**CHAP: ANIMAL CLASSIFICATION, PHYLOGENY, AND ORGANIZATION** 

**Animal Systematics** 

Molecular Approaches to Animal Systematics Kingdoms of Life

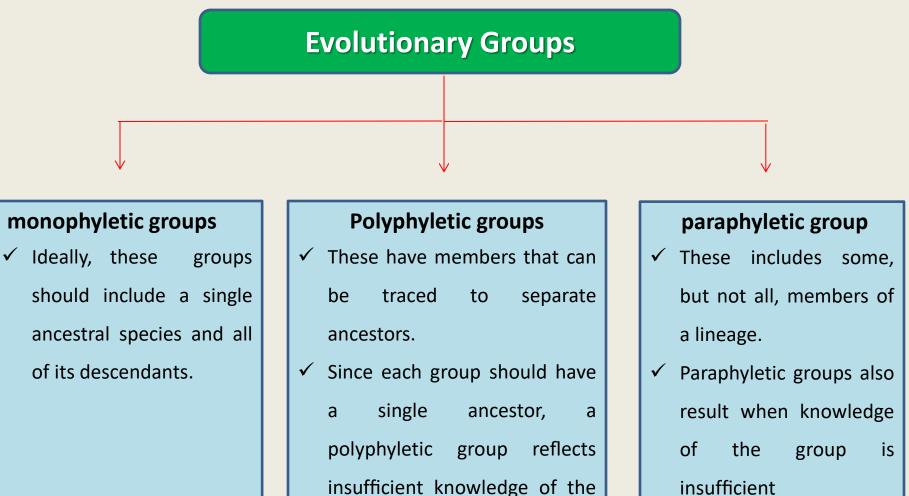
**Evolutionary Relationships and Tree Diagrams** 

**Patterns of Organization** 

**Other Patterns of Organization** 

# 1) Animal Systematics

The goal of animal systematics is to arrange animals into groups that reflect evolutionary relationships.



group.

insufficient

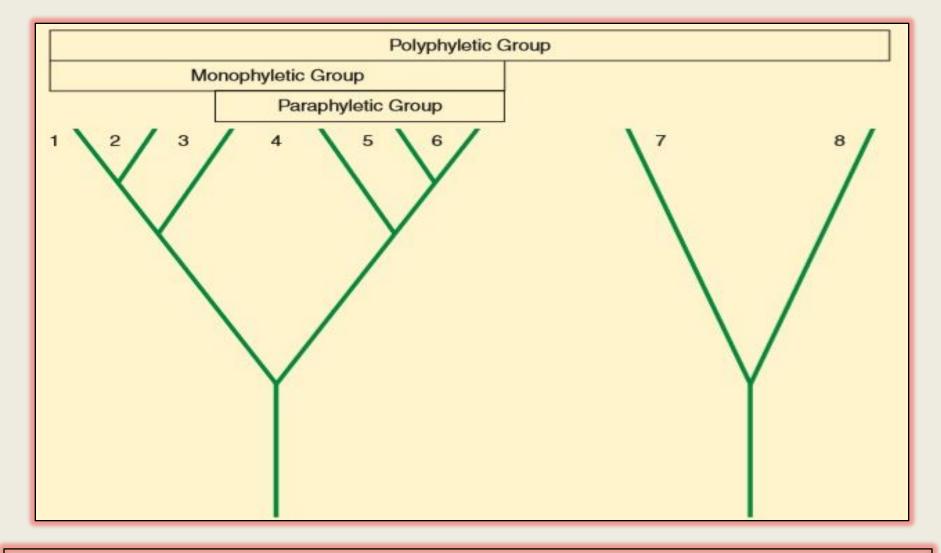


Fig: Evolutionary Groups. An assemblage of species 1–8 is a polyphyletic group because species 1–6 have a different ancestor than species 7 and 8. An assemblage of species 3–6 is a paraphyletic group because species 1 and 2 share the same ancestor as 3–6, but they have been left out of the group. An assemblage of species 1–6 is a monophyletic group because it includes all of the descendants of a single ancestor.

- ✓ As in any human endeavor, disagreements have arisen in animal systematics.
- ✓ These disagreements revolve around methods of investigation and whether

or not data may be used in describing distant evolutionary relationships.

- □ Three contemporary schools of systematics exist:
- 1) Evolutionary systematics
- 2) Numerical taxonomy
- 3) Phylogenetic systematics (cladistics).

## 1) Evolutionary systematics

- $\checkmark$  the oldest of the three approaches.
- ✓ It is sometimes called the "traditional approach," although it has certainly changed since

the beginnings of animal systematics.

✓ Evolutionary systematics often portray the results of their work on phylogenetic trees,

where organisms are grouped according to their evolutionary relationships.

□ Two kinds of similarities between organisms are recognized:

## i) homologies

### ii) analogies

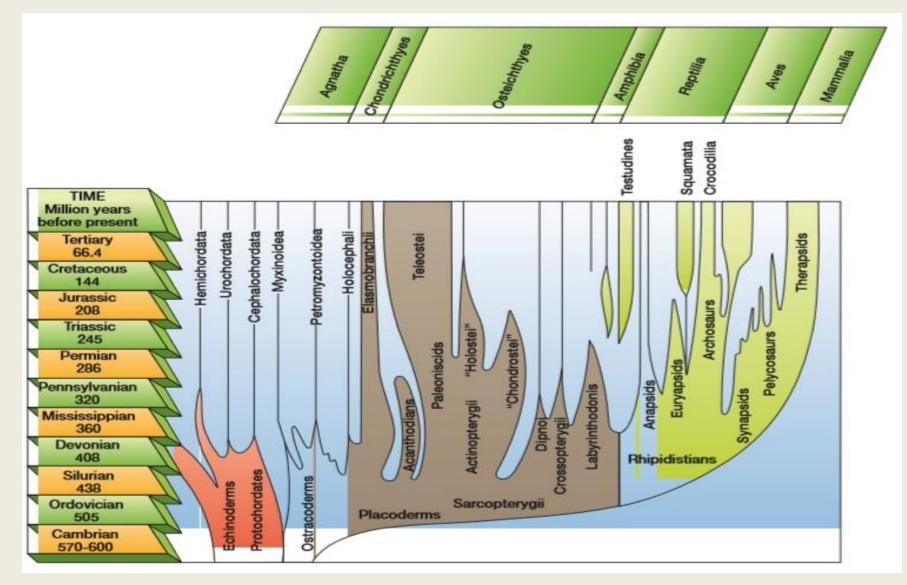


Fig: Phylogenetic Tree Showing Vertebrate Phylogeny. A phylogenetic tree derived from evolutionary systematics depicts the degree of divergence since branching from a common ancestor, which is indicated by the time periods on the vertical axis. The width of the branches indicates the number of recognized genera for a given time period. Note that this diagram shows the birds (Aves) as being closely related to the reptiles (Reptilia), and both groups as having class-level status.

#### kinds of similarities between organisms

## Homologies

Homologies are

resemblances that result

from common ancestry

- ✓ useful in classifying animals
- An example is the similarity in the arrangement of bones in the wing of a bird and the arm of a human

## Analogies

- Analogies are resemblances that result from organisms adapting under similar evolutionary pressures.
- ✓ The latter process is sometimes called convergent evolution.
- Analogies do not reflect common ancestry and are not used in animal taxonomy.
- The similarity between the wings

of birds and insects is an analogy.

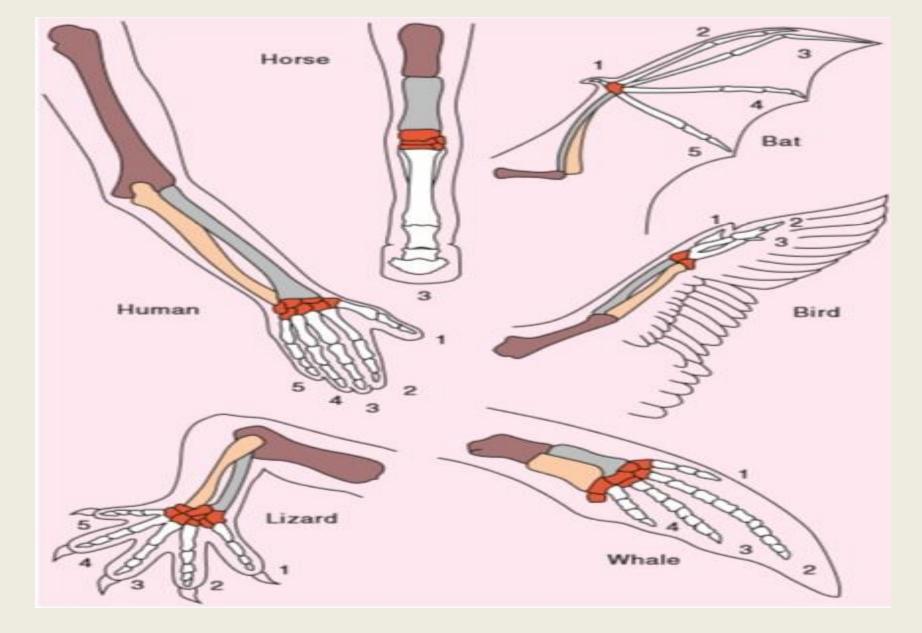


Fig: The Concept of Homology. The forelimbs of vertebrates evolved from an ancestral pattern. Even vertebrates as dissimilar as whales and bats have the same basic arrangement of bones. The digits (fingers) are numbered 1 (thumb) to 5 (little finger). Color coding indicates homologous bones.

## 2) Numerical taxonomy

- ✓ Numerical taxonomy emerged during the 1950s and 1960s
- ✓ Least popular of the three taxonomic schools
- ✓ It represents the opposite end of the spectrum from evolutionary systematics.
- ✓ Its founders believed that the criteria for grouping taxa had become too arbitrary and vague.
- ✓ Mathematical models and computer-aided techniques used by numerical taxonomists to group samples of organisms according to overall similarity.
- ✓ They do not attempt to distinguish between homologies.

### There are two main differences between the evolutionary and numerical

### taxonomy. These are:

(a) Numerical taxonomists do not distinguish between homologies and analogies. Numerical taxonomists admit that analogies exist. But they believe that telling one from the other is sometimes impossible. Therefore, the numerous homologies used in data analysis dominate the analogies.

(b) The numerical taxonomists limit discussion of evolutionary relationships to closely related . It is a major difference between evolutionary systematics and numerical

taxonomy.

## 3) Phylogenetic systematics (cladistics)

- ✓ a third approach to animal systematics.
- ✓ Goal : the generation of hypotheses of genealogical relationships among monophyletic groups of organisms
- ✓ More open to ...analysis and testing, and thus more scientific
- cladists believe that homologies of recent origin are most useful in phylogenetic studies.

#### □ Ancestral characters

 Attributes of species that are old and have been retained from common ancestors

## **Symplesiomorphies**

- "sym" together, "plesio" near, "morphe" form
- These characters are homologies that may indicate a shared ancestry, but they are useless in describing relationships within the group.

### Synapomorphies

- "syn" together, "apo" away, "morphe" form
- Characters that have arisen since common ancestry with the outgroup are called derived characters or synapomorphies

### Outgroup

 Used to help decide whether a character is ancestral or has arisen within the study group

## Clade

"klados" branch

### Cladogram

- Depict a sequence in the origin of derived characters
- Interpreted as family tree showing a hypothesis regarding monophyletic lineages

### **Hierarchical nesting**

 Groups of related organisms share suites of similar characteristics and the number of shared traits increases with relatedness

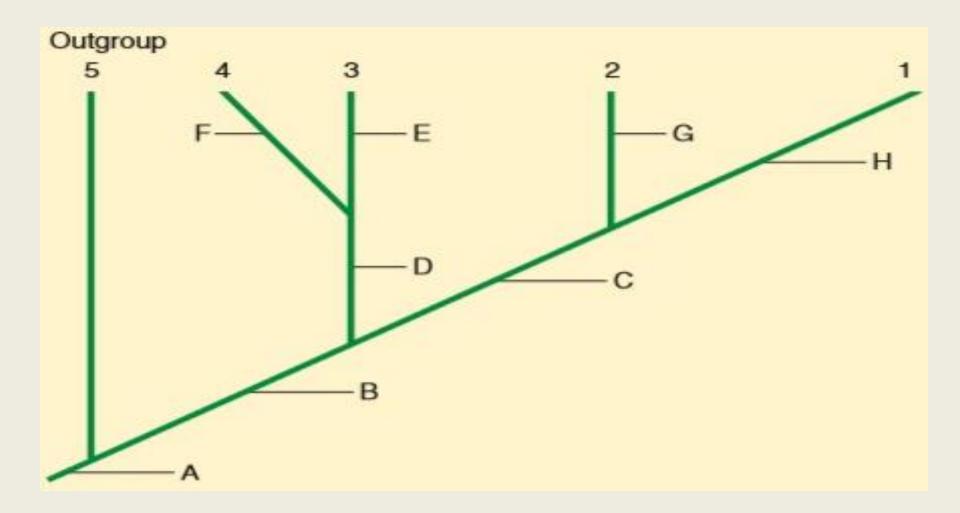


Fig: Interpreting Cladograms. This hypothetical cladogram shows five taxa (1-5) and the characters (A-H) used in deriving the taxonomic relationships. Character A is symplesiomorphic for the entire group. Taxon 5 is the outgroup because it shares only that ancestral character with taxa 1-4. All other characters are more recently derived. What single character is a synapomorphy for taxa 1 and 2, separating them from all other taxa?

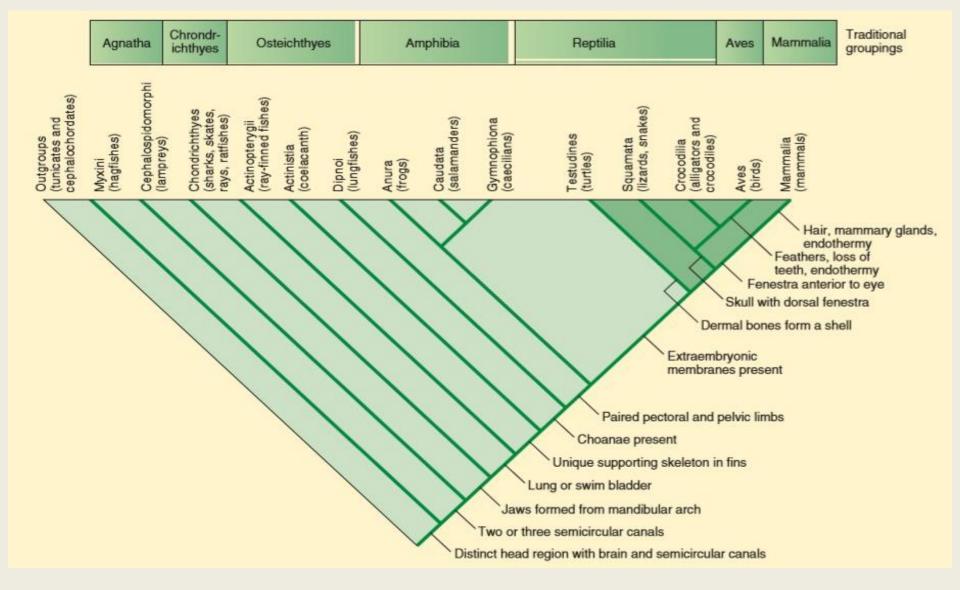


Fig: Cladogram Showing Vertebrate Phylogeny. A cladogram is constructed by identifying points at which two groups diverged. Animals that share a branching point are included in the same taxon. Notice that timescales are not given or implied. The relative abundance of taxa is also not shown. Notice that this diagram shows the birds and crocodilians sharing a common branch, and that these two groups are more closely related to each other than either is to any other group of animals.

 $\checkmark$  a synapomorphy at one level of taxonomy may be a symplesiomorphy at a

different level of taxonomy.

✓ Extraembryonic membranes is a synapomorphic character within the vertebrates

that distinguishes the reptile/bird/mammal clade. It is symplesiomorphic for

reptiles, birds, and mammals because it is ancestral for the clade and cannot be

used to distinguish among members of these three groups.

### **Cladistic analysis has shown:**

 $\checkmark$  birds are more closely tied by common ancestry to the alligators and crocodiles than

to any other group.

- ✓ According to the cladistic interpretation, birds and crocodiles should be assigned to a
  - group that reflects this close common ancestry
- ✓ Birds would become a subgroup within a larger group that included both birds and reptiles
- ✓ Cladists support their position by pointing out that the designation of "key characters" involves value judgments that cannot be tested.

## MOLECULAR APPROACHES TO ANIMAL SYSTEMATICS

## **MOLECULAR APPROACHES TO ANIMAL SYSTEMATICS**

Molecular approach includes study of molecules like protein, DNA, RNA of different species.

- **The sequence of nitrogenous bases in DNA or RNA**
- the sequences of the amino acids in proteins or the sequence of nitrogenous bases in DNA or RNA of different animals is compared.
- Genes and proteins of related animals are more similar than genes and proteins from distantly related animals.
- It gives a relatively constant mutation rate. The constant mutation rate of organisms is called molecular clock.
- The taxonomists can also estimate the time passed since divergence from a common ancestor.

### Mitochondrial DNA

Mitochondrial DNA is useful in taxonomic studies because:

(a) Mitochondria have their own genetic systems.

(b)They are inherited through cytoplasm. Mitochondria are transmitted from parent to offspring through the egg cytoplasm. Therefore it can be used to trace maternal lineages.

(c) The mitochondrial DNA involves relatively small quantities of DNA. It changes at a relatively constant rate.

## **MOLECULAR APPROACHES TO ANIMAL SYSTEMATICS**

#### Molecular and traditional techniques:

Molecular techniques have greatly helped the taxonomists. But these techniques will not

replace traditional taxonomic methods.

#### Molecular clocks run at different rates. It depends on whether one is looking at:

- (i) The sequence of amino acids in proteins.
- (ii) The sequence of bases in DNA from organelles like mitochondria
- (iii) The sequence of bases in nuclear DNA
- (iv) Data from different evolutionary lineages.

Molecular and traditional methods of investigation will always be used. These two

complement each other in taxonomic studies.

## **KINGDOMS OF LIFE**

In 1969, Robert H. Whittaker described a five-kingdom classification system based on cellular organization and mode of nutrition.

### Monera

 $\checkmark$  bacteria and the cyanobacteria.

### **Kingdom Protista**

- $\checkmark$  eukaryotic and consist of single cells or colonies of cells.
- ✓ Includes Amoeba, Paramecium etc.

### kingdom Plantae

✓ eukaryotic, multicellular, and photosynthetic.

✓ walled cells and are usually nonmotile.

## kingdom Fungi

- ✓ eukaryotic and multicellular.
- ✓ walled cells and are usually nonmotile.
- ✓ digest organic matter extracellularly and absorb the breakdown products.

## kingdom Animalia

- ✓ eukaryotic and multicellular,
- $\checkmark$  feed by ingesting other organisms or parts of other organisms.
- $\checkmark$  Their cells lack walls and they are usually motile.

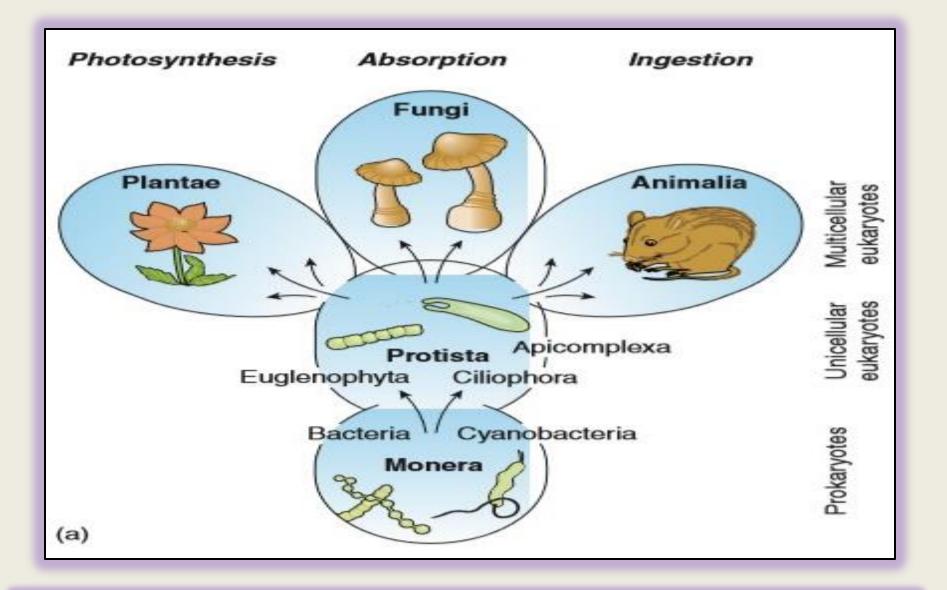


Fig: Classification of Organisms. (a) In 1969, Robert H. Whittaker described a fivekingdom classification system based on cellular organization and mode of nutrition. In recent years, new information has challenged the five kingdom classification system.

- ✓ For the first two billion years of life on the earth, the only living forms were prokaryotic microbes.
- ✓ Fossil evidence from this early period is scanty
- ✓ molecular studies of variations in base sequences of ribosomal RNA
  from more than two thousand organisms are providing evidence of

relationships rooted within this two billion-year period.

## **Ribosomal RNA**

- $\checkmark$  excellent for studying the evolution of early life on earth.
- ✓ It is an ancient molecule, and it is present and retains its function in virtually all organisms.
- ✓ ribosomal RNA changes very slowly
- ✓ This slowness of change, called evolutionary conservation, indicates that the protein-producing machinery of a cell can tolerate little change and still retain its vital function.
- $\checkmark$  closely related organisms are likely to have similar ribosomal RNAs.
- ✓ Distantly related organisms have ribosomal RNAs that are less similar, but the differences are small enough that the relationships to some ancestral molecule are still apparent.

#### Studies of ribosomal RNA have led systematists to the conclusions that:

✓ All life shares a common ancestor and that there are three major evolutionary lineages.

#### **The Archaea**

- live in extreme environments
- inhabit anaerobic environments.
- The Archaea are the most primitive life-forms known.

Ancient archaeans gave rise to two other domains of organisms:

#### **Eubacteria**

✓ true bacteria and are prokaryotic microorganisms.

#### **Eukarya**

- ✓ include all eukaryotic organisms.
- ✓ Eukarya diverged more recently than the Eubacteria from the Archaea.

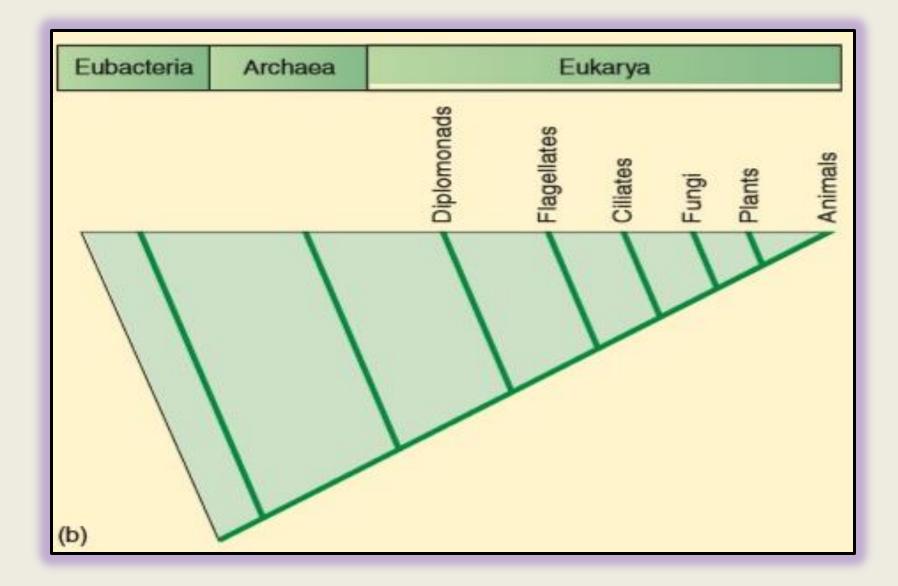


Fig: Classification of Organisms. (b) Recent studies of ribosomal RNA indicate that a grouping into three domains more accurately portrays early evolutionary relationships.