

BIO 221

Invertebrate Zoology I

Spring 2010

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Lecture 4

THE GOAL:

Identification of related taxa

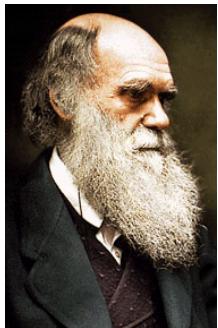
Phylogenetic Groups

Why?

**As zoologists we seek
to understand animal
relationships.**

We can accomplish this goal by reconstructing the path of animal evolution

Darwin on Classification



“Our classifications will come to be, as far as they can be so made, genealogies”
(Darwin 1859).

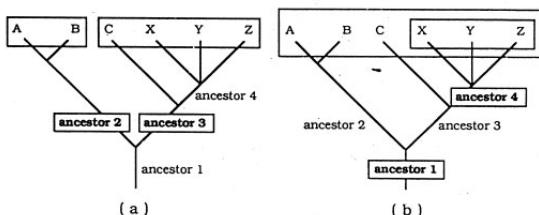
The most consistent method for identifying related taxa is to identify *synapomorphies*:

***syn* = shared**

***apo* = away from the stem**

***morph* = form**

Monophyletic Groups



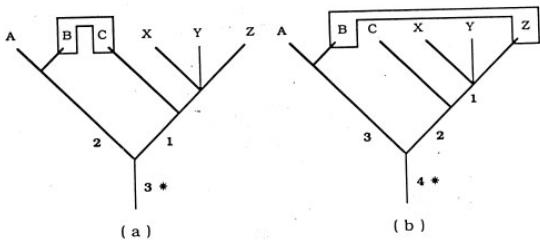
Definitions

Groups that do include all the descendants of the most recent common ancestor are said to be **monophyletic**.

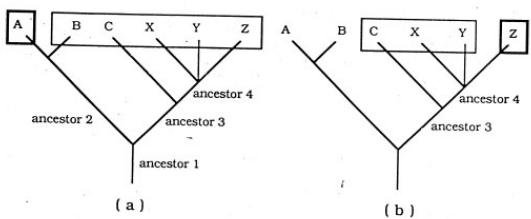
A **paraphyletic group** is a monophyletic group from which one or more of the clades is excluded to form a separate group (as in reptiles and birds).

A group that does not contain the most recent common ancestor of its members is said to be **polyphyletic** (Greek polys = many).

Paraphyletic Groups



Paraphyletic and Polyphyletic Groups



Guidepost #1:

Unless contrary evidence exists, assume that similarity represents homology.

What is an Homology?

Homology =
Tissues of
Common
Embryonic
Origin

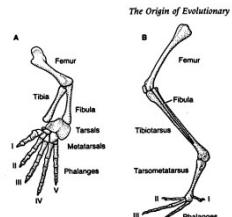


FIGURE 9
Functional reduction of parts. (A) The skeleton of the hind limb of a reptile and (B) that of a bird. In the course of evolution, the limb has become fused with the tibia and others with the metatarsals; the number of digits and phalanges is reduced, and the fibula is reduced in size. (A after Romer 1956)

Why?

***Because Evolution
appears to be a
conservative process***

1. Identical, complex structures rarely arise independently.
2. Heritable characters usually persist within lineages.

GUIDEPOSTS IN CONSTRUCTING PHYLOGENIES

- a. Unless contrary evidence exists, assume that similarities represent homologies
- b. Evidence of common ancestry is provided only by the presence of shared, derived characters (synapomorphies).

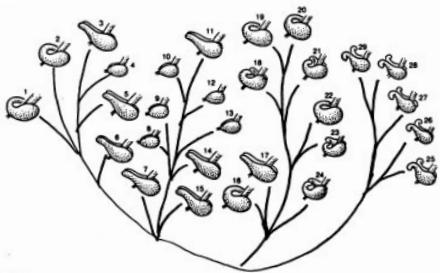
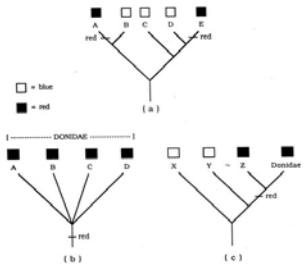


FIGURE 10
Independent origins of forms of the ejaculatory bulb in species of the *Drosophila repleta* group. The phylogeny of these species has been inferred from chromosomal evidence. Note the identical bulb shape in, for example, species 3, 5, 14, 17; 4, 10; and 1, 16, 19. (Redrawn from Throckmorton 1965)

Guidepost #2:

Evidence of common ancestry is provided only by the presence of shared, derived characters (synapomorphies)

Why?

Because convergent or parallel characters arise independently *within* lineages *after* taxa diverge.

1. Therefore, these characters only provide information about relationships *within the taxon in question*.
2. They provide no information about relationships *among taxa*.



A saclike with 4 leaflike sucking grooves and a protractile muscular mass with 4 suckers. (After Shipley and Hornell).



A scutellum in which the leaflike structures are divided up by ridges into multiple little sucking grooves.



Scutellum of the beef tapeworm, *Taenia saginata* (or *Taeniarynchus saginatus*), order Cyclophyllidae. Hu-



Pork tapeworm, *Taenia solium*. In this and other members of the family Taeniidae, the developing scolex is inverted; most of the medically important tapeworms are taeniids. (Modified after various sources)

GUIDEPOSTS IN CONSTRUCTING PHYLOGENIES

d. Identification of outgroups and character polarity

- homologous characters found among members of an in-group as well as in an outgroup are considered ancestral
- homologous characters found only among members of an in-group are considered derived.

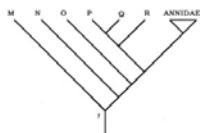
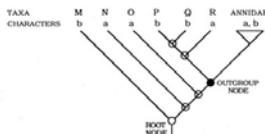


Fig. 2.20. Relationships of the Annidae clade to its closest relatives.



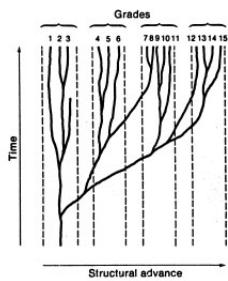


FIGURE 2
Grades and clades. A group of species (e.g., 1, 2, 3) with a recent common ancestor forms a clade; a group with the same level of structural organization (e.g., 7–11) forms a grade. Members of a grade may belong to different grades because of different evolutionary rates. (Modified from Simpson 1961)

GUIDEPOSTS IN CONSTRUCTING PHYLOGENIES

c. When information from two transformation series (characters) generate different cladograms, the most parsimonious tree (the one with the fewest character reversals) is the one accepted as true.

Table 2.2 Data matrix for determining the relationships among taxa R, S, and T.

Taxon	Character Transformation Series						
	1	2	3	4	5	6	7
X (outgroup)	0	0	0	0	0	0	0
R	1	1	0	0	1	1	1
S	1	1	1	1	1	1	1
T	1	1	1	1	0	0	0

Notes: The matrix is composed of seven character transformation series and four taxa, the outgroup X, and the ingroup R + S + T. Synapomorphies are in bold type.

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X (outgroup)	0	0	0	0	0	0	0
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T	1	1	1	1	0	0	0

Notes: The matrix is composed of seven character transformation series and four taxa, the outgroup X, and the ingroup R + S + T. Synapomorphies are in bold type.

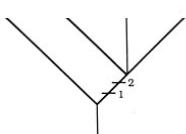


Fig. 2.14. Tree for the RSTidae, based on characters 1 and 2. This tree was produced by applying the grouping rule to character transformation series 1 and 2, then combining this information via the inclusion/exclusion rule.

Table 2.2 Data matrix for determining the relationships among taxa R, S, and T.

Taxon	Character Transformation Series						
	1	2	3	4	5	6	7
X (outgroup)	0	0	0	0	0	0	0
R	1	1	0	0	1	1	1
S	1	1	1	1	1	1	1
T	1	1	1	1	0	0	0

Notes: The matrix is composed of seven character transformation series and four taxa, the outgroup X, and the ingroup R + S + T. Synapomorphies are in bold type.

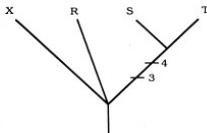


Fig. 2.15. Tree for the RSTidae, based on characters 3 and 4. This tree was produced by applying the grouping rule to character transformation series 3 and 4, then combining this information via the inclusion/exclusion rule.

Table 2.2 Data matrix for determining the relationships among taxa R, S, and T.

Taxon	Character Transformation Series						
	1	2	3	4	5	6	7
X (outgroup)	0	0	0	0	0	0	0
R	1	1	0	0	1	1	1
S	1	1	1	1	1	1	1
T	1	1	1	1	0	0	0

Notes: The matrix is composed of seven character transformation series and four taxa, the outgroup X, and the ingroup R + S + T. Synapomorphies are in bold type.

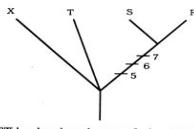


Fig. 2.16. Tree for the RSTidae, based on characters 5, 6, and 7. This tree was produced by applying the grouping rule to character transformation series 5, 6, and 7, then combining this information via the inclusion/exclusion rule.

Table 2.2 Data matrix for determining the relationships among taxa R, S, and T.

Taxon	Character Transformation Series						
	1	2	3	4	5	6	7
X (outgroup)	0	0	0	0	0	0	0
R	1	1	0	0	1	1	1
S	1	1	1	1	1	1	1
T	1	1	1	1	0	0	0

Notes: The matrix is composed of seven character transformation series and four taxa, the outgroup X, and the ingroup R + S + T. Synapomorphies are in bold type.

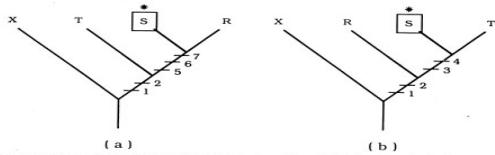


Fig. 2.17. Two logically incompatible trees produced from the information in the data matrix (Table 2.2). Taxon S (marked with an asterisk) is the problem: characters 5, 6, and 7 place it with R, while characters 3 and 4 group it with T. Both trees cluster RST together based on possession of the apomorphic form of characters 1 and 2.

The Principle of Parsimony

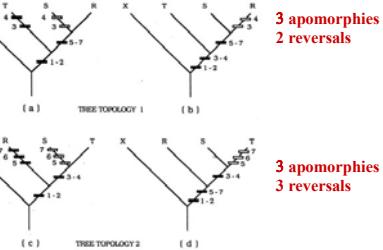


Occam's Razor: That which can be done in fewer steps is done in vain with more.

GUIDEPOSTS IN CONSTRUCTING PHYLOGENIES

c. When information from two transformation series (characters) generates different cladograms, the most parsimonious tree (the one with the fewest character reversals) is the one accepted as true.

5 apomorphies
2 convergences



5 apomorphies
3 convergences

3 apomorphies
2 reversals

■ = apomorphic character state ■ = convergence/parallelism
□ = reversal to ancestral (plesiomorph) condition

3

TYPES OF DATA USED FOR CLASSIFYING ANIMAL TAXA:

MORPHOLOGY

Anatomy
Behavior
Biochemistry
Molecules

PHYSIOLOGY

DEVELOPMENT (EMBRYOLOGY)

EXTANT/FOSSIL SPECIES

Those Dang Terms...

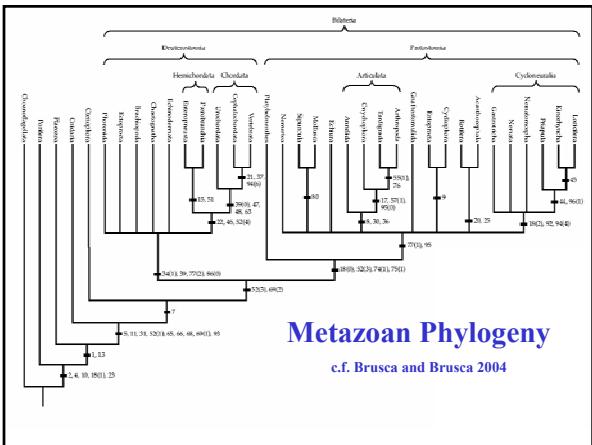
apomorphy:
derived characters
“away from the stem”

plesiomorphy:
ancestral characters
“close to the stem”

synapomorphy:
shared, derived characters

symplesiomorphy:
shared, ancestral characters

autoapomorphy:
unique, derived characters



Lower Metazoan Clades:

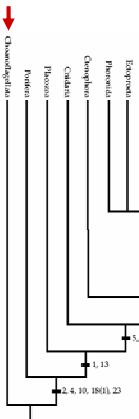
Choanoflagellata

Porifera

Placozoa

Cnidaria

Ctenophora



Lower Metazoan Clades:

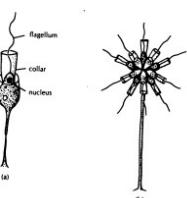
Choanoflagellata

Porifera

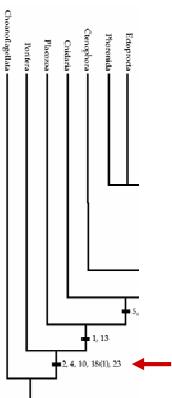
Placozoa

Cnidaria

Ctenophora



Choanoflagellates



Lower Metazoan Clades:

Choanoflagellata

Porifera

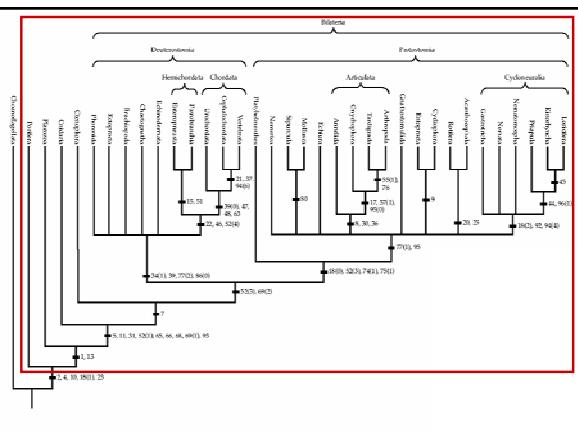
Placozoa

Cnidaria

Ctenophora

Porifera and Metazoa

- a. Are distinct from choanoflagellates by:
 - 2. Multicellularity
 - 4. Epithelial tight junctions
 - 10. Collagen fibers in body
 - 18(1). Development w/ "radial" cleavage.
 - 23. Spermatozoa



Lower Metazoan Clades:

Choanoflagellata

Porifera

Placozoa

Cnidaria

Ctenophora

Porifera

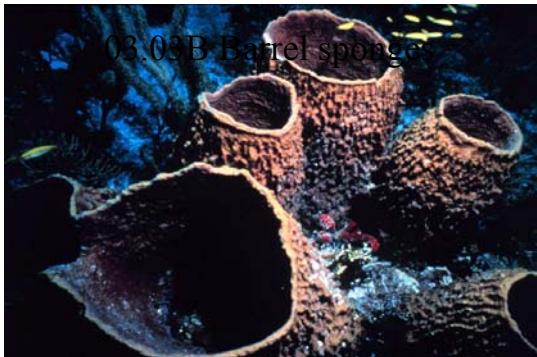
a. Are distinct from the Placozoa by:

Have collar cells (absent in Metazoa)

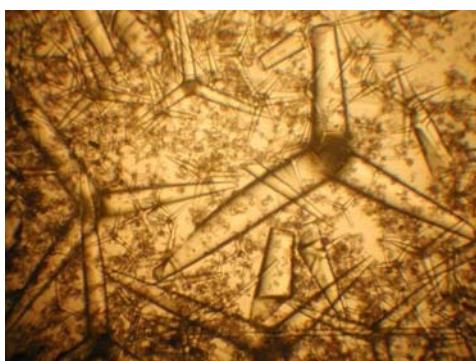
Lack striated ciliary rootlets (present in Metazoa)

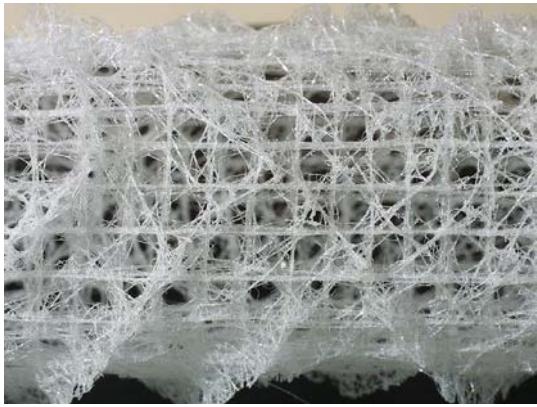
b. Also have the following apomorphies

1. Aquiferous system
2. Layered construction
3. Spicules



Sponge Spicules



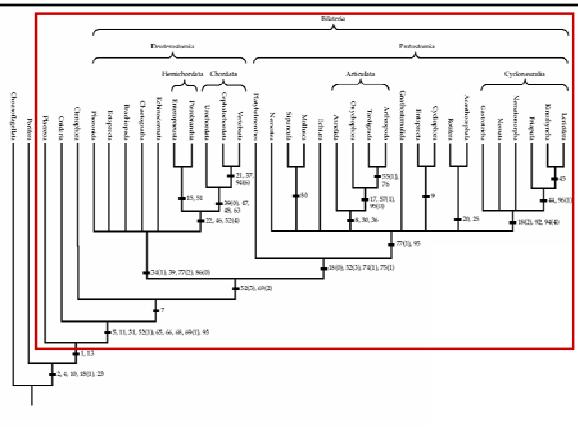


Placozoa and other Metazoa

This clade includes all animals
(multicellular heterotrophs)

a. Synapomorphies:

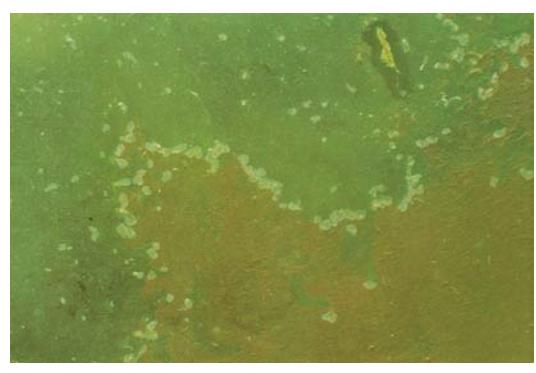
- 1. Absence of collar cells
- 13. Striated ciliary rootlets

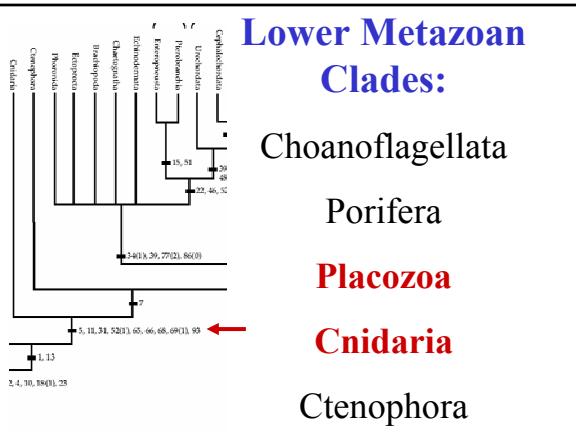


Tricoplax adhaerens



Tricoplax adhaerens





Cnidaria and Other Metazoa

Includes the major animal phyla –

- b. Synapomorphies
 - 5. – Gap junctions between cells
 - 11. – Organized gonads
 - 31 – Ectoderm and endoderm (gastrulation)
 - 52(1) – Nervous system with at least a nerve net.
