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Evidence of evolution

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While on board HMS *Beagle*, [Charles Darwin](#) collected numerous specimens, many new to science, which supported his later theory of evolution.

In biology, **evidence of evolution** or **evidence for evolution** is generally any of an available body of facts or information that supports the theory of [evolution](#). Complications arise because several different meanings are associated with "Evolution." In a broad sense, "evolution" refers simply to any heritable change in a population of organisms over time. More specifically,

"evolution" may refer to [Charles Darwin](#)'s overall theory of evolution, which itself comprises two theories each addressing a different aspect of evolutionary change: The theory of [descent with modification](#) addresses the *pattern* of the change, while the theory of modification through [natural selection](#) addresses the *process* or mechanism of the change.

The theory of descent with modification postulates that all [organisms](#) have descended from one or a few common ancestors through a continuous process of branching. The theory of natural selection offers one possible mechanism, natural selection, as the directing or creative force behind the perceived pattern of evolution.

Some people, emphasizing the division of evolutionary change into two types—[macroevolution](#) above the species level and [microevolution](#) within species—assert that the evidences of natural selection as the causal agent of evolutionary change are found only on the microevolutionary level. Others, perceiving the distinction between macro- and microevolution as an artificial construct, assert that natural selection is a single continuous process encompassing not only major changes above the species level but also change within species. Those holding this latter perspective tend to consider all evidence of evolution as support for the comprehensive theory of evolution that includes both the pattern of descent with modification and the mechanism of modification through natural selection.

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Evidences from [fossils](#), biogeography, [homology](#), and genetics are among those used to support the theory of descent with modification. Evidences also are applied to support the theory of

natural selection on the microevolutionary level. Evidence that would apply to natural selection at the macroevolutionary level, however, necessarily is based on extrapolation from evidence on the microevolutionary level. This article highlights primarily evidence for evolution on the macroevolutionary level applied to the theory of descent with modification.

Overview

As broadly and commonly defined in the scientific community, the term [evolution](#) connotes heritable changes in populations of organisms over time, or changes in the frequencies of [alleles](#) over time. In this sense, the term does not specify any overall pattern of change through the ages, nor the process whereby change occurs, and it refers not to individual organisms but to populations of organisms through successive generations.

However, the term evolution often is used with narrower meanings. It is not uncommon to see the term equated to the specific theory that all organisms have descended from common ancestors, which is also known as the [theory of descent with modification](#). Less frequently, evolution sometimes is used to refer to one explanation for the process by which change occurs, the [theory of modification through natural selection](#). In addition, the term evolution occasionally is used with reference to a comprehensive theory that includes both the non-causal pattern of descent with modification and the causal mechanism of natural selection.

In reality, in Darwin's comprehensive theory of evolution, there actually can be elucidated at least five major, largely independent theories, including these two main theories (Mayr 1982). Other theories offered by Darwin deal with (3) evolution as such (the fact of evolution), (4) the gradualness of evolution, and (5) population speciation.

Theory of descent with modification

The "theory of descent with modification" is the major theory covering the pattern of evolution—that is, it is descriptive and treats non-causal relations between ancestral and descendant [species](#), orders, phyla, and so forth. The theory of descent with modification, also called the "theory of common descent," postulates that all organisms have descended from common ancestors by a continuous process of branching. In other words, in a restrictive sense, all life evolved from one kind of organism or from a few simple kinds, and each species arose in a single geographic location from another species that preceded it in time. Each [taxonomic](#) group—whether it be as limited in scope as a subspecies of fish or as extensive in scope as all St. Bernard dogs, all [whales](#), all [mammals](#), all [vertebrates](#), or all [human beings](#) throughout history—shares a common ancestor or pair of common ancestors. In the broadest sense of the terminology, descent with modification simply means that more recent forms result from modification of earlier forms.

One of the major contributions of [Charles Darwin](#) was to catalog evidence for the theory of descent with modification, particularly in his book *Origin of Species*. In the years since the book was published, biologists have added so substantially to the original body of evidence compiled by Darwin that most biologists consider the "pattern of evolution," that is, descent with modification—at least in the broader sense that more recent taxa came by modification from

earlier forms, without specifying one or only a few original forms—to be well documented. In support of this view, the common evidences put forward are the [fossil](#) record, the distribution patterns of existing species, genetic correlations, and comparison of homologous structures.

The tangled roots and branches of the tree of life

While the theory of descent with modification in the broad sense is supported, the conventional paradigm that the history of life maps as the "tree of life"—a tree beginning with one universal common ancestor as the trunk and then progressively branching, with modern species at the twig ends—is being re-drawn at both the base of the trunk and the branches. These revisions arise as scientists gain more understanding about the "hidden" world of microbes (unicellular organisms and [viruses](#)).

The great diversity, abundance, and ubiquity of the single-celled organisms ([bacteria](#), [archaea](#), and some protists) has gained widespread recognition in recent years, and considerable progress has been made in incorporating that knowledge into the story of evolution. In contrast, the place of viruses in the story of evolution remains much more speculative.

There are proposals that the tree of life instead of being simple at its base, may be considerably more complex. Sequencing the genomes of specific organisms yields support for the view in which tracing the ancestry of life back through time leads to something more like a bush representing the ongoing exchange of genetic material between diverse single-celled organisms—some of them with a nucleus and some without it—sharing genetic material tracing back further perhaps to a momentary convergence in a first nucleated cell (a first eukaryote) comprising some of the key genetic code that has been preserved even to humans today. Current evidence suggests that the eukaryote structure itself was a fusion product of the two different kinds of non-nucleated organisms—[archaea](#) and [bacteria](#)—with the archaea forming the nucleus and the bacteria the surrounding cytoplasm.

Before the formation of eukaryotes, the archaea and the bacteria shared genetic material within, as well as between, their two great domains through horizontal gene transfer. By this model, the momentary constricting of the trunk of the tree of life when the eukaryote was formed might be envisioned as a single trunk emerging from a great root structure that has been variously called a ring or a bush or a network representing one or probably two common gene pools (Rivera and Lake 2004, Bacterial/Prokaryotic Phylogeny).

The bush or network aspect of the ancestral track is consistent with the concept of evolution by endosymbiosis as proposed by biologist Lynn Margulis. She writes that "all visible organisms, plants, animals, and fungi evolved by 'body fusion.' Fusion at the microscopic level led to the integration and formation of ever more complex individuals." In the Margulis model, prokaryotes are a vast reservoir of diverse functions and metabolisms, including those that through cellular fusions have produced not only the first eukaryote, but also the energy-generating [mitochondria](#), the [photosynthetic chloroplasts](#), [flagella](#), and [cilia](#). Beyond these most basic of cellular components, Margulis sees evidence of such "syntrophogenesis" in the successive acquisition of greater functionality in more complex organisms. Examples range from the rugged [lichen](#) as a fusion of a [fungus](#) and a photosynthetic [alga](#) (or a blue-green bacterium) to the

leguminous plants dependent on nitrogen-fixing bacteria in their roots, the "higher" termites carefully tending the fungi they eat, and cows with their separate "stomach" housing bacteria converting grass eaten by the cows to a form the cows can digest (Margulis and Sagan 2002).

Viruses add a new dimension to the story of evolution. Generally identified as not living and dependent on cells for reproduction, viruses, it now seems, have from early on and continuing to today played an active role in the exchange of genetic material both between unicellular and multicellular organisms. Needing the cellular machinery to multiply, viruses are adept at inserting their short genome into the host organism's genome, whether the host is unicellular or multicellular. While some viruses commandeer the cell's genetic machinery solely for reproducing the virus then spread when the cell bursts, other viruses insert their genome into the host genome and then linger without significantly disrupting the cell until some later time when the cell or its descendants experiences stress. This slow-acting viral invasion, called lysogenic viral infection, is, for example, what transforms an otherwise innocuous bacteria into the one that causes cholera.

Higher on the tree of life, some scientists speculate, both viruses and unicellular organisms can transfer genes between distantly related organisms on different branches. Such horizontal gene transfers connecting different branches have been called "vines" on the tree of life (Kunin, Goldovsky, Darzentas, and Ouzounis 2005).

Other complicating factors are proposed based on the relatively sudden appearance of phyla during the [Cambrian explosion](#) and on evidence that certain types of animals may have originated more than once and in different places at different times (Whittington 1985; Gordon 1999; Woese 1998; Wells 2000).

Theory of modification through natural selection

The second major evolutionary theory is the "theory of modification through natural selection," also known as the "theory of natural selection." It involves mechanisms and causal relationships; in other words, the "process" by which evolution took place to arrive at the pattern. Natural selection may be defined as the mechanism whereby biological individuals that are endowed with favorable or deleterious traits reproduce more or less than other individuals that do not possess such traits. According to this theory, natural selection is the directing or creative force of evolution.

The theory of natural selection was the most revolutionary and controversial concept advanced by Darwin. It comprises three components: (a) purposelessness (no higher purpose, just the struggle of individuals to survive and reproduce); (b) philosophical [materialism](#) (matter is seen as the ground of all existence with mind being produced by or a function of the material brain); and (c) the view that evolution is not progressive from lower to higher, but just an adaptation to local environments; it could form a man with his superior brain or a [parasite](#), but no one could say which is higher or lower (Luria, Gould, and Singer 1981).

In reality, most evidence presented in support of evolution is actually evidence for the theory of descent with modification. Concrete evidence for the theory of modification by natural selection

is limited to [microevolution](#)—that is, evolution within populations or species. For example, modification by natural selection is observed as various species of bacteria develop increased [pesticide](#) resistance. Artificial selection within populations or species also provides evidence, such as in the production of various breeds of animals by selective breeding, or varieties of plants by selective cultivation.

Evidence that natural selection directs the major transitions between taxa and originates new designs (macroevolution), however, necessarily involves extrapolation from evidences on the microevolutionary level. That is, it is inferred that if moths can change their color in 50 years, then new designs or entire new genera can originate over millions of years. It is further inferred that if geneticists see population changes for [fruit flies](#) in laboratory bottles, then given eons of time, [birds](#) can evolve from [reptiles](#), and [fish](#) with jaws from jawless ancestors.

Evidence for the theory of descent with modification

For the broad concept of evolution ("any heritable change in a population of organisms over time"), evidences of evolution are readily apparent on a microevolutionary level. These include observed changes in domestic crops (creating a variety of [maize](#) with greater resistance to disease), bacterial strains (development of strains with resistance to [antibiotics](#)), laboratory animals (structural changes in fruit flies), and flora and fauna in the wild (color change in particular populations of peppered moths and polyploidy in plants).

It was Charles Darwin, however, in the *Origin of Species*, who first marshaled considerable evidences for the theory of descent with modification on the macroevolutionary level. He did this within such areas as [paleontology](#), [biogeography](#), morphology, and [embryology](#). Many of these areas continue to provide the most convincing proofs of descent with modification even today (Mayr 1982; Mayr 2001). Supplementing these areas are molecular evidences.

[Stephen Jay Gould](#) (1983) notes that the best support for the theory of descent with modification actually comes from the observation of imperfections of nature, rather than perfect adaptations:

All of the classical arguments for evolution are fundamentally arguments for imperfections that reflect history. They fit the pattern of observing that the leg of Reptile B is not the best for walking, because it evolved from Fish A. In other words, why would a rat run, a bat fly, a porpoise swim and a man type all with the same structures utilizing the same bones unless inherited from a common ancestor?

Gould provides a good characterization of the common way of thinking about the evidence of evolution. Yet, it may be of interest to note that he is not offering a scientific analysis or proof. Rather, he suggests that only one hypothesis could make sense of the evidence—inheritance from a common ancestor, a common ancestor that presumably also possessed the same structures and same bones. This places Gould and the biology he characterizes in the position of depending on there being no counterexamples and no viable alternative hypotheses. For a discussion of a counterexample, see [Homology](#).

Questioning the evidence

Those who would question the persuasiveness or legitimacy of evidence offered in support of the theory of descent with modification at the macroevolutionary level tend to be those who are seeking to reconcile earth's life and geology with their own sense of religion or spirituality. Various views of religion or spirituality have led people to insert into the discussions on evolution such views as: a young earth required by a literal interpretation of a scripture; a cosmic consciousness infusing all of the natural world; a cosmic designer shaping the pattern and products of evolution; or even a cosmic parent creating a human child in the cosmic parent's image.

Young-earth or "scientific" [creationists](#) maintain that modern organisms did not descend from common ancestors, and that modern organisms' only historical connectedness is in the mind of God. Scientific creationists promulgate the view that living organisms are immutable, and were all created by God in a short time period, on an earth whose age is generally measured in thousands of years. The substantial fossil record is dismissed in various ways, including as a trick of God or as an artifact from the Great Flood (with some organisms sinking faster than others and thus settling onto a lower fossil plane). Although some individual presentations by scientific creationists are quite sophisticated, the overall theory of scientific creationism runs counter to an enormous body of evidence and thus is strongly criticized by most of the scientific community.

Specific critiques of the theory of descent with modification have been made for most of the evidences of evolution, including the fossil record, structural and embryological homologies, and patterns of geographical distribution of species. The critiques tend to rely on the view that conventional evidences of evolution if viewed closely do not really support the conclusion there has been a continuous line of descent with modification from one or a few ancestors to the full array of life on earth today. The key word in several critiques is "continuous:" although the evidence may be suggestive of continuity, it becomes proof of continuity only in conjunction with an additional naturalistic premise. The premise is that all of the many gaps in the evidence must have been spanned by the same material processes that have already been observed. Hence, throughout the evolutionary process, only materialistic processes have been involved in producing the continuity of lineages extending from one or a few primeval ancestors to the earth's present hugely diverse flora and fauna, including humans.

While some people who believe in God and the essential spiritual nature of human beings are comfortable with a fully materialistic evolutionary process, others intuitively sense that there must have been a substantial spiritual dimension to the workings of the evolutionary process. Such latter people are likely the source of many of the concrete critiques of the commonly-presented evidences of evolution. Examples of these critiques are attached, one each, to the following detailed elaborations in the sections on "Limitations of fossil evidence," "Homologous structures," "Vestigial organs," and "Evidence from embryology."

Evidence from paleontology



An insect trapped in [amber](#).

Overview

[Fossil](#) evidence of prehistoric organisms has been found all over the earth. Fossils are traces of once living organisms. Fossilization of an organism is an uncommon occurrence, usually requiring hard parts (like bone), and death where [sediments](#) or volcanic ash may be deposited. Fossil evidence of organisms without hard body parts, such as shell, bone, teeth, and wood stems, is rare, but exists in the form of ancient microfossils and the fossilization of ancient burrows and a few soft-bodied organisms. Some insects have been preserved in resin. The age of fossils can often be deduced from the geologic context in which they are found (the strata); and their age also can be determined with radiometric dating.

The comparison of fossils of extinct organisms in older geological strata with fossils found in more recent strata or with living organisms is considered strong evidence of descent with modification. Fossils found in more recent strata are often very similar to, or indistinguishable from living species, whereas the older the fossils are, the greater the difference from living organisms or recent fossils. In addition, fossil evidence reveals that species of greater complexity have appeared on the earth over time, beginning in the [Precambrian](#) era some 600 millions of years ago with the first [eukaryotes](#). The fossil records support the view that there is orderly progression in which each stage emerges from, or builds upon, preceding stages.

Fossils

When organisms die, they often decompose rapidly or are consumed by scavengers, leaving no permanent evidences of their existence. However, occasionally, some organisms are preserved. The remains or traces of organisms from a past [geologic age](#) embedded in [rocks](#) by natural processes are called [fossils](#). They are extremely important for understanding the evolutionary

history of life on Earth, as they provide direct evidence of evolution and detailed information on the ancestry of organisms. [Paleontology](#) is the study of past life based on fossil records and their relations to different geologic time periods.

For fossilization to take place, the traces and remains of organisms must be quickly buried so that weathering and decomposition do not occur. Skeletal structures or other hard parts of the organisms are the most commonly occurring form of fossilized remains (Martin 1999). There are also some trace "fossils" showing molds, casts, or imprints of some previous organisms.

As an animal dies, the organic materials gradually decay, such that the [bones](#) become porous. If the animal is subsequently buried in mud, [mineral](#) salts will infiltrate into the bones and gradually fill up the pores. The bones will harden into stones and be preserved as fossils. This process is known as petrification. If dead animals are covered by wind-blown [sand](#), and if the sand is subsequently turned into mud by heavy [rain](#) or [floods](#), the same process of mineral infiltration may occur. Apart from petrification, the dead bodies of organisms may be well preserved in [ice](#), in hardened resin of [coniferous](#) trees ([amber](#)), in tar, or in anaerobic, [acidic peat](#). Examples of trace fossils, an impression of a form, include [leaves](#) and footprints, the fossils of which are made in layers that then harden.

Fossils are important for estimating when various lineages developed. As fossilization is an uncommon occurrence, usually requiring hard body parts and death near a site where sediments are being deposited, the fossil record only provides sparse and intermittent information about the evolution of life. Evidence of organisms prior to the development of hard body parts such as shells, bones, and teeth is especially scarce, but exists in the form of ancient microfossils, as well as impressions of various soft-bodied organisms

Fossil records



Fossil [trilobite](#). Trilobites were hard-shelled [arthropods](#), related to living [horseshoe crabs](#) and [spiders](#), that first appeared in significant numbers around 540 mya, [dying out](#) 250 mya.

It is possible to observe sequences of changes over time by arranging fossil records in a chronological sequence. Such a sequence can be determined because fossils are mainly found in [sedimentary rock](#). Sedimentary rock is formed by layers of silt or mud on top of each other; thus, the resulting rock contains a series of horizontal layers, or strata. Each layer contains fossils that are typical for a specific time period during which they were made. The lowest strata contain the oldest rock and the earliest fossils, while the highest strata contain the youngest rock and more recent fossils.

A succession of animals and plants can also be seen from fossil records. Fossil evidence supports the theory that organisms tend to progressively increase in complexity. By studying the number and complexity of different fossils at different stratigraphic levels, it has been shown that older fossil-bearing rocks contain fewer types of fossilized organisms, and they all have a simpler structure, whereas younger rocks contain a greater variety of fossils, often with increasingly complex structures.

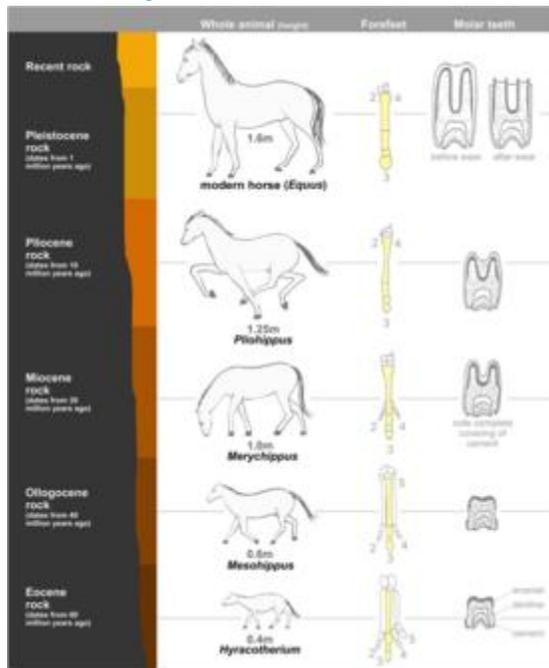
In the past, geologists could only roughly estimate the ages of various strata and the fossils found. They did so, for instance, by estimating the time for the formation of sedimentary rock layer by layer. Today, by measuring the proportions of [radioactive](#) and stable elements in a given rock, the ages of fossils can be more precisely dated by scientists. This technique is known as radiometric dating.

Throughout the fossil record, many species that appear at an early stratigraphic level disappear at a later level. This is interpreted in evolutionary terms as indicating the times at which species originated and became [extinct](#). Geographical regions and climatic conditions have varied throughout the Earth's history. Since organisms are adapted to particular environments, the constantly changing conditions favored species that adapted to new environments.

According to fossil records, some modern species of plants and animals are found to be almost identical to the species that lived in ancient geological ages. They are existing species of ancient lineages that have remained morphologically (and probably also [physiologically](#)) somewhat unchanged for a very long time. Consequently, they are called "living fossils" by laypeople. Examples of "living fossils" include the tuatara, the [nautilus](#), the [horseshoe crab](#), the [coelacanth](#), the [ginkgo](#), the Wollemi pine, and the [metasequoia](#).

Despite the relative rarity of suitable conditions for fossilization, approximately 250,000 fossil species are known (Gore 2006). The number of individual fossils this represents varies greatly from species to species, but many millions of fossils have been recovered: For instance, more than three million fossils from the last [Ice Age](#) have been recovered from the La Brea Tar Pits (NHMLA 2007) in Los Angeles. Many more fossils are still in the ground, in various geological formations known to contain a high fossil density, allowing estimates of the total fossil content of the formation to be made. An example of this occurs in South Africa's Beaufort Formation (part of the Karoo Supergroup, which covers most of South Africa), which is rich in [vertebrate](#) fossils, including [therapsids](#) (reptile/mammal transitional forms) (Kazlev 2002).

Evolution of the horse



Evolution of the horse showing reconstruction of the fossil species obtained from successive rock strata. The foot diagrams are all front views of the left forefoot. The third metacarpal is shaded throughout. The teeth are shown in longitudinal section.

Due to a substantial fossil record found in North American sedimentary deposits from the early [Eocene](#) to the present, the [horse](#) is considered to provide one of the best examples of evolutionary history (phylogeny).

This evolutionary sequence starts with a small animal called the *Hyracotherium* that lived in North America about 54 million years ago, then spread across to Europe and Asia. Fossil remains of *Hyracotherium* show it to have differed from the modern horse in three important respects: It was a small animal (the size of a [fox](#)), lightly built and adapted for running; the limbs were short and slender, and the feet elongated so that the digits were almost vertical, with four digits in the forelimbs and three digits in the hindlimbs; and the incisors were small, the molars having low crowns with rounded cusps covered in enamel.

The probable course of development of horses from *Hyracotherium* to *Equus* (the modern horse) involved at least 12 [genera](#) and several hundred [species](#). The major trends seen in the development of the horse to changing environmental conditions may be summarized as follows:

- Increase in size (from 0.4m to 1.5m);
- Lengthening of limbs and feet;
- Reduction of lateral digits;
- Increase in length and thickness of the third digit;

- Increase in width of incisors;
- Replacement of premolars by molars; and
- Increases in tooth length, crown height of molars.

A dominant [genus](#) from each geological period has been selected to show the progressive development of the horse. However, it is important to note that there is no evidence that the forms illustrated are direct descendants of each other, even though they are closely related.

Limitations of fossil evidence

The fossil record is an important but intrinsically limited source of evidence of the evolutionary history of organisms. The vast expanse of geological time and the rarity of fossilization prescribes that the fossil record can at best offer clues to the broad patterns of evolution. Even the detailed history of transitions from an ancestral horse (Eohippus) to the modern [horse](#) (Equus), which has been characterized as being "articulately represented," remains sketchy despite the identification of "at least 12 genera and several hundred species." Such extensive fossils offer no evidence of direct ancestor-descendant relations that would need to be proven to prove the notion of continuous descent from a common ancestor.

The horse ancestor fossil record is considered to be the most detailed fossil record of all. For most modern species, however, there is a general lack of gradually sequenced intermediary forms. There are some fossil lineages that appear quite well-represented, such as from therapsid reptiles to the mammals, and between what are considered the land-living ancestors of the whales and their ocean-living descendants (Mayr 2001). [Archaeopteryx](#) has been viewed by many as representing an intermediate stage between reptiles and birds. Generally, however, [paleontologists](#) do not find a steady change from ancestral forms to descendant forms. Rather, they find discontinuities, or gaps in most every phyletic series (Mayr 2002). This has been explained both by the incompleteness of the fossil record and by proposals of speciation that involve short periods of time, rather than millions of years. Notably, there are also gaps between living organisms, with a lack of intermediaries between whales and terrestrial mammals, between reptiles and birds, and between flowering plants and their closest relatives (Mayr 2002). [Archaeopteryx](#) has recently come under criticism as a transitional fossil between reptiles and birds (Wells 2000).

There is a gap of about 100 million years between the early [Cambrian](#) period and the later [Ordovician](#) period. The early Cambrian period was the period from which numerous invertebrate fossils are found. These include: sponges, [cnidarians](#) ([jellyfish](#)), [echinoderms](#) (eocrinoids), [mollusks](#) ([snails](#)), and [arthropods](#) ([trilobites](#)). In the later Ordovician period, the first animal that really possessed the typical features of [vertebrates](#), the [Australian fish](#), *Arandaspis* appeared. Thus few, if any, fossils of an intermediate type between [invertebrates](#) and vertebrates have been found, although likely candidates include the Burgess Shale animal, *Pikaia gracilens*, and its Maotianshan Shales relatives, *Myllokunmingia*, *Yunnanozoon*, *Haikouella lanceolata*, and *Haikouichthys*.

Some of the reasons for the incompleteness of fossil records are:

- In general, the probability that an organism becomes fossilized after death is very low;
- Some species or groups are less likely to become fossils because they are soft-bodied;
- Some species or groups are less likely to become fossils because they live (and die) in conditions that are not favorable for fossilization to occur in;
- Many fossils have been destroyed through erosion and tectonic movements;
- Some fossil remains are complete, but most are fragmentary;
- Some evolutionary change occurs in populations at the limits of a species' ecological range, and as these populations are likely to be small, the probability of fossilization is lower (punctuated equilibrium);
- Similarly, when environmental conditions change, the population of a species is likely to be greatly reduced, such that any evolutionary change induced by these new conditions is less likely to be fossilized;
- Most fossils convey information about external form, but little about how the organism functioned;
- Using present-day biodiversity as a guide suggests that the fossils unearthed represent only a small fraction of the large number of species of organisms that lived in the past.

Critique of fossil evidence

One argument against using the fossil record as a support for evolutionary theory is that while the fossil record provides "consistent evidence of systematic change through time" (NAS 1999), its intrinsic irregularity and inconsistency precludes accumulation of the record of any continuous lineage. In terms of directly successive generations, the fossil record presents us with great gaps. Claiming such a spotty record as evidence of a lineage that is continuous through slow and gradual change requires assumptions for which there is no scientific evidence. Among scientists, one of the strong critics of the prevailing view that the fossil record indicates continuous, gradual change between species is Lynn Margulis. She writes, in collaboration with Dorian Sagan, that the many scientific insights of the 20th century show "that the luxuriant living diversity surrounding us *did not* evolve gradually, as the students of the fossil record so vociferously tell us. Precious little evidence in the sedimentary rocks exists for small steps that connect one species gradually to its descendants. . . . The discontinuous record of past life shows clearly that the transition from one species to another occurs in discrete jumps" (Margulis and Sagan 2002). Margulis proposes to explain the discrete jumps in part by endosymbiosis through which one organism comes to incorporate into its genome all or part of the genome of its former symbiont.

Evidence from comparative anatomy

Overview

The study of comparative anatomy also yields evidence that has been used to support the theory of descent with modification. For one, there are structures in diverse species that have similar internal organization yet perform different functions. [Vertebrate](#) limbs are a common example of such *homologous structures*. [Bat](#) wings, for example, are very similar to human hands. Also similar are the forelimbs of the penguin, the porpoise, the rat, and the [alligator](#). In addition, these features derive from the same structures in the [embryo](#) stage. As queried earlier, "why would a

rat run, a bat fly, a porpoise swim and a man type” all with limbs using the same bone structure if not coming from a common ancestor (Gould 1983).

Likewise, a structure may exist with little or no function in one organism, while a very similar structure in other species may have a clear and essential function. These structures are called [vestigial organs](#) or vestigial characters. The wings of flightless birds, such as the [ostrich](#) and [emu](#), and the remnant eyes of moles, some blind salamanders, and blind cave fish are examples. Such structures would be the prediction of the theory of descent with modification, suggesting that organisms with a vestigial structure share a common ancestry with organisms that have the same feature in a fully functional form.

For the point of view of classification, it can be observed that various species exhibit a sense of "relatedness," such as various catlike mammals, which can be put in the same family (Felidae), dog-like mammals can be put in the same family (Canidae), and bears are in the same family (Ursidae). These and other similar mammals can be combined into the same order (Carnivora). This sense of relatedness, from external features, fits the expectations of the theory of descent with modification.

Comparative study of the anatomy of groups of [plants](#) reveals that certain structural features are basically similar. For example, the basic components of all [flower](#) blossoms are sepals, petals, stigma, style, and ovary; yet the size, color, number of parts, and specific structure are different for each individual species.

Phylogeny, the study of the ancestry (pattern and history) of organisms, yields a phylogenetic tree to show such relatedness (or a cladogram in other taxonomic disciplines).

[Homologous structures](#)

Main article: [Homology \(biology\)](#)

If widely separated groups of organisms are originated from a common ancestry, they are expected to have certain basic features in common. The degree of resemblance between two organisms should indicate how closely related they are:

- Groups with little in common are assumed to have diverged from a common ancestor much earlier in geological history than groups that have a lot in common;
- In deciding how closely related two animals are, a comparative anatomist looks for [structures](#) that are fundamentally similar, even though they may serve different functions in the adult.
- In cases where the similar structures serve different functions in adults, it may be necessary to trace their origin and embryonic development. A similar developmental origin suggests they are the same structure, and thus likely to be derived from a common ancestor.

In biology, [homology](#) is commonly defined as any similarity between structures that is attributed to their shared ancestry. [Darwin](#) meant something different when he used "homology" in his theory of [evolution](#). He was using the term with its classical meaning as it was coined by [Richard Owen](#) in the 1840s. Historically, homology was defined as similarity in structure and position, such as the pattern of [bones](#) in a bat's wing and those in a porpoise's flipper (Wells 2000).

Conversely, the term *analogy* signified functional similarity, such as the wings of a bird and those of a [butterfly](#).

Homology in the classical sense, as similarity in structure and position of anatomical features between different organisms, was an important evidence used by Darwin. He used similarity in structures between diverse organisms—such as the similar skeletal structures (utilizing same bones) of the forelimbs of [humans](#), [bats](#), [porpoises](#), [birds](#), and [cats](#)—as evidence of [evolution by common descent](#) (theory of descent with modification).

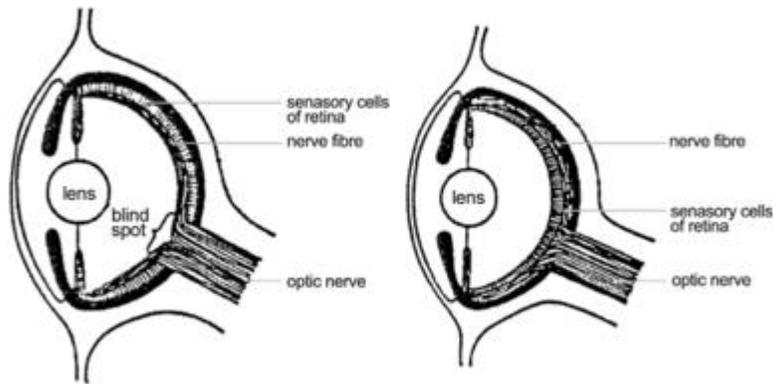
However, it would be incorrect to state that homology, as presently defined, provides evidence of evolution because it would be circular reasoning, with homology defined as similarity due to shared ancestry. Mayr (1982) states, "After 1859 there has been only one definition of homologous that makes biological sense... Attributes of two organisms are homologous when they are derived from an equivalent characteristic of the common ancestor." One of Darwin's own examples of homology offers an example of the hazard of presuming common ancestry based on structural similarity. The bird's wing structure is no longer included routinely as an example of homology because the presumed common ancestor of birds with mammals is too distant. That presumed common ancestor was a fish whose pectoral fins are thought to have been the common precursor structure of both mammal forelimbs and bird wings.

When a group of organisms share a homologous structure that among the members of the group is variously specialized to perform a variety of functions in order to adapt to different environmental conditions and modes of life, that phenomenon is known as [adaptive radiation](#). The gradual spreading of organisms with adaptive radiation is known as divergent evolution. Examples of divergent evolution are seen in the mammalian pentadactyl limb, insect mouth parts, and other arthropod appendages.

The mammalian pentadactyl limb appears in a remarkable range of variations—from the human with arms supporting four fingers and an opposable thumb and with legs terminating in the five-toed foot, to the horse with four legs terminating in elaborations of only the third digit (third "finger" or "toe"), and the bat with webbed skin stretched from the "arm" bones and the four "finger" bones while the separate "thumb" bone as well as a five "toe" bones in the small foot each feature a claw used for gripping. Insect mouth parts similarly vary widely in their shape and function—from the strong biting and chewing capabilities of the grasshopper to the sucking capabilities of the butterfly and the piercing and sucking capabilities of the mosquito. As members of the phylum [Arthropoda](#), meaning "jointed foot," insects demonstrate in the variety of their appendages—not only of their mouth parts, but also their legs and antennae—a pattern of adaptive variation of the appendages that is seen widely throughout the phylum.

See also [Homology of structures in evolution](#)

Analogous structures and convergent evolution



Inverted retina of vertebrate (left) and non-inverted retina of octopus (right). An example of convergent evolution and a counterexample to the Darwinian concept of homology. The remarkable similarity in the organs suggests they are homologous, but they cannot be so because they have no common ancestor with an equivalent characteristic.

Under similar environmental conditions, fundamentally different structures in different groups of organisms may undergo modifications to serve similar functions. This phenomenon is called [convergent evolution](#). Similar structures, physiological processes, or mode of life in organisms apparently bearing no close phylogenetic links but showing adaptations to perform the same functions are described as [analogous](#), for example:

- Wings of [bats](#), [birds](#), and [insects](#);
- the jointed legs of [insects](#) and [vertebrates](#);
- tail fin of [fish](#), [whale](#), and [lobster](#);
- [eyes](#) of the [vertebrates](#) and [cephalopod mollusks](#) ([squid](#) and [octopus](#)). The above drawing of the two retinas illustrates difference between an inverted and non-inverted retina, the sensory cells lying beneath the nerve fibers. This results in the sensory cells being absent where the optic nerve is attached to the eye, thus creating a blind spot. The octopus eye has a non-inverted retina in which the sensory cells lie above the nerve fibers. There is therefore no blind spot in this kind of eye. Apart from this difference the two eyes are remarkably similar, an example of convergent evolution.

Vestigial organs

Main article: [Vestigial organ](#)

A further aspect of comparative anatomy is the presence of [vestigial organs](#). [Organs](#) that are smaller and simpler in structure than corresponding parts in the ancestral species, and that are usually degenerated or underdeveloped, are called vestigial organs. From the point of view of descent with modification, the existence of vestigial organs can be explained in terms of changes in a descendant species, perhaps connected to changes in the environment or modes of life of the

species. Those organs are thought to have been functional in the ancestral species but to have since become unnecessary and non-functional. Examples are the vestigial hind limbs of [whales](#), the haltere (vestigial hind [wings](#)) of [flies](#) and [mosquitos](#), vestigial wings of flightless birds such as [ostriches](#), and the vestigial [leaves](#) of some xerophytes (e.g. [cactus](#)) and parasitic plants (e.g. dodder). It must be noted however, that vestigial structures have lost the original function but may have another one. For example, the halteres in dipterists help balance the insect while in flight and the wings of ostriches are used in mating rituals.

The human **vermiform appendix**, an appendage of the cecum (the ascending colon) has long been claimed by [evolutionary](#) biologists as an example of a vestigial organ. It has been compared with the [rabbit's](#) appendix, which is large and apparently functional as an aid in digesting [cellulose](#). The modern discovery of useful functions for the human [appendix](#) is still somewhat controversial in the field of human [physiology](#). Evidence has been uncovered for useful functions of the appendix in both fetal and adult humans. These include producing important compounds in [fetuses](#) (biogenic amines and peptide hormones), serving an immune function by working as a [lymphatic](#) organ in adults, and providing a safe haven for useful [bacteria](#) (Rowland 2007; Zahid 2004; AP 2007). The evidence of these functions calls into question the designation of the vermiform appendix as a vestigial organ. Other commonly listed examples of vestigial elements in humans include [ear muscles](#), wisdom teeth, and the formation of goose bumps as a fear response.

Evidence from embryology

The field of embryology has long been claimed as a source of evidence supporting descent with modification. The assertion has been that the [embryos](#) of related animals are often quite similar to each other, often much more similar than the adult forms, and hence the embryos provide evidence of their descent from common ancestors. For example, it is held that the development of the human embryo correlates closely with comparable stages of other kinds of [vertebrates](#) ([fish](#), [salamander](#), tortoise, chicken, pig, cow, and rabbit). Furthermore, it is asserted that mammals such as cows and rabbits are more similar in embryological development than with [alligators](#). The drawings of early vertebrate embryos by [Ernst Haeckel](#) have often been offered as proof of these presumed correlations even though the accuracy of those same drawings has been widely refuted (Gilbert 2006).

It has further been asserted that features, such as the "gill pouches" in the mammalian embryo resembling those of fish, are most readily explained as being remnants from the ancestral fish, which were not eliminated because they are embryonic "organizers" for the next step of development.

Wells (2000) has criticized embryological evidence on several points. For one, it is now known that Ernst Haeckel exaggerated the similarities of vertebrate embryos at the midpoint of embryological development, and omitted the earlier embryological stages when differences were more pronounced. Also, embryological development in some [frog](#) species looks very similar to that of [birds](#), rather than other frog species. Remarkably, even as revered an evolutionist as Ernst Mayr, in his 2001 text *What Evolution Is*, used Haeckel drawings from 1870, which he knew

were faked, noting "Haeckel (sp.) had fraudulently substituted dog embryos for the human ones, but they were so similar to humans that these (if available) would have made the same point."

Evidence from geographical distribution

Overview

The geographic distribution of plants and animals offers another commonly cited evidence for evolution (common descent). The fauna on [Australia](#), with its large [marsupials](#), is very different from that of the other continents. The fauna on [Africa](#) and [South America](#) are very different, but the fauna of Europe and North America, which were connected more recently, are similar. There are few mammals on oceanic islands. These findings support the theory of descent with modification, which holds that the present distribution of flora and fauna would be related to their common origins and subsequent distribution. The longer the separation of continents, as with Australia's long isolation, the greater the expected divergence is.

Writing in 1982, Mayr states that "the facts of biogeography ... were eventually used by Darwin as his most convincing evidence in favor of evolution."

Continental distribution

Biologists have discovered many puzzling facts about the presence of certain species on various [continents](#) and [islands](#) ([biogeography](#)).

All organisms are adapted to their environment to a greater or lesser extent. If the abiotic and biotic factors within a habitat are capable of supporting a particular species in one geographic area, then one might assume that the same species would be found in a similar habitat in a similar geographic area, e.g. in [Africa](#) and [South America](#). This is not the case. Plant and animal species are discontinuously distributed throughout the world:

- Africa has short-tailed (Old World) monkeys, [elephants](#), [lions](#), and [giraffes](#).
- South America has long-tailed monkeys, [cougars](#), [jaguars](#), and [llamas](#).

Even greater differences can be found if [Australia](#) is taken into consideration though it occupies the same [latitude](#) as South America and Africa. [Marsupials](#) like the [kangaroo](#) can be found in Australia, but are totally absent from Africa and are only represented by the [opossum](#) in [South America](#) and the Virginia Opossum in North America:

- The [echidna](#) and [platypus](#), the only living representatives of primitive egg-laying mammals ([monotremes](#)), can be found only in Australia and are totally absent in the rest of the world.
- On the other hand, Australia has very few placental mammals except those that have been introduced by human beings.

Explanation



: The world map showing (A) land bridges between continents in past geologic time with black lines and arrows representing the spread of modern mammals from a probable origin in the northern hemisphere into the southern continents and (B) water barriers (straits) formed due to the submergence of land bridges. Once isolated by the water barriers at straits, the animals in each continent have shown adaptive radiation to evolve along their own lines.

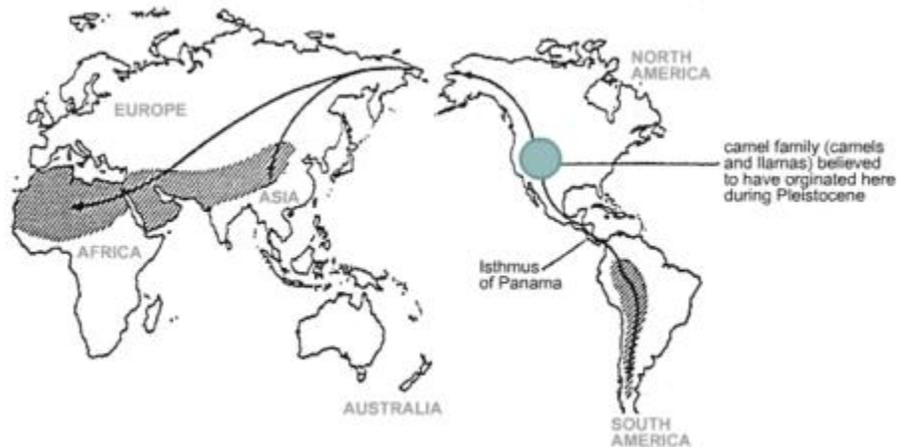
The theory of descent with modification offers an explanation for the observed geographical distributions of fauna. According to this, the main groups of modern [mammals](#) arose in the Northern Hemisphere and subsequently, at a time of low sea level when the intercontinental land bridges were exposed, migrated in three major directions :

- To South America via two land bridges: one connecting Asia with North America and one (the Isthmus of Panama) connecting North America with South America. A large number of families of South American marsupials became extinct as a result of competition with these Northern Hemisphere counterparts.
- To Africa via the land bridge connecting Europe and Africa at today's Gibraltar.
- To Australia via the South East Asia peninsula and islands, which at a time of low sea level formed a continuous land bridge extending to Australia.

The shallowness of the Bering Strait today means that a lowering of the sea level in the past would have readily exposed a land bridge between the two northern continents permitting a relatively easy passage of animals between the two continents. Such a perspective offers a ready explanation of the present-day similarity of the faunas of Eurasia and North America. But once they got down into the southern continents, they presumably became isolated from each other by various types of barriers.

- The submerging of the Isthmus of Panama: Isolates the South American fauna.
- The [Mediterranean Sea](#) and the North African desert: Partially isolate the African fauna.
- The submerging of the original connection between Australia and South East Asia: Isolates the Australian fauna

Evidence for migration and isolation



Map of the world showing distribution of present members of camel. Solid black lines indicate possible migration routes that would have crossed land bridges at a time of low sea level.

[Camels](#) and their relatives, the [llamas](#), are found on two continents, with true camels in Asia and Africa, and llamas in South America (Mayr 2001). There are no camels in North America. Based on descent with modification, it would be expected that camels once existed in North America but became extinct. Indeed, there was the discovery of a large fossil fauna of [Tertiary](#) camels in North America (Mayr 2001).

One proposal for the fossil record for the [camel](#) is that camels started in North America, from which they migrated across the Bering Strait into Asia and hence to Africa, and through the Isthmus of Panama into South America. Once isolated, they evolved along their own lines, producing the modern camel in Asia and Africa, the llama in South America, and becoming extinct in North America.

Continental drift

The same kinds of fossils are found from areas known to have been adjacent to one another in the past, but which, through the process of [continental drift](#), are now in widely divergent geographic locations. For example, fossils of the same types of ancient [amphibians](#), [arthropods](#), and [ferns](#) are found in South America, Africa, India, Australia, and Antarctica, which can be dated to the [Paleozoic Era](#), at which time these regions were united as a single landmass called [Gondwana](#). Sometimes the descendants of these organisms can be identified and show unmistakable similarity to each other, even though they now inhabit very different regions and climates.

Oceanic island distribution

Most small isolated islands only have native species that could have arrived by air or water: Birds, [insects](#), and [turtles](#). The few large mammals present today were brought by human settlers

in boats. Plant life on remote and recent volcanic islands like Hawaii could have arrived as airborne spores or as seeds in the droppings of birds. After the explosion of Krakatoa a century ago and the emergence of a steaming, lifeless remnant island called Anak Krakatoa (child of Krakatoa), plants arrived within months and within a year there were moths and spiders that had arrived by air. Scarcely more than a century later the island has nearly completely recovered—to the extent that it is now difficult to distinguish the island ecologically from others nearby that have been there for millions of years.

Evidence from biochemistry

Evidence for common descent may be found in traits shared between all living organisms. In Darwin's day, the evidence of shared traits was based solely on visible observation of morphologic similarities, such as the fact that all birds—even those which do not fly—have wings. Today, the theory of common descent is supported by genetic similarities. For example, every living cell makes use of [nucleic acids](#) as its genetic material, and uses the same twenty [amino acids](#) as the building blocks for [proteins](#). All organisms use the same genetic code (with some extremely rare and minor deviations) to specify the nucleic acid sequences that form proteins. The universality of these traits strongly suggests common ancestry, because the selection of these traits seems somewhat arbitrary.

Similarly, the metabolism of very different organisms is based on the same biochemistry. For example, the [protein](#) cytochrome c, which is needed for aerobic respiration, is universally shared in aerobic organisms, suggesting a common ancestor that used this protein. There are also variations in the amino acid sequence of cytochrome c, with the more similar molecules found in organisms that appear more related ([monkeys](#) and [cattle](#)) than between those that seem less related (monkeys and [fish](#)). The cytochrome c of chimpanzees is the same as that of humans, but very different from that of bread mold. Similar results have been found with blood proteins.

Other uniformity is seen in the universality of [mitosis](#) in all cellular organisms, the similarity of [meiosis](#) in all sexually reproducing organisms, the use of [ATP](#) by all organisms for energy transfer, and the fact that almost all plants use the same chlorophyll molecule for [photosynthesis](#).

The closer that organisms appear to be related, the more similar are their respective genetic sequences. That is, comparison of the genetic sequence of organisms reveals that phylogenetically close organisms have a higher degree of sequence similarity than organisms that are phylogenetically distant. Comparison of the DNA sequences allows organisms to be grouped by sequence similarity, and the resulting phylogenetic trees are typically congruent with traditional [taxonomy](#), and are often used to strengthen or correct taxonomic classifications. Sequence comparison is considered a measure robust enough to be used to correct erroneous assumptions in the phylogenetic tree in instances where other evidence is scarce. For example, neutral human DNA sequences are approximately 1.2 percent divergent (based on substitutions) from those of their nearest genetic relative, the [chimpanzee](#), 1.6 percent from [gorillas](#), and 6.6 percent from [baboons](#) (Chen and Li 2001; Cooper et al. 2003).

Further evidence for [common descent](#) comes from genetic detritus such as pseudogenes, regions of DNA that are orthologous to a gene in a related organism, but are no longer active and appear

to be undergoing a steady process of degeneration. Such genes are called "fossil" genes. Since [metabolic](#) processes do not leave fossils, research into the evolution of the basic cellular processes is done largely by comparing the biochemistry and genetics of existing organisms.

The proteomic evidence also supports the universal ancestry of life. Vital [proteins](#), such as the [ribosome](#), DNA polymerase, and RNA polymerase, are found in everything from the most primitive bacteria to the most complex mammals. The core part of the protein is conserved across all lineages of life, serving similar functions. Higher organisms have evolved additional protein subunits, largely affecting the regulation and protein-protein interaction of the core. Other overarching similarities between all lineages of extant organisms, such as [DNA](#), [RNA](#), [amino acids](#), and the lipid bilayer, give support to the theory of common descent. The [chirality](#) of DNA, RNA, and amino acids is conserved across all known life. As there is no functional advantage to right- or left-handed molecular chirality, the simplest hypothesis is that the choice was made randomly by early organisms and passed on to all extant life through common descent.

Evidence for theory of natural selection

On the [microevolutionary](#) level (change within species), there are evidences that [natural selection](#) does produce evolutionary change. For example, changes in [gene](#) frequencies can be observed in populations of [fruit flies](#) exposed to selective pressures in the laboratory environment. Likewise, systematic changes in various [phenotypes](#) within a species, such as color changes in [moths](#), has been observed in field studies.

However, evidence that natural selection is the directive force of change in terms of the origination of new designs (such as the development of [feathers](#)) or major transitions between higher taxa (such as the evolution of land-dwelling [vertebrates](#) from fish) is not observable.

The conventional view of [evolution](#) is that [macroevolution](#) is simply microevolution continued on a larger scale, over large expanses of time. That is, if one observes a change in the frequencies of spots in guppies within 15 generations, as a result of selective pressures applied by the experimenter in the laboratory, then over millions of years one can get [amphibians](#) and [reptiles](#) evolving from [fish](#) due to natural selection. If a change in beak size of finches is seen in the wild in 30 years due to natural selection, then natural selection can result in new phyla if given eons of time.

Indeed, the only concrete evidence for the [theory of modification by natural selection](#)—that natural selection is the causal agent of both microevolutionary *and* macroevolutionary change—comes from microevolutionary evidences, which are then extrapolated to macroevolution. However, the validity of making this extrapolation has been challenged from the time of [Darwin](#), and remains controversial today.

Challenges to the theory of natural selection come from both the scientific and religious communities. In some cases, key arguments against natural selection being the main or sole agent of evolutionary change come from evolutionary scientists. Some see microevolution as decoupled from macroevolution in terms of mechanisms, with natural selection being incapable of being the creative force of macroevolutionary change (Luria, Gould, and Singer 1981).

Historically, the strongest opposition to [Darwinism](#), in the sense of being a synonym for the theory of natural selection, has come from those advocating [religious](#) viewpoints. In essence, the chance component involved in the creation of new designs, which is inherent in the theory of natural selection, runs counter to the concept of a [Supreme Being](#) who has designed and created humans and all phyla. Chance (stochastic processes) is centrally involved in the theory of natural selection. As noted by [Mayr](#) (2001), chance plays an important role in two steps. First, the production of genetic variation "is almost exclusively a chance phenomena." Secondly, chance plays an important role even in "the process of the elimination of less fit individuals," and particularly during periods of [mass extinction](#). This element of chance counters the view that the development of new evolutionary designs, including [humans](#), was a progressive, purposeful creation by a Creator God. Rather than the end result, according to the theory of natural selection, human beings were an accident, the end of a long, chance-filled process involving adaptations to local environments. There is no higher purpose, no progressive development, just [materialistic](#) forces at work. Such views are squarely at odds with many religious interpretations.

A key point of contention between the worldviews is, therefore, the issue of variability—its origin and selection. For a Darwinist, random [genetic mutation](#) provides a mechanism of introducing novel variability, and natural selection acts on the variability. For those believing in a creator God, the introduced variability is not random, but directed by the Creator, although natural selection may act on the variability, more in the manner of removing unfit organisms than in any creative role. Some role may also be accorded differential selection, such as [mass extinctions](#). Neither of these worldviews—random variation and the purposeless, non-progressive role of natural selection, or purposeful, progressive variation—are conclusively proved or unproved by scientific methodology, and both are theoretically possible.

At question has always been the sufficiency of extrapolation to the macroevolutionary level. As [Mayr](#) (2001) notes, "from Darwin's day to the present, there has been a heated controversy over whether macroevolution is nothing but an unbroken continuation of microevolution, as Darwin and his followers have claimed, or rather is disconnected from microevolution."

The following are evidences of natural selection, albeit at the microevolutionary level.

Laboratory evidences of natural selection

In the laboratory, [biologists](#) have demonstrated natural selection on the microevolutionary level involving organisms with short lifecycles, such as [fruit flies](#), guppies, and [bacteria](#), which allow testing over many generations.

[Endler](#) (1980) set up populations of guppies (*Poecilia reticulata*) and their predators in artificial ponds in the laboratory, with the ponds varying in terms of the coarseness of the bottom gravel. Guppies have diverse markings (spots) that are heritable variations and differ from individual to individual. Within 15 generations in this experimental setup, the guppy populations in the ponds had changed according to whether they were exposed to coarse gravel or fine gravel. The end result was that there was a greater proportion of organisms with those markings that allowed the guppies to better blend in with their particular environment, and presumably better avoid being seen and eaten by predators. When predators were removed from the experimental setup, the

populations changed such that the spots on the guppies stood out more in their environment, likely to attract mates, in a case of [sexual selection](#).

Likewise, [bacteria](#) grown in a Petri dish can be given an antibiotic, such as [penicillin](#), that is just strong enough to destroy most, but not all, of the population. If repeated applications are used after each population returns to normal size, eventually a strain of bacteria with antibiotic resistance may be developed. This more recent population has a different [allele](#) frequency than the original population, as a result of selection for those bacteria that have a genetic makeup consistent with antibiotic resistance.

Evidences in the field for natural selection

In the field, natural selection on the microevolutionary level has also been demonstrated. Both antibiotic-resistant bacteria and populations of pesticide-resistant [insects](#) have been frequently observed in the field. Since the introduction of house sparrows in North America in 1852, they have developed different characteristics in different locations, with larger-bodied populations in the north. This is assumed to be a heritable trait, with selection based on colder weather in the north.

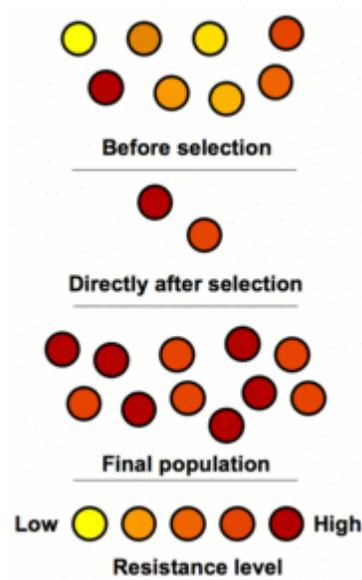
Industrial melanism

In [England](#), a systematic color change in the peppered moth, *Biston betularia*, has been observed over a 50-year period, although there is some controversy whether this can be attributed to [natural selection](#) (Wells 2000). In this case, two forms of peppered moths exist, melanic and non-melanic forms. Field studies during this five decade period suggest that melanic forms increased in proportion in polluted areas because of the phenomenon of industrial melanism. This shift toward darker melanic forms is attributed to an heightened predation by [birds](#) of the light-colored moths, because the lighter forms could more easily be seen on the tree trunks that have been increasingly darkened from pollution. However, Wells (2000) pointed out that there are flaws in the studies, including the fact that peppered moths do not normally alight on tree trunks, and there are even inverse correlations with pollution in many situations.

Galapagos finches

A well-known field example of microevolution attributed to natural selection is the study done by Peter Grant and B. Rosemary Grant (2002) on Galapagos finches. They studied two populations of finches on a Galapagos island and observed changes in body size and beak traits. For example, after a drought, they recorded that survivors had slightly larger beaks and body size. This is an example of an allele change in populations—microevolution. It is also an apparent example of natural selection, with natural selection defined according to Mayr (2001) as, "the process by which in every generation individuals of lower fitness are removed from the population." However, the Grants also found an oscillating effect: When the rains returned, the body and beak sizes of the finches moved in the opposite direction.

Bacterial resistance



Schematic representation of how antibiotic resistance is enhanced by natural selection. The top section represents a population of [bacteria](#) before exposure to an antibiotic. The middle section shows the population directly after exposure, the phase in which selection took place. The last section shows the distribution of resistance in a new generation of bacteria. The legend indicates the resistance levels of individuals.

A commonly cited example of natural selection in action is the development of antibiotic resistance in [microorganisms](#). [Antibiotics](#) have been used to fight [bacterial](#) diseases since the discovery of [penicillin](#) in 1928 by [Alexander Fleming](#). However, the widespread use of antibiotics has led to increased microbial resistance against antibiotics, to the point that the methicillin-resistant *Staphylococcus aureus* (MRSA) has been described as a "superbug" because of the threat it poses to health and its relative invulnerability to existing drugs.

Natural populations of bacteria contain, among their vast numbers of individual members, considerable variation in their genetic material, primarily as the result of [mutations](#). When exposed to antibiotics, most bacteria die quickly, but some may have mutations that make them a little less susceptible. If the exposure to antibiotics is short, these individuals will survive the treatment. This selective elimination of "maladapted" individuals from a population is natural selection in action.

These surviving bacteria will then reproduce again, producing the next generation. Due to the elimination of the maladapted individuals in the past generation, this population contains more bacteria that have some resistance against the antibiotic. At the same time, new mutations occur, contributing new genetic variation to the existing genetic variation. Spontaneous mutations are very rare, very few have any effect at all, and usually any effect is deleterious. However, populations of bacteria are enormous, and so a few individuals may have beneficial mutations. If

a new mutation reduces their susceptibility to an antibiotic, these individuals are more likely to survive when next confronted with that antibiotic. Given enough time, and repeated exposure to the antibiotic, a population of antibiotic-resistant bacteria will emerge.

Recently, several new strains of MRSA have emerged that are resistant to vancomycin and teicoplanin. The appearance of vancomycin resistant *Staphylococcus aureus*, and the danger it poses to hospital patients is considered a direct result of evolution through natural selection. This exemplifies a situation where medical researchers continue to develop new antibiotics that can kill the bacteria, and this leads to resistance to the new antibiotics.

A similar situation occurs with pesticide resistance in [plants](#) and [insects](#). The appearance of DDT resistance in various forms of *Anopheles* mosquitoes, and the appearance of myxomatosis resistance in breeding rabbit populations in Australia are all considered similar evidence of the existence of evolution in situations of evolutionary selection pressure in species in which generations occur rapidly.

Hawthorn fly

Another example involves the hawthorn fly, *Rhagoletis pomonella*, a native of North America also known as the apple maggot fly, which appears to be undergoing sympatric speciation. Different populations of hawthorn fly feed on different fruits. A new population spontaneously emerged in North America in the nineteenth century sometime after [apples](#), a non-native species, were introduced. The apple-feeding population normally feeds only on apples and not on the historically preferred fruit of hawthorns. Likewise the current hawthorn feeding population does not normally feed on apples. A current area of scientific research is the investigation of whether or not the apple-feeding race may further evolve into a new species. Some evidence, such as the facts that between the two variants [allele](#) frequencies at six out of thirteen allozyme loci are different, that hawthorn flies mature later in the season and take longer to mature than apple flies, and that there is little evidence of interbreeding (researchers have documented a 4 to 6 percent hybridization rate) suggests this possibility. (See Berlocher and Bush 1982; Berlocher and Feder 2002; Bush 1969; McPheron, Smith, and Berlocher 1988; Prokopy, Diehl, and Cooley 1988; Smith 1988).

Artificial selection

Analogously to natural selection, for thousands of years, humans have artificially manipulated changes within species through artificial selection. By selecting for preferred characteristics in [cattle](#), [horses](#), grains, and so forth, various breeds of [animals](#) and varieties of [plants](#) have been produced that are different often in significant respects from their ancestors.

Evidence from studies of complex iteration

[Computer science](#) allows the iteration of self changing complex systems to be studied, allowing a mathematical approach to understanding the nature of the processes behind evolution. Based on human concepts, such computer programs have provided theoretical evidence for the possibility

of natural selection directing macroevolutionary changes and insights into possible hidden causes of known evolutionary events (Adami et al. 2000; Earl and Deem 2004; Stemmer 1994).

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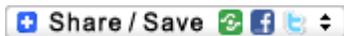
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Biogeography: Polar Bears and Penguins

Polar bears live in the Arctic, but not the Antarctic. For penguins, the picture is reversed. The pattern of [organisms](#) around the globe -- the absence of some species from environments that would suit them, and closer relationships between species that are geographically near each other than between species that inhabit similar environments -- is persuasive evidence of the evolutionary origin of [biodiversity](#).
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[Darwin](#), [Wallace](#) and the other 19th century naturalists who traveled widely were fascinated by the distribution of animals and plants in their habitats around the world. Why do the Galapagos Islands of South America and the Cape Verde Islands off Africa have strikingly different fauna and flora, despite having similar environments? Why does the Arctic have polar bears and Antarctica penguins?

These patterns impressed Darwin deeply. To him, they argued that species arose in single centers by descent with modification from existing species, and that their geographic range was limited by their ability to migrate to other suitable environments.

The distribution of flora and fauna of the oceanic islands provided Darwin with some of his strongest arguments. The islands contain a small number of species because immigration from the mainland was difficult, he said. Some categories of life are absent altogether, such as batrachians -- frogs, toads, and newts -- even though they would seem to be adapted for such habitats. The reason? They are killed by saltwater, so could not reach the islands by migration. Terrestrial mammals aren't found on oceanic islands more than 300 miles from the mainland. But bats, with their long-distance flying ability, are plentiful.

Another point: Most of the species on islands, while distinct from other species, are most closely related to species on the nearest mainland. Therefore, Darwin said, the island inhabitants must have migrated from the original, mainland area where the species originated. That explains why the species on the Galapagos Islands most closely resemble those on the nearby South American mainland, and those in the Cape Verdes resemble those of west Africa.

Aside from the islands, Darwin was intrigued by unusual distributions of animals and plants across the continents. He concluded that changes in locations of climatic zones over time -- the advance and retreat of glaciers, for example -- could explain some of the patterns in animals' habitats.

Just as intriguing to Darwin, and even more apparent now, is the fact that fossils of possible ancestors of living species are often found in the same parts of the globe where their descendants live today. Darwin observed this in the South American fossils he collected, relatives of today's capybaras and armadillos. Apes today live only in Africa and Asia, and that is where the fossils most resembling modern apes are also found. There are no apes, fossil or living, known from anywhere in the Americas.

These same patterns are just as impressive today. And since Darwin's day, advances in scientific understanding have shown how accurate his conclusions were. For example, [plate tectonics](#), undreamed of when Darwin was forming his ideas, fits elegantly into Darwin's theory as another major influence on dispersal, helping to produce the patterns in the distribution of both fossils and living organisms seen around the world in modern times.

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EVOLUTION CREATION

Evolution: Converging Lines of Evidence

by [P. Wesley Edwards](#) • December 30, 2011 • 0 Comments

The strength of any theory comes not from a single measurement or a single confirmed prediction, but from the theory's many predictions being confirmed by many *independent* tests, samples, and methods. Often, attacks on evolutionary theory take the form of showing that some measurement technique is not infallible, or that some measurement technique depends on assumptions that could be wrong. Examples, of course, include creationist criticisms of radiometric dating, which is a common technique for dating rocks.

When the creationist adds to these types of criticisms the charge that there are some things evolutionary theory cannot explain, it can seem to some that evolutionary theory is a weak, speculative hypothesis. But as we will show below, scientific theories aren't strong because the measurement techniques that confirm them are perfect, or because they have no open questions. If this were the case, *all* science would be weak and speculative.

The best way to illustrate the fundamental problem with the creationist critique is by way of an analogy. Let's say I'm the prosecuting attorney in a felony case, and my case depends on placing the suspect in a certain location between 4:55 PM and 5:05 PM, during which the suspect shot someone. Now let's say twenty of my witnesses happened to look at their watches (a combination of analog and digital watches) when they saw the suspect shoot. Seventeen other witnesses separately recall seeing the suspect shoot just as the 5 O'clock news was coming on in each of their apartments in the neighboring building. Twenty six other witnesses saw the suspect shoot just as the 5 O'clock whistle blew at the nearby quarry.

Now, imagine the defense carefully pointing out that watches have been known to be wrong. Watches, he stresses to the jury, are *not* infallible. He proudly brings in people to testify that they have made mistakes at some point in their lives about the time of day because their watch's battery had run down, or their watch had gotten wet, or damaged by various means. As for the 5 O'clock news, the defense points out that scheduling errors in TV programming have been known to cause shows to come on more than five minutes after or five minutes before their scheduled time, and he even finds a TV producer to testify about a time that this did, in fact, happen. And as for the quarry, the defense was able to find several expert witnesses (people who blow whistles at quarries) to testify that there had been times when they blew the whistle at more than five minutes before or after the scheduled time, at each of their respective quarries.

As is obvious in this example, it is not enough for the defense to show that the methods used by each of the prosecution's witnesses are fallible ways of telling the time. Not only is it *extremely* unlikely that something was wrong with *everyone's* measurement of the same event, but even if everyone were in error, we would hardly expect them to be in *agreement with each other*—especially when the measurements involve *unrelated technologies and methods*. Creationist criticisms of the evidence that support evolutionary theory or modern geology (e.g., dating rock samples) are often analogous to this defense attorney's criticism of the evidence supporting the prosecution's case. To take the defense's (and creationists') criticisms seriously would literally mean that we could not tell time at all simply because watches are individually imperfect. But in science that fallibility has been specifically taken into account through the use of multiple samples and multiple independent measurement methods. Just like our imaginary prosecutor, scientists look for independent corroboration before they consider a theory to be well supported.

In the case of rock dating, and in all significant aspects of evolutionary theory, we have just this type of wide agreement spanning many different methods and many different samples (far more samples and methods, in fact, than described in the courtroom

analogy). This first article will focus on just five of the many independent, corroborating lines of evidence that confirm evolutionary theory, with a focus on one of its key hypotheses: Descent with Modification. The definition of this hypothesis (taken from the subject refresher article on Evolution in Freethought Debater) follows:

The descent with modification component of evolutionary theory is that all life forms can trace their lineages back to earlier classes of life forms in a branching, "nested" hierarchy (forming what looks like a bush or tree, as in the "Tree of Life"), which can ultimately be traced back to the beginning of life on earth...During the long period since that time, changes in body plans have accumulated in diverse directions to make all the differences we now see between all life forms. To continue the tree analogy, you can start from the tip of any arbitrarily chosen twig and follow it back to the point where it joins another twig, the point of origin of the two (or more) twigs. That now thicker twig or branch can then be traced back to where it joins another branch. This process can be repeated until you ultimately reach the trunk. Applied to evolution, each twig and branch represents a particular lineage; the points where there is a joining of those twigs and branches represents the common ancestor of all the lineages that can be traced back to that point.

The importance of recognizing the cross checking nature of science cannot be overstated. When one forgets that this is the basis of good theory, one can quickly lose sight of the "forest for the trees," and literally end up haggling over irrelevant *individual* cases in which a result was unexpected or inconsistent with the theory. However, some exceptions are, in fact, *expected* so long as they can be shown to be "outlier" results (random or statistically rare errors) that do not significantly affect the conclusion drawn from all of the data taken as a *whole*. This is exactly why statistics plays such a large role in analyzing scientific data, and why scientific results are usually stated along with a statistical level of certainty.

It is perhaps understandable why creationists make these sort of irrelevant criticisms of outlier results. Unlike actual science, creationism does "not seek organizational relationships or look for relationships in terms of universal physical laws."¹ Instead, by definition, they exist to defend a point of view—a view rooted in absolute certainty in an unchanging Truth (with a capital T).

The lines of evidence we will briefly look at are the fossil record in the geologic column; the classification of living forms based on comparative anatomy; biochemistry; embryology; and finally, biogeography. As you review the evidence notice how the independently corroborating nature of the different lines of evidence precludes any appeal to "there was this one fossil they couldn't explain" or "someone once made a mistake in classifying an animal," or even, "there was once this hoax. . ." As in the court case example, the proof is in the *wide statistical agreement* of many measurements spanning all of these methods, not in any single data point.

Fossil Record

The geologic column, which is the identification and classification of the different rock layers (strata), was essentially completed by 1815, almost 50 years before Darwin's theory. Importantly, this work was done by the *creationists* of the time. They noticed that each rock strata contained a distinct collection of animals and plants. So unique and consistent were these fossil collections in each of the layers, that certain fossils in them could then be matched to fossils in other continents to locate that layer within the geologic column (index fossils). It is important to notice that this all predates Darwin and is completely independent of any assumptions about evolution. Inexplicably, a common creationist complaint is that the geologic column presupposes the truth of evolution, which in turn presupposes the truth of the geologic column, resulting in a circular argument for evolution. But as this very short history should already make clear, the geologic column makes no assumptions about evolution since it was established by *before* there even was a theory of evolution.

By comparing the fossil contents from the lower layers (or strata) to the higher ones, these pre-Darwin creationists (such as Cuvier, the father of paleontology and a deeply religious creationist) could see a pattern in which an individual life form would appear in one layer and then be replaced in the next layer up by multiple variations on that original, single form. These layers were often themselves followed by layers in which all or most of those variations (and variations of variations) suddenly and completely disappeared. These creationists also noticed that the deeper the fossil, the less recognizable it was. As one moved higher, the forms became increasingly recognizable. As these scientists examined more and more strata, this cycle of emergence followed by branching variations continued.

Again, this pattern was recognized before Darwin's theory, though the pattern was assumed not to reflect any kind of relationship through descent. Based on their observations, these creationists (and basically all geologists were creationists at this time) concluded that God must have inflicted not one, but a series of cataclysms, each followed by a new creation. However, as they collected ever more data, they realized that there had to have been ever more of these cataclysm and creation events.

To recap, at this point in pre-Darwinian history the geologic column had been established with the lower layers understood to be older than the higher layers. The actual ages of the layers remained unknown, however, but were assumed to be consistent with a literal reading of the Bible. Also, at this point in history, it was apparent that a slice through the earth—like cutting through a layer cake to reveal the layers—revealed not a hodgepodge mix of living and extinct forms (as one might expect from a world-wide deluge), but an extremely ordered and consistent pattern of fossils throughout the world. That ordered and consistent pattern was that a form would appear in one layer, and in higher layers that same form would be replaced by similar though different forms, which became progressively more different in even higher strata. This typically ended in the wide-spread disappearance of many of the forms, and then this cycle of appearance followed by a kind of "radiation" would start over. One thing that was also apparent even then was that the higher the layer in which a fossil was found, the more recognizable the fossil usually was, while at lower

layers the forms were less recognizable, and harder to tell apart and categorize. For example, it is easy to tell mammals from reptiles today, but if one goes deep enough, mammals and reptiles become essentially indistinguishable (e.g., you find groups like the Therapsids, which were one of the mammal-like reptiles that blended features of both groups). Creationists, like Cuvier, argued that the data could be explained by a series of divine cataclysms and creations, the last of which was the Biblical Flood.

Classification of Living Forms

Setting aside fossils altogether for a moment, but keeping the observed pattern we saw in mind, let us separately look at what happens when we classify today's living forms based on their physical forms and structures (called "morphology"). A fair question to ask before classifying living things is, "What characteristics should we use: size, weight, what?" Well, the pre-Darwinian, Linnaeus, who came up with the animal naming system we still use today, grouped animals by overall large-scale anatomical similarity, though this left some room for arbitrary decisions about what should be considered "similar." Later, the anti-Darwinian, Richard Owen, argued that if a feature could be shown to be the same structure modified for different purposes—as revealed by comparative anatomy and embryological development—then the animals should be classified closer together. The more such structures were shared, the closer would be the classification. He called such structures "homologous," while structures that looked *superficially* the same, but were based on completely *different* structures and embryological development, he called "analogous."

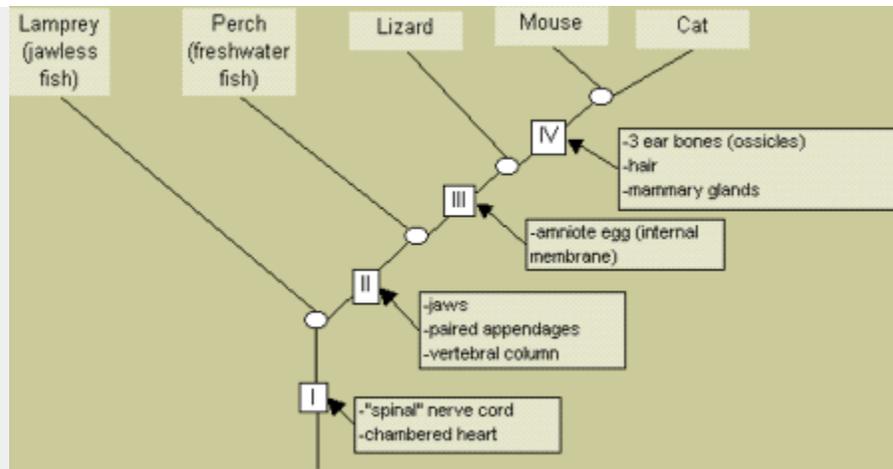
This homology / analogy distinction works very well because by using it one can *predict* other things that the animals would also have in common. This approach allows one to gain new insights. If you had classified by size alone, say, you wouldn't gain any additional insights, and would know little more than the just size of the animal. It's interesting to ask *why* this approach makes for such effective predictions. For Owen, and the creationist establishment of the time, the answer was that homologous structures revealed part of God's plan: He used relatively few basic templates that He modified to create all the species. Different species that shared homologous structures were based on the same template, but each had customized modifications to meet the functional needs of the individual "kinds."

Owen's approach, however, also produces observations that conflict with expectations based on God's having created each kind directly. If each kind were separately created, then there would be no restriction preventing God from mixing and matching useful structures. If God designed a structure to serve a purpose, then all species could benefit from that originally perfect design. There would be no *constraint* on God that says once He designs a useful structure, He can *only* give it to other species that happen to share with that first species a set of *completely unrelated characteristics*. For example, there would not be a rule that says God can only give three middle ear bones to species that have milk-producing (mammary) glands.

An all-powerful Designer should have at least as much flexibility as human designers. Things designed and manufactured by humans show no such restrictions. Design ideas are shared across widely different "kinds" of human creations. This is quickly apparent when you try to create a classification of modern computers or aircraft based on their shared components. For example, Global Positioning Satellite (GPS) technology can now be found on helicopters, biplane crop dusters, high performance fighter aircraft, and even rental cars and fishing boats. If you had earlier created a hierarchical classification that had winged aircraft as the basis for one branch and wingless (e.g., helicopter) aircraft as the basis for another, you would now have to add GPS to both branches. In other words, GPS technology would not be *nested* within just one branch, but would *cut across* the branches. As a result, one cannot create a stable, hierarchical classification for human-created things in which sets of characteristics are nested one within the other.

On the other hand, if each species is related through common descent, and not individually created, then we would expect that a classification of them based on shared structures *would* reveal just such a nested hierarchy of structures. We would expect this since the structural inheritance of each branch is different and any new structures have to be built from the materials at hand; that is, they have to derive from these inherited "components." As a result, any new structures would be confined to the one lineage in which it first appeared, and to its descendent branches. Consequently, we wouldn't expect to see structures *cutting across* the branches, as we did in the GPS example.

When we classify living life forms we see the nested hierarchy predicted by Descent with Modification. For example, consider the following classification (cladogram)² of a few representative, but disparate forms:



Note the pattern in the sharing of characteristics. They are not mixed and matched, but are “nested” one within the other. For example, within the whole group all forms share a chambered heart; nested within those having a chambered heart is a group that additionally has a vertebral column; within the group that has both a chambered heart and vertebral column are nested those that additionally have mammary glands (i.e., you only get mammary glands if you have a chambered heart and vertebral column). The characteristics appearing at a branch point are confined to all the branches above it; they *never cut across* to other branches. This nested pattern is very characteristic of all life on earth.

Descent with Modification also makes some additional, more specific predictions about the morphology of living forms. First, since species can only work within their structural inheritance to solve adaptive problems, we would expect that as descendent species in one lineage branch out into different niches (some that involve flying and others swimming, for example), that their adaptations will involve different modifications of the same underlying structures. These are the homologies we discussed earlier, and they are a specific prediction of the Descent with Modification hypothesis. A corollary prediction of this view is that we would never actually find the “winged horse” seen in mythology, since that would involve entirely new appendages appearing “out of thin air,” as it were, rather than coming from existing structures. This is why, for example, flying birds and mammals had to modify two of their four inherited appendages to get wings; that is, they had to modify their “arms” to make wings.

Second, where species from *different* lineages find themselves filling the same environmental niche (for example, living in different parts of the world and filling the bamboo-eating niche) we would expect to see cases of *different* structures being used for *similar* functions (as opposed to *similar* structures being used for *different* functions in the homology example); that is, we would expect to see different lineages solve the *same* adaptive problems with *different* structures—structures which reflect each lineage’s unique inheritance. Such cases are examples of “analogies,” (or “convergent evolution” as it’s often called today) and are also predicted by Descent with Modification. But a further interesting prediction of this theory is that some analogous structures will be *inferior* to others in fulfilling similar functions. This is expected under this theory, since the inherited components of some lineages will make better designs easier to “get to” than the components inherited in other lineages.

In the case of homologies, we see exactly what is predicted. For example, the forelimbs of all mammals are composed of the same bones arranged in similar ways. It’s only the proportions of these bones that differ. For example, compare the bones of bat, human, and dolphin. While each fills a very different niche, and uses these bones for very different functions, they all have the scapula, humerus (upper arm), radius (forearm bone 1), ulna (forearm bone 2), carpals (wrist), metacarpals (hand), and phalanges (fingers). Again, only their proportions differ. Creationists often say that there are similar structures for similar functions, but if that’s true, then why does the bat’s wing have far more structural similarity with the human *hand* than it does with a bird’s wing?

In the case of analogies we see again exactly what is predicted. For example, the shark (a fish), Ichthyosaur (an extinct swimming reptile), penguin (a bird), and dolphin (a mammal) all have forelimbs adapted for swimming. Outwardly, these forelimbs look very, very similar; however, the internal structures are radically different: the dolphin’s fin has more in common with the bat’s wing and the human hand (including the same five finger bones) than it does with the Shark’s purely cartilaginous fin (no bones at all). This makes sense in the evolutionary context given that the genetic inheritance in the fish lineage didn’t have bone to work with when the sharks first appeared. So, again, the Creationist claim of “similar structures for similar functions” is falsified. What we typically see is different structures for similar functions and similar structures for different functions.

The Australian marsupials are a particularly startling example of this kind of convergent evolution (different structures adapted to solve the same functional needs). There are marsupial versions of mice, flying squirrels, moles, ground hogs, rabbits and wolves, just to name a few. As different as they are from each other, they still have more in common with each other than to any placental mammal. For example, the marsupial mouse has more in common with the marsupial wolf than it does with the placental mouse with which we are all familiar. (This Australian example is discussed in more detail below.)

Owen's supernatural "cost-control" explanation for these patterns is an *ad hoc* theory tacked on after the fact to explain data that contradicts the predictions of a theory based on an all-powerful Designer creating each "kind" separately. Worse, his explanation requires one to contradict God's omnipotence and omniscience. People such as Owen apparently felt that God used relatively few templates for reasons of efficiency in the design process, in the same way that GM, for example, would not want to design each car from scratch due its being an inefficient use of limited and expensive resources. Of course, it is entirely unclear how one is to reconcile this explanation with the notion of an all-powerful, all-knowing, and perfect Creator, who presumably isn't operating under such resource constraints. Unless there was a second act of creation after the "Fall" (one in which inferior designs were introduced) then one can only conclude that many "kinds" were rendered imperfect *from the very beginning (i.e., before the Fall)*, since many of the analogous structures we see in the different "kinds" are not equally effective in serving similar functions.

An all-powerful and perfect creator who created each kind directly would be expected to have originally used the optimal design when the same function was needed. If any inefficient functionality that we see today was due to "degeneration" following the "Fall," then this would appear as resulting from defects appearing in a *common* structure, not from the use entirely *different* structures, which would reflect a choice that had been made from the *very beginning*.

Relationship to Fossil Record and Descent with Modification

Now, let's go back to the fossil record. If the nested hierarchy we see in living forms reveals the particular design approach of a Creator who made all "kinds" at the *same time*, then there should be no connection between the characteristics of life forms (like having 3 ear bones) and the depth of the rock layers in which these characteristics first appear. In other words, if all species were created at the same time, then there should be no correlation between elapsed time and the appearance of *characteristics* that define each species.

On the other hand, if all life is related through the process of descent with modification, then there *should* be a very specific correlation between time and characteristics; which is to say, there should be a correlation between the depth of rock strata, and the first appearance of structural characteristics in the fossils of those layers. How should they correlate? Remember that a structural characteristic that is shared by more branches, such as jaws or a vertebral column, should first appear in layers that are deeper than those containing the first appearance of any nested characteristic. For example, the earliest appearance of animals possessing 3-ear bones (ossicles) should appear higher in the rock layers (i.e., in younger rock formations), than the earliest appearance of animals with vertebral columns.

This pattern is *exactly* what is found in the fossil record. Referring back to our earlier tree with the lamprey, perch, lizard, mouse, and cat (which was made independently of fossils) what we find in the fossil record is that the jawless fishes (agnaths) first appeared in the deepest layers, followed in higher layers by the first appearance of bony fishes, followed in yet higher layers by the first appearance of reptiles, which in still higher layers were followed by the first appearance of mammals. The theory of Descent with Modification not only predicts this, but is alone in being able to explain it in a productive way (that is, based on a theory with testable predictions and not by invoking Divine, mystical, or magical causes and purposes, which can be made to fit *any* data—which, of course, means it can explain *no* data).

Note that I said "first" appearance. Obviously jawless fishes are still with us, as are the reptiles, and even the much earlier forms of life like blue-green algae. Too often one hears comments like, "...but if we evolved from them, then why are they still here." It should be clear from the discussion so far that such a view represents a serious misunderstanding of descent with modification and evolution. A parent species does not have to go extinct before a child species can emerge. To take just one simple example, a child species can emerge when the parent species is split into two by the disappearance of, say, a land bridge, creating two islands where there had been just one. The two groups might now diverge into two species, though one of the species may show almost no change from the original population, while the other shows dramatic change. This could be the result of very different environmental pressures on each of the two groups.

To recap so far, we see that a tree of life made from comparative anatomy of living forms, which has nothing to do with timing or fossils, independently correlates to a tree of life based only on the appearance of characteristics as you go from deeper to shallower rock strata.

Biochemistry

Now if Descent with Modification is the right explanation of the these two independent phenomena, (i.e., the pattern in fossil record and the pattern in living organisms) then any newly discovered features should continue to corroborate these same patterns, while perhaps adding even more detail and filling in open questions.

Since Darwin's time, the life and geological sciences have exploded, complete with the emergence of whole new sciences that Darwin could never have imagined, such as molecular genetics, plate tectonics, and geochronology (rock dating). Any good falsifiable theory should not only hold up under the scrutiny of these new sciences, but thrive and contribute to this progress of knowledge. Looking at the new field of molecular genetics, what happens if we try to make yet *another* "tree of life" diagram, but based only on DNA, independent of anatomy and independent of the fossil record? If we end up with a tree of life that is completely

different from the diagrams we got based on fossils and comparative anatomy, then Descent with Modification will have a big problem.

DNA

Briefly, DNA is a molecule on which is strung a code made up of just a four-letter alphabet. For example, part of the whole string might read, "...GCCTTACGGA..." where the whole string is actually about 3 billion letters long in human DNA. When that code is read across the entire DNA, one ends up with a recipe for a growing a life form. This four-letter alphabet really represents the four chemical "bases," each of whose initials are A, T, G, and C (adenine, thymine, guanine, and cytosine).

Until the DNA copies itself (a process called "replication"), this string of letters exists as one side of a two-sided zipper-like structure called a double helix. The other side of the zipper is the mirror image of the left, where T is the mirror of A, and C is the mirror of G. When a cell divides, this zipper unzips into two halves. Each half then builds a new sister half, letter by letter: Ts attract As, As attract Ts, etc. When all is done and said, we end up with two complete "zippers," each identical to the original single zipper before it split.

Now, each group of three letters makes a "word," (e.g., CCA is a word, or UCU, etc.). These three-letter words are called "codons" and come in two basic types: instructions for building things, or exons; and regulatory instructions, or introns, which can sometimes be thought of as punctuation marks or "stop reading," "start reading" instructions. In the case of exons, each three-letter word corresponds to a particular building block of a protein molecule. These building blocks are called amino acids. A protein is essentially a string of amino acids in a particular sequence all hooked up end-to-end. Proteins in living things are made up of very long sequences of just 20 different types of amino acids. The DNA code for making the whole protein is an example of a "gene," each of which can be thousands of letters long.

A genetic mutation amounts to A, U, G, or C (actually the U stands for uracil, which is used instead of T in RNA, where RNA is an intermediate step before the protein-building process) being accidentally "flipped" to something else, or having a one or more letters deleted, added, reversed, or put somewhere else in the sequence. For example, if the word UCA becomes UCG, then there is no effect since they both code for the same amino acid: serine. However, if the first position is flipped, turning UCA into GCA, then the amino acid in this part of the completed protein will be alanine instead of serine. This change to the protein may or may not affect the way it functions or the final "fitness" of the completely grown life form.

Some mutations may prevent the protein from even forming at all, such as a mutation affecting one of the "punctuation marks." If this happens, the entire gene of some thousands of those letters (A, C, T, U) are rendered useless, or "dead." (Of course, from the standpoint of affecting offspring, and therefore evolution, the only mutations that matter are those that affect the DNA copies that go into the sex cells, since only they are going to be used to grow another organism.)

In the interest of space, I've tried to limit this introduction to genetics to only those points bearing directly upon our discussion. Hopefully I've described enough of it to make the significance of the next point clear: *only around 5% of DNA actually codes for building anything, the rest are the introns along with a vast amount of dead or "pseudo" genes.* This means that most random mutations will have no impact because they will land in this vast sea of ignored dead genes. (All introns, including these dead genes, are actually cut out to leave only the exons just before the instructions are read prior to building proteins.)

Keeping in mind that some 95% of the genetic code is nonfunctional, and also keeping in mind that random mutations appear on a fairly regular basis, we can expect that mutations affecting these dead areas of the DNA will tend to spread throughout the breeding population. The reason they will tend to spread is that specific mutations are very rare, and they have *no effect on survivability (since the dead genes don't do anything)*. Consequently, as the creature possessing this mutation reproduces, it will likely pass it on and it will multiply over the generations. If one could find very old DNA of a particular species, and compare it to new DNA from that same species, one would expect the newer DNA to show an accumulation of these types of mutations. Even more importantly, if that earlier population had split into two, say by a land bridge being cut creating two islands from one, then each of the two descendant populations should be accumulating mutations *independently* of each other—getting more and more different from each other over time—since mutations in one group cannot spread to the other group. The bigger the accumulated difference, the longer the time they have been separated.

Earlier we created a tree based on comparative anatomy, and saw that it corresponded closely to a tree independently built from the fossil record. In that example, we looked at representatives from disparate branches, but similar anatomical and fossil classifications of just the primates invariably show that the great apes are very close to each other and to humans, with monkeys being more distantly related, and lemurs further still (i.e., "more distantly related" means it represents an earlier split, in the same way that the perch, in our earlier diagram, represents a lineage that split off prior to the lizard's lineage).

With our understanding of genetic mutation and of the large amount of non-functional DNA we can make yet another "tree of life." One way to build a tree based on genetic differences is to "unzip" the chromosomes of different species, and take the left half of one species and see how well it bonds to the right half of the other species. Naturally the bonding will be 100% for the same species. The greater the genetic similarity, the tighter the bond (measured by heat required to re-separate them). Here are the results from this DNA-DNA binding technique ³:

Species	Percent DNA Binding
Human	100
Chimpanzee	100
Gibbon	94
Rhesus monkey	88
Tarsier	65
Lemur	47
Mouse	21
Chicken	10

This certainly isn't expected if each kind were separately created, especially when you consider that the vast majority of the sequences have *nothing to do with function*. The dead genes, however, provide much more powerful corroboration of evolution than does this impressive result.

Shared Typographical Errors

The discovery of the high proportion of dead or "pseudo" genes provides corroboration of the Descent with Modification hypothesis in a startlingly different way. To see how, let's start with an analogy.

Imagine you are a teacher grading essays. The essays are each a response to the same question you posed to the whole class. You, of course, made clear to the students that they are to work separately, and that they are not to copy each other's work. So how do you tell whether matching passages in some of the returned essays were plagiarized or were just the result of a coincidentally similar choice of words in response to the same question? What if 30 consecutive words were identical? Well, that certainly is not likely, but what if in addition all the punctuation marks also matched exactly? Well, now things are looking even worse for student honesty; but what if in addition to all of that, grammatical, spelling, and punctuation *errors* match exactly between the two passages and in exactly the same locations? Well now the odds of a coincidence are so small as to be considered zero. An extension of this kind of analysis can also reveal whether one person copied from another, or if two students each separately copied from the same third source, and whether each of those "child" copies were themselves copied by others, etc. The "junk" genes, of which so much of DNA is made, allow just this type of analysis on gene "copying" between species.

As mentioned earlier, mutations can prevent a gene from making anything at all. A gene is just a long run of code (often made up of thousands of the code letters A, T, C, and G) that when read produces, for example, an entire protein. If mutations occur at critical locations, then that protein may not be made at all. Such a mutation would render the whole string of code, of some thousands of letters, "dead." Since only a few errors in a string of thousands can make a gene non-functional, then an analysis of the string can often reveal what the gene *originally* coded for.

For example, humans and the other primates require vitamin C in their diets. In humans and primates, vitamin C (ascorbic acid) deprivation will lead to debilitating diseases such as scurvy. "So what?" you ask? Well, this dependence on vitamin C is the exception among mammals, since, besides primates and the guinea pig, other mammalian species produce an enzyme protein that allows their bodies to synthesize their own vitamin C. This enzyme protein is called LGGLO (which, if you must know, stands for L-gulonogamma-lactone-oxidase). Now, the LGGLO gene that codes for this protein has been identified.

Under the evolutionary hypothesis all mammals inherited the LGGLO gene from a common ancestor. Any mutation that would render this gene nonfunctional in any of this common ancestor's descendent species would be pretty rare, and when it did occur it would be fatal unless the gene were no longer needed, such as if the diets of those affected species just happened to be rich in vitamin C. Now what if one of these descendent species develops a mutation in the LGGLO gene that "kills" the gene—that is, makes it a dead gene? Well, as I mentioned above, this would only be a problem if the diet of this species is not rich in vitamin C. But what if this species with a dead LGGLO does have a diet rich in vitamin C, and it branches into multiple descendent species of

its own over the course of evolution? Well, now we have a testable prediction. If Descent with Modification is true, we would expect that this same dead gene would appear in each of those descendent species. In the case of the primates those descendent species are alive today, and include us. The prediction is confirmed: that broken relic of a once working LGGLO gene has indeed been found in humans and in the other primates.⁴

Now humans and the other primates are believed to share a recent common ancestor based on an enormous array of other converging lines of evidence that have *nothing to do* with the LGGLO gene—such as morphological, other genetic, molecular, and fossil lines of evidence. So the additional fact that humans and primates as a *group* need vitamin C in their diets, and the fact that this condition is extremely rare among the mammals, suggests yet another very specific testable prediction—namely, that the particular genetic “typo” that makes this LGGLO gene “dead” would be the exact *same* typo in humans as it is in the other primates. The reason we would expect this is that any number of potential defects can “kill” a gene, so if the defect occurred independently in each primate, then it would be extremely unlikely to be the result of the same typo each time—and it would certainly be completely mysterious why such a cluster of independent events would target the primates as a *group* when it is extremely rare among all mammals. This “identical typo” prediction for the primates/human relationship has now been confirmed: “A small section of the GLO pseudogene sequence was recently compared from human, chimpanzee, macaque and orangutan; all four pseudogenes were found to share a common crippling single nucleotide deletion that would cause the remainder of the protein to be translated in the wrong triplet reading frame.”⁵

It is important to see that the strength of this prediction in no way depends on primates being the *only* group of species with a dead LGGLO gene. The strength of the prediction comes from two powerful facts: first, that the mutation is extremely *rare* among mammals but found in *all* primates as a *group* (why would this be if the primates are not related?); and second, that for primates as a *group* the gene is not just dead, but dead from *precisely the same genetic typographical error*. Now it shouldn’t be very surprising if we find a dead LGGLO gene in some other mammalian species that does not share a common ancestor with the primates, so long as it is a rare find. This is so because it is certainly conceivable for a mutation that kills the LGGLO gene to appear *independently* in another lineage; however, the strong expectation is that if it did occur independently, then the genetic typo involved would be a *different* typo from the one found in the primates. This is the expectation, for example, in the case of the guinea pig, which is an example of another rare occurrence of a mammalian species with a dead LGGLO gene.

So the LGGLO case is yet another powerful independent line of evidence that converges with so many others. The creationist has to explain not just how each of these lines of evidence might be wrong, but how, if they are wrong, they all point to the same answer. Convergence makes appeals to potential errors extremely implausible since it relies on either a fantastic coincidence (that all these errors are just coincidentally consistent with a single theory), or a fantastic conspiracy (that all international universities have been secretly colluding to hide the truth for over a century). If the LGGLO case is an example of degeneration after the Fall, then why did it just happen to primates and humans as a *group* in such a way as to independently corroborate that identical grouping constructed from all the other *independent* sources already mentioned (fossil layering, morphology, etc.)—was it to “test our faith”?

A functional gene that is rendered useless and then persists as a dead gene in the population is rare because most such errors are fatal or horribly debilitating (In the case of LGGLO, the primate diet was rich in vitamin C, so its loss was not a disadvantage). A more common error found is that of gene duplication, which occurs during the DNA replication process. It is as if in copying a book someone copies the same paragraph or page twice. Since one gene is functional, and the copy usually defective and nonfunctional (i.e., dead), mutations can accumulate in the defective copy without affecting the animal carrying it, since they have a second working copy. Consequently, more of this type of dead gene is found than is the other type.

One example (of many) of duplicated dead genes is the gene that codes for an enzyme that is involved in the metabolism of steroid hormones. Right next to this gene in humans is a defective copy of the *same gene*; that is, it’s a non-functional, “dead” copy of the still functional gene right next to it. Many mutations can render the copy dead; in this case, the particular typo that ruins this gene copy is the deletion of a particular string of just 8 letters (out of a much, much larger number of letters). Now, Chimpanzees have the same dead gene and here is the “smoking gun”: Chimpanzees have the exact same 8 letter deletion.⁶ *This is important: they don’t just have the same dead gene, they have the same typographical error that we do in a very large “book” of letters.*

Any appeal to “similar design for similar function” is irrelevant here since these are *non-functional* errors. Any appeal to “degeneration since the Fall” is also irrelevant, unless one is to assume that God intervenes directly to cause this degeneration by first creating redundant copies of a gene and then targeting particular letters out of many thousands in the genetic code, and *only in those animals that are grouped closely together based on comparative anatomy and fossil layering*. Keep in mind that this is only one of many examples of specific typos in the same locations of dead genes that are shared between humans and primates.

Of course, God can *do anything* (which is why saying “Because God did it that way” explains nothing), but if He did, it only serves to create false corroboration of evolution. If we allow for that type of explanation, then we can just as easily accept that the universe was created ten minutes ago with our memories in tact, and that all evidence to the contrary is either a test, or just “because God did it that way for His reasons, which we are too lowly to comprehend”. Again, not only can *anything* be believed under such an approach, but it also denies us any insights in to the workings of nature since it undermines *all* of science.

What else did all those dead genes code for?

Those dead and dormant genes code for some strange things, indeed—but unsurprising from an evolutionary framework. For example, embryonic tissue from the jaw of a chicken was induced to grow teeth.⁷ Please pause and consider the significance of this: *genes for teeth are in the chicken's DNA*, but ignored because the chemical signal that activates them no longer occurs. Of course, this experiment proves that the genes for teeth *are in there*. Why a creator would give chickens the genes for teeth, but keep them turned off, is something difficult to image without the help of a qualified creationist.

To recap up to this point, we've seen that a conclusion of descent with modification is corroborated by a tree of life based *only* comparative anatomy; and again independently corroborated by a tree based *only* on the position of extinct species in the fossil layers; and again independently corroborated by a tree based *only* on DNA, which is made up largely of code that doesn't do anything; and again independently corroborated by the pattern of shared identical typographical errors in the dead genes found in DNA; and again independently corroborated by the kinds of things those dead genes used to code for—things like teeth in chickens, which fits with where chickens are in a tree of life with respect to their toothed, reptilian ancestors.

Embryology

Earlier I described DNA as a kind of recipe. This analogy is apt because the form of the final organism depends on the precise timing of various other genes during embryological development. Indeed, embryological structures are an important factor in identifying homologous structures (as they were for the earlier taxonomists such as the anti-Darwinian, Richard Owen, mentioned above).

A gene typically doesn't create an anatomical feature all by itself; instead, the feature arises from the action of the gene working in concert with many other genes, and with each operating under a complex schedule of timing. Modifications of genes that control timing can cause some features to be suppressed, others to be dramatically modified, and still others that are partially developed at one stage of embryological development to be completely erased at a later stage. Because genes work in this manner, we would expect that the developing embryo will sometimes reveal certain aspects of its evolutionary past.

Examples of this include the whalebone whale and the anteater, both of whom develop teeth in an early embryological stage only to reabsorb them in a later embryological stage *before* birth.⁸ (Actually, this example also demonstrates the presence of teeth genes in yet more toothless animals, like the chicken.) Terrestrial salamanders at one stage develop both fins and gills, but then lose them *before* hatching.

Not only do examples like this show the presence of silent genes for characteristics alien to the definition of the species in which we find them, but these dormant traits are consistent with the placement of these animals in the tree of life as having descended from species that did express these traits: birds descended from toothed reptiles, amphibians descending from an ancestral fish, etc.

Of course, this embryological process may not cause complete disappearance of ancestral traits as it did in the above examples. When they don't completely disappear, but are still nonfunctional, the structures are described as "vestigial." Flightless beetles, for example, have wings that remain forever sealed under permanently fused wing covers. Even Darwin commented on many such examples, including that of the rudimentary hind legs found in Boa Constrictors. Seeming to anticipate that some might claim these to have an as yet unknown function, Darwin asked, "why...have they not been retained by other snakes, which do not possess even a vestige of these same bones?"⁹

Biogeography

This final section is perhaps the most straightforward and certainly one of the most persuasive stand-alone bits of evidence that support Descent with Modification (in other words, even if it weren't corroborated by all the independent lines of evidence we've discussed so far). Based on Descent with Modification, if one species is the descendent of another, then there had to be some geographical continuity from where the parent species is found to where the child species is found—they had to be able to get there.

Of course, if this geographical continuity were broken at some point in the past, then there are predictable consequences—but only if Descent with Modification is true. Without going into the many examples of biodiversity that support Descent with Modification, I will focus only on the Australia example, since it alone is such an overwhelmingly persuasive example—particularly against any notion that all of today's air-breathing species came from one point on the globe, such as from an "Ark."

Deeper layers of the fossil record show that marsupial mammals (pouched mammals like the kangaroo) were more common than placental mammals (mammals like us that gestate their young inside their bodies with the use of a placenta). During this time (i.e., in these layers) some parts of the world were populated *only* by marsupial mammals, including the land mass that would eventually become Australia. Shallower (more recent) layers of the fossil record show that placental mammals had displaced the marsupials over much of the earth.

But what if a barrier appeared before the expanding placentals could invade a particular area that had been occupied only by marsupials? For example, what if a peninsula that had been occupied only by marsupials, became an island *before* the new placentals migrated there? Well, Descent with Modification would predict that the isolated marsupials might not only survive, but fill many, if not all, of the same ecological niches that placental mammals occupy elsewhere in the world. In other words, they would evolve many *analogies* to placentals, and only in one place: their isolated island.

Of course, this is exactly what we see in Australia. In the table below¹⁰, keep in mind that all of the animals in the Marsupial column are more closely related to each other than they are to their counterparts in the other column. This is an extremely telling observation; it really should make you say, “Wow!”

Consider that the Tiger cat is more closely related to the marsupial mouse than it is to the Bob Cat, which looks superficially almost the same. The same can be said about the Tasmanian Wolf, which looks almost identical to a “regular” wolf, but is also in fact a closer relative to the Marsupial mouse, who for all the world looks like a “regular” mouse.

Placental	Marsupial
Wolf	Tasmanian Wolf
Flying Squirrel	Flying Phalanger
Mouse	Marsupial Mouse
Mole	Marsupial Mole
Anteater	Numbat
Bob Cat	Tasmanian Tiger Cat
Lemur	Spotted Cuscus

Keep in mind that all these marsupial species exist in only *one part* of the world. Fascinating to be sure, though this is not only *explained* by Descent with Modification, it is practically *expected*. Moreover, it adds yet another independent cross-check of the tree you get based only on the comparative anatomy of marsupials and placentals, which, in turn, is independently cross-checked by the tree drawn only from the layer positions of fossils, which is cross-checked by the tree based on biochemistry, etc., etc.

On the other hand, this is not only completely inexplicable under the creationist “model,” but it actually *falsifies* that “model.” What can the creationist say about such a pattern in biogeography? All they can say is that God created parallel versions of each of these animals (which alone contradicts “similar structures for similar functions”), that they left the Ark at the same time from Mt. Ararat and that somehow the marsupial mouse, Tasmanian wolf, Tiger Cat and the many, many other marsupial species (not shown in the table) that exist only in Australia all cooperated as a *group* to get to get to Australia ahead of all placental mammals. As Philip Kitcher puts it,

Some marsupials—wombats, koalas, and marsupial moles, for example—move very slowly. Koalas are sedentary animals, and it is difficult to coax them out of the eucalyptus trees on which they feed...The idea of any of these animals engaging in a hectic dash around the globe is patently absurd (On the evolutionary account, of course, they are all descendents of ancestral marsupials who had millions of years to reach their destinations)¹¹

If they all started at the same time in the same place, as the creationists claim, what was it about their lack of a placenta that made them move as a *group, predator and prey, large and small* ahead of very fast placental predators to just this one part of the globe? Without a direct Divine assist, it’s hard to imagine a coherent explanation.

Conclusion

Let's think back to the original example of the court case that we discussed at the very beginning. Can analog watches be wrong? Of course. Can certain fossils be misidentified, or identified as coming from the wrong layers? Of course. Can digital watches make mistakes? Definitely. Are animals sometimes misclassified based on their anatomies? Definitely. What about the timing of the 5 O'clock news—is it *infallible*? Definitely not. What about the reading of DNA sequences—is it infallible? Definitely not.

But just as in the court case, such criticisms miss the whole point. In the court case example, we don't believe the suspect is guilty *just* because of what someone's watch said, or *just* because someone heard the 5 O'clock news coming on at 5 O'clock, or just because someone heard the 5 O'clock whistle blow. We believe it, because what someone's watch said was the *same thing* as what the timing of the 5 O'clock news was telling us, which was the *same thing* as what the timing of the 5 O'clock whistle was telling us. In other words, we believe because of the *agreement* between multiple independent sources (not to mention the agreement between multiple samples from the same source—e.g., many watches of different types).

When you find yourself talking about highly technical minutia regarding some particular measurement or method, remember that one particular measurement or one particular method is not why scientists believe that evolution is true. The critic of Evolution has to show not how a measurement or method may be wrong (we all know *that*), but how all of the thousands of different measurements using many different independent methods come up with the *same wrong answer*. In the court case, ask yourself what the odds are that all those analog and digital watches were all broken in different ways, but still all said 5 O'clock at the same time; and further that this matched the mis-scheduling of the 5 O'clock news, which in turn, coincided with the mis-scheduling of the 5 O'clock whistle. This conspiracy of errors would have to ensure that as a group they all agreed it was 5:00 PM when it was really, say, 2:02 PM.

It is in fact likely that errors *will* be made, precisely for the reasons creationists give: these techniques are *not perfect*. However, if the prosecution is to have a convincing case, errors should appear as a couple of watches that said it was 4:35 or 5:20, with one perhaps saying it was 11:00 AM, but with the overwhelming majority of independent measurements and methods showing tight agreement around 5 O'clock, plus or minus a minute or two. Naturally that would be extremely convincing, and the errors would be recognized as statistical outliers—due precisely to the known fallibility of *individual* measurements. This is precisely why science doesn't consider any theory strong on a few data points, but only when there are a many data points and a good deal of independent corroboration. Keep in mind that errors and unexpected results *are reported* with the rest of the data. This is how science accounts for the fallibility of measurements, and the imperfections of individual scientists.

So it is with evolution. To the creationist one has to ask: How did all the possible errors that *could* happen in any separate case not only *did* happen, but conspired together so that as a *group* they would have tight agreement around the *same* wrong answer? That is what we mean by independent corroboration; that is what we mean when we say that a theory is well supported by the evidence; and that is what the critic needs to explain. Indeed, his or her alternative theory must not only explain the same phenomena, but must *account for that agreement*, and not simply point to the obvious fact that mistakes can be made, or that some questions remain, as they do in every field of science.

¹ Arthur N. Strahler, *Science and Earth History: The Evolution / Creation Controversy* (Buffalo: Prometheus Books, 1987), p. 108.

² Adapted from Joel Cracraft, "Systematics, Comparative Biology, and the Case Against Creationism," in *Scientists Confront Creationism*, ed. Laurie R. Godfrey (New York: W. W. Norton & Company, 1983), p. 171.

³ Adapted from Strahler, p. 352

⁴ Edward E. Max, "Plagiarized Errors and Molecular Genetics," *Creation/Evolution* XIX (1986) , p. 34. Reprinted and updated 7/12/99 in TalkOrigins.

⁵ Ibid.

⁶ Kawaguchi, *American Journal of Human Genetics* 50:766-80 (1992), cited in Max.

⁷ E.J. Ckollar and C. Fisher, *Science* 207:993 (1980) cited in Douglas J. Futuyma, *Science on Trial: The Case for Evolution* (Sunderland: Sinaur Associates, 1995), p. 48.

⁸ Stephen Jay Gould, "Evolution as Fact and Theory," in *Science and Creationism*, ed. Ashley Montagu (New York: Oxford University Press, 1984), p. 122.; see also, Futuyma, p. 189.

⁹ Quoted in Futuyma, p. 49.

¹⁰ Adapted from Tim M. Berra, *Evolution and the Myth of Creationism* (Stanford: Stanford University Press, 1999), Fig. 16.

¹¹ Philip Kitcher, *Abusing Science: The Case Against Creationism* (Cambridge: The MIT Press, 1993), pp. 141.

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MIMICRY

M.Tevfik Dorak, M.D., Ph.D.

Mimicry is the resemblance of one organism (mimic) to another (model) such that these two organisms are confused by a third organism (receiver). The model and mimic are not usually taxonomically related. In molecular mimicry, pathogenic organism (or a parasite) mimics a molecule of the host so that it escapes recognition as foreign (a kind of aggressive mimicry, see below). An evolving mimicry takes advantage of previously evolved communication signals and responses between organisms (for example, between a predator and a warningly colored prey). To be successful and beneficial to the mimic, the model should be an abundant species whose noxious characteristics have left a lasting impression on predator.

Batesian mimicry: First described by the British naturalist Henry Walter Bates in 1852. He found two unrelated but similarly marked families of Brazilian forest butterflies one of which (model) was poisonous to the birds and the other palatable ones (mimic) survived because of the resemblance to the poisonous ones. They usually mimic the aposematic coloration of the model species. In this kind of mimicry, the mimicking organism has evolved some features of a poisonous organism but is not poisonous itself. This is essentially equivalent to camouflage. Batesian mimicry is particularly common among insects. The mimicry by grasshoppers of poisonous tiger beetle is another example from the insect world. Theoretically, selection only favors the mimic if it is less common than the model. The fitness of the mimics is negatively frequency-dependent.

Mullerian mimicry: The German zoologist Fritz Muller proposed an explanation to Bates's paradox in 1878. Bates had observed a resemblance among several unrelated butterflies all of which were inedible. This paradoxical observation puzzled him. Muller realized that the explanation might lie in the advantage to one inedible species in having a predator learn from another. Once the predator has learned to avoid the particular conspicuous warning coloration with which it had its initial contact, it would then avoid all other similarly patterned species, edible or inedible. Maximum protection is gained by Mullerian mimics when all individuals have the same signal (signal standardization). The number of individuals sacrificed in educating the predators is spread over all of the species sharing the same warning pattern (called mimicry rings). This tendency of inedible and noxious species to evolve to have the same or similar warning signals is called Mullerian mimicry. One example is the black and yellow striped bodies of social wasps, solitary digger wasps and the caterpillars of the cinnabar moths. Mullerian mimicry could be considered not to be true mimicry because the receiver is not actually deceived and it is not obvious which organism is the model and which one is the mimic.

Aggressive mimicry: The organism mimics a signal that is attractive or deceptive to its prey. The examples are the egg mimicry by cuckoos and praying mantis mimicking flowers and vegetation to attract insects (a wolf in sheep's clothing). Another example is that cuckoo bees lay their eggs in the nests of humblebees, which they closely resemble. Host mimicry by parasites, in which the host is both the model and receiver, is an extension of aggressive mimicry. Most examples occur in birds and between viruses and their hosts including humans.

[A lecture on mimicry from University College of London](#)

[Examples of Mimicry in Sea Animals](#)

[An article by Lev-Yadun on Aposematic Coloring in Plants](#)

[A high school activity on Mimicry with a list of examples](#)

[Female mimicry in garter snakes by Mason & Crews, 1985 & by Shine et al, 2001](#)

[Motion camouflage by Dragon Flies \(New Scientist\)](#)

[Crypsis & Mimicry Images](#) [Insect Mimicry](#) [The Art of Deception](#)

[Encyclopedia Britannica article on mimicry \(subscribers only\)](#)

[Animal Imposters: PBS video](#) [Adaptations for Survival in the Sea: ORG Video](#)

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SOME ADAPTATIONS & IMPERFECTIONS

CHECK THE CATEGORY COLUMN APPROPRIATE FOR EACH FEATURE

AD=adaptation

CO=contrivance

VE=vestigial feature

AT=atavism

FEATURES	AD	CO	VE	AT
1. Our spinal column				
2. Our larynx, its lower position				
3. Our eustachian tube				
4. Human tails				
5. "Wisdom Teeth"				
6. Our ear-wagging muscles				

7. Sickle-cell Anemia				
8. Flippers of seals and sea lions				
9. Tree kangaroos: legs and feet				
10. Anteaters' teeth in embryos only				
11. Salamanders: gills and fins on embryos only				
12. Hollow bones in flying birds				
13. Hollow bones in flightless birds				
14. Cave dwelling animals: sightless eyes				
15. Male Booby birds: nesting material - for courting only				
16. Some beetles: useless wings beneath wing covers				
17. Some whales, sometimes with pelvis, thigh bones				
18. Teeth in some baleen whales (embryos only)				
19. Pythons, boa constrictors: with pelvis & tiny limbs				
20. Panda's "thumb" (6th digit from wrist bone)				

21. Extra Horse Toes

SOME ADAPTATIONS & IMPERFECTIONS: Details & Key

Read or relate the following details to the class while showing the check-table on the overhead projector.

Codes shown at end of each item below is the expected category to be checked on table.

1. **Our spinal column**, clearly homologous to the "suspension bridge" support structure in tetrapods, must serve as a vertical load-bearing column in people, bringing an abundance of classic back problems when its support is compromised. (CO)
2. **Our larynx**: Occupies a lower level than it does in other animals (creating a larger space in our throat and pharynx for tongue movements and other changes for generating complex subtle sounds (speech), but creates a liability in that our food path crosses the air path, making us more likely to choke compared to other animals, since food can become more easily caught in our air path. (CO)
3. **Our Eustachian tube** (ear canal), homologous to a gill cleft in fishes, serves to equalize air pressure on opposite sides of our eardrum. Small changes in air pressure (due to altitude change, or other cause), can bring severe ear pain, especially if the tube is swollen closed due to a cold, and is often subject to infection. (CO)
4. **Human tail**: Always on our embryo (VE). Sometimes, babies are born with a fleshy tail (AT).
5. **Our "wisdom teeth"** (3rd molars), sometimes never develop, often become impacted, may require surgical removal. Is this "wise design", or the unfortunate result of reduced facial projection as the teeth reduced in size over the course of human evolution? (VE)
6. **Our ear-wagging muscles**. (VE)
7. **Sickle Cell Anemia**: caused by a molecular mechanism which, in a moderate (heterozygous) dose, protects against malaria, but in its full dose (homozygous recessive), produces disabling disease of sickle cell anemia. (CO)
8. **The flippers of seals and sea lions** are clearly homologous to the legs of tetrapods, and work quite well in the water, but make for very clumsy locomotion on land. (CO)
9. **Tree kangaroos** show limited adaptations of their limbs to their arboreal existence, but they're still relatively clumsy in the trees, and they are also not as fit for activity on the ground as their ground-dwelling relatives. (CO)
10. **Anteaters develop teeth** during fetal development and then lose them before birth.

(VE)

11. **Terrestrial salamanders develop gills and fins** but only during fetal development. (VE)

12. **Flying birds possess hollow bones.** (AD)

13. **Flightless birds** (e.g. ostriches, moa, emus, penguins) **also possess hollow bones.** In terrestrial birds, hollow bones cannot provide nearly the structural support found in other terrestrial vertebrates.(VE)

14. **Many cave-dwelling animals possess sightless eyes.** (VE)

15. **Male booby birds** court females with nesting material then mate with them, throw the nesting material away, and the females lay their eggs on the bare ground. (VE)

16. **Some beetles have useless wings** sealed beneath wing covers (elytra). (VE)

17. **Certain whales sometimes possess a pelvis and thigh bones.** (AT)

18. **Some baleen whales have teeth** (embryos only) (VE)

19. **Pythons and boa constrictors possess a pelvis and tiny limbs.** (VE)

20. **Panda's thumb:** sixth "digit" formed from a wrist bone. While it is functionally a digit, it is structurally different from the digits of all other mammals. (CO)

21. **Extra toes found occasionally on horses:** Usually duplicates of the main (3rd) toe, but sometimes they develop from the enlarged "splint" bones (vestigial toes 2 and 4). (AT)

REMEMBER, THE EMPHASIS HERE: Notice the **MANY IMPERFECTIONS** in living things (not so much their categories); are these most likely the result of poor design, poor engineering, or normal evolution?

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[SOME ADAPTATIONS AND IMPERFECTIONS:](#)

Blank Table
Details and Key

(SAME AS SHOWN ABOVE)

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Evolution theory explains how organisms have changed over time.



The fossil fish *Priscacara liops* found in sediments dating from the Eocene epoch (55.8 ± 0.2 to 33.9 ± 0.1 mya) in present day Green River, a tributary of the Colorado, USA. Photo: Wikimedia Commons.

Scientific understanding requires both facts and theories that can explain those facts in a coherent manner. Evolution, in this context, is both a fact and a theory. It is an incontrovertible fact that organisms have changed, or evolved, during the history of life on Earth. And biologists have identified and investigated mechanisms that can explain the major patterns of change.

There are four major patterns of change.

Patterns in Nature

The field of evolutionary biology seeks to provide explanations for four conspicuous patterns that are manifest in nature. The first three concern living species, whereas the fourth relates to fossils.

Genes are linked to how organisms look and behave.

Genetic variation. There is tremendous genetic diversity within almost all species, including humans. No two individuals have the same DNA sequence, with the exception of identical twins or clones. This genetic variation contributes to phenotypic variation — that is, diversity in the outward appearance and behavior of individuals of the same species.

Organisms must adapt to their environment to survive.

Adaptation. Living organisms have morphological, biochemical, and behavioral features that make them well adapted for life in the environments in which they are usually found. For example, consider the hollow bones and feathers of birds that enable them to fly, or the cryptic coloration that allows many organisms to hide from their predators. These features may give the superficial appearance that organisms were designed by a creator (or engineer) to live in a particular environment. Evolutionary biology has demonstrated that adaptations arise through selection acting on genetic variation.

Species evolved along different paths from a common ancestor.

Divergence. All living species differ from one another. In some cases, these differences are subtle, while in other cases the differences are dramatic. Carl Linnaeus (1707-1778) proposed a classification that is still used today with slight changes. In the modern scheme, similar species are grouped into genera, similar genera into families, and so on. This hierarchical pattern of relationship produces a tree-like pattern, which implies a process of splitting and divergence from a common ancestor.

Fossils provide evidence of evolutionary changes.

Fossil species . Fossils are the mineralized remnants or impressions of once-living organisms. Many fossils, such as trilobites and dinosaurs, belong to groups that no longer exist on the face of the Earth. Conversely, many modern species appear similar to other fossils, yet fossils of the modern species are absent from rocks of corresponding ages. The age of the Earth is estimated to be about 4.5 billion years, with the earliest bacterial fossils about 3.5 billion years old. Fossils from around 550 million years ago (the Cambrian period) show a diverse assemblage of multicellular animals.

The origin of life remains an unsolved mystery.

Evolutionary biology provides a scientific framework for understanding the changes that have occurred since the first life forms arose on Earth several billion years ago. Biochemists, geologists, and physicists seek natural explanations for the origin of life on Earth. While progress has been made in this area, the origin of life remains an interesting, but unanswered, question.

When species evolve, their genetic makeup changes.

Offspring with genetic mutations are different from their parents.

Genes can be shuffled between organisms.

Not all mutations become fixed in a population.

Natural selection guarantees that the fittest are most likely to pass on their genes.

Mechanisms of Evolution

Biological evolution results from changes over time in the genetic constitution of species. Genetic changes often, but not always, produce noticeable changes in the appearance or behavior of organisms. Evolution requires both the production of variation and the spread of some variants that replace others.

Genetic variation arises through two processes, mutation and recombination. Mutation occurs when DNA is imperfectly copied during replication, leading to a difference between a parent's gene and that of its offspring. Some mutations affect only one bit in the DNA; others produce rearrangements of large blocks of DNA.

Recombination occurs when genes from two parents are shuffled to produce an offspring, as happens regularly in sexual reproduction. Usually the two parents belong to the same species, but sometimes (especially in bacteria) genes move between more distantly related organisms.

The fate of any particular genetic variant depends on two processes, drift and selection. Drift refers to random fluctuations in gene frequency, and its effects are usually seen at the level of DNA. Ten flips of a coin do not always produce exactly five heads and five tails; drift refers to the same statistical issue applied to the transmission of genetic variants across generations.

The principle of natural selection was discovered by Charles Darwin (1809-1882), and it is the process by which organisms become adapted to their environments. Selection occurs when some individual organisms have genes that encode physical or behavioral features that allow them to better harvest resources, avoid predators, and such relative to other individuals that do not carry the same genes. The individuals that have these useful features will tend to leave more offspring than other individuals, so the responsible genes will become more common over time, leading the population as a whole to become better adapted.

Distinct species diverge from one ancestor and can no longer interbreed.

The process that many people find most confusing about evolution is speciation, which is not a separate mechanism at all, but rather a consequence of the preceding mechanisms played out in time and space. Speciation occurs when a population changes sufficiently over time that it becomes convenient to refer to the early and late forms by different names. Speciation also occurs when one population splits into two distinct forms that can no longer interbreed. Reproductive isolation does not generally happen in one generation; it may require many thousands of generations when, for example, one part of a population becomes geographically separated from the rest and adapts to a new environment. Given time, it is inevitable that two populations that live apart will diverge by mutation, drift, and selection until eventually their genes are no longer compatible for successful reproduction.

Evidence for Evolution, and its Significance in our Lives

It is impossible to review all the evidence for evolution in a short article such as this. However, the following offers a sample of the kinds of evidence that have been discovered and confirmed repeatedly by scientists. These examples also illustrate the importance of this evidence for science and society more generally.

Fossils are the most easily observed evidence for evolution.

Evidence from fossils. Based on myriad similarities and differences between living species, evolutionary biology makes predictions about the features of ancestral forms. For example, numerous features indicate that birds are derived from reptilian ancestors. By contrast, these data reject the possibility that birds were derived from other groups, such as flying insects. Scientists have discovered fossil birds with feathers and legs like modern birds, but which also have teeth, clawed digits on their forelimbs, and a tailbone like their reptilian ancestors. Fossils are especially important evidence for evolution because, with little effort, each of us can use our eyes and minds to observe and interpret the dinosaur and other ancient fossils in public museums.

DNA profiles show evolutionary relationships among species.

Evidence from genetics. The genomes of all organisms contain overwhelming evidence for evolution. All living species share the same basic mechanism of heredity using DNA (or RNA in some viruses) to encode genes that are passed from parent to offspring, and which are transcribed and translated into proteins during each organism's life. Using DNA sequences, biologists quantify the genetic similarities and differences among species, in order to determine which species are more closely related to one another and which are more distantly related. In doing so, biologists use essentially the same evidence and logic used to determine paternity in lawsuits. The pattern of genetic relatedness between all species indicates a branching tree that implies divergence from a common ancestor. Within this tree of life, there are also occasional reticulations where two branches fuse, rather than separate. (For example, mitochondria are organelles found in the cells of plants and animals. Mitochondria have their own genes, which are more similar to genes in bacteria than to genes on the chromosomes in the cell nucleus. Thus, one of our distant ancestors arose from a symbiosis of two different cell types.) The genetic similarity between species, which exists by virtue of evolution from the same ancestral form, is an essential fact that underlies biomedical research. This similarity allows us to begin to understand the effects of our own genes by conducting research on genes from other species. For example, genes that control the process of DNA repair in bacteria, flies, and mice have been discovered to influence certain cancers in humans. These findings also suggest strategies for intervention that can be explored in other species before testing on humans.

Evolution is evident today in how bacteria evolve to resist antibiotics.

Evolution in action. Evolutionary change continues to this day, and it will proceed so long as life itself exists. In recent years, many bacterial pathogens have evolved resistance to antibiotics used to cure infections, thereby requiring the development of new and more costly treatments. In some frightening cases, bacteria have evolved resistance to every available antibiotic, so there is no longer any effective treatment. In the case of HIV, which causes AIDS, significant viral evolution occurs within the course of

infection of a single patient, and this rapid evolution enables the virus to evade the immune system. Many agricultural pests have evolved resistance to chemicals that farmers have used for only a few decades. As we work to control diseases and pests, the responsible organisms have been evolving to escape our controls. Moreover, scientists can perform experiments to study evolution in real time, just as experiments are used to observe dynamic processes in physics, chemistry, and other branches of biology. To study evolution in action, scientists use organisms like bacteria and fruitflies that reproduce quickly, so they can see changes that require many generations.

Conclusions

Conclusions: Current evidence and historical data show that evolution is both a fact and a theory.

Evolutionary biology is a strong and vigorous field of science. A theoretical framework that encompasses several basic mechanisms is consistent with the patterns seen in nature; and there is abundant evidence demonstrating the action of these mechanisms as well as their contributions to nature. Hence, evolution is both a theory and a set of established facts that the theory explains.

Like every other science, there is scientific debate about some aspects of evolution, but none of these debates appear likely to shake the foundations of this field. There exists no other scientific explanation that can account for all the patterns in nature, only non-scientific explanations that require a miraculous force, like a creator. Such super-natural explanations lie outside of science, which can neither prove nor disprove miracles. Science provides us with a compelling account and explanation of the changing life on Earth. It should also remind us of our good fortune to have come into being and our great responsibility to ensure the continuity of life.

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