

# Biogeography. Lecture 13

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March 9, 2016



# Outline

## Taxonomy

- Basic principles

- The structure of diversity



# Taxonomy

## Basic principles

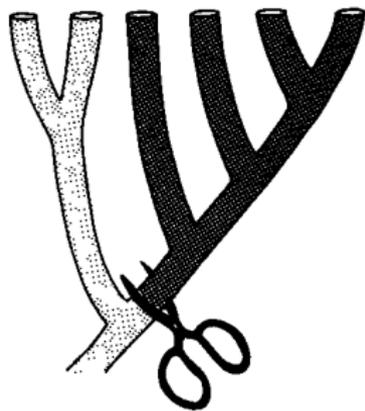


# How to describe the natural order: principles of classification

- ▶ Traditional method (mind model), phenetic (multivariate statistics), and cladistic (phylogenetic, now mostly molecular—objective but based on few samples)
- ▶ Results: ranked classifications, cloud ordinations, trees (dendrograms)
- ▶ Conversion from clouds to classification: hiatus
- ▶ Conversion from tree to classification raises the problem of monophyletic, paraphyletic and polyphyletic groups
- ▶ Time estimation from fossils and molecules might replace ranks



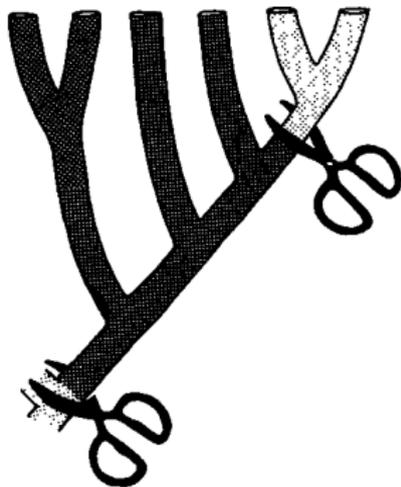
# Monophyly, paraphyly, polyphyly



**Monophyletic**

one and  
only one cut

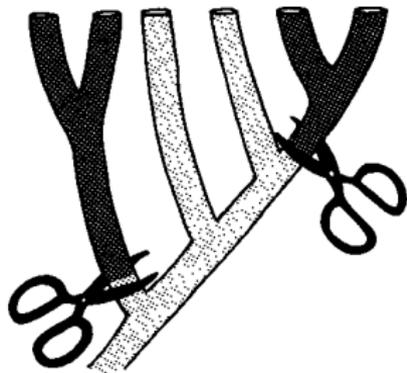
One branch



**Paraphyletic**

one cut below the  
group and one or more  
cuts higher up

A piece of a branch



**Polyphyletic**

more than one cut  
below the group

More than one  
piece of a branch

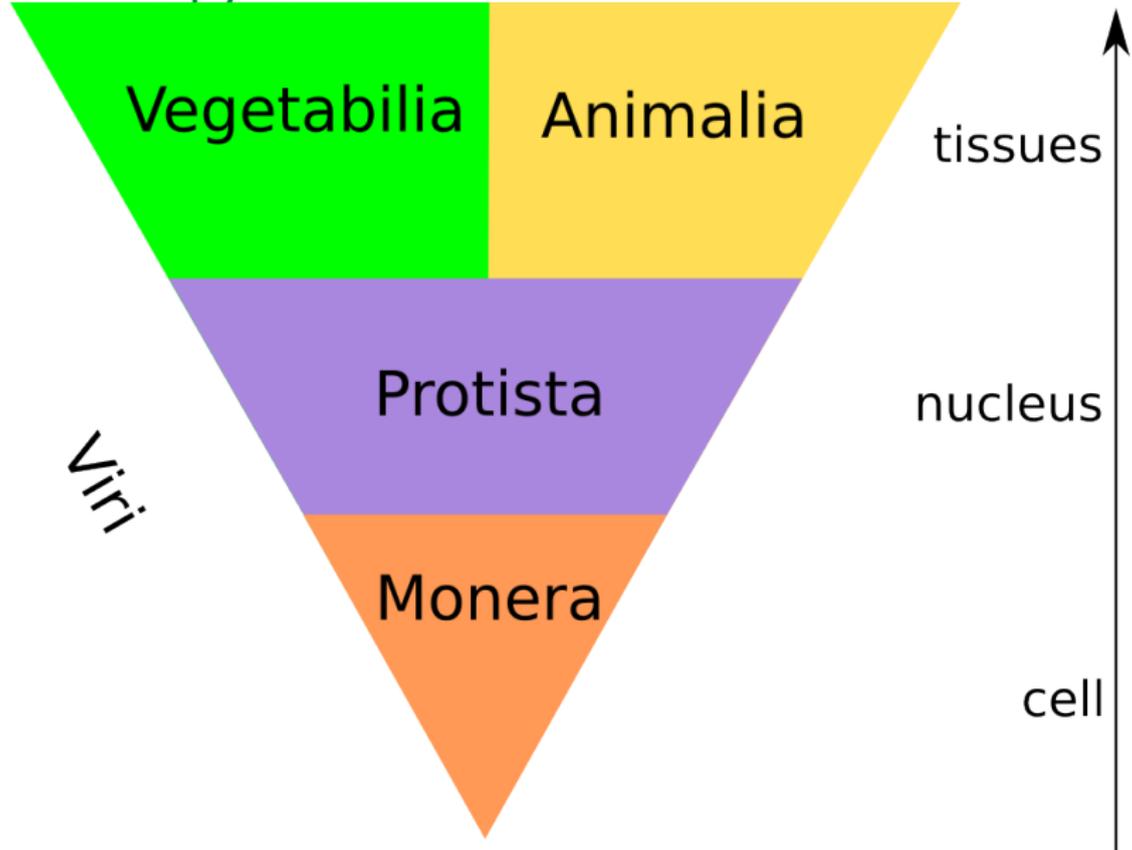


# Taxonomy

## The structure of diversity



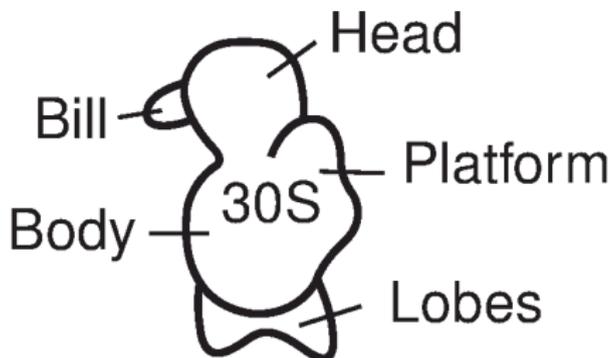
# Taxonomic pyramid



Kingdoms and domains. Kingdoms are traditional (pyramid), domains are molecular cladistic. We usually hear about three domains but recent publications introduced two domains concept.



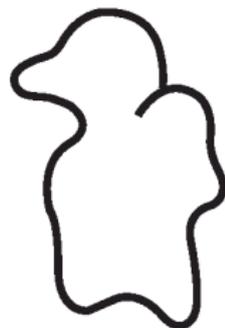
## Structure of ribosomes of three domains



*Bacteria*



*Archaea*



*Eukarya*



# Williams et al., 2013

## REVIEW

doi:10.1038/nature12779

### An archaeal origin of eukaryotes supports only two primary domains of life

Tom A. Williams<sup>1</sup>, Peter G. Foster<sup>2</sup>, Cymon J. Cox<sup>3</sup> & T. Martin Embley<sup>1</sup>

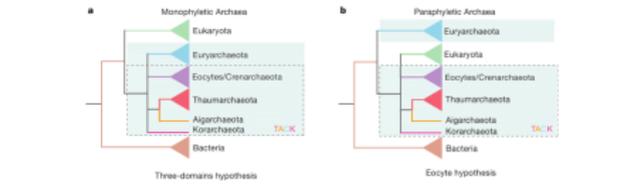
The discovery of the Archaea and the proposal of the three-domains 'universal' tree, based on ribosomal RNA and core genes mainly involved in protein translation, catalysed new ideas for cellular evolution and eukaryotic origins. However, accumulating evidence suggests that the three-domains tree may be incorrect: evolutionary trees made using newer methods place eukaryotic core genes within the Archaea, supporting hypotheses in which an archaeon participated in eukaryotic origins by founding the host lineage for the mitochondrial endosymbiont. These results provide support for only two primary domains of life—Archaea and Bacteria—because eukaryotes arose through partnership between them.

Since their discovery by Carl Woese and his co-workers in 1977, the Archaea have figured prominently in hypotheses for eukaryotic origins<sup>1,2</sup>. Although similar to Bacteria in terms of cell structure, molecular phylogenies for ribosomal RNA and a small core of genes, that mainly have essential roles in protein translation<sup>3</sup>, suggested that the Archaea were more closely related to the eukaryotic nuclear lineage; that is, to the host cell that acquired the mitochondrion<sup>4</sup>. The idea that Archaea and eukaryotes are more closely related to each other than either is to Bacteria depends on analyses suggesting that the root of the tree should be placed on the bacterial stem, or within the Bacteria<sup>5–11</sup>, implying that the prokaryotes—cells that lack a nucleus—are a paraphyletic group<sup>12</sup>. The main question now debated is whether core components of the eukaryotic nuclear lineage descended from a common ancestor shared with Archaea, as in the three-domains tree<sup>13</sup> (Fig. 1), which is also often called the 'universal tree' or 'tree of life'<sup>14–17</sup>, or from within the Archaea, as proposed by archaeal-host hypotheses for eukaryotic origins<sup>18</sup>. The archaeal-host scenario with the greatest phylogenetic support is the eocyte hypothesis<sup>19</sup>, which proposes a sister-group relationship between eukaryotes and the

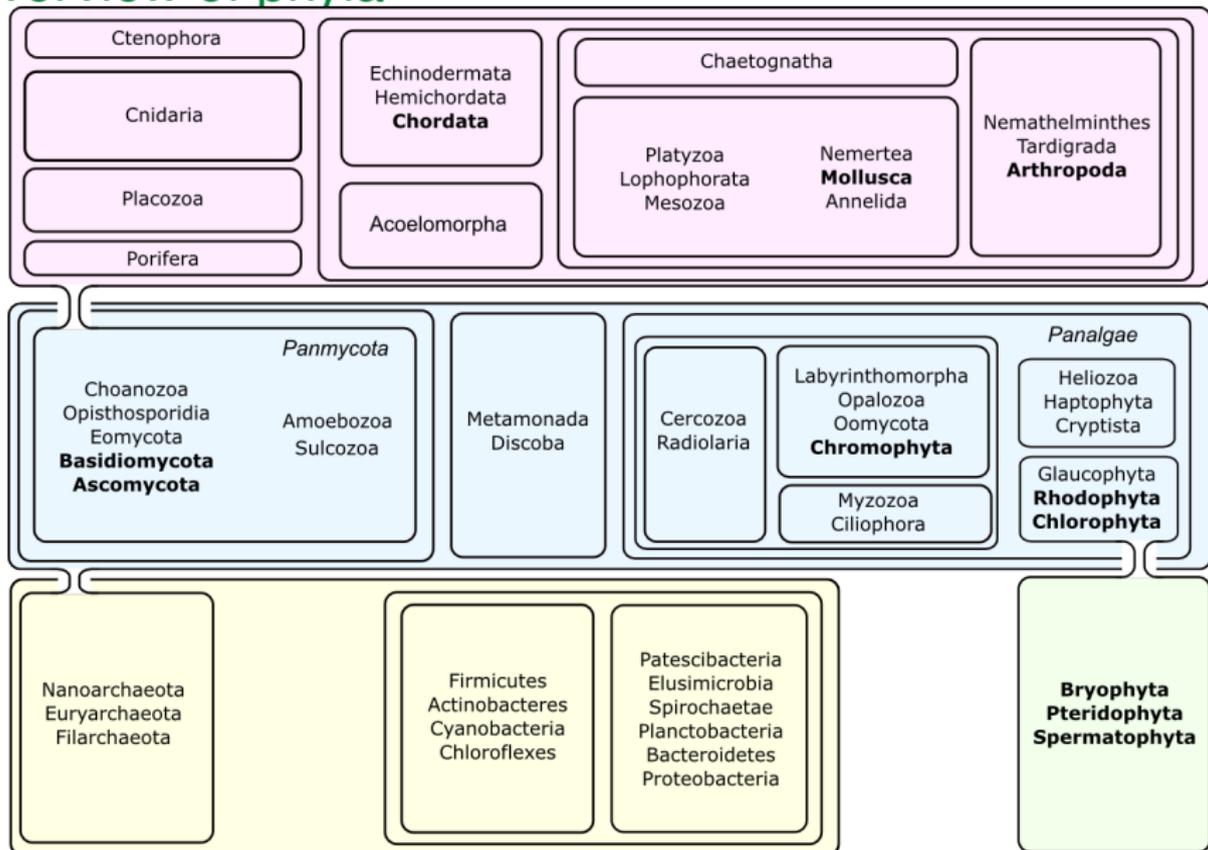
eocytes (or Crenarchaeota<sup>20</sup>), one of the major archaeal divisions (Fig. 1). However, the three-domains-eocyte debate remains controversial because different phylogenetic methods have delivered different results, often from the same data<sup>19</sup>. This disagreement is due, at least in part, to the difficulties associated with resolving ancient divergences in phylogenetic trees.

#### Challenges of reconstructing ancient relationships

A major issue in reconstructing ancient relationships is the strength and quality of historical signal remaining after the millions of years since the divergence of Archaea and eukaryotes. The earliest fossils identified as eukaryotic appeared by about 1.8 billion years ago<sup>21</sup>, over this enormous span of time, the accumulation of multiple substitutions in DNA and protein sequences might have erased any signal that would allow the relationship between archaeal and eukaryotic core genes to be established<sup>22</sup>. However, more recent simulations and empirical studies suggest that there are reasons to be cautiously optimistic that this is not the case: functional constraints vary across real DNA and protein sequences so that sites evolve at different rates<sup>22–25</sup>. Fast-evolving sites are indeed



# Overview of phyla



# Summary

- ▶ There are seven main taxonomic ranks



# For Further Reading



**A. Shipunov.**

*Biogeography* [Electronic resource].

2014—onwards.

Mode of access:

[http://ashipunov.info/shipunov/school/biol\\_330](http://ashipunov.info/shipunov/school/biol_330)



**Biological classification.**

[http:](http://en.wikipedia.org/wiki/Biological_classification)

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