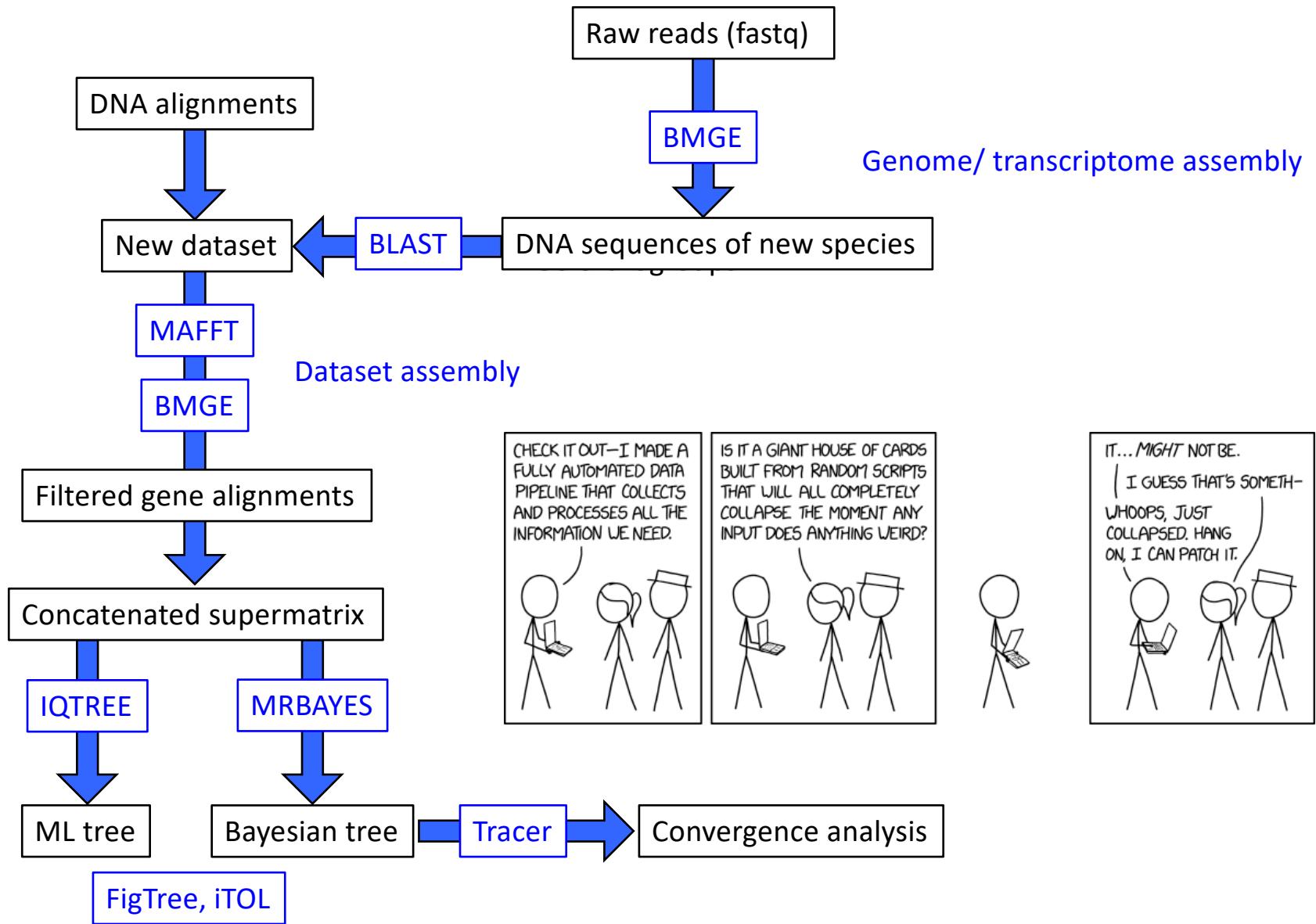


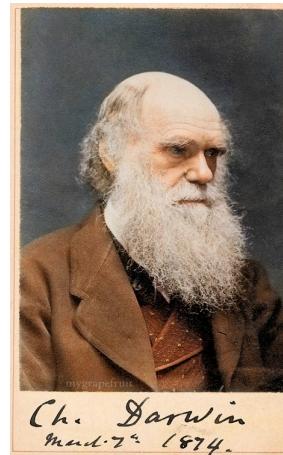
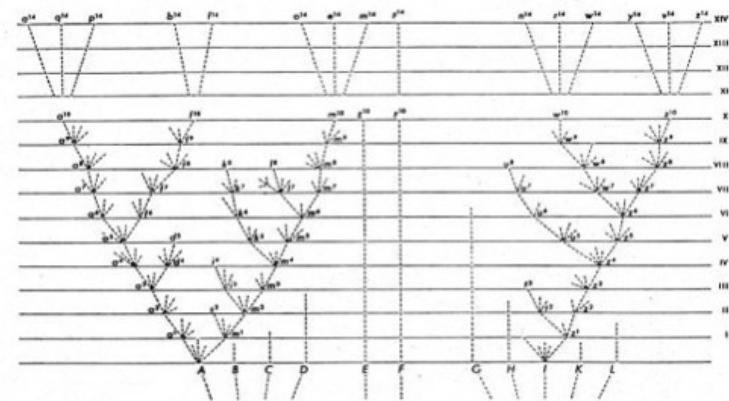
Pipeline

Phylogenetic analysis

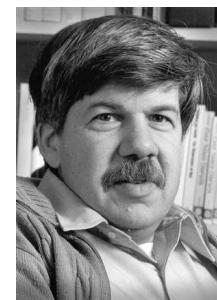
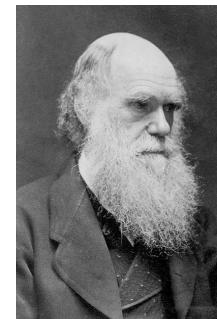


"I am fully convinced that species are not immutable; but that those belonging to what are called the same genera are lineal descendants of some other and generally extinct species, in the same manner as the acknowledged varieties of any one species are the descendants of that species. Furthermore, I am convinced that natural selection has been the most important, but not the exclusive, means of modification."

— Charles Darwin,
On the Origin of Species 1859



- Ancestor-descent relationships imply we can use trees to express evolutionary relationships
- Evolution is an historical science (contingency)
- Evolution is a population process



"Nothing in biology makes sense, except in the light of evolution.

Without that light it becomes a pile of sundry facts - some of them interesting or curious but making no meaningful picture as a whole"

– Theodosius Dobzhansky

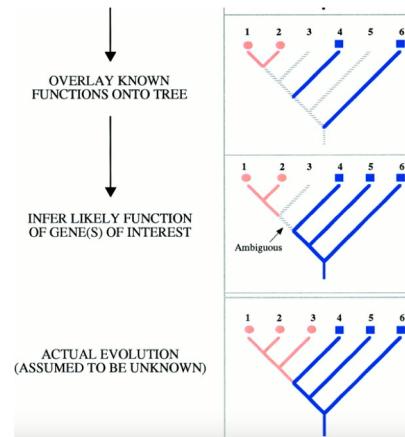
Definitions

Phylogenomics: Improving Functional Predictions for Uncharacterized Genes by Evolutionary Analysis

Jonathan A. Eisen¹

Department of Biological Sciences, Stanford University, Stanford, California 94305-5020 USA

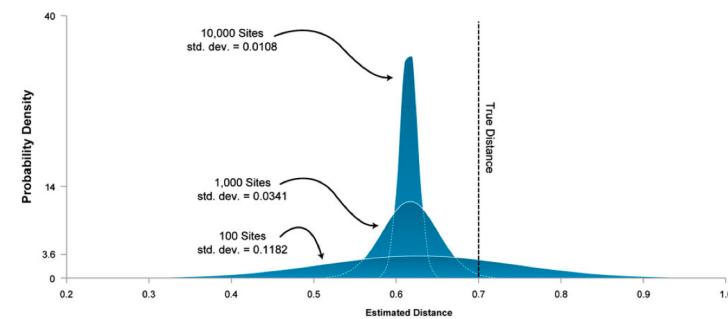
Eisen 1998 Genome Res



Phylogenomics

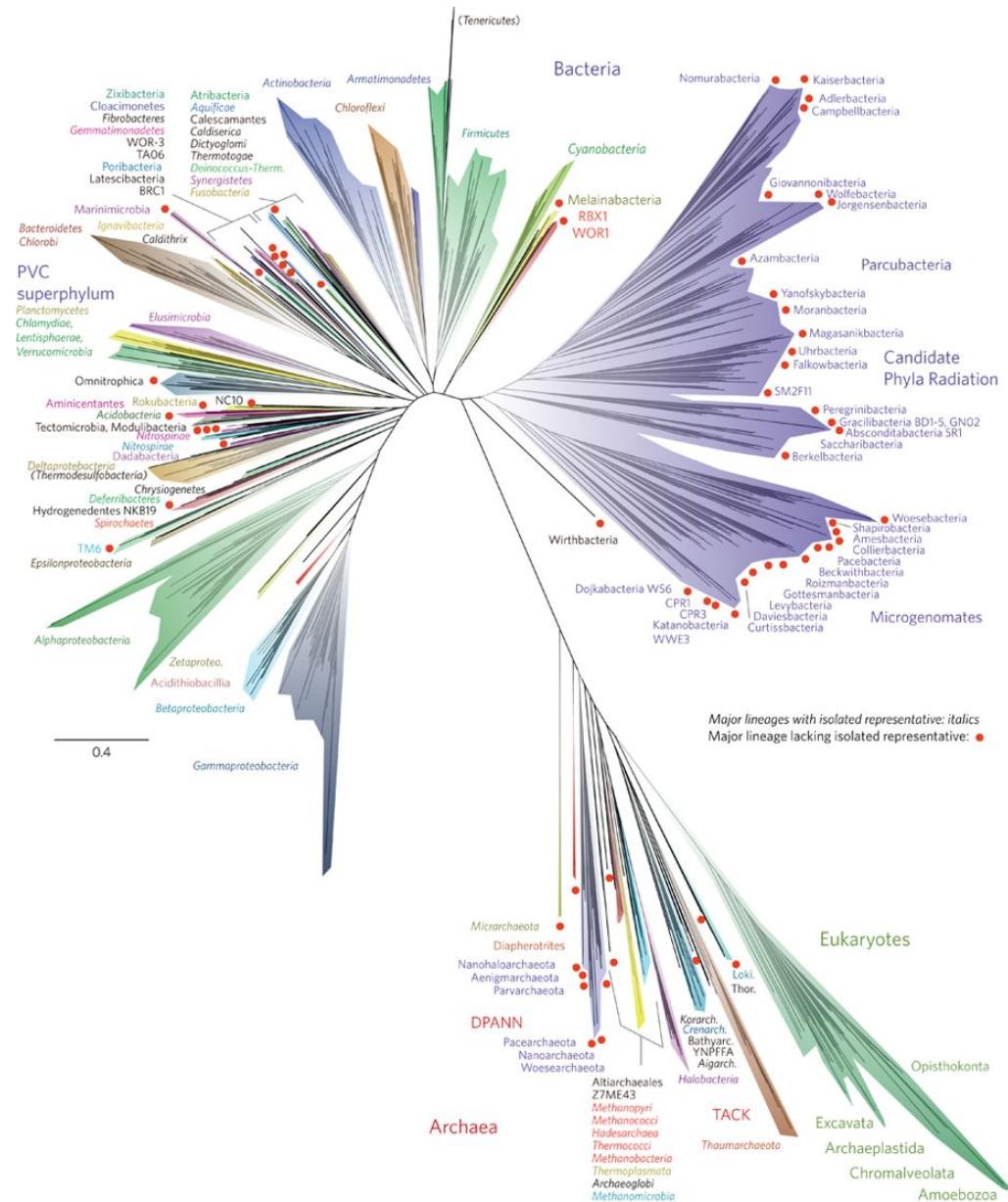
From Wikipedia, the free encyclopedia

Phylogenomics is the intersection of the fields of **evolution** and **genomics**.^[1] The term has been used in multiple ways to refer to analysis that involves **genome** data and evolutionary reconstructions. It is a group of techniques within the larger fields of **phylogenetics** and genomics. Phylogenomics draws information by comparing entire genomes, or at least large portions of genomes.^[2] Phylogenetics compares and analyzes the sequences of single genes, or a small number of genes, as well as many other types of data.



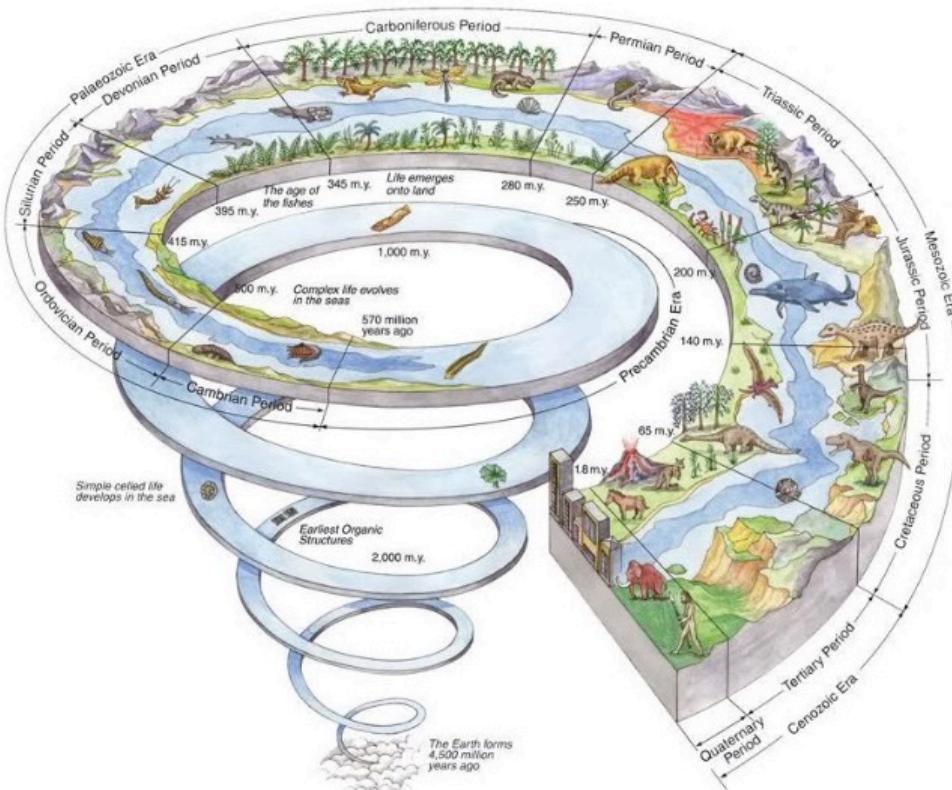
Kumar et al. 2012 Mol Biol Evol

Tree of Life



Hug et al. 2016 Nat Microbiol

Phylogenomics: “molecular archaeology”



YOUR GENETIC TEST RESULTS
ARE BACK. APPARENTLY YOU'RE
PART OF AN UNBROKEN LINEAGE
STRETCHING BACK BILLIONS OF
YEARS TO THE EARLY EARTH!



Understand evolution of traits: morphology, behaviour, etc.

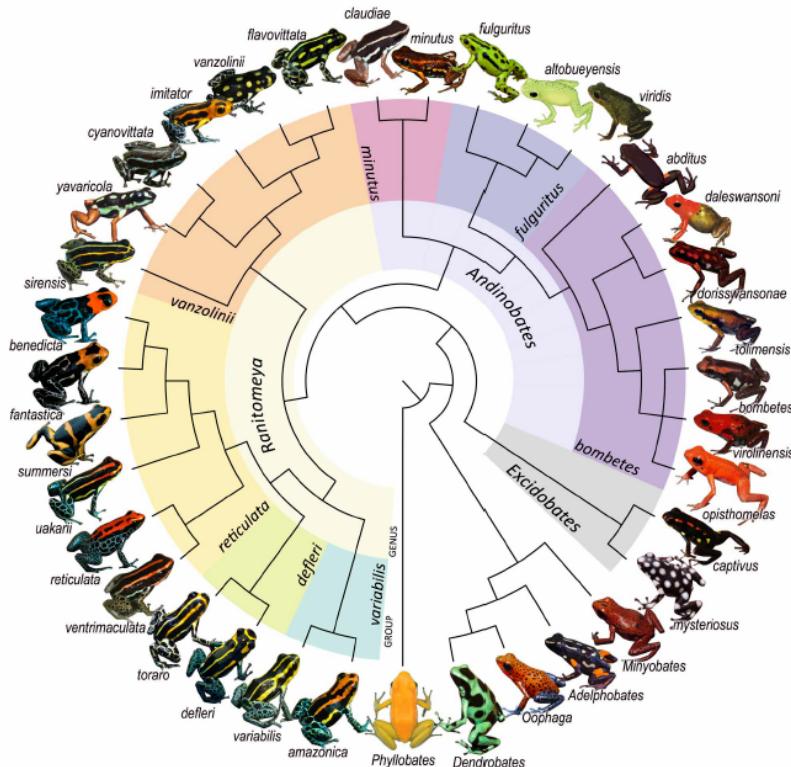
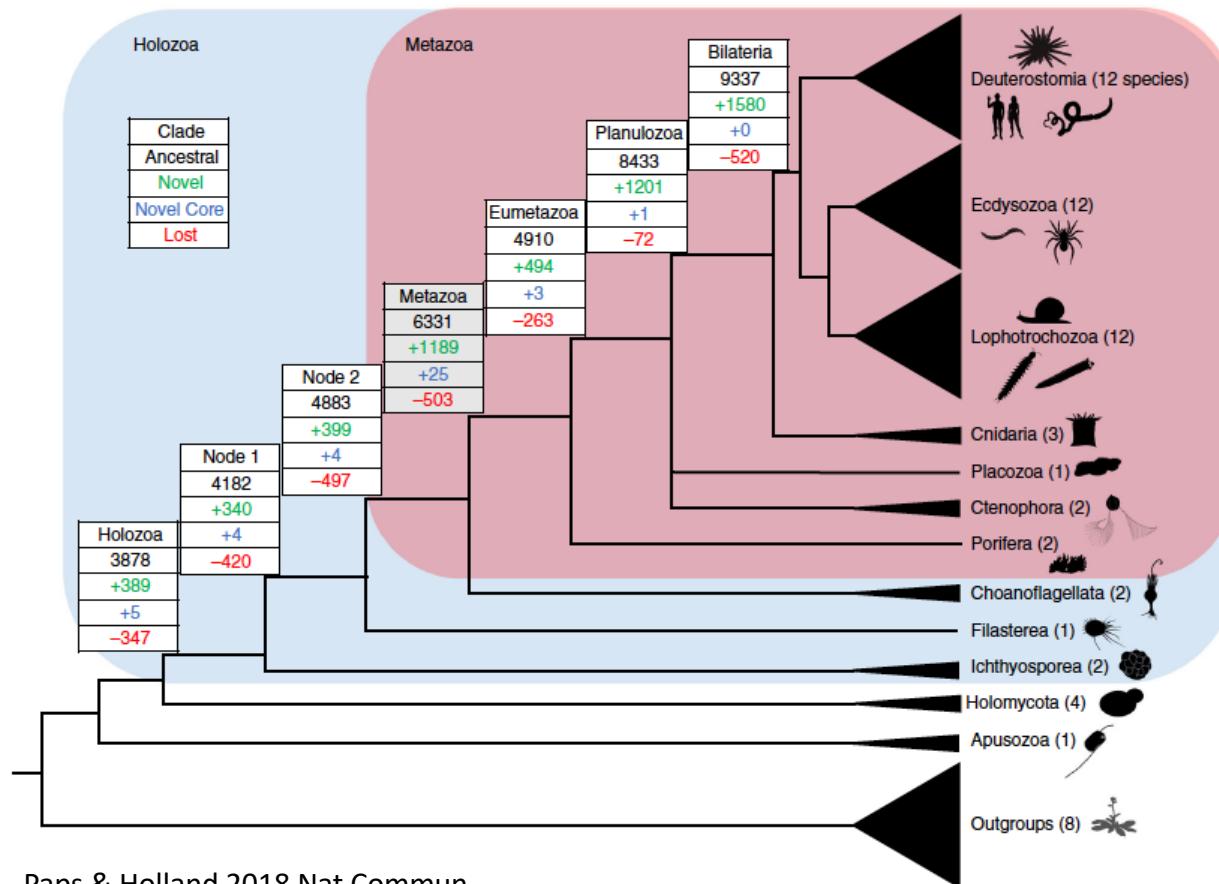


Figure 1. Mimetic forms of *Ranitomeya imitor* and its Müllerian co-mimics.
Top row, the mimic *Ranitomeya imitor*: left, "Varadero" blotched morph; right, striped morph. Bottom row, the models: left, the aptly named *R. fantastica*; right, *R. variabilis*. Photos courtesy of Evan Twomey.

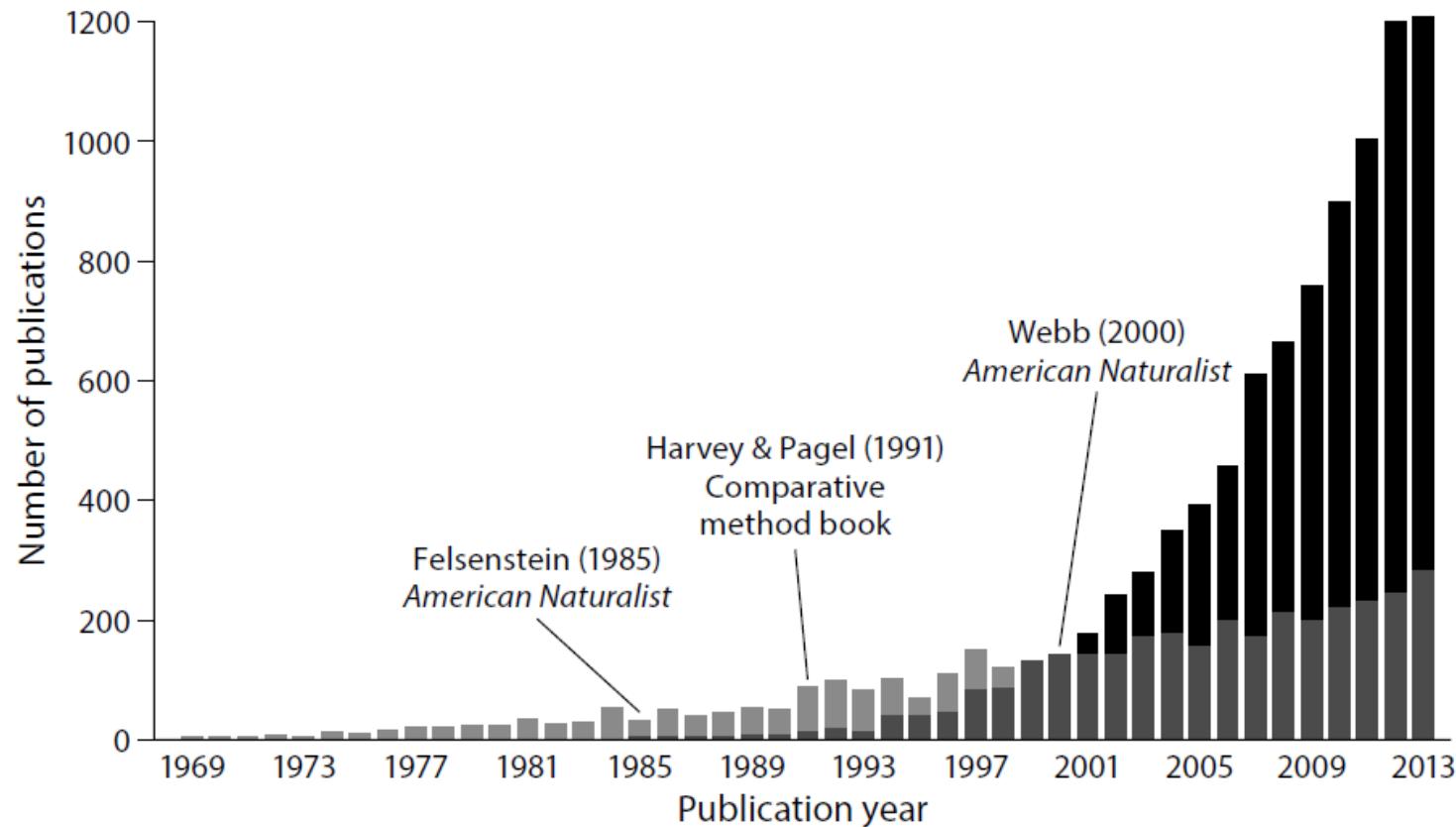
Mallet 2014 Curr Biol
Brown et al. 2011 Zootaxa

Evolution of genomes and gene families

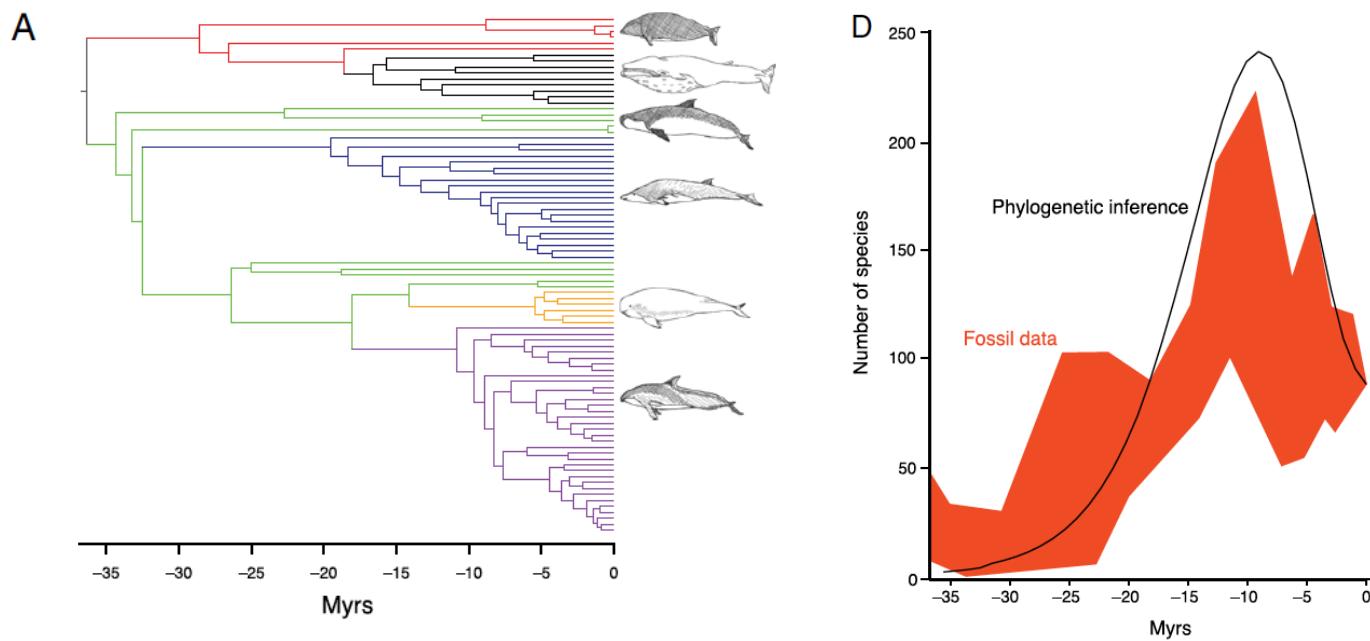


Paps & Holland 2018 Nat Commun

Testing hypothesis in Ecology with phylogenies

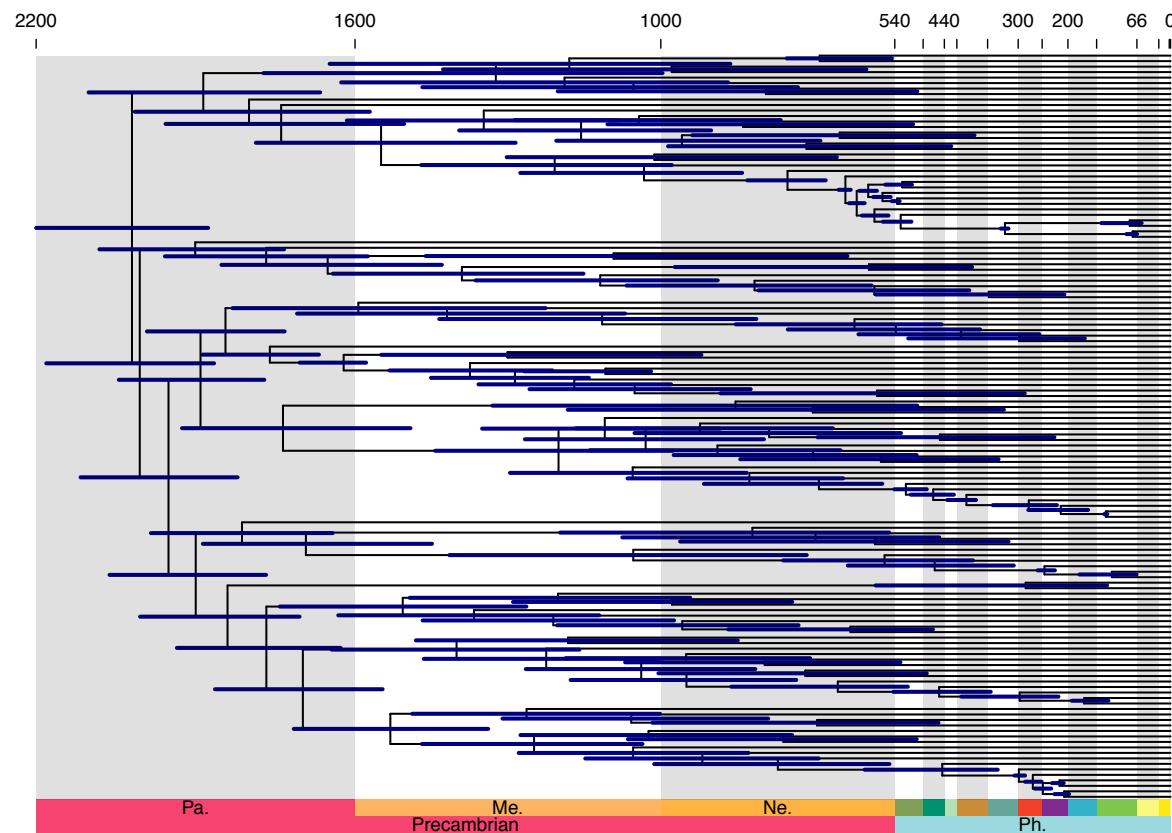


Testing hypothesis: Macroevolution



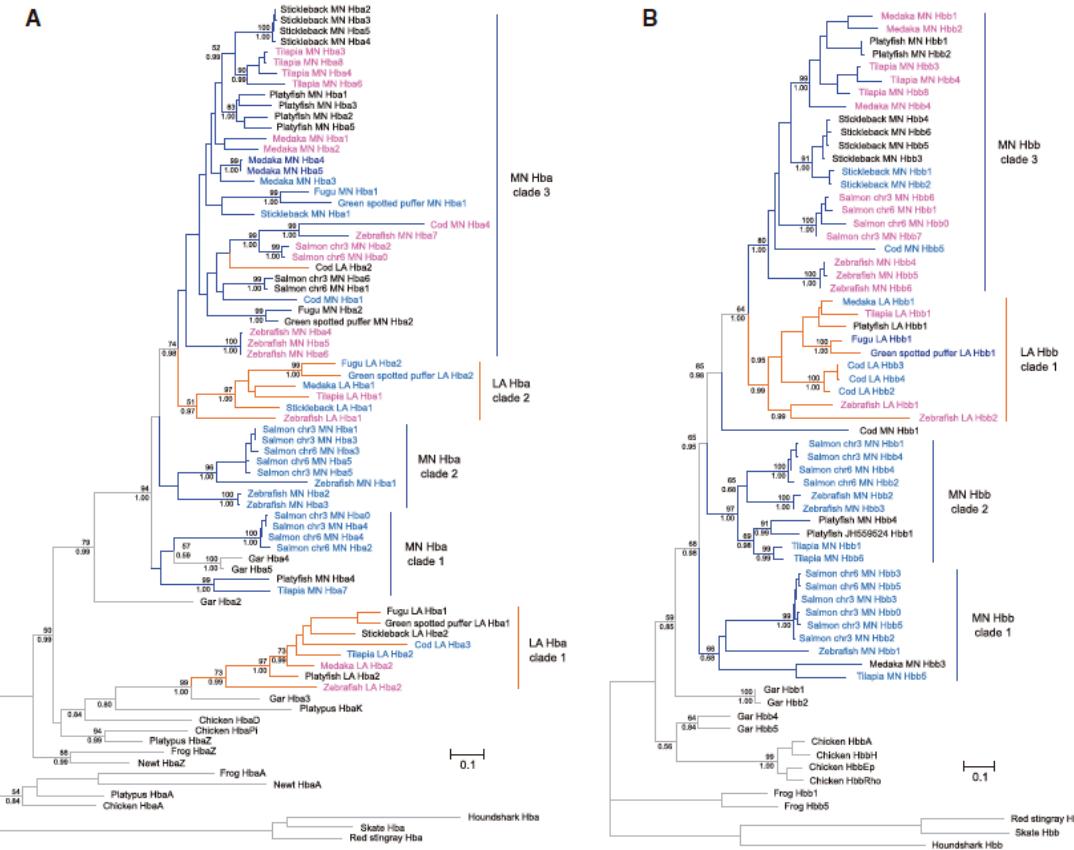
Morlon et al. 2011 PNAS

Molecular clock



Strassert et al.

Evolution of genomes and gene families



Opazo et al. 2013
Mol Biol Evol

Reconstruction of ancestral character states

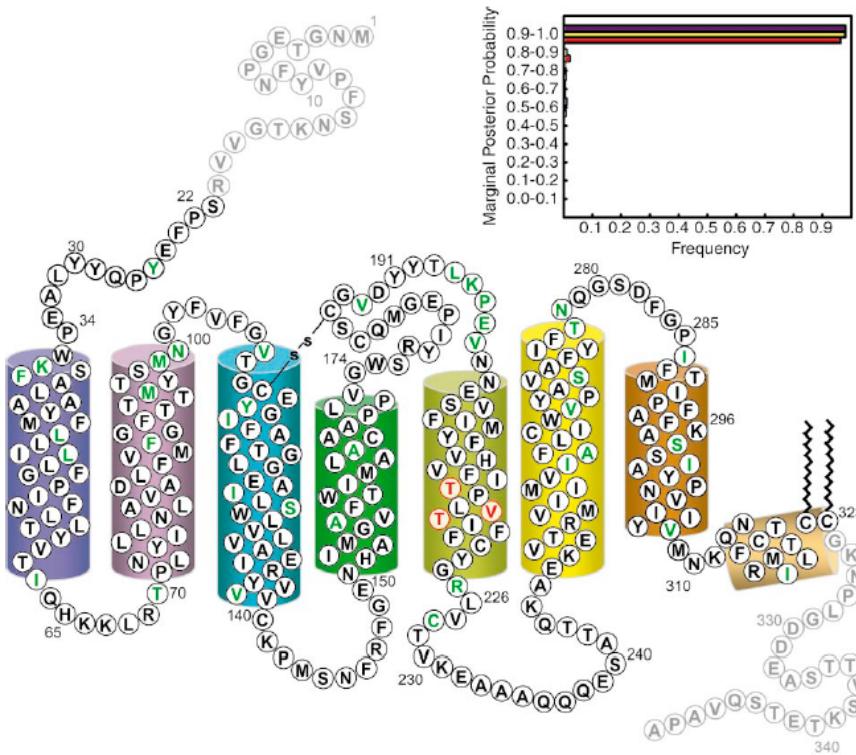


FIG. 2.—Protein sequence of the reconstructed ancestral archosaur rhodopsin drawn as a schematic on the basis of the crystal structure for bovine rhodopsin (Palczewski et al. 2000). Sites that differ among the best three reconstructions, for which variants were also synthesized, are marked in red. The 38 residues that differ from bovine or alligator rhodopsin are marked in green. Inset, frequencies of marginal posterior probabilities calculated for the most likely amino acid reconstruction at each site of the ancestral archosaur rhodopsin sequence. These posterior probabilities, which represent the likelihood of having reconstructed the correct amino acid, under the assumptions of the model used, were calculated for the best-fitting nucleotide (HKY+Γ, purple bars), codon (F61+Γ, yellow bars), and amino acid (Jones+F+Γ, red bars) models.

Chang et al. 2002
Mol Biol Evol

Study of natural selection

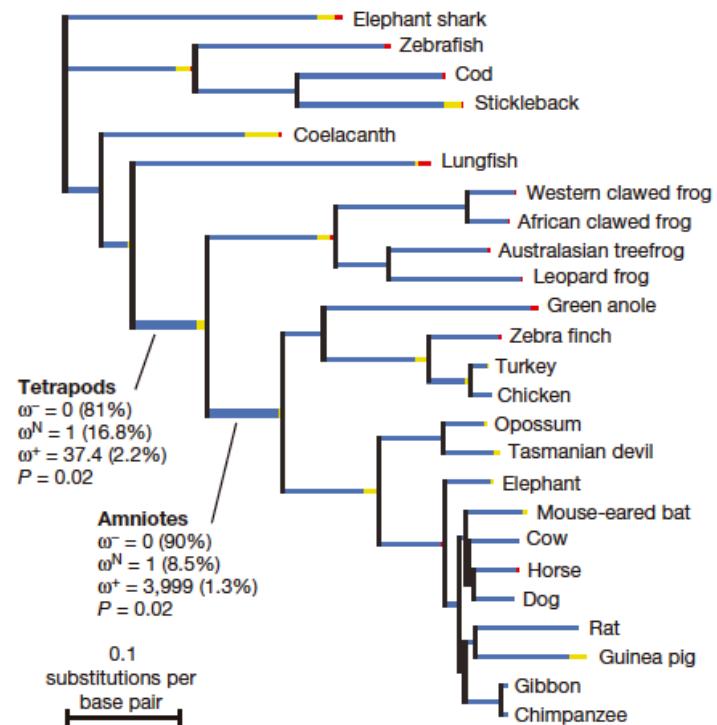
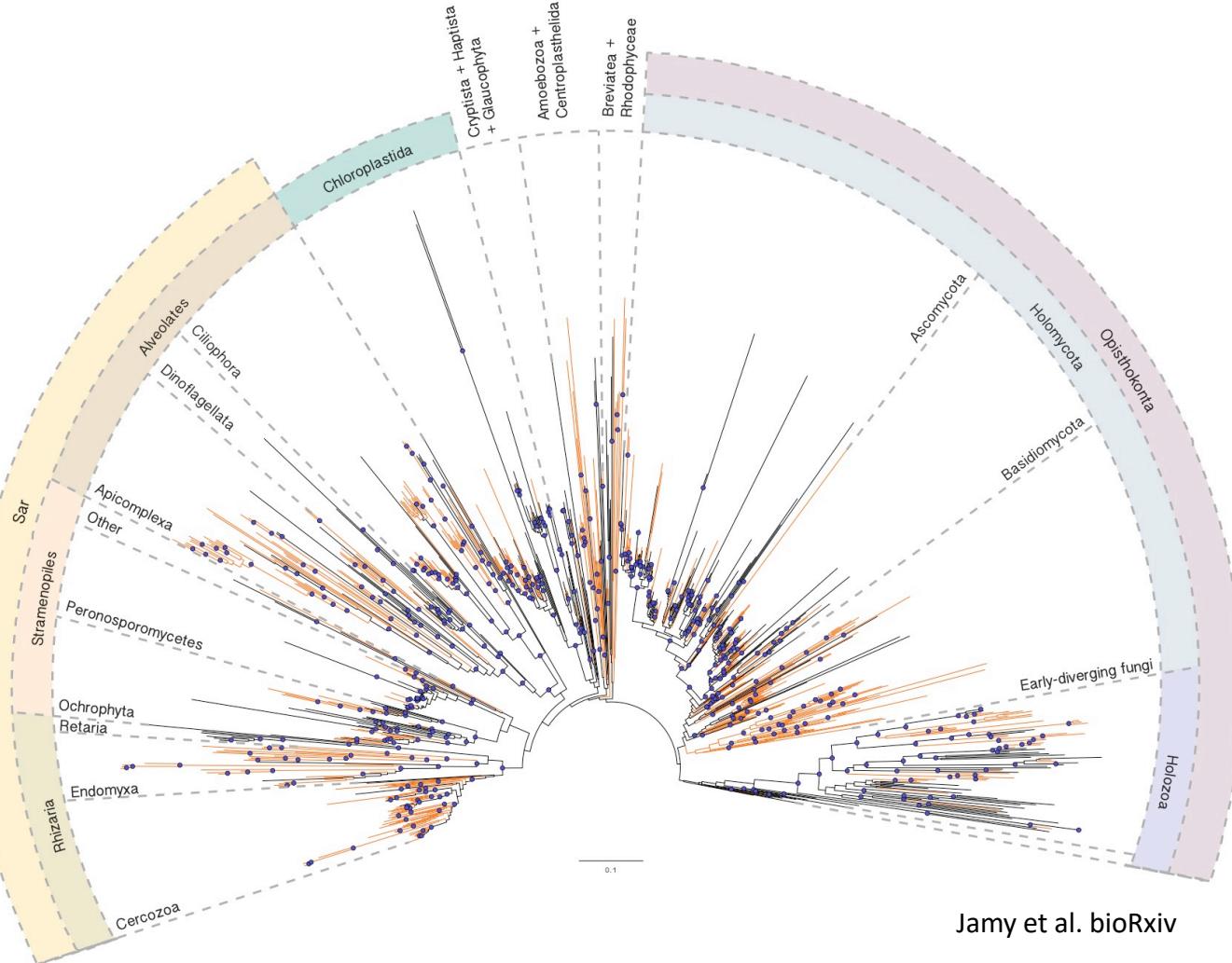


Figure 3 | Phylogeny of *Cps1* coding sequences is used to determine positive selection within the urea cycle. Branch lengths are scaled to the expected

Amemiya et al.
2013 Nature

Classification, metagenomics



Jamy et al. bioRxiv

Epidemiology, criminology, medicine

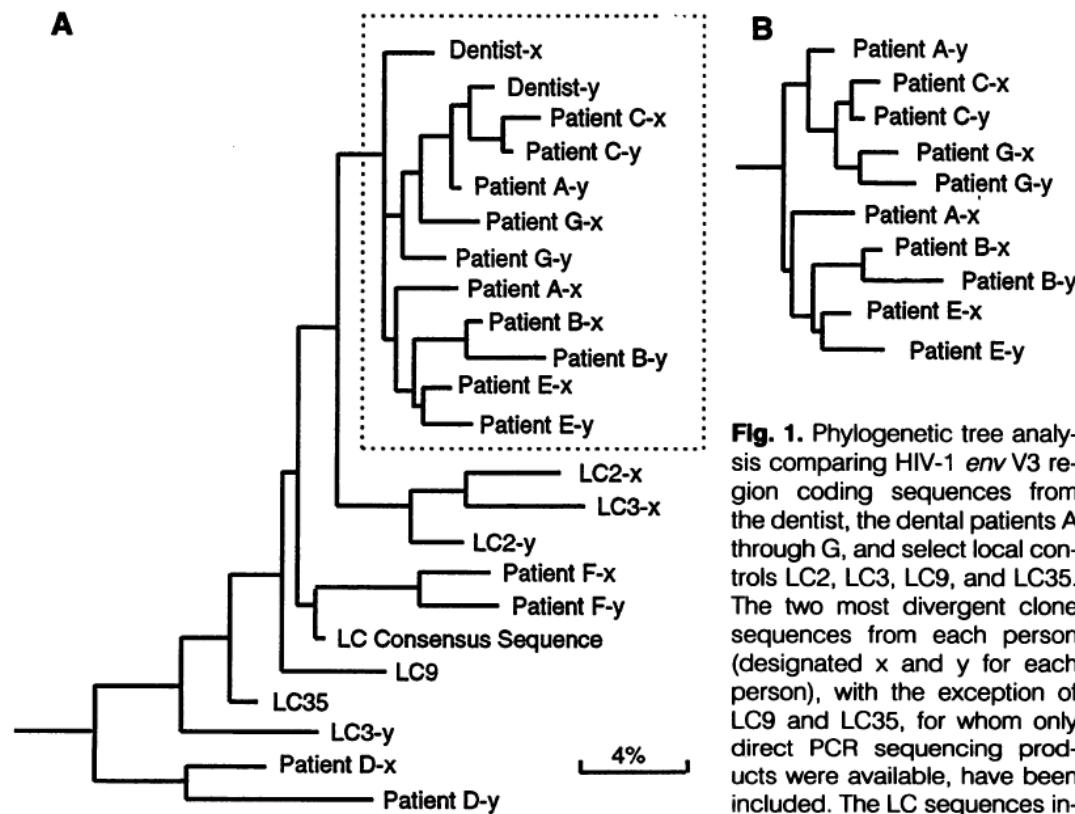


Fig. 1. Phylogenetic tree analysis comparing HIV-1 *env* V3 region coding sequences from the dentist, the dental patients A through G, and select local controls LC2, LC3, LC9, and LC35. The two most divergent clone sequences from each person (designated x and y for each person), with the exception of LC9 and LC35, for whom only direct PCR sequencing products were available, have been included. The LC sequences included were those found by

Ou et al. 1992
Science

Cancer genomics

Rapid evolution and biogeographic spread in a colorectal cancer

Joao M Alves^{1,2,3}, Sonia Prado-Lopez^{1,2,3}, Jose Manuel Cameselle-Teijeiro^{4,5}, David Posada^{*1,2,3}

