



THE CLASSIFICATION OF LIFE: FROM LINNAEAN TAXONOMY TO DNA BARCODING

For centuries, people have been interested in naming and classifying living things, but with an estimated 10 – 100 million different species on Earth, this is no small task. Traditional **taxonomy** (the identification, naming and classification of living things) based on physical characteristics such as size, shape, colour, and anatomical structure - has identified fewer than 2 million of our planet's species. New molecular technologies such as DNA barcoding are helping scientists to raise this number. This is a story of two revolutions, 250 years apart, which together provide the keys to understanding Earth's biodiversity.

The Birth of Modern Taxonomy

As far as 18th century scientists go, Carl Linnaeus (1707-1778) was a Swedish super star. His contributions revolutionized taxonomy and the Linnaean taxonomic system is still being used today.

Before Linnaeus left his mark, classification nomenclature used long, cumbersome strings of Latin descriptors. For example, the honeybee's full scientific name was *Apis pubescens, thorace subgriseo, abdomine fusco, pedibus posticus glabris, untrinque margine ciliatus*. It doesn't exactly roll off the tongue. Linnaeus simplified and standardized this nomenclature into the **binomial system** (two-name system) of **genus** and **species** that we, *Homo sapiens*, are familiar with today. Following the Linnaean system, the honeybee acquired the much simpler scientific name of *Apis mellifera*. The oldest valid names of plants and animals are derived from Linnaeus' publications *Species Plantarum* (1753) and *Systema Naturae* (10th ed., 1758).

The terms *genus* and *species* were borrowed from the ancient Greek philosopher and zoologist Aristotle (384-322 B.C.E.). He observed and classified animals with similar characteristics into broad groups that he called *genera* and then determined the species within the genera. Aristotle's early classification system was the most comprehensive and insightful of its time. Notably, his distinction between animals with (red) blood versus those without corresponds broadly to our current distinction between vertebrates and invertebrates.

For more information about what constitutes a species, read the background: [What is a Species?](#)

Linnaeus also changed the way that organisms, especially plants, were classified. Like his taxonomic predecessors, he grouped plants according to their shared physical characteristics, but instead of looking at the entire plant, he focused on the anatomy of their reproductive system. By simplifying the classification criteria, Linnaeus made botanical taxonomy much more manageable.

Linnaeus classified both plants and animals into broad **kingdoms**, and continued subdividing into **classes**, **orders**, genera (singular: genus) and finally species. Sound familiar? This system became the standard for generations of biologists and has remained the backbone of our modern classification

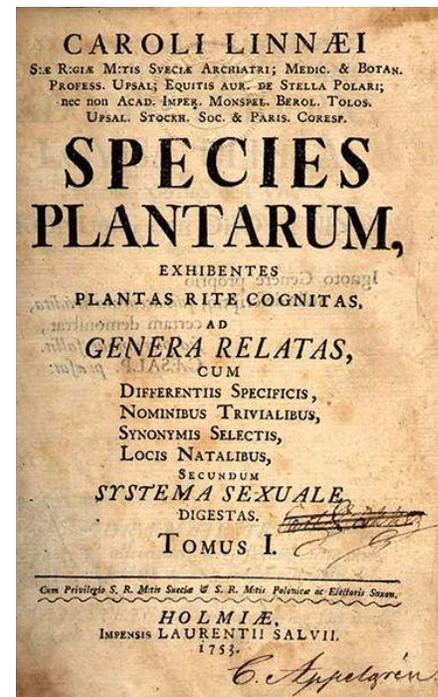


Figure 1: *Species Plantarum* (1753) by Carl Linnaeus.

http://commons.wikimedia.org/wiki/File:Species_plantarum_001.jpg Public domain image on Wikimedia Commons)



system, with ongoing refinement. For an example of how taxonomists identify different earthworm species, using a traditional **taxonomic key**, click [here](#).

A Fly (or three) in the Taxonomic Ointment

Although the Linnaean classification system is still used today, it has a few challenges. First, any classification system based on **morphology** (physical characteristics), no matter how nuanced, will run into problems when specimens are damaged or incomplete. If the defining morphological features of a plant or animal are not intact, identification may be impossible.

Second, many species have different **developmental stages** with radically different morphologies. A familiar example is a caterpillar that undergoes metamorphosis into a butterfly – same species, but a totally different appearance (see Figure 2 A and 1B below).

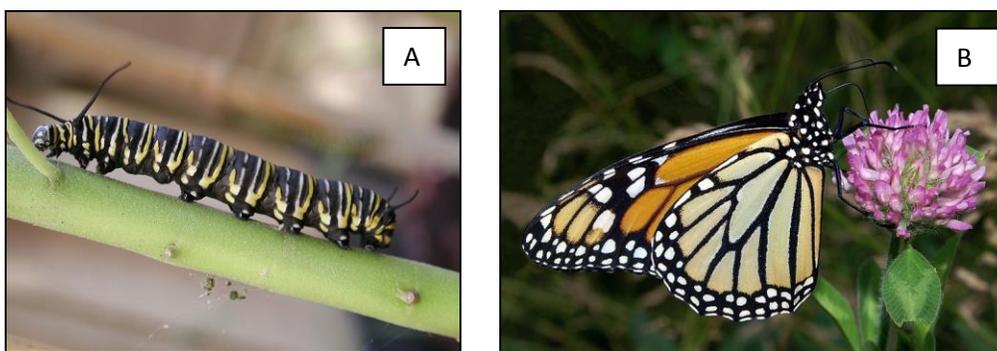


Figure 2A: Monarch butterfly caterpillar.

(http://commons.wikimedia.org/wiki/File:Monarch_caterpillar_on_swan_plant_branchlet.jpg Public domain image on Wikimedia Commons)

Figure 2B: Adult Monarch butterfly.

(http://commons.wikimedia.org/wiki/File:Monarch_In_June_6787d.jpg Public domain image on Wikimedia Commons)

The Monarch butterfly caterpillar (Figure 2A, left) and the adult Monarch butterfly (Figure 2B, right) are two morphologically distinct stages in the development of a single species (*Danaus plexippus*).

Third, there is the opposite problem of **cryptic species**, or different species that are morphologically indistinguishable. [Cryptic species](#) are found among birds, butterflies, fish, frogs, elephants, mosquitoes, plants and many other animal groups. Figure 3A and 3B is a good example of cryptic species – the Northern and Southern Leopard frog.



Figure 3A: Northern Leopard Frog (*Rana pipiens*)

([http://commons.wikimedia.org/wiki/File:Northern_Leopard_Frog_\(Lithobates_pipiens\).jpg](http://commons.wikimedia.org/wiki/File:Northern_Leopard_Frog_(Lithobates_pipiens).jpg) Public domain image from Wikimedia Commons)

Figure 3B: Southern Leopard Frog (*Rana sphenocephala*)

(http://commons.wikimedia.org/wiki/File:Rana_sphenocephala.jpg Public domain image from Wikimedia Commons)



As you can imagine, reliable Linnaean species identification requires an expertly trained taxonomist, and even then there's a practical limit to how many different species one person can discriminate!

The Second Taxonomic Revolution – DNA Barcoding

In 2003, University of Guelph scientist Paul Hebert introduced a new species identification technique based on DNA sequencing (for more information about DNA sequencing techniques, see the [Sanger Sequencing Backgrounder](#)). Called **DNA barcoding**, it is analogous to the way that Universal Product Codes (UPC) use variation in a group of black bars to create unique identifiers for consumer products. DNA barcoding uses genetic variation at the molecular level, in an organism's DNA, to discriminate between different species.

The recipe book for all living things is written in DNA code, specifically the nitrogenous bases called Adenine (A), Cytosine (C), Thymine (T), and Guanine (G), which bond together in **base pairs** (A+T and C+G) to connect two strands of DNA into the famous double helix structure. The sequence of A, C, T, and G molecules in certain genes is variable between different species, but not between individuals belonging to the **same** species. A species' DNA barcode is simply the sequence of A, C, T, and G molecules for a standardized stretch of DNA. It provides a unique **molecular identifier**.

To barcode animals, scientists use a 648-base pair region of the cytochrome c oxidase 1 gene (*CO1*), which is encoded in mitochondrial DNA. This region is easy to amplify by **Polymerase Chain Reaction** (PCR), short enough to be sequenced quickly and cheaply, and long enough to reliably detect variation between, and therefore identify, about 98% of all animal species. For more information about PCR, see the [PCR Backgrounder](#).

The situation is trickier for plant barcoding, because *CO1* doesn't show enough variation between different plant species to be a discriminating barcode. After several years of experimentation and discussion, scientists decided to use regions from two different chloroplast genes, *matK* and *rbcL*. *MatK* has a good level of inter-species variation, but it is technically hard to sequence. *RbcL* has a lower level of variation, but it is easy to sequence. Using both sequences can accurately identify about 70% of plant specimens – not as well as *CO1* for animals, but scientists are working to improve the plant barcode every day.

DNA barcoding enhances traditional taxonomy, because it overcomes all the potential pitfalls associated with morphological identification. DNA is a very tough molecule, and can be recovered from damaged, degraded and incomplete specimens. A species' genetic code never changes throughout its development or life cycle, no matter how much its morphology changes. Conversely, no matter how much cryptic species look alike, they will always have variation at the DNA level.

The Big Picture

The Consortium for the Barcode of Life ([CBOL](#)), based at the Smithsonian Institution in the U.S., is leading the international barcoding community toward its goal of creating a reference library of 5 million standardized DNA barcode sequences that could identify 500 thousand different species – all by the end of 2015!

The University of Guelph, birthplace of DNA barcoding, is home to a major hub of this International Barcode of Life ([iBOL](#)) initiative. The Biodiversity Research Institute of Ontario at the University of Guelph develops barcoding tools, analyzes specimens, and maintains a public reference library of barcodes called the Barcode of Life Database ([BOLD](#)). BOLD currently has molecular and morphological data for over 1.6 million specimens that represent over 150 thousand named species.

The applications of DNA barcoding are widespread. In October 2011, the U.S. Food and Drug Administration approved barcoding for industrial applications such as testing seafood and herbal medicines to prevent consumer fraud. It is also being developed to identify insect predators of the Colorado potato beetle, which is highly damaging to potato, tomato and pepper crops. By barcoding the gut contents of candidate predators to see which ones digest a lot of Colorado potato beetles, scientists can identify insects that could be used for biological control.

Perhaps the biggest picture of all is the use of traditional taxonomy and DNA barcoding to increase our understanding of Earth's biodiversity. This is not just scientific 'stamp collecting.' With so many ecosystems threatened by climate change, pollution and development, it is critically important that we identify our planet's cohabitants and understand both the distribution and interconnectedness of living things. Protecting biodiversity would be a scientific triumph – and would certainly make Linnaeus proud.



Figure 4: Plant Diversity.
(http://commons.wikimedia.org/wiki/File:Diversity_of_plants_image_version_3.png Public domain image on Wikimedia Commons)