

Inheritance or convergence? The winding paths of species evolution

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How can we explain that some species are more alike than others? Species are the product of their history: evolution. They represent the leaves of the tree of life, which emerges from a main trunk symbolizing their ancestor common to all. Two closely related species in this tree have therefore recently separated from each other - they have a recent common ancestor - and often resemble each other. Two species far away in the tree are therefore generally very different because they have followed independent evolutionary branches. However, some pairs of historically distant but very morphologically similar species are counter-examples. In fact, these intriguing similarities are the product of the repeated adaptation of species to the same environmental conditions. These evolutionary convergences are major elements that make it possible to affirm that adaptation is a fundamental force in the evolution of living organisms.

A remarkable feature of the living world is the very great diversity of forms it takes. Individuals are often grouped into species, which makes it easy to describe this biodiversity. Thus, a certain diversity of species forms within mammals can be observed in the images in Figure 1. But some species are more alike than others. Thus, the polar bear looks much more like the brown bear than the gorilla.

1. First cousins are more alike than distant cousins

Species have long been described from a fixist point of view. Assumption that there is neither transformation nor drift of living species, nor is there any profound modification of the Universe. point of view, *i.e.* as immutable entities, "essences"

that were *a priori* thought by the divine (see [What is biodiversity?](#)). At the end of the 18th and beginning of the 19th centuries, scientists such as Lamarck (1744-1829), Wallace (1823-1913) and Darwin (1809-1882, see focus on [Darwin](#)) revolutionized this traditional vision of biodiversity by proving that living species evolved from their origins (see [Lamarck and Darwin: two divergent visions of the living world](#)) and that they were therefore all descended from a single common ancestor. How does this discovery help us to better understand the similarities between species?

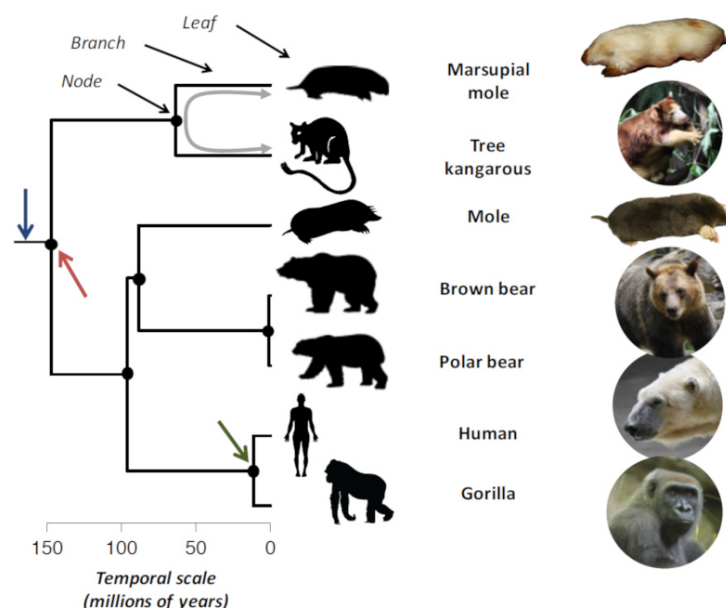


Figure 1. An example of phylogenetic tree. Seven mammalian species (out of almost 5000 existing species) represent the leaves of the phylogenetic tree that describes their evolutionary relationships. The horizontal scale is given in millions of years. The blue arrow indicates the root of the tree, the red arrow its first node, which is also the ancestor common to all species of the tree (147 million years). The green arrow indicates the ancestor common to gorillas and humans, who are assumed to have lived 11.5 million years ago. The double grey arrow represents the phylogenetic distance between a tree kangaroo and a marsupial mole (twice the age of the common ancestor, or $2 \times 63 = 126$ million years). The phylogenetic tree is derived from the study by Bininda-Emonds et al [2]. [Source: © F. Mazel except European mole (Didier Descouens) and marsupial mole (Michael J. Barritt)]

The evolution of species can thus be represented as a phylogenetic tree. Schematic representation of the kinship relationships between groups of living beings. Each node of the tree represents the common ancestor of its descendants. The name it bears is that of the clade formed by the brotherly groups that belong to it, not that of the ancestor, which remains impossible to determine. The tree may or may not be rooted, depending on whether the ancestor common to all leaves has been identified. (Figure 1) which reconstructs "the historical course of the descendants of organized beings" [1]. He thus describes the **interrelationships** between species. Each branch of the tree has **leaves**, the current species. Each **node** of the tree represents the common ancestor of the species above it. This tree is adjusted on a time scale - often in millions of years - and time flows from the root (from left to right from the blue arrow in Figure 1) [2]. The root represents an ancestral species, common to all the leaves of the tree. In the example in Figure 1, it is divided into two daughter branches (red arrow) around 147 million years old [3], which themselves branch off several times before reaching the current species, the leaves. The gorilla and man represent two closely related leaves, *i.e.* they have a relatively recent common ancestor (green arrow) compared to that between man and, for example, the polar bear. If species evolve randomly (hypothesis 1) at a constant rate over time, they will therefore be all the less similar because they separated a long time ago. For example, man and gorilla have only been able to accumulate differences for 11.5 million years, while man and polar bear have been different for 91 million years, reflecting the great similarity between gorilla and man in relation to the polar bear. Phylogenetic distances represent an index of overall similarity between two taxa. This is the amount of evolution between the sequences and their ancestors. (Figure 1) between species (grey arrow) therefore give a good idea of the expected morphological similarity between two species: the more closely two species are phylogenetically related, the more likely they will be to resemble each other.

2. Some counter-examples...

However, there are counter-examples: evolutionarily distant species can look strikingly similar, as is the case between some large groups of marine animals, plants or mammals.

2.1. Marine animals

Radiated finfish (e.g. tuna) [4] and cetaceans (marine mammals including whales and dolphins) separated about 430 million

years ago [5]. However, don't they share a similar general appearance? On this subject, Darwin [6] already noted that:

"For animals, belonging to two most distinct lines of descent, may readily become adapted to similar conditions, and thus assume a close external resemblance; but such resemblances will not reveal -will rather tend to conceal their blood-relationship to their proper lines of descent. [...] thus the shape of the body and fin-like limbs [...] being adaptations in both classes for swimming through the water..."

Darwin suggests here that both groups have, over evolution, developed a hydrodynamic form and fins that allow them to move efficiently in the water.

2.2. Underground mammals

Mole-like animals (Figure 1) exist in mammals in different parts of the world. Thus, the European mole is present in part of Eurasia while the marsupial mole is present in Australia. These species have a similar burrowing shape, adapted to underground life (Figure 1). They all have a stocky "sausage-shaped" body - without a distinguishable neck - equipped with powerful forelegs with large claws for efficient digging. They have all more or less lost their external sensory organs (external ear, sight). The similarity between these "moles" does not come from a common heritage, that is, from a common ancestor with a mole shape. Indeed, the marsupial mole is phylogenetically closer to a kangaroo than to a European mole (Figure 1), which is closer to man than the marsupial mole. Thus, the "mole" form has appeared several times in evolution of mammals.

2.3. Cushion plants



Figure 2. Cushion plants. The figure shows four cushioned species: *Androsace helvetica* (A), *Saxifraga marginata* (B), *Silene acaulis* (C) and *Benthamiella patagonica* (D). These species belong, respectively, to the families Primulaceae, Saxifragaceae, Caryophyllaceae and Solanaceae (found mainly in America). [Source: photos © Joseph Fourier Alpine Station (SAJF)]

Cushion plants are plants forming more or less compact rounded domes (Figure 2, [7]). This very particular morphology is allowed by the presence of very narrow internodes (stem between two successive leaves) and small leaves. In France, these organisms can be found on high mountains with harsh, cold and windy climates. In fact, the plant's very compact structure protects the roots and stems from abrupt temperature variations, but also from cold and wind, allowing the plant to survive in extreme conditions. The evolution of plants into pillow shapes has occurred many times in history, since once again pillow plants are found in very different families and in all regions of the world with arctic or alpine climates (Figure 2).

2.4. "Cactoid" plants



Figure 3. Cactoid plants. The figure shows three groups with cactus-shaped species: (1) the Cactaceae family: general view and detail view (Fig. 3A and 3B, *Demnoza rhodacantha*, Patagonia [Photo © R. Douzet, SAJF]); (2) the Euphorbiaceae family: general view and detail view (Fig. 3C and 3D, *Euphorbia officinarum*, Morocco. [Photo © Jean Paul Pelletier, www.teline.fr]) and (3) *Stapélias*: general and detailed view (Fig. 3E & 3F, *Apteranthes joannis*, Morocco [Source: photos © Sébastien Sant and © Jean-Paul Pelletier, www.teline.fr])

Cactoid plants, *i.e.* cactus-shaped plants, are plants with a characteristic appearance (Figure 3) that live in arid regions. They sometimes have leaves transformed into thorns that allow them to limit water loss and protect themselves from herbivores. In addition, they all contain tissues to store water. In the American deserts, cactus take this particular form, while euphorbia and ampelia species replace them in Africa (Figure 3). These three groups of plants belong to independent evolutionary groups and have therefore not inherited their very particular form, but have acquired it, independently, during evolution.

2.5. Carnivorous plants



Figure 4. Carnivorous plants. The figure shows three species of carnivorous plants: *Drosophyllum lusitanicum* (A, B), *Drosera capensis* (C), and *Heliamphora chimantensis* (D). These species belong, respectively, to the families *Drosophyllaceae*, *Drosophyllaceae* and *Saraceniaceae*. [Source : photos: Carsten Niehaus, Noah Elhardt and Andreas Eils, respectively, via Wikipedia Commons]

Carnivorous plants are plants with the ability to attract and capture small animals such as insects (Figure 4). In France, they are found in environments that are often low in nitrogen, such as peat bogs. Wetlands colonized by vegetation, whose particular ecological conditions have allowed the formation of a soil characterized by its very high content of organic matter, little or no decomposition, of plant origin. A peatland is a particular and fragile ecosystem whose characteristics make it a carbon sink, despite methane emissions, because there is more synthesis of organic matter than degradation. (see [Peatlands and marshes, remarkable wetlands](#)). By digesting these captured animals, carnivorous plants have found a solution to recover large quantities of nitrogen and thus compensate for the lack of available nitrogen in the soil. These plants are found in phylogenetically distant families, suggesting that carnivory has been acquired several times and independently in the evolution of the plants. While the evolutionary convergence of the function - recovering nitrogen from animals - is evident between these species, the structures developed to achieve it are more variable. For example, insects can be immobilized in an adhesive substance, which has appeared several times during evolution (Figures 4A and 4B) or trapped in an urn (Figure 4C). In the latter case, plants have developed a different structure for capturing animals, thus illustrating the famous "tinkering with evolution": to achieve the same function, several structures are possible.

3. When natural selection "blurs the tracks"

Thus, although some species may be very distant phylogenetically, they may have **converged** towards a similar morphology, to adapt to similar environmental constraints. The hypothesis of a random evolution that took place previously (hypothesis 1) therefore does not seem to be able to explain these phenomena of adaptation of living organisms to their environment. A major contribution of Darwin (1859) was precisely to propose the mechanism allowing the adaptation of species: **natural selection**.

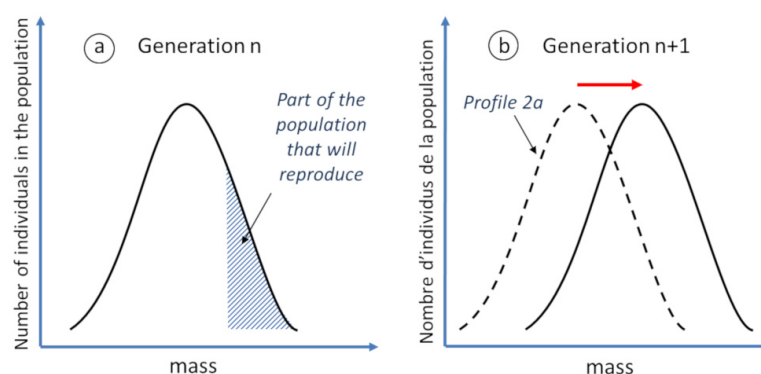


Figure 5. Illustration of the natural selection process. A given species has some variability (of mass as in this example) in a generation *n* (box a) only part of the individuals will reproduce (hatched part of box 2a), because their mass allows them to do so (better survival and/or fertility). Mass is an at least partially hereditary character so the next generation sees its average mass increase.

~~The first necessary condition is the existence of a certain diversity of forms within a species itself, for example individuals of more or less compact cushion plants (Figure 5A). It is precisely this diversity that was ignored by the fixists, for whom it represented only "errors of copying" the divine essence of the species. However, this diversity is real: just look at the diversity within the human species.~~

4. Synthesis

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Just imagine that each individual of a species gives two descendants to each generation. If we start from a single individual, after twenty generations, the population will have reached the size of 2^{20} individuals, i.e. more than one million and after a hundred generations, several billion of billions... which is a priori impossible on a planet with important but limited resources. Thus, only a limited number of individuals of the species will contribute to the next generation. If these characteristics are **heritable**, then they will gradually spread throughout the population and the species will gradually evolve over generations (Figure 5B).

Similarities between species can therefore be the result of historical heritage or evolutionary convergence. To be able to distinguish between the two hypotheses, it is therefore necessary to have a phylogeny of the species and to measure their morphological and anatomical characteristics. Historically, phylogenetic trees were built from morphological data, which survive in an environment where living characters are more and more difficult to reproduce. For example, in an increasingly harsh environment, it is conceivable that only the most compact cushion plant individuals survive long enough to reproduce more. For example, in an increasingly harsh environment, it is conceivable that only the most compact cushion plant individuals survive long enough to reproduce more. For example, in an increasingly harsh environment, it is conceivable that only the most compact cushion plant individuals survive long enough to reproduce more.

The last few decades have seen the advent of DNA molecule sequencing and its use in phylogeny. Molecular similarities are much less subject to these evolutionary convergences, and if properly used they are therefore a tool of choice for reconstructing phylogenetic relationships between species. The comparison of heritable old taxonomic classifications (and text) Relative to taxonomy and hierarchical classifications of living beings (and text) on morphology and phylogenetic classifications from molecular data will highlight evolutionary convergences. It is, in a way, a synergy between old and new approaches in evolution.

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References and notes

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[1] Darlu P. & Tassy P. (1993) *Phylogenetic reconstruction. Concepts and Methods*. Series "Theoretical Biology", No. 7. Masson, Paris (online book on the website of the Sorbonne University: <http://www.sorbonne-universite.fr/bibliothèque/ouvrages/philosophie/philosophie-theorique/philosophie-theorique-concepts-et-methodes>)

[2] Bininda-Emonds O.R., Cardillo M., Jones K.E., Jones K.E., MacPhee R.D., Beck R.M., Grenyer R., Price S.A., Vos R.A., Gittleman J.L. & Purvis A. (2007) *The delayed rise of present-day mammals*. Nature, 446, 507-512.

If these characteristics are **heritable**, then they will gradually spread throughout the population and the species will gradually evolve over generations (Figure 5B).

[3] The dates are from the study by Bininda-Edmonds *et al* (reference 2). These dates are speculative and reflect the current state of knowledge in mammalian phylogeny, and are therefore subject to modification as new discoveries are made.

[4] "Fish" includes cartilaginous fish (sharks and rays), radiated finfish (e.g. trout or tuna), hagfish, lampreys and lungfish. They no longer form a group used in systematics (but - rightly - still in cooking), because the common ancestor of "fish" is not exclusive to them. For example, the ancestor common to trout and shark is also the common ancestor of man. The "fish" do not therefore represent an evolutionary lineage of their own, but rather a concatenation of several distinct groups.

[5] <http://www.timetree.org>. These dates are speculative and reflect the current state of knowledge in phylogeny, and are therefore subject to modification as new discoveries are made.

[6] Darwin C. (1859) *On the origins of species by means of natural selection*. London: Murray, 247.

[7] see also www.cushionplants.eu

