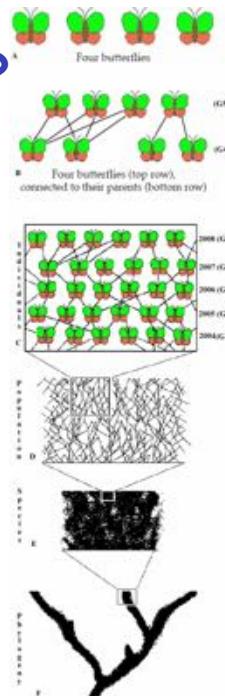


Molecular Phylogenetics

EEOB 563

What is a phylogenetic tree?

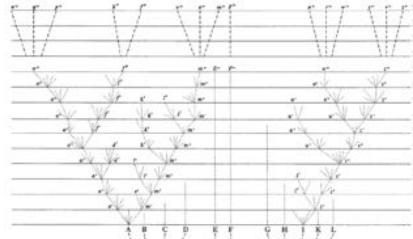
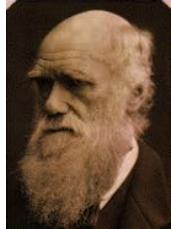
- A tree is a mathematical structure which is used to model the actual evolutionary history of a group of sequences or organisms.
- The actual pattern of historical relationships is an evolutionary tree which we try to estimate



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.



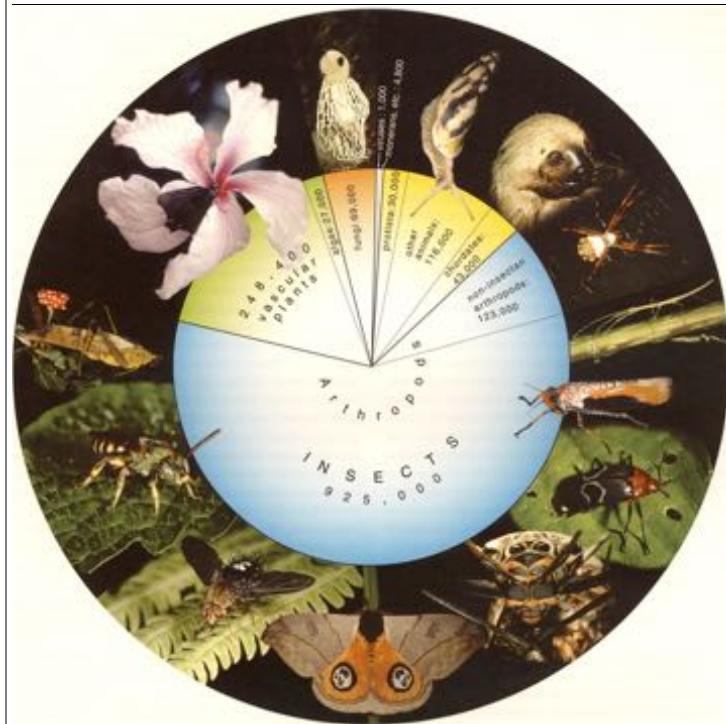


"The time will come I believe, though I shall not live to see it, when we shall have fairly true genealogical (phylogenetic) trees of each great kingdom of nature"

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.

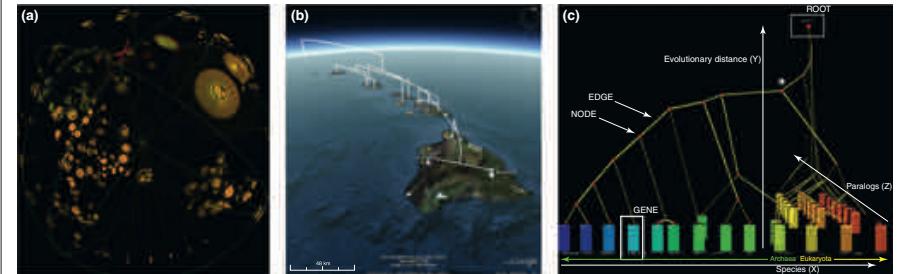


The Project Reference Database (PRD) is a catalog of molecular barcode Small Subunit rRNA sequences with associated metadata.

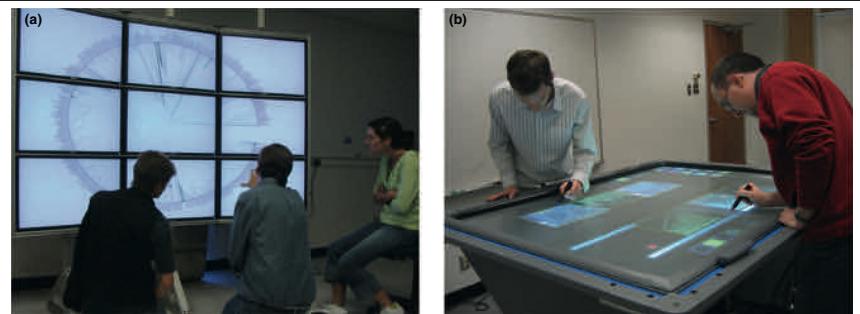
The Chaperonin-60 (Chaperonin-60) is a barcode for bacteria that enables the Assembly of Metagenomic Sequence Data (AMSA).

The Effect of Geographical Scale of Sampling on DNA Barcoding.

Akira Community Resources Events Partners News

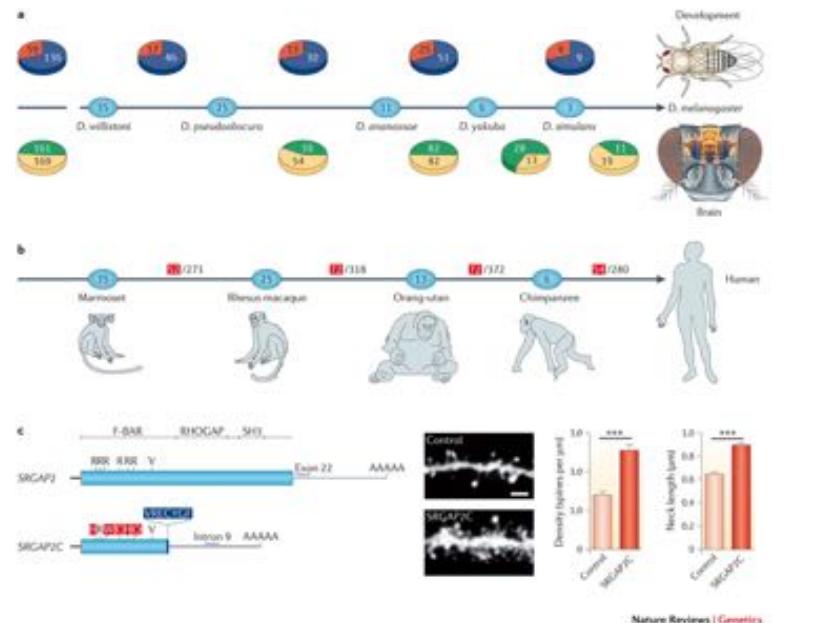


TRENDS in Ecology & Evolution



TRENDS in Ecology & Evolution

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

Why molecular phylogenetics?



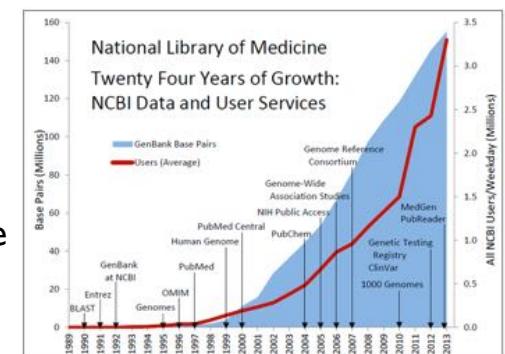
- The stream of heredity makes phylogeny: in a sense, it is phylogeny. Complete genetic analysis would provide the most priceless data for the mapping of this stream. *George G. Simpson, 1945*



- "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”

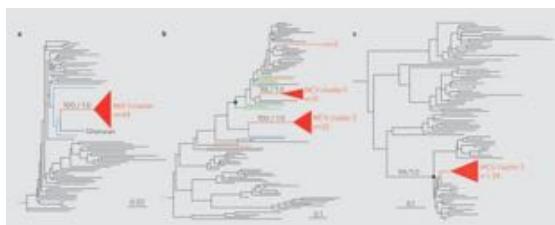
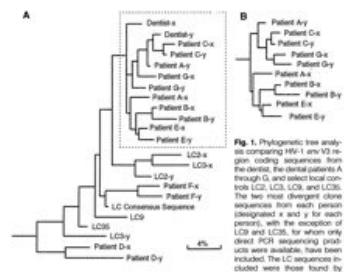


Applications of Phylogenetic Analysis

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



Disease Transmission and Medical Forensics



Molecular Epidemiology of HIV Transmission in a Dental Practice

Chin-Yih Ou, Carol A. Ciesielki, Gerald Myers, Claudio I. Bandea, Chi-Cheng Luo, Bette T. M. Korber, James I. Mullins, Gerald Schochetman, Ruth L. Berkelman, A. Nikki Economou, John J. Witte, Lawrence K. Furman, Glen A. Satten, Kersti A. Machnick, James W. Curran, Harold W. Jaffe, Laboratory Investigation Group,* Epidemiologic Investigation Group†

Ou et al. 1992

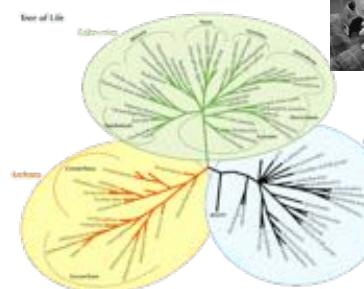
Nature 444: 836-837 (14 December 2006) doi:10.1038/nature05364; Received 4 November 2006; Accepted 24 November 2006; Published online 6 December 2006

Molecular Epidemiology: HIV-1 and HCV sequences from Libyan outbreak

Tulio de Oliveira¹, Oliver G. Pyleus¹, Andrew Rambaut², Marco Salemi³, Sharon Casas⁴, Massimo Ciuccozzi⁵, Giovanni Rezza⁶, Guido Castelli-Gattinara⁶, Roberta D'Arrigo⁷, Massimo Amicosante⁸, Luc Perrini⁹, Vittorio Colizzi¹⁰, Carlo Federico Perno¹⁰ and Benghazi Study Group¹⁰

In 1998, outbreaks of human immunodeficiency virus type 1 (HIV-1) and hepatitis C virus (HCV) infection were reported in children attending Al-Fateh Hospital in Benghazi, Libya. Here we use molecular phylogenetic techniques to analyse new virus sequences from these outbreaks. We find that the HIV-1 and HCV strains were already circulating and prevalent in this hospital and its environs before they were in March 1998 of the original medical staff (five Bulgarian nurses and a Palestinian doctor) who stand accused of transmitting the HIV strain to the children.

Discovering new life forms



Proc. Natl. Acad. Sci. USA
Vol. 104, No. 11, pp. 5088–5090, November 19, 2007
Evolution

Environmental Genome Shotgun Sequencing of the Sargasso Sea

J. Craig Venter,^{1,*} Karin Remington,¹ John F. Heidelberg,³ Aaron L. Halpern,² Doug Rusch,² Jonathan A. Eisen,³ Donghyun Won,¹ Ian Paulsen,¹ Michael L. Hettich,³ William Nelson,³ Derrick J. Joung,² Samuel Levy,² Anthony H. Korey,² Michael W. Lomas,² Ken Neilson,² Owen White,³ Jeremy Peterson,³ Jeff Hoffman,³ Rachel Parsons,⁶ Holly Baden-Tillson,³ Cynthia Pfannkoch,³ Yu-Hui Rogers,⁴ Hamilton O. Smith¹

Font Color Legend
IBEA-SAR samples
Other environmental samples
Cultured species

— Proteorhodopsin-like 4
— Proteorhodopsin-like 3
— Proteorhodopsin-like 2
— Proteorhodopsin
— Proteorhodopsin-like 1
— IBEA-SAR Novel Opsins 1-4
— Halorhodopsins
— Fungal Opsin
— Bacteriorhodopsins
— Sensory Opsins

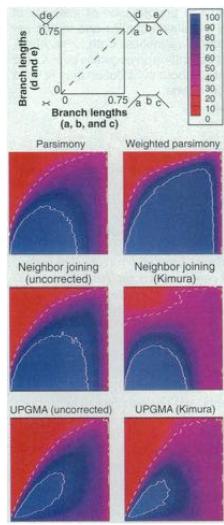
Applications of Phylogenetic Analysis

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- Biotechnology
- Agriculture
- Conservation

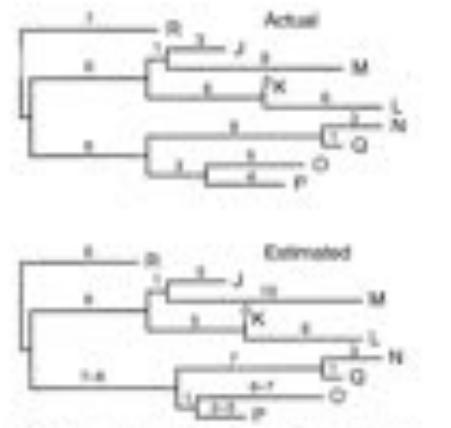
"Simple identification via phylogenetic classification of organisms has, to date, yielded more patent filings than any other use of phylogeny in industry."
Bader et al. (2001)



How do we know that phylogenetics work?

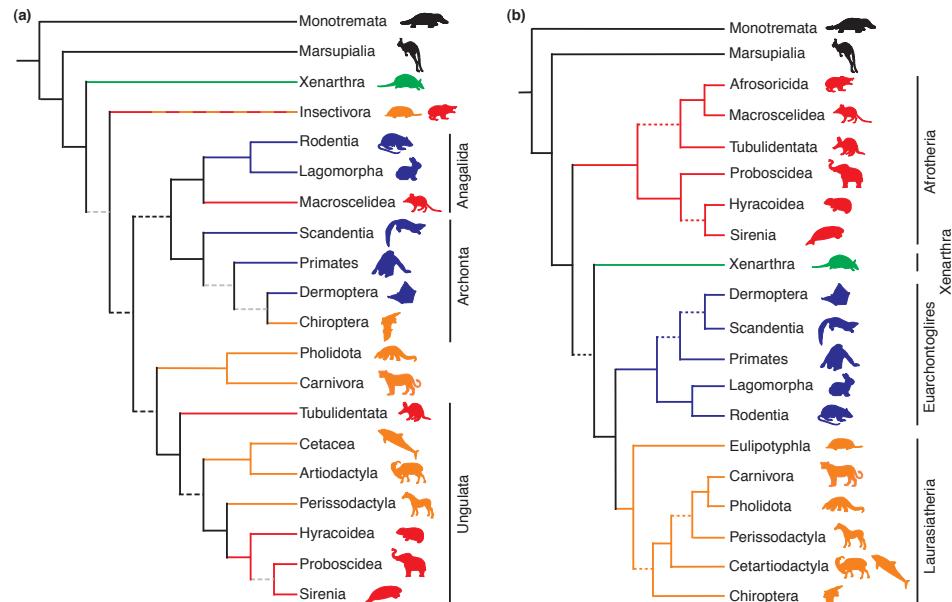


a) simulations

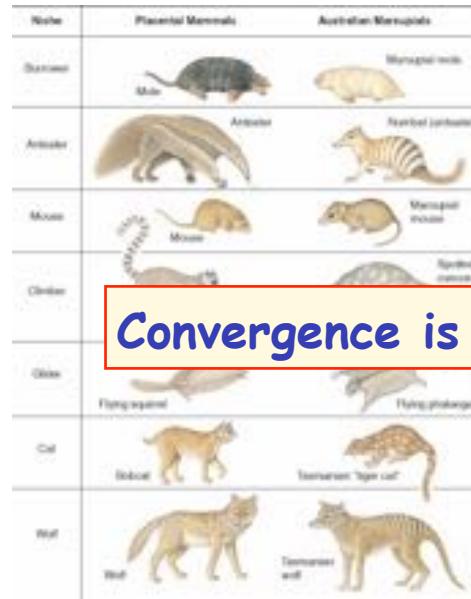


b) experimental phylogenies

■ ARTICLE <https://doi.org/10.1038/nature03279> Application and Accuracy of Molecular Phylogenies
David M. Hillis, John P. Huelsenbeck, Clifford W. Cunningham



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

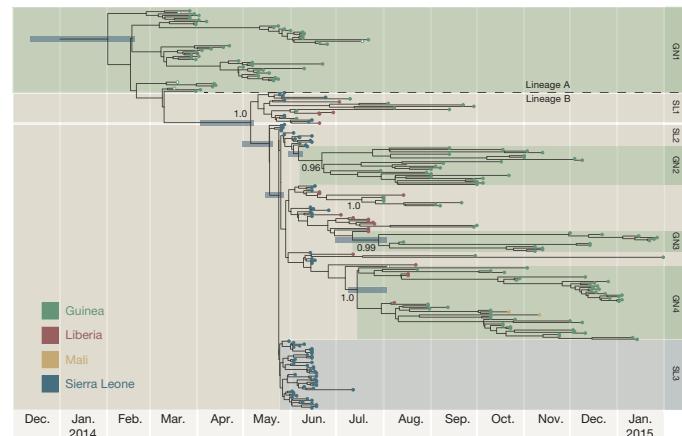


Figure 3 | A time-scaled phylogenetic tree of 262 EBOV genomes from Guinea, Sierra Leone, Liberia and Mali. Shown is a maximum clade credibility tree constructed from 10,000 trees sampled from the posterior distribution with mean node ages. Clades described in Gire *et al.* are identified here (SL1, 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.

ARTICLE

doi:10.1038/nature14447

Complex archaea that bridge the gap between prokaryotes and eukaryotes

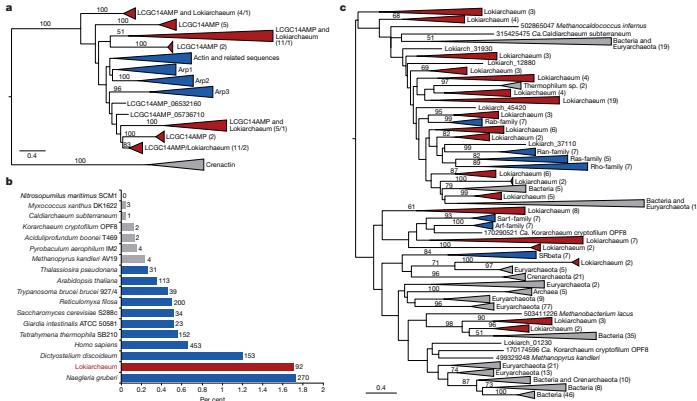


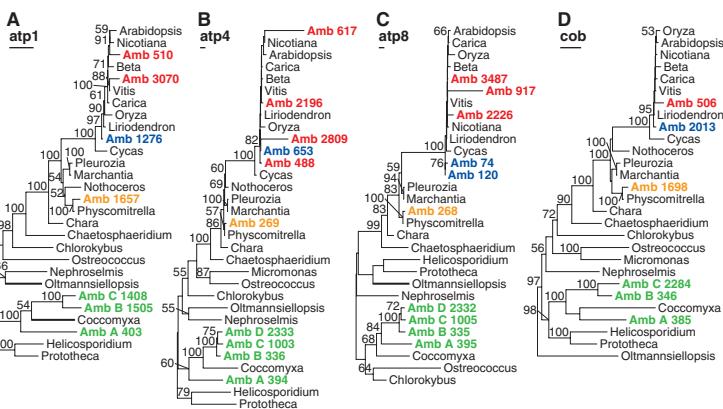
Figure 3 | Identification and phylogeny of small GTPases and actin orthologues. a, Maximum-likelihood phylogeny of 378 aligned amino acid

Figure 1. The relationship between the proportion of patients with a history of smoking and the proportion of patients with a history of alcohol abuse.

RESEARCH ARTICLES

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

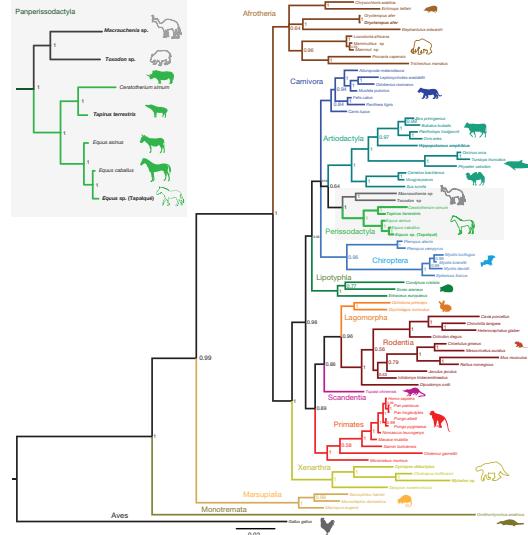
Danny W. Rice,¹ Andrew J. Alverson,^{1*} Aaron O. Richardson,¹ Gregory J. Young,^{1,†} M. Virginia Sanchez-Puerta,^{1,‡} Jérôme Munzinger,^{2,§} Kerrie Barry,³ Jeffrey L. Boore,^{3||} Yan Zhang,⁴ Claude W. dePamphilis,⁴ Eric B. Knox,¹ Jeffrey D. Palmer^{1,¶}



LETTER

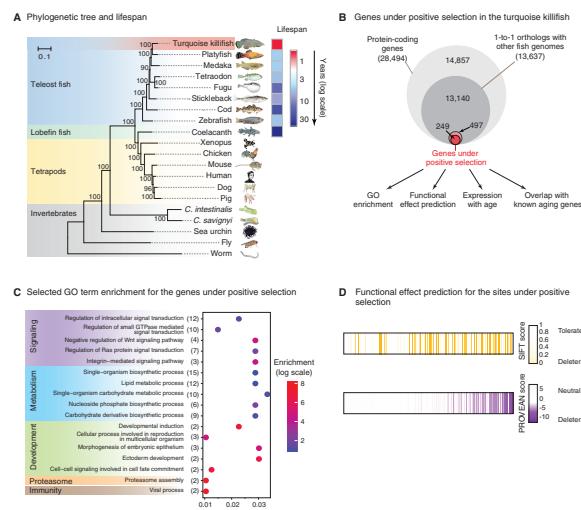
doi:10.1038/nature1424

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



Resource

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



LETTER

doi:10.1038/nature15697

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

