

Biogeography. Lecture 14

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Outline

Taxonomy

Basic principles



Taxonomy

Basic principles



Intermediate ranks. Subspecies and cultivars. Shortcuts: “sp.”, “spp.”, “s. l.” (wide sense), “s. str.” (strict sense), “i. s.” (position unknown)



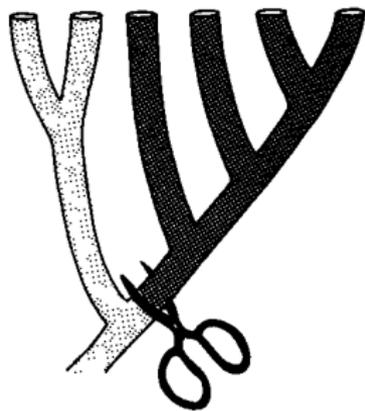
α -taxonomy: species description and β -taxonomy: work with existing descriptions. How many species? 2,000,000 described; the feasible estimation is 4–5,000,000. There are also 20,000,000 names—most of them are synonyms and homonyms.



How to describe the natural order: principles of classification. Hiatus: distance between “clouds”. Traditional (model in mind), phenetic (multivariate statistics), and cladistic (phylogenetic) approaches. The last is now mostly molecular (objective but based on few samples). Dendrograms (trees). Monophyletic, paraphyletic and polyphyletic groups. Time estimation.



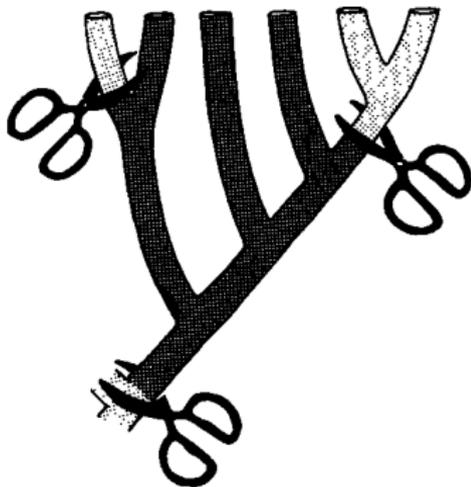
Monophyly, paraphyly, polyphyly



Monophyletic

one and
only one cut

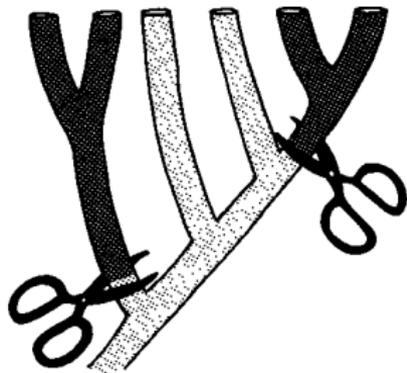
One branch



Paraphyletic

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

A piece of a branch



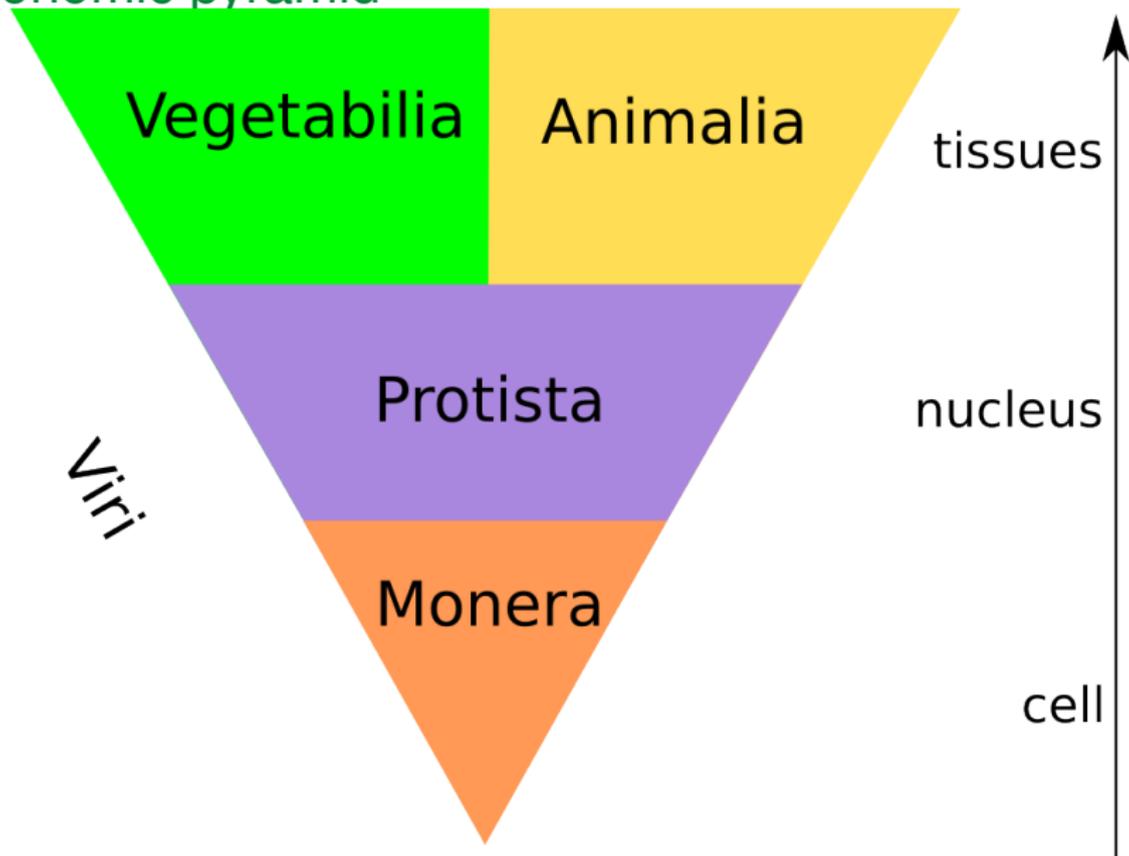
Polyphyletic

more than one cut
below the group

More than one
piece of a branch



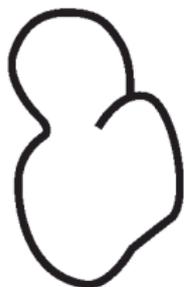
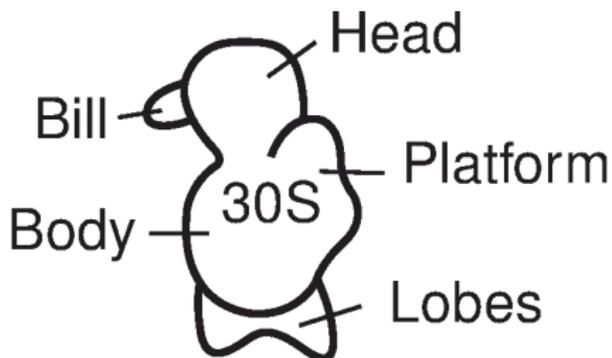
Taxonomic pyramid



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



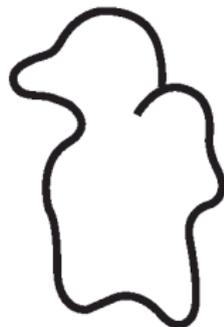
Structure of ribosomes of three domains



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. Williams¹, Peter G. Foster², Cymon J. Cox¹ & T. Martin Embley¹

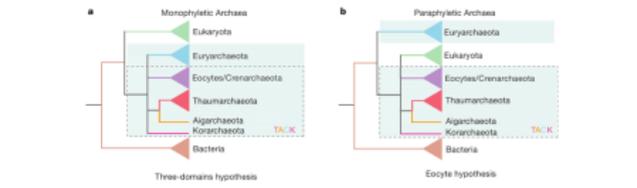
The discovery of the Archaea and the proposal of the three-domains 'universal' tree, based on ribosomal RNA and core genes mainly involved in protein translation, catalysed new ideas for cellular evolution and eukaryotic origins. However, accumulating evidence suggests that the three-domains tree may 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^{1,2}. 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 translation³, suggested that the Archaea were more closely related to the eukaryotic nuclear lineage; that is, to the host cell that acquired the mitochondrion⁴. 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^{5–11}, implying that the prokaryotes—cells that lack a nucleus—are a paraphyletic group¹². 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 tree¹³ (Fig. 1), which is also often called the 'universal tree' or 'tree of life'^{14–17}, or from within the Archaea, as proposed by archaeal-host hypotheses for eukaryotic origins¹⁸. The archaeal-host scenario with the greatest phylogenetic support is the eocyte hypothesis¹⁹, which proposes a sister-group relationship between eukaryotes and the

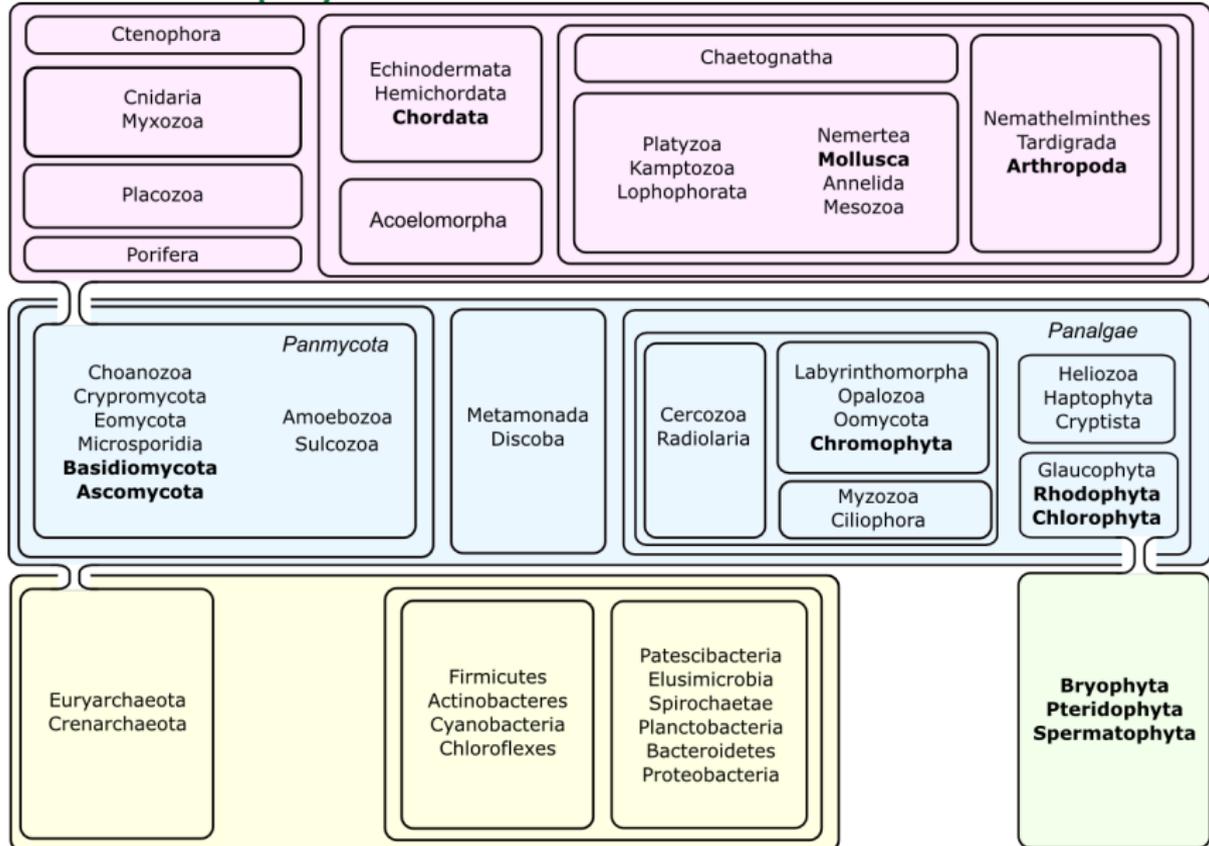
eocytes (or Crenarchaeota²⁰), one of the major archaeal divisions (Fig. 1). However, the three-domains-eocyte debate remains controversial because different phylogenetic methods have delivered different results, often from the same data¹⁹. This disagreement is due, at least in part, to the difficulties 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 ago²¹, 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 established²². 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^{22–25}. Fast-evolving sites are indeed



Overview of phyla



Summary

- ▶ There are seven main taxonomic ranks
- ▶ There are four kingdoms of living organisms



For Further Reading



A. Shipunov.

Biogeography [Electronic resource].

2014—onwards.

Mode of access:

http://ashipunov.info/shipunov/school/biol_330



Biological classification.

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

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

