<u>**Evolution and Biodiversity Laboratory**</u>

Taxonomy

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Recent estimates of biodiversity suggest that earth may house 5 - 50 million species or more. To date, about 1.4 million species (including 750,000 insects, 250,000 plants and 41,000 vertebrates) have been scientifically described and classified. To effectively study the myriad organisms that inhabit the biosphere, we attempt to classify organisms into groups that reflect their evolutionary relationships.

I. Two Interrelated Sciences

Taxonomy is the science of describing and naming living organisms and classifying them into cohesive, evolutionary units called **taxa** (singular = **taxon**). A scientist whose area of expertise is taxonomy is known as a **taxonomist**.

Systematics is the science of determining evolutionary relationships among living organisms. A scientist whose area of expertise is systematics is known as a **systematist**.

Taxonomy is used as a tool within systematics.
In today's lab, you will learn to use some of the tools of both taxonomy and systematics.
We will start with taxonomy and taxonomic keys.

A. The Taxon

A **taxon** is a group of organisms that represents a cohesive, evolutionary unit.

Biological **nomenclature** is the application of names to organisms recognized as part of a particular taxon. From most to least inclusive, the major **taxonomic ranks** are shown in Figure 1.

Every described, named organism is nested into a complete hierarchy, from species (**least inclusive**) through domain (**most inclusive**).

This classification and nomenclature system, known as ***systema naturae***, was devised by Swedish botanist **Carl Linne** who published it in 1735. Linne Latinized his own name to **Carolus Linnaeus**, and we remember him today as **Linnaeus**, the father of modern taxonomy.

- **The scientific name of an organism consists of its genus and species.**
- **The genus is capitalized and the specific epithet is in lower case.**
- **The names are <u>Latin</u> or are <u>Latinized</u>, and so must be *italicized*.**
- **For example, the genus of our species is Homo.**
- **Our species is sapiens.**
- **The scientific name of our species is *Homo sapiens*.**

A **monophyletic taxon** reflects true evolutionary relationships by including all descendants of a single common ancestor. Various lines of evidence can be used to determine the degree of common ancestry between two taxa, including comparison of

- morphology
- nucleic acid sequences
- protein sequences
- embryo development
- etc.

As new technologies arise, our ability to study evolutionary relationships evolves.

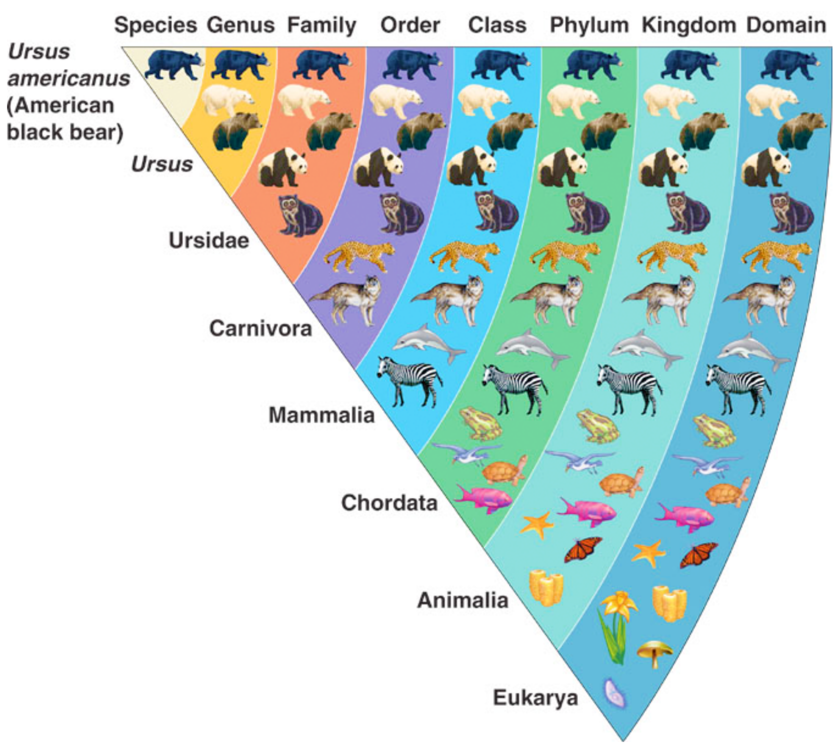

Figure 1. The Linnaean taxonomic hierarchy. Each Domain contains related Kingdoms. Each kingdom consists of related phyla. Each phylum consists of related classes, classes of related orders, orders of related families, families of related genera (singular: genus) and genera of related species. Between the major taxonomic ranks may be larger and smaller taxa such as subkingdoms, superphyla, subclasses, infraorders, subspecies, etc.

A taxon is generally considered to have **three aspects**: **name**, **rank**, and **content**.

1. The taxon's name

Mammalia is the name of the taxon containing all animals that have fur and mammary glands. Carnivora is the name of the taxon containing all flesh-eating mammals with specialized cutting teeth called carnassials. *Canis lupus* is the name of the taxon containing all gray wolves.

All taxonomic names are Latin or are Latinized.

2. The taxon's rank

A taxon's rank reflects its relative level of inclusiveness (i.e., how many other taxa it contains). The most inclusive rank is Domain. The least inclusive rank is species.

A taxon's rank has no more biological significance than its name. It serves only to help the biologist locate the taxon within its hierarchy.

For example, the taxon "**Eukarya**" is currently assigned the rank of **domain**.
The taxon "**Mammalia**" is currently assigned the taxonomic rank of **class**.
A taxon's rank can change as new data become available.

The *relative* rank of a taxon is more relevant than the rank itself.
For example, it is *more* important to remember that all members of *Felis* are classified within the larger taxon "Carnivora," and that all carnivores are classified within the still larger taxon "Mammalia." It is *less* important to to recall that "Carnivora" is an order and "Mammalia" is a class.

Many institutions use a **rankless system** in which a taxon is described only by its name. An author using this system will write "Mammalia" rather than "Class Mammalia".

3. The taxon's content.

A taxon's content is simply the living organisms classified within it.
The taxon Rodentia contains all rodents. The taxon *Homo* contains related species of humans, all of which except *Homo sapiens* are now extinct. Organisms contained in the same taxon share a common evolutionary origin. Therefore, **unlike a taxon's name or rank, the taxon's content is biologically significant.**

B. The Taxonomic Key: A Tool for Identification

When an investigator wishes to identify an unknown specimen, a **taxonomic key** is used.
A taxonomic key consists of **paired statements/descriptions** based on phenotypic traits of organisms being identified in the key. Because the key branches in two at each stage, is called a **dichotomous key** (from the Greek *dicho* meaning "in two" or "split" and *tom*, meaning "cut").

In today's lab, you will learn to (1) use and (2) create a taxonomic key to identify unknown organisms.