

The Encyclopedia of Life is an unprecedented effort to gather scientific knowledge about all life on earth—multimedia, information, facts, and more. [Learn more at eol.org](http://eol.org).

What is a Species?



Author:
Leo Shapiro, Encyclopedia of
Life, Smithsonian Institution

Photo credit: *Breutelia affinis* by Arthur Chapman, Flickr: EOL Images. CC BY-NC-SA

What is a species? At first glance, the answer to this question may appear to be straightforward: a species is a distinct "kind" of animal, plant, fungus, or other organism. But where does one species end and another begin? How do we define or recognize the boundary between two species? Biologists have long debated this question on both philosophical grounds and practical grounds. How should we define species ideally? Given the limits of our information about the biology and evolutionary history of most organisms, what practical criteria can we use to consistently define species?

Perhaps the most widely accepted species concept is known as the Biological Species Concept (BSC). According to this definition, proposed by the evolutionary biologist Ernst Mayr in the mid-20th century, species are groups of actually or potentially interbreeding natural populations which are reproductively isolated from other such groups. Within this definition, a species represents a set of individuals connected by gene exchange ("gene flow") that is genetically isolated from all other such sets of individuals. There is gene flow among individuals within a species, but not between different species. This lack of gene exchange means that different species can evolve independently.

Other approaches to defining and thinking about species have focused on lineages in branching evolutionary trees, with ancestral species splitting into two different lineages and the tips of the branches representing the species that are with us today. The focus on reproductive isolation (biological species concept) versus the relationships among branches in evolutionary trees (lineage-based species concepts) represents two perspectives on the speciation process (the origin of new species) that are not mutually exclusive.

Today, most biologists are more interested in understanding the process of speciation than in trying to find a strict species definition that is always applicable. Speciation is usually a gradual process, so it is not unusual to encounter populations that are only partly reproductively isolated. This means that individuals from diverged lineages may still exchange genes to a limited degree, perhaps even to the extent that they will merge again. These situations are challenging for both the biological species concepts and lineage species concepts. Although some people may wish for a black-and-white criterion for defining species, this is unrealistic. By analogy, imagine a population of maturing humans. Most individuals will be easily recognized as children or adults, but some will be difficult to categorize and these difficult individuals might be tagged differently by different people using different criteria (e.g., different physical characteristics, different measures of emotional maturity, etc.). Similarly, most individual birds or snails or mushrooms can be readily categorized as belonging to one species or another, but exceptions are not rare.

Recognizing Species

In practice, direct information on reproductive isolation or evolutionary relationships between groups of individuals is often unavailable. Because reproductively isolated lineages are genetically isolated, they evolve independently and tend to accumulate genetic differences (and therefore morphological and other differences). Scientists can use these differences to infer reproductive isolation without direct evidence on gene exchange. Historically, and still today, careful analysis of morphology (physical characteristics) has been used to infer which groups are probably reproductively isolated and represent independently evolving lineages. In recent decades, newly available DNA sequence data has provided a rich new source of data for both assessing evidence of gene exchange in recent generations (relevant to biological species concept status) and estimating the evolutionary relationships (relevant to lineage species concepts) among living organisms.

The question of what constitutes a species can clearly be a very complex one, and in many cases it may not be obvious where a species boundary should be drawn. Nevertheless, more often than not the organisms we encounter can reasonably be placed in distinct "bins". This is why field guides work well most of the time.

Inferring Evolutionary Relationships Among Organisms

For a variety of reasons, figuring out the relationships among species is much more complex than simply grouping by similarity in appearance. For example, two organisms that are not closely related (such as a cactus and a euphorb) may resemble each other because they have evolved similar adaptations for similar environmental conditions (this phenomenon is known as "convergent evolution"). Alternatively, two individuals that appear morphologically identical may nevertheless belong to distinct reproductively isolated species--with reproductive isolation based, for example, on different sex pheromones or mating behaviors (distinct species that are morphologically indistinguishable, or nearly so, to human scientists are known as "cryptic species").

While morphological data are clearly extremely useful for investigating the evolutionary relationships among organisms, morphology can be limited or misleading. In recent years, DNA sequence data have become central to most studies of evolutionary relationships. Although the quantity of available data that can be obtained from comparing DNA sequences is very large, inferring evolutionary relatedness based on simple similarity in DNA sequence is similarly problematic. DNA consists of long strings of chemical units, or nucleotides, of just four types (abbreviated as G, A, C, and T). As DNA is copied across generations the base at each position may mutate among these four nucleotides, making the history challenging to reconstruct when we look at the result of this history by sequencing the DNA of current-day species. These challenges have spurred the development of very sophisticated analytical methods, beyond the scope of this overview, for reconstructing the evolution of DNA and other characters from hypothetical common ancestors to the organisms alive today. By applying these methods, with ever increasing amounts of computer power and quantities of genetic data as technology advances, scientists' understanding of the relationships among organisms continues to improve at a rapid rate.