the evolutionary history of each organism.

Genes evolve at different rates because, although mutation is a random event, some proteins are much more tolerant of changes in their amino acid sequence than

3-dimensional structures of proteins molecules and their amino acids sequences link organisms to a common ancestor!

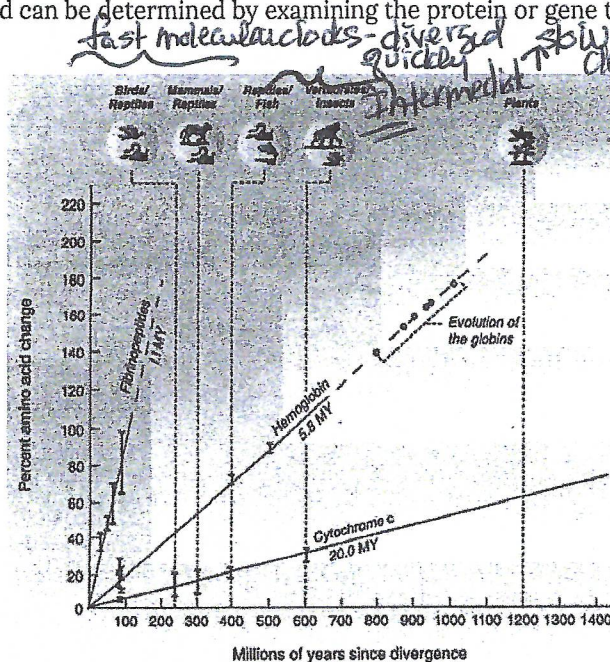
Molecular Structure (DNA and proteins) is a powerful tool now being used to study evolutionary relationships

* Sequencing the nucleotides that make up DNA has improved and we can use genes to reconstruct evolutionary history of organisms

are other proteins. For this reason, the genes that encode these more tolerant, less constrained proteins evolve faster. The average rate at which a particular kind of gene or protein evolves gives rise to the concept of a "molecular clock." Molecular clocks run rapidly for less constrained proteins and slowly for more constrained proteins, though they all time the same evolutionary events.

The figure on this page compares three molecular clocks: for cytochrome c proteins, which interact intimately with other macromolecules and are quite constrained in their amino acid sequences; for the less rigidly constrained hemoglobins, which interact mainly with oxygen and other small molecules; and for fibrinopeptides, which are protein fragments that are cut from larger proteins (fibrinogens) when blood clots. The clock for fibrinopeptides runs rapidly; 1 percent of the amino acids change in a little longer than 1 million years. At the other extreme, the molecular clock runs slowly for cytochrome c; a 1 percent change in amino acid sequence requires 20 million years. The hemoglobin clock is intermediate.

The concept of a molecular clock is useful for two purposes. It determines evolutionary relationships among organisms, and it indicates the time in the past when species started to diverge from one another. Once the clock for a particular gene or protein has been calibrated by reference to some event whose time is known, the actual chronological time when all other events occurred can be determined by examining the protein or gene tree.



Species that diverged longer ago have more differences in their corresponding proteins, reflecting changes in the amino acids over time. Proteins evolve at different rates depending on the constraints imposed by their functions. Cytochrome c, a protein involved in energy transfer, is tightly constrained and changes slowly. Fibrinopeptides, which are involved in blood clotting, are much less constrained, with hemoglobin an intermediate case. The estimates for times of divergence shown here are based on 1971 data and have changed slightly since then (see table on page 13).

An interesting additional line of evidence supporting evolution involves se-

Molecular Clock:
Average rate at which a particular gene or protein evolves.

- 1) fibrinopeptides - fast molecular clock.
- 2) hemoglobin - intermediate
- 3) cytochrome c - molecular clock runs very slowly

We looked at amino acid sequences on our PPT - find the slide. The organisms whose amino acid sequences were almost the same were related. They have a more recent, common ancestor.

fast molecular clocks - diverged quickly
intermediate
slow molecular clock - diverged slowly

(diverged slowly)

(diverged slowly)

2 purposes of molecular clocks:

- 1) determines the evolutionary relationship among organisms
- 2) indicates the time in the past when species started to diverge from one ancestor.

When species have more differences in their proteins, it means they diverged longer ago - more rapidly. They diverged faster into new species.

When species have fewer differences in their amino acids (proteins) it means they did not diverge or evolve fast from their common ancestor. It takes much longer for them to diverge into a new species.