

How Biologists Classify Organisms...

(pg 113 - 119)

The science of classifying is called “**taxonomy**”. Classifying organisms allows us to determine evolutionary history (who is ancestrally related to who).

Several sources of evidence are used to help us achieve this...

1. **Comparative Anatomy**

Comparison of body structures that looks for similarity of design in different species (“**homologous structures**”). Finding similarly built structures lets us “infer” that creatures are related

2. **Fossils**

Radioactive dating techniques are used to determine a rock layers age, and we infer the fossils in that rock layer existed a certain time ago. We can determine the “**relative age**” of creatures. (What came before / after what)

3. Embryonic Development

Early in their development, embryos show many characteristics that are lost during later development. Embryos that develop in similar ways, or show similar characteristics are related.

4. Comparative Biochemistry

DNA is a body's blueprint for making proteins, so if different species make the same proteins, we can infer they carry the same "genes" that code for those proteins, and are related.

5. DNA Evidence

How similar is the order of the base sequence inside DNA molecules when you compare different species? The more similar they are, they more close the relationship. Also allows us to estimate when one group split / branched from another group.

Phylogeny.....hypotheses on paper about how groups are related, what common ancestors may have been, and how descendants may have arose. These diagrams are called **phylogenetic trees** (oldest species on the bottom, younger on top)

Cladistics.....grouping species together because they share a common ancestor. Each species still contains a part of that ancestor, but also gains new differences due to evolution and genetic mutation.

Cladistics diagrams are simple stick drawings of how groups may have split from (diverged) the ancestor species.

- Value...
- one species has something valuable, we know where to seriously look for more
 - better understand why some diseases are shared by different species

Modern Classification Techniques STSE on-line

Our modern system of taxonomy was developed in the 1700's by **Carolus Linnaeus**.....

- checklists of physical characteristics was used to identify organisms...the first “**taxonomic keys**”
 - a **dichotomous key** is one that uses pairs of contrasting choices to direct the reader through a series of steps to finally identify what something is. Based on permanent physical characteristics.

“**Creating a Dichotomous Key**”, page 110

- used a system of **taxa**, nested groups, and assigned a two part name to each identified species....**binomial nomenclature**

Kingdom -

Phylum

Class

Order

Family

Genus

Species

...and the 2 part name...

Genus species

Examples ?

This type of system provides consistency in naming, unlike “common names”, which vary from place to place for the same organism.



Ex. Common names for this fish...

Brook trout
Speckled trout
Speckle
Brookie
Squaretail
Mud trout
Sea trout
River char

But there's only one scientific name... Salvelinus fontinalis

Another reason why the binomial system and hierarchical system is used.....it is very flexible, allowing us to add new groups at each level, or even an entirely new Kingdom when we need to...as new evidence directs us to.

There's always exceptions.....**VIRUSES**
(page 122)

- 160 groups, 21 infect humans
- not made of cells, and don't have any cell organelles
- can't reproduce themselves
- no energy needs, no excretion

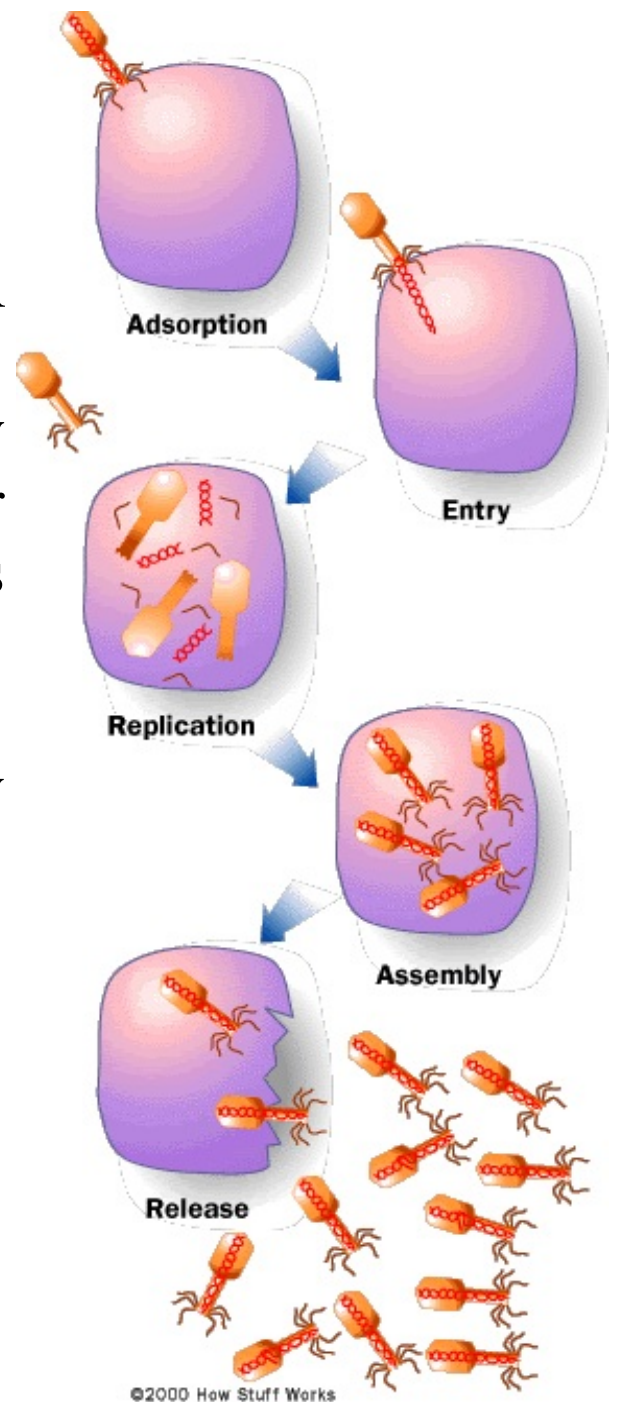
Made of an outer, protein “**capsid**”, which contains a DNA or RNA molecule. Acts as a mobile gene, whose container attaches to specific receptors on its target cell.

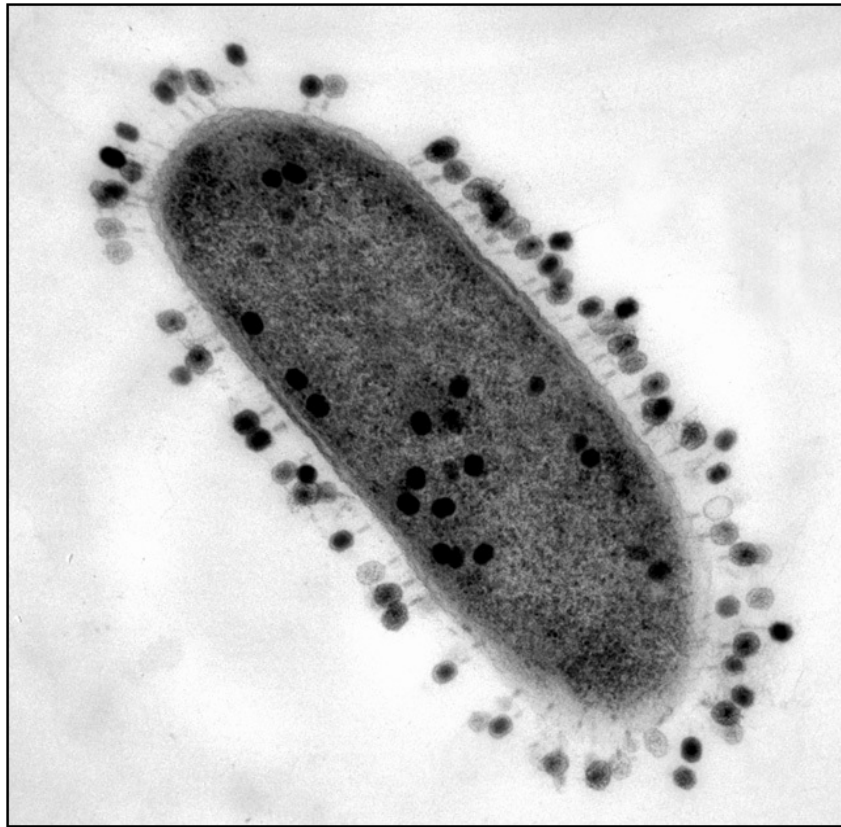
Virus cycle...the “lytic cycle” or “lysogenic cycle”

- attachment
- injection of DNA or RNA
- the host cell doesn't know this isn't its own DNA or RNA, reads it, produces more viruses until
- the cell is full of new viruses,
- then bursts (“cell lysis”)

About 30 minutes

About 200 new viruses





Viruses are classified based on how they work...

Bacteriophages - attack bacterial cells in the way described, not plants or animals

Retroviruses - inject RNA, read and used to make DNA by the host cell, incorporated into the cell DNA, copied when the cell is copied....a timebomb

Provirus - injects DNA, and acts like the retrovirus

This knowledge of viruses is used in recombinant DNA (rDNA) technology. We use empty virus capsids, put in the DNA / RNA we want to introduce into a cell, give this virus a supply of target cells, and let it do its thing. We have made cells that contain our “inserted gene”...they now make something we want, or can be placed into other organisms.