

Molecular Phylogenetics

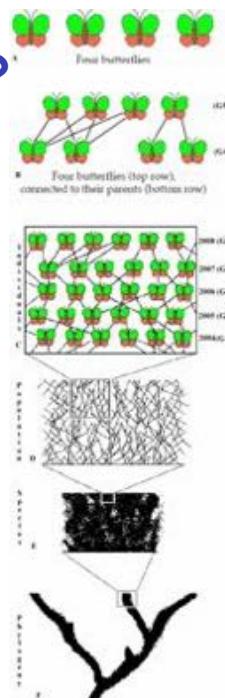
EEOB 563

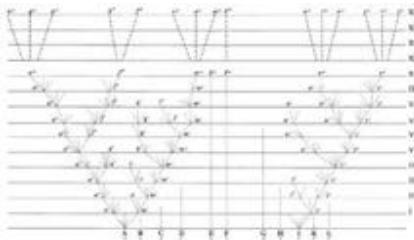
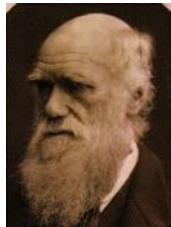
Phylogeny (from phylum – tribe, and genesis – origin)

- the term introduced by E. Haeckel in the second half of the XIX century and now has two somewhat different meanings.
- (1) Phylogeny in wide sense is a historical development of organisms
- (2) Phylogeny in narrow sense includes not all aspects of historic development, but only succession of branching of a genealogical (i.e. a phylogenetic) tree.
- Usually represented by a phylogenetic tree.

What is a phylogenetic tree?

- A tree is a mathematical structure which is used to model the actual evolutionary history of a group of sequences or organisms.
- The actual pattern of historical relationships is an evolutionary tree which we try to estimate



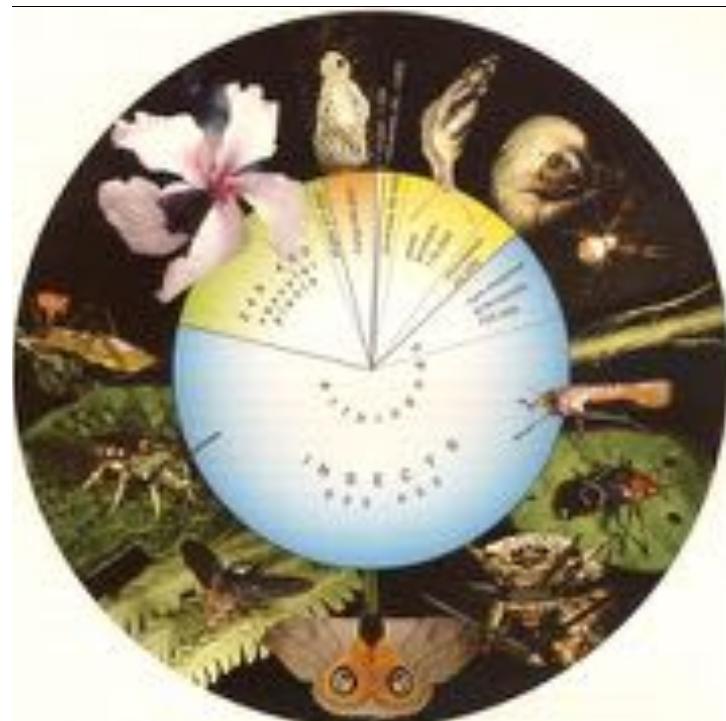


"The time will come I believe, though I shall not live to see it, when we shall have fairly true genealogical (phylogenetic) trees of each great kingdom of nature"

Darwin's letter to Thomas Huxley (1857)

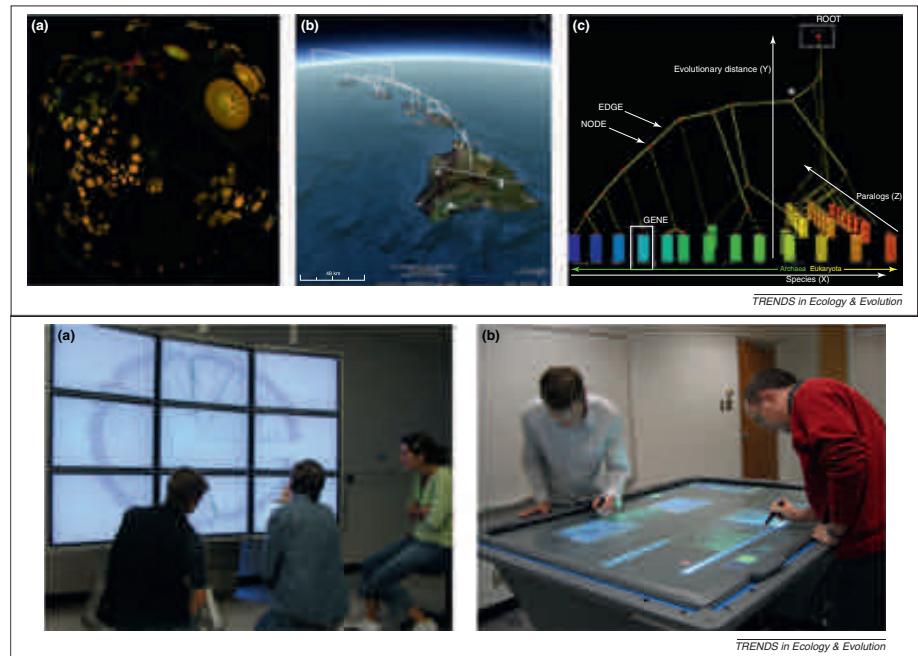
"... there is, after all, one true tree of life [...]. It exists. It is in principle knowable. We don't know it all yet. By 2050 we should —or if we do not, we shall have been defeated only at the terminal twigs, by the sheer number of species."

Dawkins (2003), *A Devil's Chaplain*

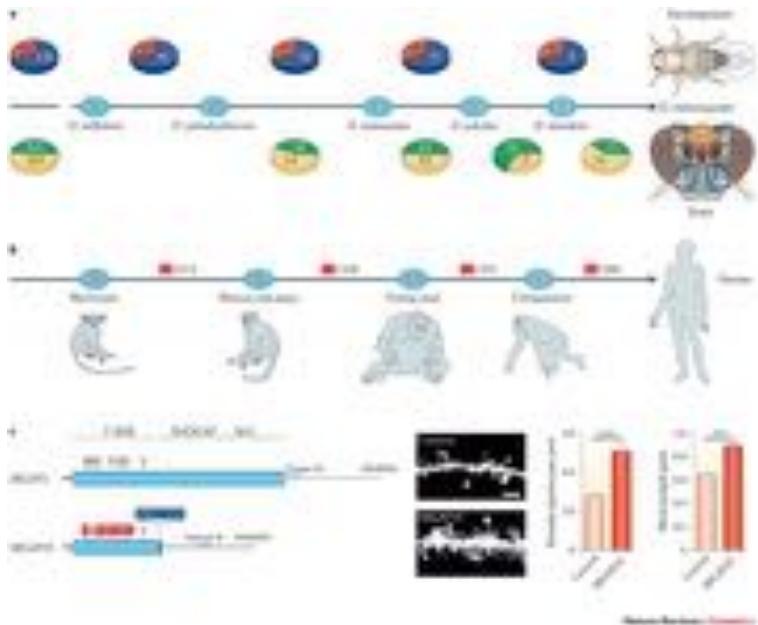


The AToL initiative (Assembling the Tree of Life) is a large research effort sponsored by the National Science Foundation. Its goal is to reconstruct the evolutionary origins of all living things.

The screenshot shows the homepage of the Barcode of Life website. At the top, there's a banner with a monarch butterfly wing. Below the banner, there's a search bar and some navigation links. The main content area has several sections: "How to DNA Barcoding", "Barcode of Life Data Bank", and "About Us". There are also links to "Species", "Genes", and "Tools". The overall design is clean and modern.



Space, time, form: viewing the Tree of Life
Roderic D.M. Page



a | The phylogeny shows the distributions of new *Drosophila* spp. genes involved in development⁴⁶ (above) and in the brain⁷⁶ (below) in various evolutionary stages within the past 36 million years⁸¹.



J. Theoret. Biol. (1965) 8, 357–366

Molecules as Documents of Evolutionary History

EMILE ZUCKERKANDL AND LINUS PAULING

Why molecular phylogenetics?



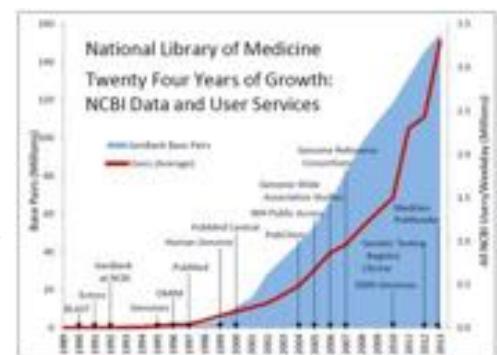
- The stream of heredity makes phylogeny: in a sense, it is phylogeny. Complete genetic analysis would provide the most priceless data for the mapping of this stream. *George G. Church*



- "I do not fully understand why we are not proclaiming the message from the housetops ... We finally have a method that can sort homology from analogy." *Stephen J. Gould , 1985*

Molecules as documents of evolutionary history

- "We may ask the question where in the now living systems the greatest amount of information of their past history has survived and how it can be extracted"
- "Best fit are the different types of macromolecules (sequences) which carry the genetic information"

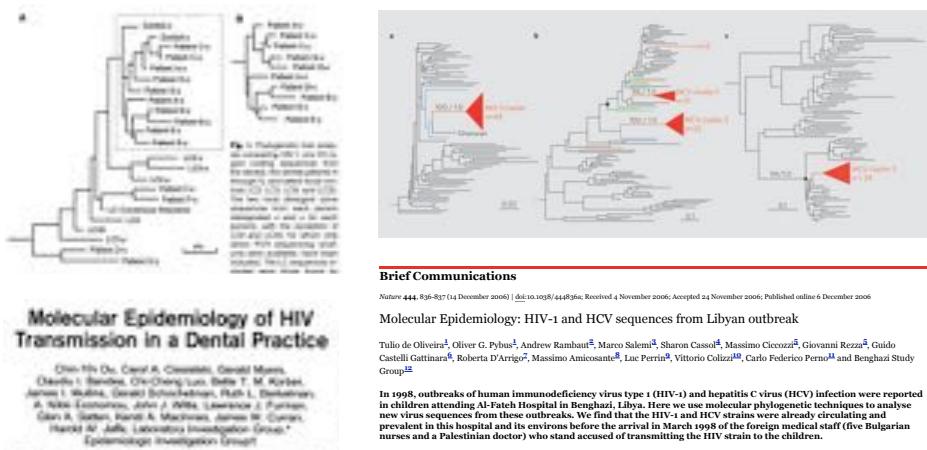


Applications of Phylogenetic Analysis

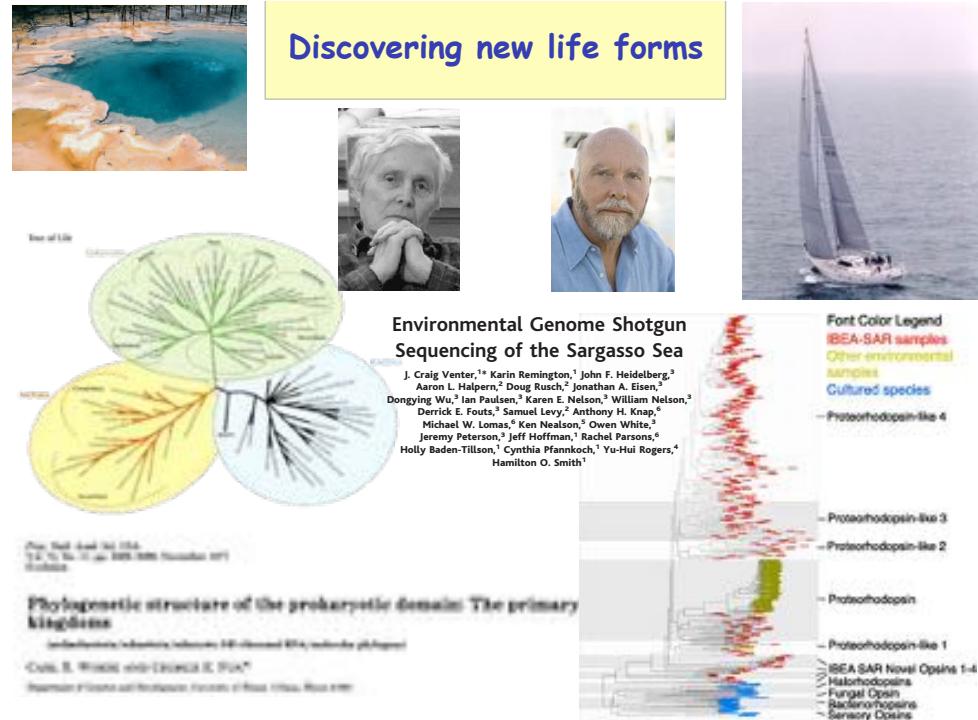
- Systematics and classification
- Discovering new life forms
- Phylogeography and speciation
- Molecular evolution
- Genomics
- Epidemiology and forensics
- Biotechnology
- Agriculture
- Conservation



Disease Transmission and Medical Forensics



Ou et al. 1992



Applications of Phylogenetic Analysis

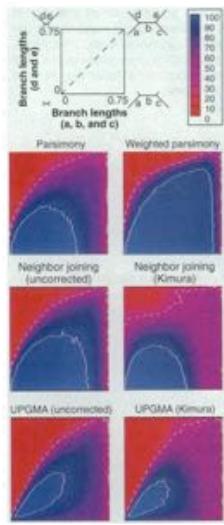
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"Simple identification via phylogenetic classification of organisms has, to date, yielded more patent filings than any other use of phylogeny in industry."

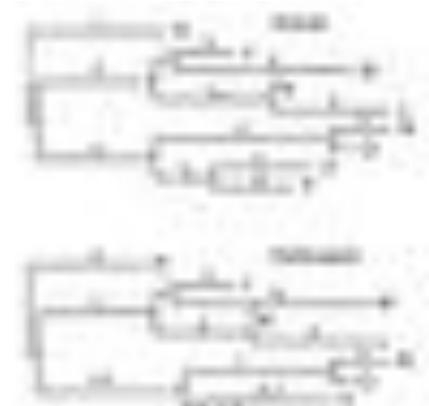
Bader et al. (2001)



How do we know that phylogenetics work?



a) simulations

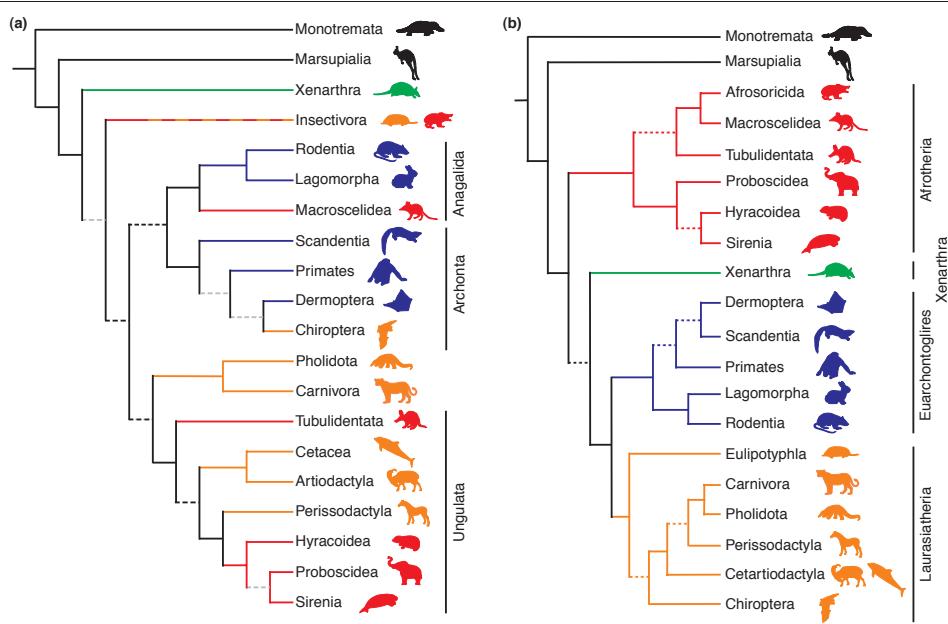


b) experimental phylogenies

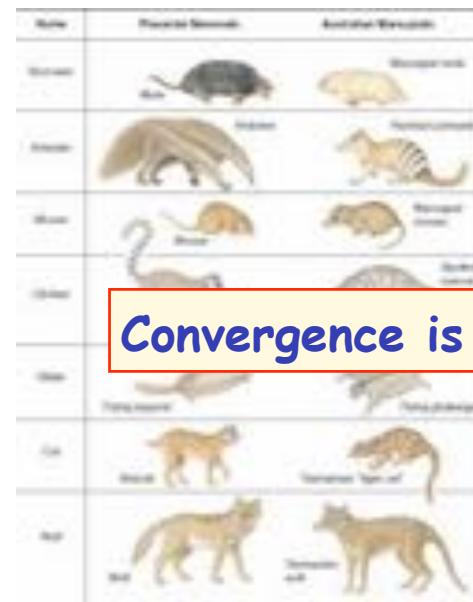
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Application and Accuracy of Molecular Phylogenies

David M. Hillis, John P. Huelsenbeck, Clifford N. Cunningham



TRENDS in Ecology & Evolution
Springer et al. 2004



Convergence is widespread!



Springer et al. 2004

LETTER

OPEN
doi:10.1038/nature14594

Temporal and spatial analysis of the 2014–2015 Ebola virus outbreak in West Africa

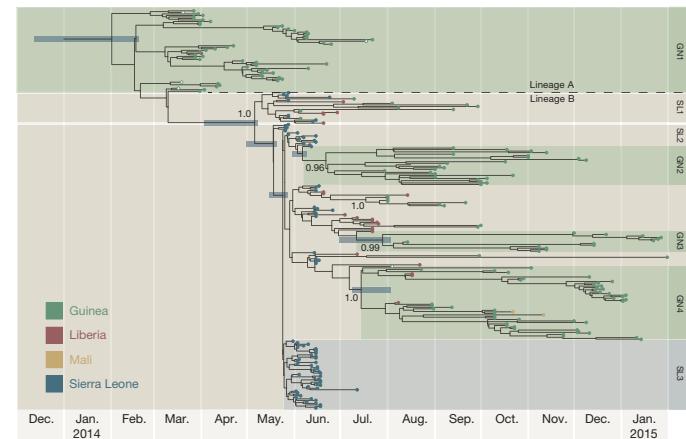
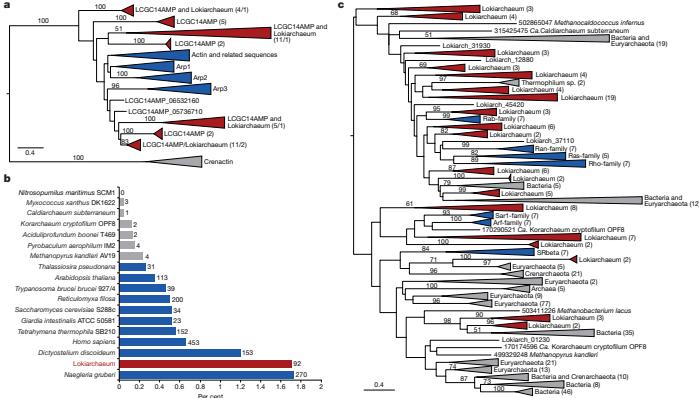


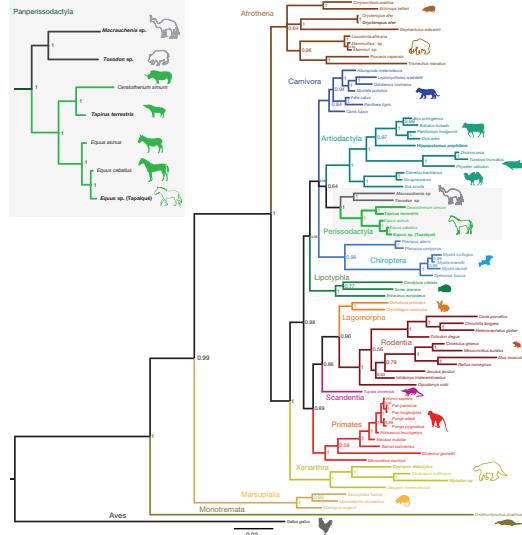
Figure 3 | A time-scaled phylogenetic tree of 262 EBOV genomes from Guinea, Sierra Leone, Liberia and Mali. Shown is a maximum clade credibility tree constructed from 10,000 trees sampled from the posterior distribution with mean node ages. Clades described in Gire *et al.* are identified here (SL1, SL2 and SL3) as well as a number of lineages predominantly circulating in Guinea and posterior probability support is given for these. For certain key node ages, 95% credible intervals are shown by horizontal bars.

Complex archaea that bridge the gap between prokaryotes and eukaryotes



archaeal and bacterial species. Numbers refer to total amount of small GTPases and actin orthologues. **a**, Maximum likelihood phylogeny of 378 aligned amino acid sequences. **b**, Percentage of predicted proteome per cent. **c**, Maximum likelihood phylogeny of 150 aligned archaeal and bacterial species. Numbers refer to total amount of small GTPases and actin orthologues.

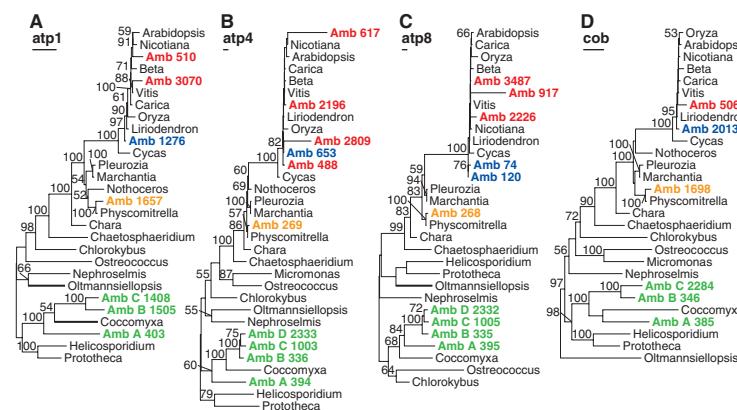
Ancient proteins resolve the evolutionary history of Darwin's South American ungulates



RESEARCH ARTICLES

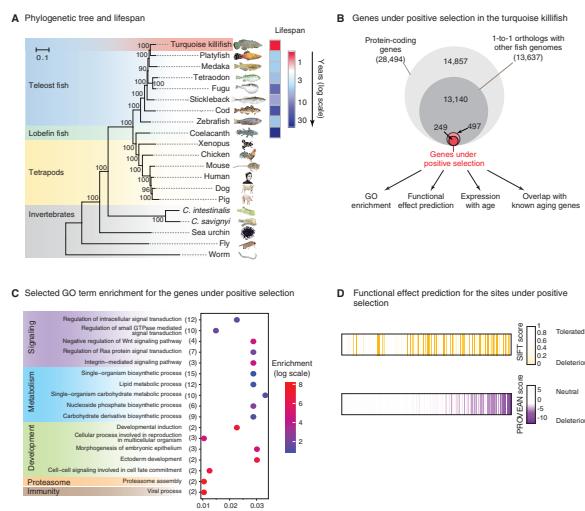
Horizontal Transfer of Entire Genomes via Mitochondrial Fusion in the Angiosperm Amborella

Danny W. Rice,¹ Andrew J. Alverson,^{1,*} Aaron O. Richardson,¹ Gregory J. Young,^{1†} M. Virginia Sanchez-Puerta,^{2,‡} Jérôme Munzinger,^{2,§} Kerrie Barry,² Jeffrey L. Boore,^{3||} Yan Zhang,³ Claude W. dePamphilis,³ Eric B. Knox,³ Jeffrey D. Palmer^{1¶}



Cell

The African Turquoise Killifish Genome Provides Insights into Evolution and Genetic Architecture of Lifespan



A comprehensive phylogeny of birds (Aves) using targeted next-generation DNA sequencing

