

Evidence for evolution.

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Introduction

Evolution is a key unifying principle in biology. As Theodosius Dobzhansky once said, “Nothing in biology makes sense except in the light of evolution.”¹

But what, exactly, are the features of biology that make more sense through the lens of evolution? To put it another way, what are the indications or traces that show evolution has taken place in the past and is still happening today?

Evolution happens on large and small scales

Before we look at the evidence, let's make sure we are on the same page about what evolution is. Broadly speaking, **evolution** is a change in the genetic makeup (and often, the heritable features) of a population over time. Biologists sometimes define two types of evolution based on scale:

- **Macroevolution**, which refers to large-scale changes that occur over extended time periods, such as the formation of new species and groups.
- **Microevolution**, which refers to small-scale changes that affect just one or a few genes and happen in populations over shorter timescales.

Microevolution and macroevolution aren't really two different processes. They're the same process – evolution – occurring on different timescales. Microevolutionary processes occurring over thousands or millions of years can add up to large-scale changes that define new species or groups.

The evidence for evolution

In this article, we'll examine the evidence for evolution on both macro and micro scales.

First, we'll look at several types of evidence (including physical and molecular features, geographical information, and fossils) that provide evidence for, and can allow us to reconstruct, macroevolutionary events.

At the end of the article, we'll finish by seeing how microevolution can be directly observed, as in the emergence of pesticide-resistant insects.

Anatomy and embryology

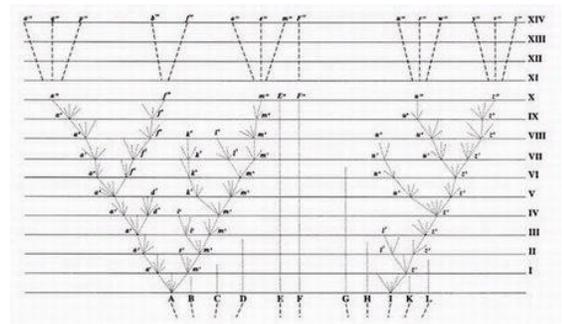
Darwin thought of **evolution** as "descent with modification," a process in which species change and give rise to new species over many generations. He proposed that the evolutionary history of life forms a branching tree with many levels, in which all species can be traced back to an ancient common ancestor.

In this tree model, more closely related groups of species have more recent common ancestors, and each group will tend to share features that were present in its last common ancestor. We can use this idea to "work backwards" and figure out how organisms are related based on their shared features.

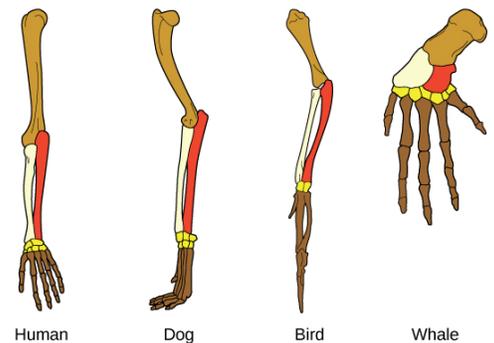
Homologous features

If two or more species share a unique physical feature, such as a complex bone structure or a body plan, they may all have inherited this feature from a common ancestor. Physical features shared due to evolutionary history (a common ancestor) are said to be **homologous**.

To give one classic example, the forelimbs of whales, humans, birds, and dogs look pretty different on the outside. That's because they're adapted to function in different environments. However, if you look at the bone structure of the forelimbs, you'll find that the pattern of bones is very similar across species. It's unlikely that such similar structures would have evolved independently in each species, and more likely that the basic layout of bones was already present in a common ancestor of whales, humans, dogs, and birds.



Branching diagram that appeared in Charles Darwin's *On the origin of species*, illustrating the idea that new species form from pre-existing species in a branching process that occurs over extended periods of time.



The similar bone arrangement of the human, bird, and whale forelimb is a structural homology. Structural homologies indicate a shared common ancestor.

Image credit: "Understanding evolution: Figure 7." by OpenStax College, Biology, CC BY 4.0

Some homologous structures can be seen only in embryos. For instance, all vertebrate embryos (including humans) have gill slits and a tail during early development. The developmental patterns of these species become more different later on (which is why your embryonic tail is now your tailbone, and your gill slits have turned into your jaw and inner ear)². Homologous embryonic structures reflect that the developmental programs of vertebrates are variations on a similar plan that existed in their last common ancestor.

Sometimes, organisms have structures that serve no apparent function but are homologous to useful structures in other organisms. These reduced or nonfunctional structures, which appear to be evolutionary "leftovers," are called **vestigial structures**. Examples of vestigial structures include the tailbone of humans (a vestigial tail), the hind leg bones of whales, and the underdeveloped legs found in some snakes (see picture at right)³.

Analogous features

To make things a little more interesting and complicated, not all physical features that look alike are marks of common ancestry. Instead, some physical similarities are **analogous**: they evolved independently in different organisms because the organisms lived in similar environments or experienced similar selective pressures. This process is called **convergent evolution**. (To *converge* means to come together, like two lines meeting at a point.)

For example, two distantly related species that live in the Arctic, the arctic fox and the ptarmigan (a bird), both undergo seasonal changes of color from dark to snowy white. This shared feature doesn't reflect common ancestry – i.e., it's unlikely that the last common ancestor of the fox and ptarmigan changed color with the seasons⁴. Instead, this feature was favored separately in both species due to similar selective pressures. That is, the genetically determined ability to switch to light coloration in winter helped both foxes and ptarmigans survive and reproduce in a place with snowy winters and sharp-eyed predators.

Determining relationships from similar features

In general, biologists don't draw conclusions about how species are related on the basis of any single feature they think is homologous. Instead, they study a large collection of features (often, both physical features and DNA sequences) and draw conclusions about relatedness based on these features as a group. We will explore this idea further when we examine phylogenetic trees.

Molecular biology

Like structural homologies, similarities between biological molecules can reflect shared evolutionary ancestry. At the most basic level, all living organisms share:

- The same genetic material (DNA)
- The same, or highly similar, genetic codes
- The same basic process of gene expression (transcription and translation)
- The same molecular building blocks, such as amino acids

These shared features suggest that all living things are descended from a common ancestor, and that this ancestor had DNA as its genetic material, used the genetic code, and expressed its genes by transcription and translation. Present-day organisms all share these features because they were "inherited" from the ancestor (and because any big changes in this basic machinery would have broken the basic functionality of cells).

Although they're great for establishing the common origins of life, features like having DNA or carrying out transcription and translation are not so useful for figuring out *how* related particular organisms are. If we want to determine which organisms in a group are most closely related, we need to use different types of molecular features, such as the nucleotide sequences of genes.

Homologous genes

Biologists often compare the sequences of related genes found in different species (often called **homologous** or **orthologous** genes) to figure out how those species are evolutionarily related to one another.

The basic idea behind this approach is that two species have the "same" gene because they inherited it from a common ancestor. For instance, humans, cows, chickens, and chimpanzees all have a gene that encodes the hormone insulin, because this gene was already present in their last common ancestor.

In general, the more DNA differences in homologous genes (or amino acid differences in the proteins they encode) between two species, the more distantly the species are related. For instance, human and chimpanzee insulin proteins are much more similar (about 98% identical) than human and chicken insulin proteins (about 64% identical), reflecting that humans and chimpanzees are more closely related than humans and chickens⁵.

Biogeography

The geographic distribution of organisms on Earth follows patterns that are best explained by evolution, in combination with the movement of tectonic plates over geological time. For example, broad groupings of organisms that had already evolved before the breakup of the supercontinent [Pangaea](#) (about 200 million years ago) tend to be distributed worldwide. In contrast, broad groupings that evolved after the breakup tend to appear uniquely in smaller regions of Earth. For instance, there are unique groups of plants and animals on northern and southern continents that can be traced to the split of Pangaea into two supercontinents (Laurasia in the north, Gondwana in the south).

The evolution of unique species on islands is another example of how evolution and geography intersect. For instance, most of the mammal species in Australia are marsupials (carry young in a pouch), while most mammal species elsewhere in the world are placental (nourish young through a placenta). Australia's marsupial species are very diverse and fill a wide range of ecological roles. Because Australia was isolated by water for millions of years, these species were able to evolve without competition from (or exchange with) mammal species elsewhere in the world.

The marsupials of Australia, Darwin's finches in the Galápagos, and many species on the Hawaiian Islands are unique to their island settings, but have distant relationships to ancestral species on mainlands. This combination of features reflects the processes by which island species evolve. They often arise from mainland ancestors – for example, when a landmass breaks off or a few individuals are blown off course during a storm – and diverge (become increasingly different) as they adapt in isolation to the island environment.

Fossil record

Fossils are the preserved remains of previously living organisms or their traces, dating from the distant past. The fossil record is not, alas, complete or unbroken: most organisms never fossilize, and even the organisms that do fossilize are rarely found by humans. Nonetheless, the fossils that humans have collected offer unique insights into evolution over long timescales.

How can the age of fossils be determined? First, fossils are often contained in rocks that build up in layers called **strata**. The strata provide a sort of timeline, with layers near the top being newer and layers near the bottom being older. Fossils found in different strata at the same site can be ordered by their positions, and "reference" strata with unique features can be used to compare the ages of fossils across locations. In addition, scientists can roughly date fossils using [radiometric dating](#), a process that measures the radioactive decay of certain elements.

Fossils document the existence of now-extinct species, showing that different organisms have lived on Earth during different periods of the planet's history. They can also help scientists reconstruct the evolutionary histories of present-day species. For instance, some of the best-studied fossils are of the horse lineage. Using these fossils, scientists have been able to reconstruct a large, branching "family tree" for horses and their now-extinct relatives. Changes in the lineage leading to modern-day horses, such as the reduction of toed feet to hooves, may reflect adaptation to changes in the environment.

Image credit: "[Equine evolution](#)," by H. Zell, [CC BY-SA 3.0](#)

Summary

Multiple types of evidence support the theory of evolution:

- Homologous structures provide evidence for common ancestry, while analogous structures show that similar selective pressures can produce similar adaptations (beneficial features).
- Similarities and differences among biological molecules (e.g., in the DNA sequence of genes) can be used to determine species' relatedness.
- Biogeographical patterns provide clues about how species are related to each other.
- The fossil record, though incomplete, provides information about what species existed at particular times of Earth's history.
- Some populations, like those of microbes and some insects, evolve over relatively short time periods and can be observed directly.

