Examples of Phylogenetic Reconstruction

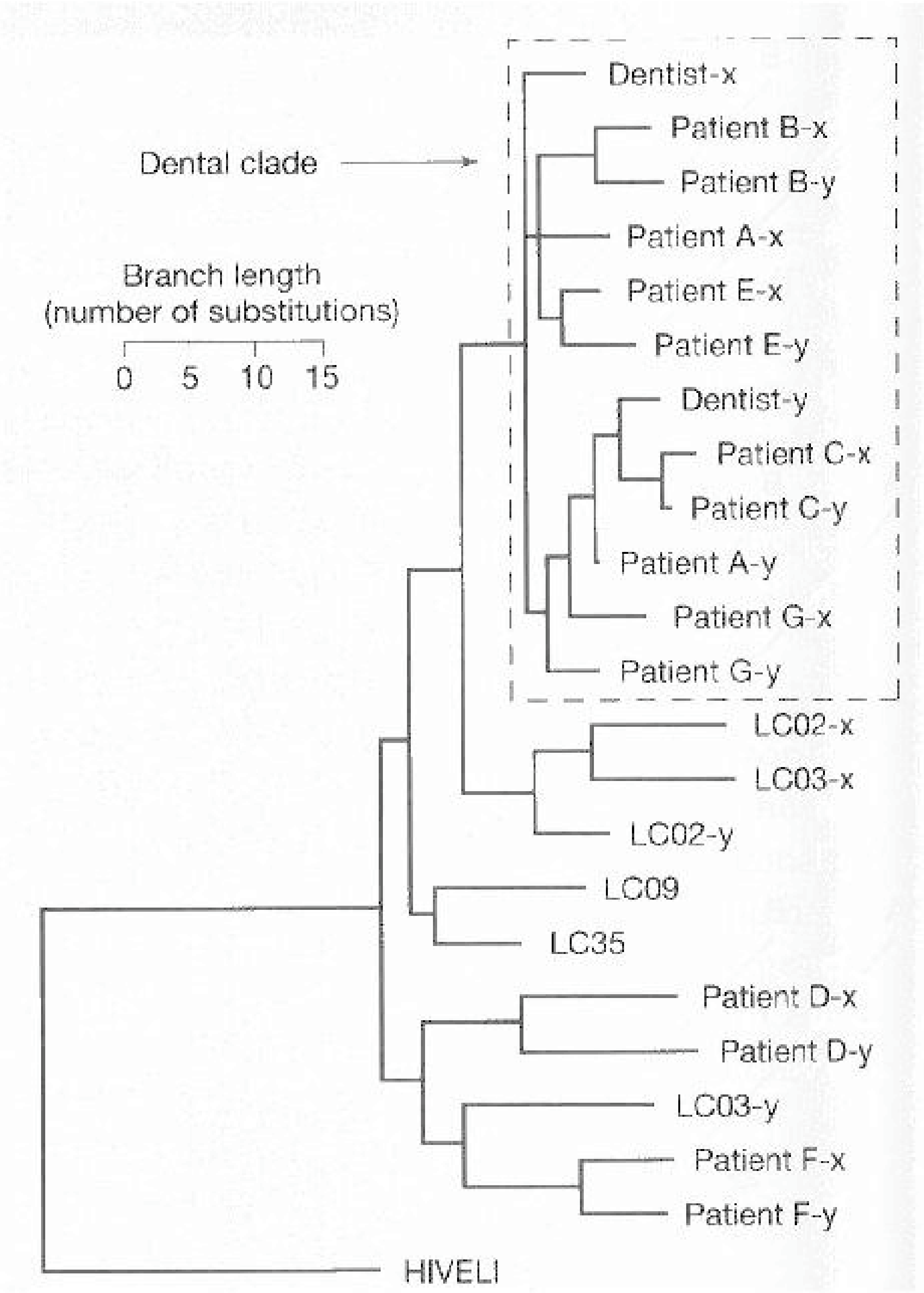
1. HIV transmission

Recently, an HIV-positive Florida dentist was suspected of having transmitted the HIV virus to his dental patients.

Although a number of his patients were HIV-positive, it was unclear whether they had been infected by visiting the dentist.

The Centers for Disease Control sequenced the gp120 gene from viruses in the dentist, his HIV-positive patients, and a number of HIV-positive people from the same community.

This data was analysed by Ou et al (1992) and reanalysed using a number of methods (parsimony, distance, maximum likelihood) by Hillis et al (1994):



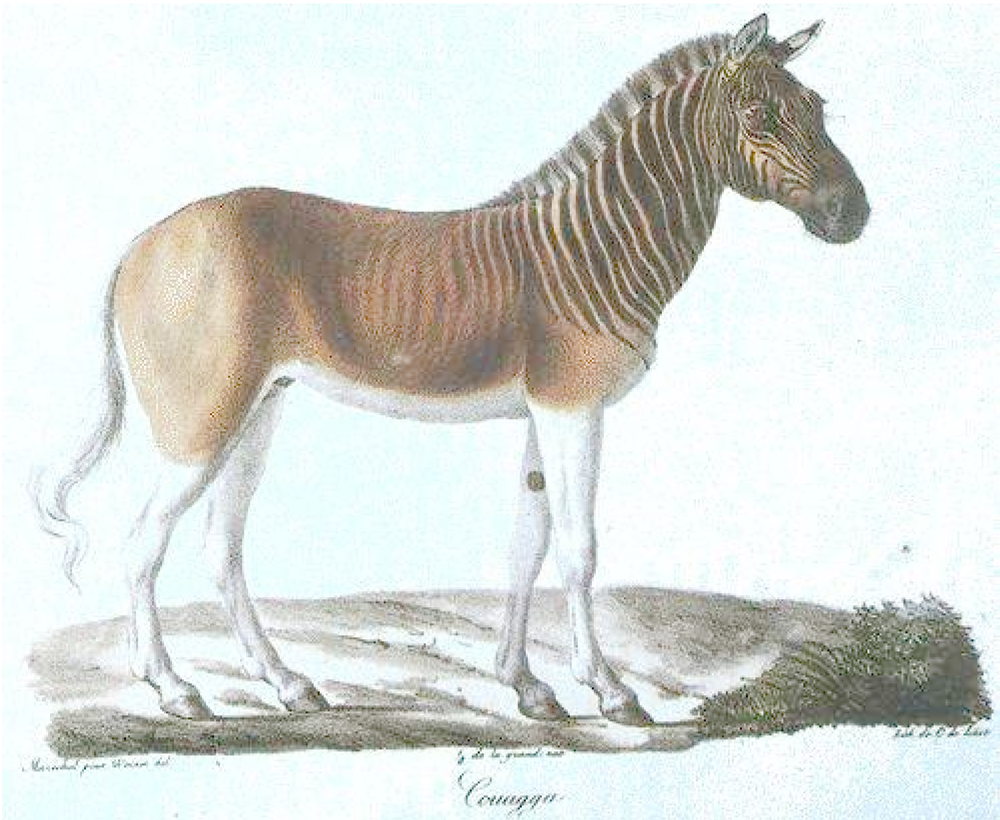
(From Freeman and Herron, 1998; x and y represent different viruses sampled from the same individual)

All methods supported the existence of a "dental clade" (dashed box), which suggests that the dentist’s HIV strain is ancestral to those found in patients A, B, C, E, and G.

This case was very important in publicizing the need for careful, sterile techniques in dental and medical practise.

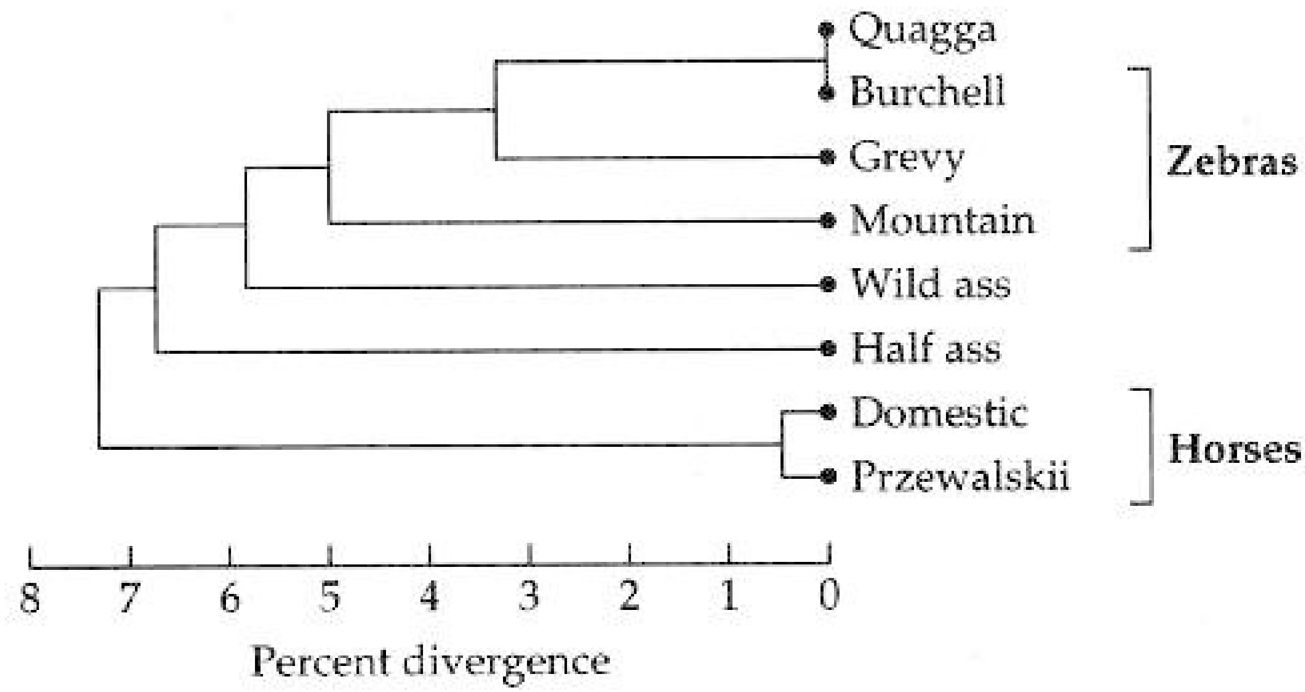
2. Ancient DNA

In 1984, Higuchi et al succeeded in isolating DNA from the 140-year old skin of a quagga, a species in the horse genus which had gone extinct with the death of the last quaaga in the Amsterdam Zoo on August 12 1883.



Numerous changes happen to ancient DNA, including pyrimidine modifications, missing bases, and intermolecular cross-links.

Although these changes make it difficult to obtain DNA for analysis, enough mitochondrial DNA was obtained to reconstruct the following phylogeny (Paabo et al, 1989):



(From Li, 1997)

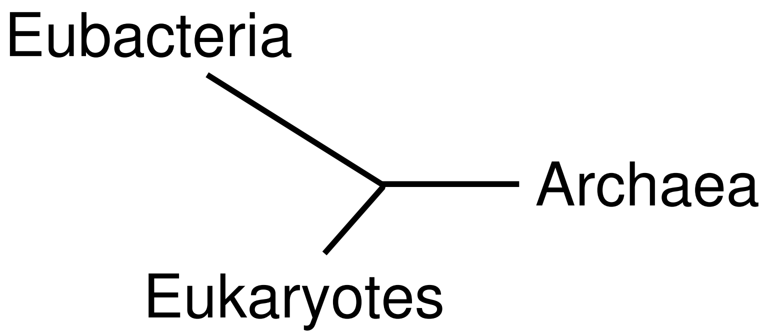
Rather than being closely related to the domestic horse, this phylogeny supports the view that the quagga is closely related to the Burchell's zebra (and is perhaps even a subspecies).

3. The Tree of Life

Recently, our view of the major groupings of living organisms has undergone a major revision, following the revelation that three major branches of life exist.

The traditional view divided living organisms into two main domains: eukaryotes and bacteria.

Molecular phylogenies of eukaryotes and bacteria suggested instead that a third group, the Archaea, exist as well.

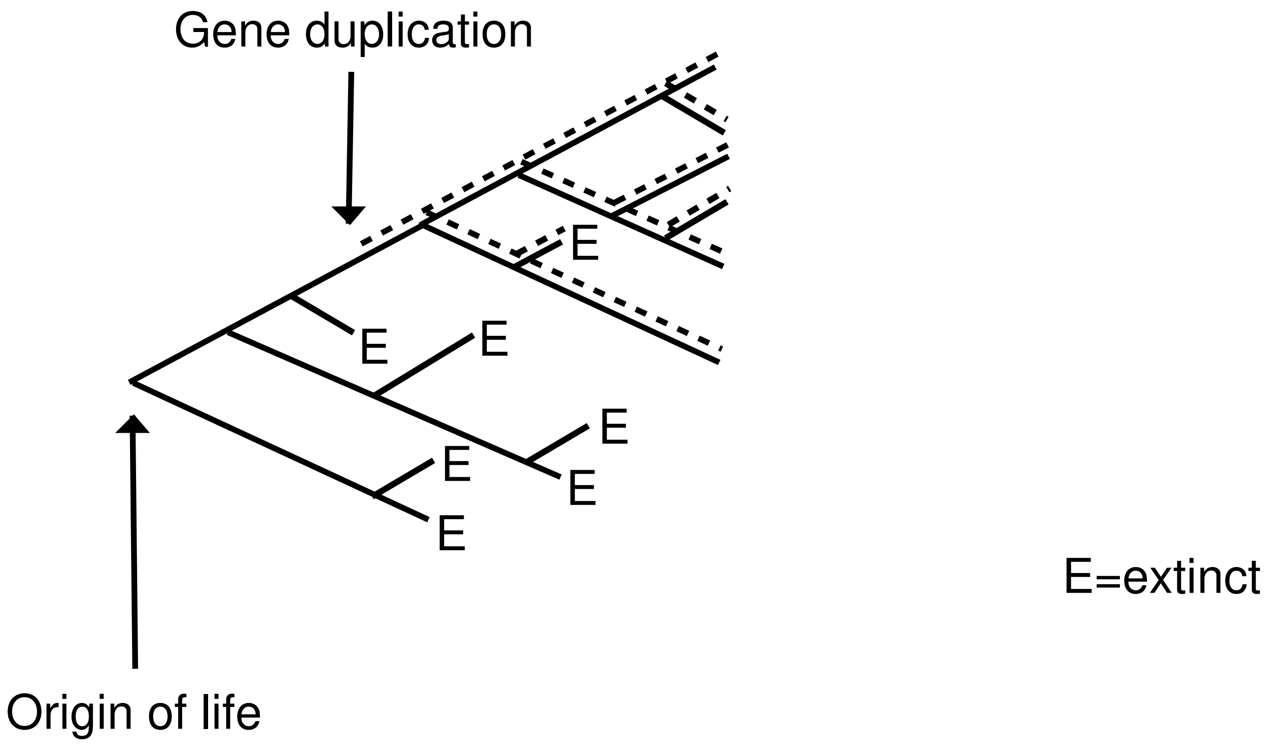


The Archaea include a number of prokaryotes living in harsh environments, including thermophiles ("heat-loving") and halophiles ("salt-loving") prokaryotes.

But how can we root the universal tree of life without an outgroup?

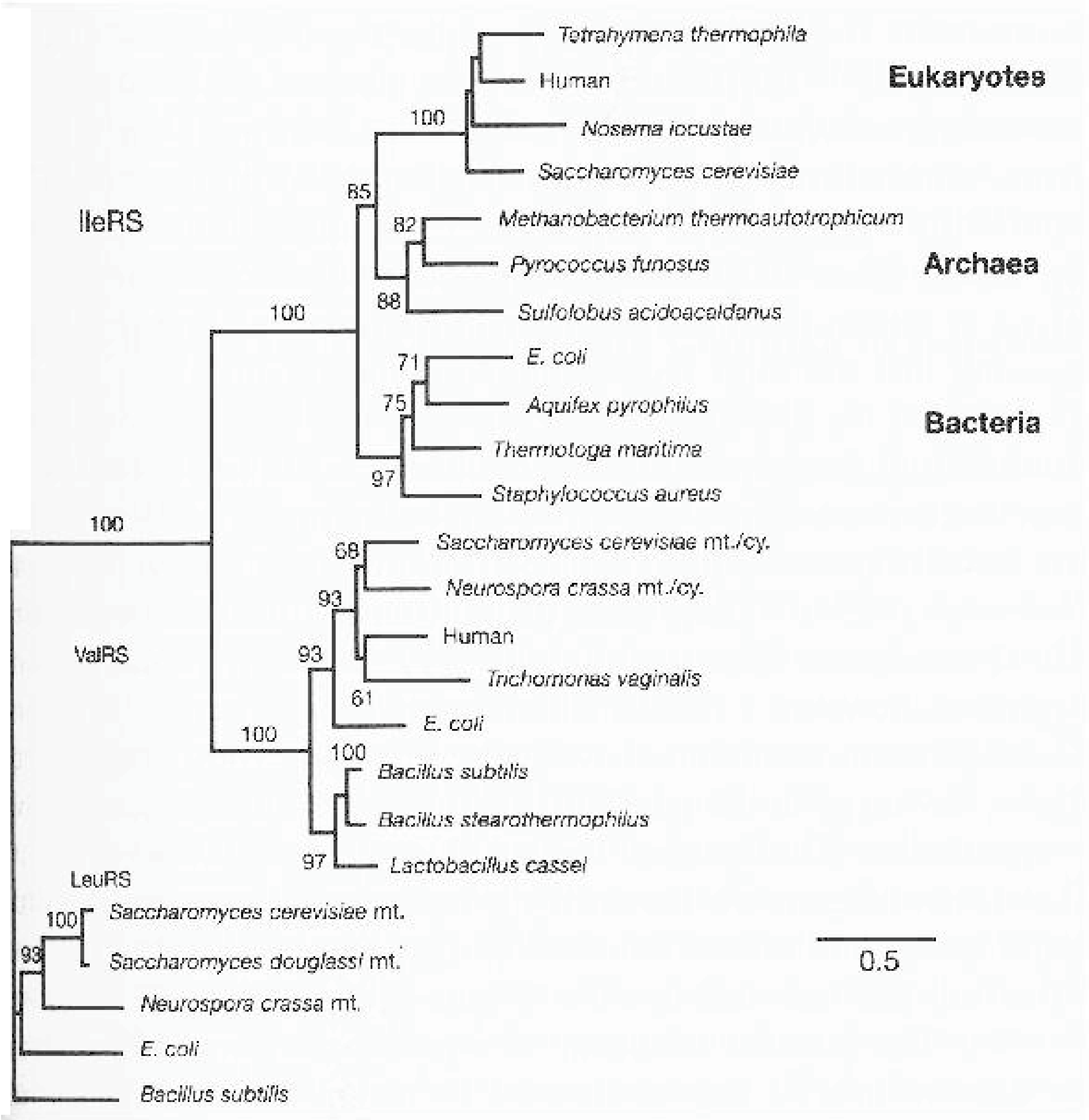
Ingeniously, Schwartz and Dayhoff suggested that a pseudo-outgroup exists in the form of duplicated genes.

If a gene duplicated before the diversification of all the branches of organisms currently alive, then the two genes will share a common ancestor before this diversification and one gene can be used to root the other.



To root the tree of life, Brown and Doolittle (1995) used aminoacyl-tRNA synthetase genes, which add amino acids to tRNAs.

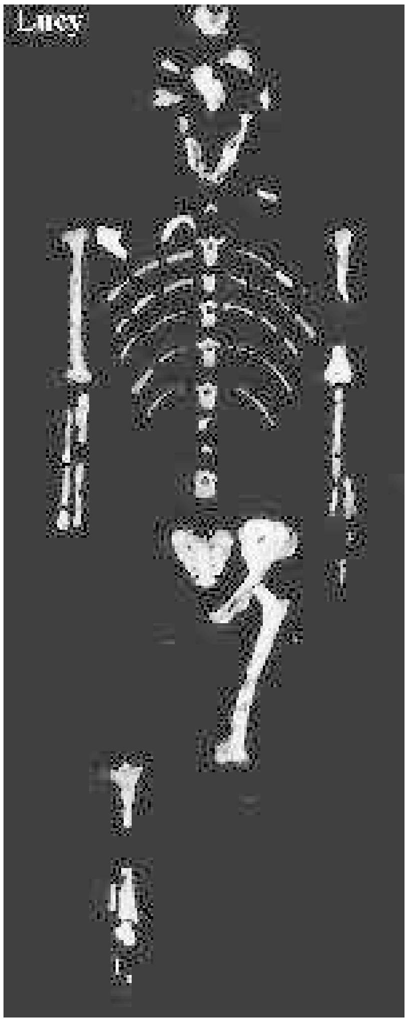
The aminoacyl-tRNA synthetase genes that add isoleucine (IleRS), valine (ValRS), and leucine (LeuRS) are structurally similar and are thought to represent very early gene duplication events.



(From Freeman and Herron, 1998)

Similar studies in other laboratories using different genes confirms this phylogeny, suggesting that the closest relatives to eukaryotes are the Archaea.

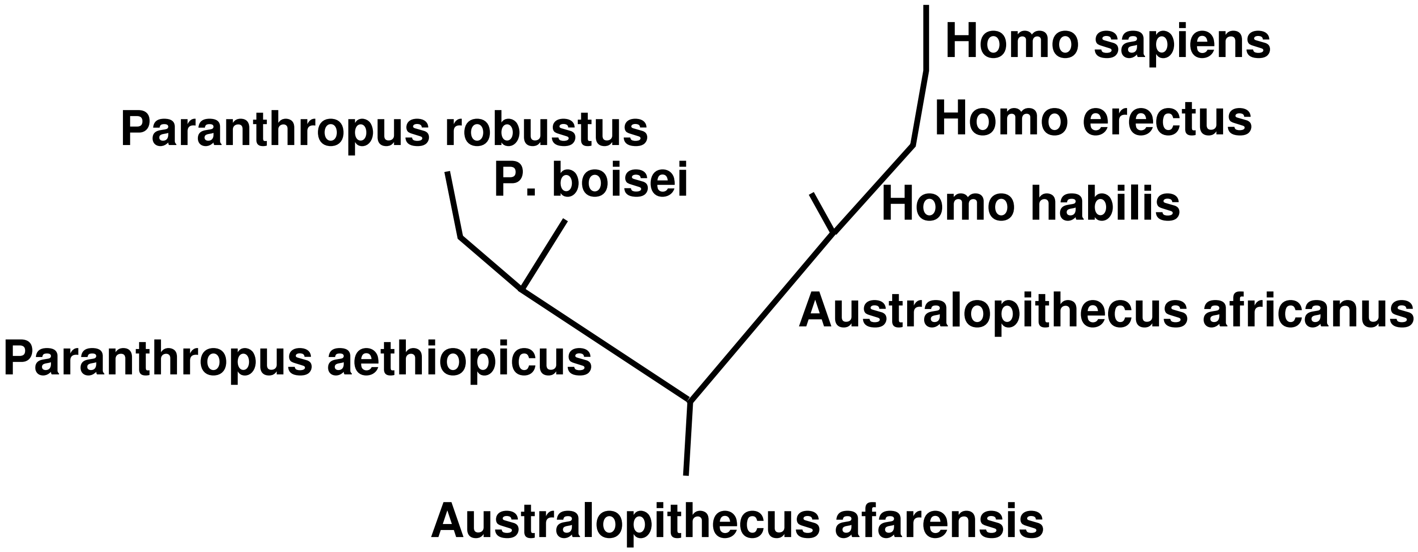
4. Mitochondrial Eve



The earliest fossils in the genus *Homo* have been found in African deposits nearly two million years old.

These early hominids, *Homo habilis*, form a link between older, more ape-like *Australopithecus* species (e.g. "Lucy") and more modern precursors to humans, *Homo erectus*.

Fossil *Homo erectus* specimens are found during a period from 1.6 MYA to 0.3 MYA, with the later specimens appearing more and more similar to *Homo sapiens* fossils which date back to 0.4 MYA.

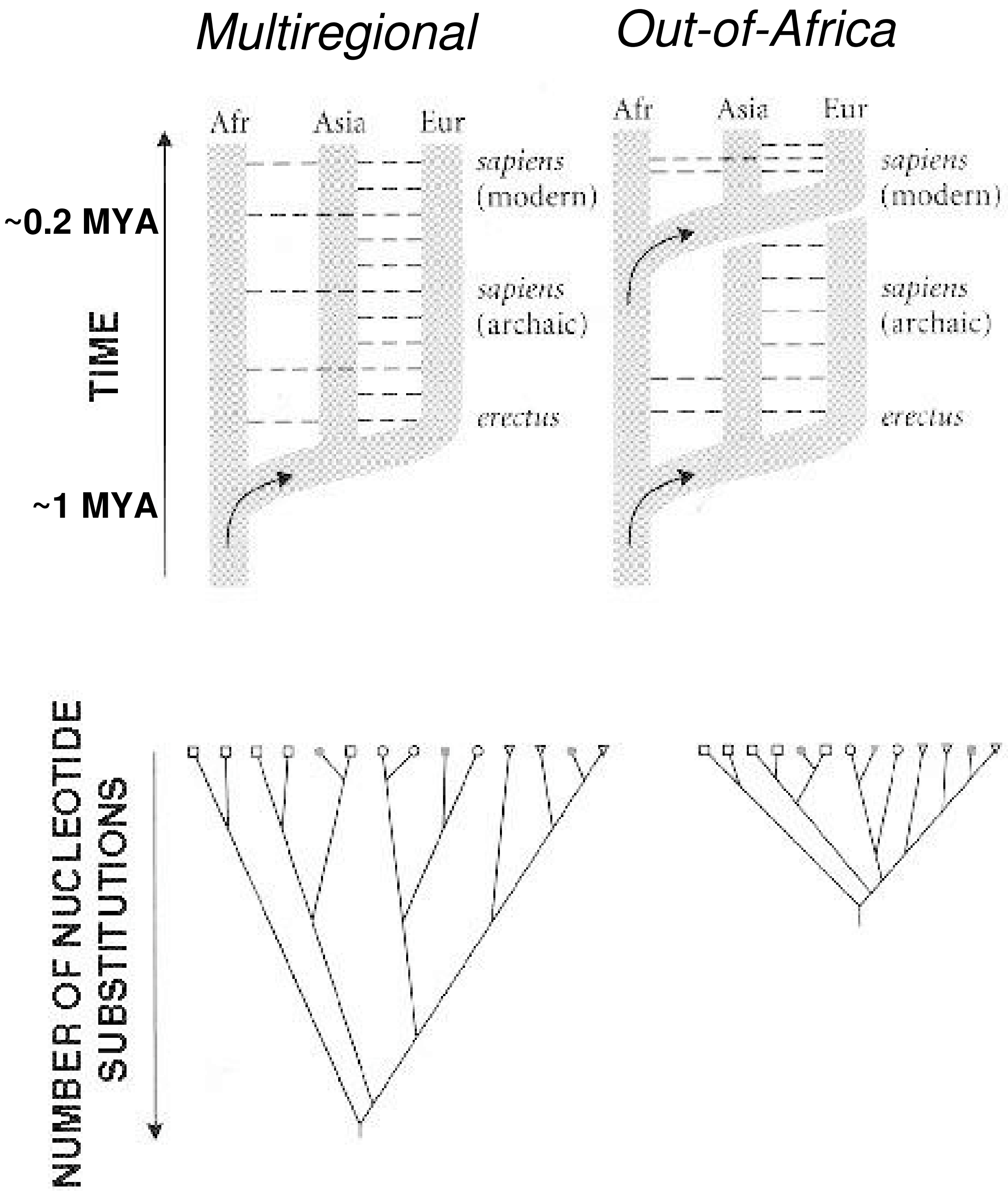


"On average, brain size (cranial capacity) increases throughout hominid history, although not at a constant rate, and there are progressive changes, from [*Australopithecus*] *afarensis* to [*Australopithecus*] *africanus* to [*Homo*] *erectus* to [*Homo*] *sapiens*, in many other features, such as the teeth, face, pelvis, hands, and feet...Although many issues remain unresolved, the most important point is fully documented: *modern humans evolved from an ape-like ancestor*"

-- Futuyma (1998), p. 733

How modern *Homo sapiens* are related to the *Homo erectus* populations that existed throughout Africa and Asia has been a subject of much debate.

The two primary views are the *multiregional* hypothesis and the *out-of-Africa* hypothesis:



(From Futuyma, 1998; dashed lines suggest gene flow)

The multiregional hypothesis claims that modern *Homo sapiens* evolved from precursors throughout Africa and Asia, with gene flow ensuring that modern traits were common to all populations.

The out-of-Africa hypothesis claims that modern *Homo sapiens* evolved fairly recently from a population within Africa and then migrated out of Africa to form modern *Homo sapiens*.

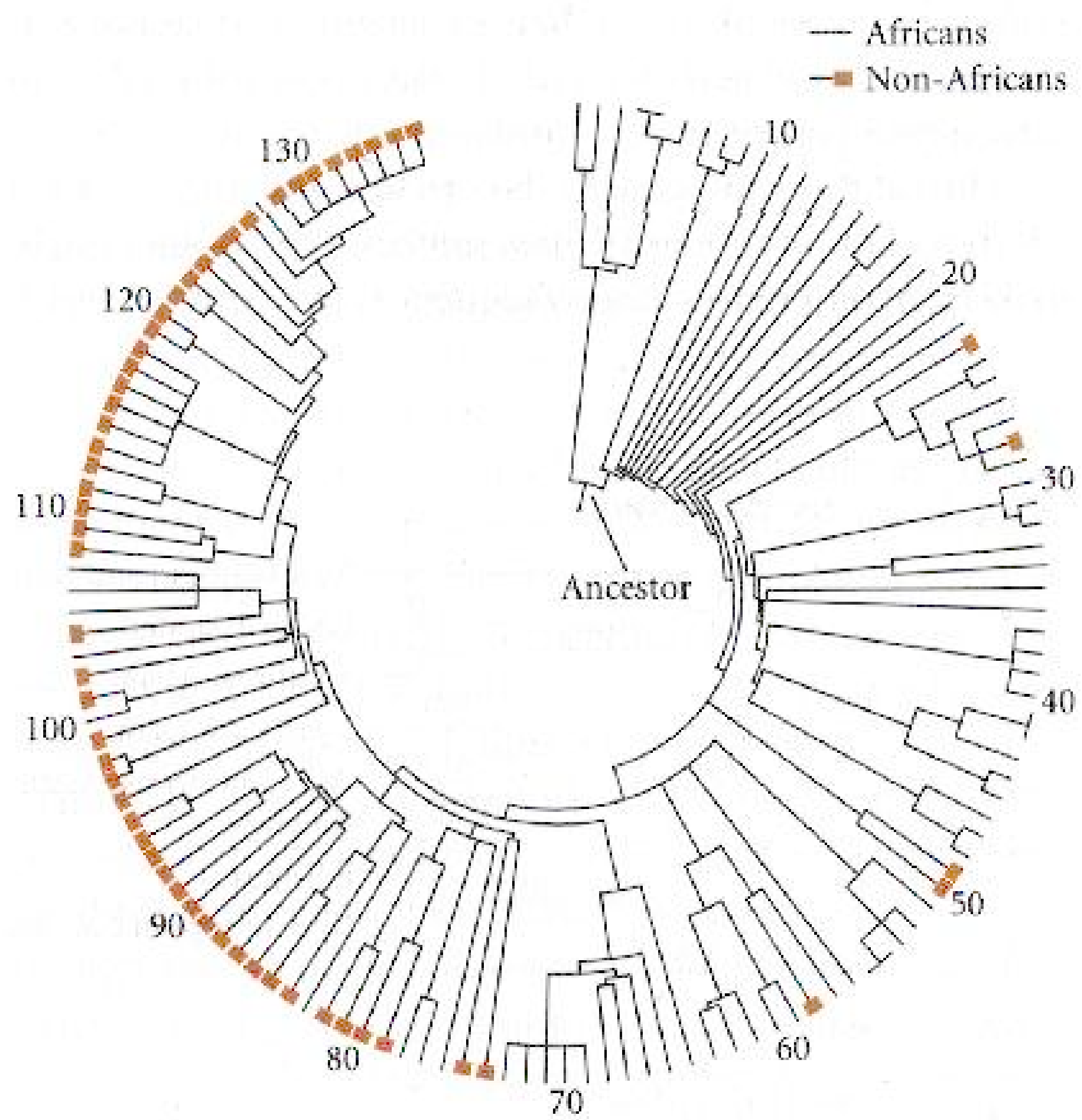
The two hypotheses lead to very different predictions:

	Multiregional	Out-of-Africa
Most recent common ancestor:	>1,000,000 YA	~ 200,000 YA
Genetic diversity:	High	Low

Cann et al (1987) and Vigilant et al (1991) used phylogenies estimated from mitochondrial DNA to test the above hypotheses.

For example, Vigilant et al (1991) sequenced two rapidly evolving segments of the mitochondrial genome from 189 individuals.

From this data, they constructed a tree using parsimony:



The time until the most recent common ancestor of these sequences (the "Mitochondrial Eve") was estimated to have lived 166,000 - 249,000 years ago, consistent with the out-of-Africa hypothesis.

In addition, the greatest genetic diversity was found in Africa, suggesting that modern *Homo sapiens* did evolve in Africa, with other geographical regions containing only some of the mitochondrial genomes present in Africa.

This study was critisized for a number of reasons, most importantly that only one tree was presented within the paper. Many trees were equally parsimonious and some did not support an African origin for humans.

Other studies soon followed:

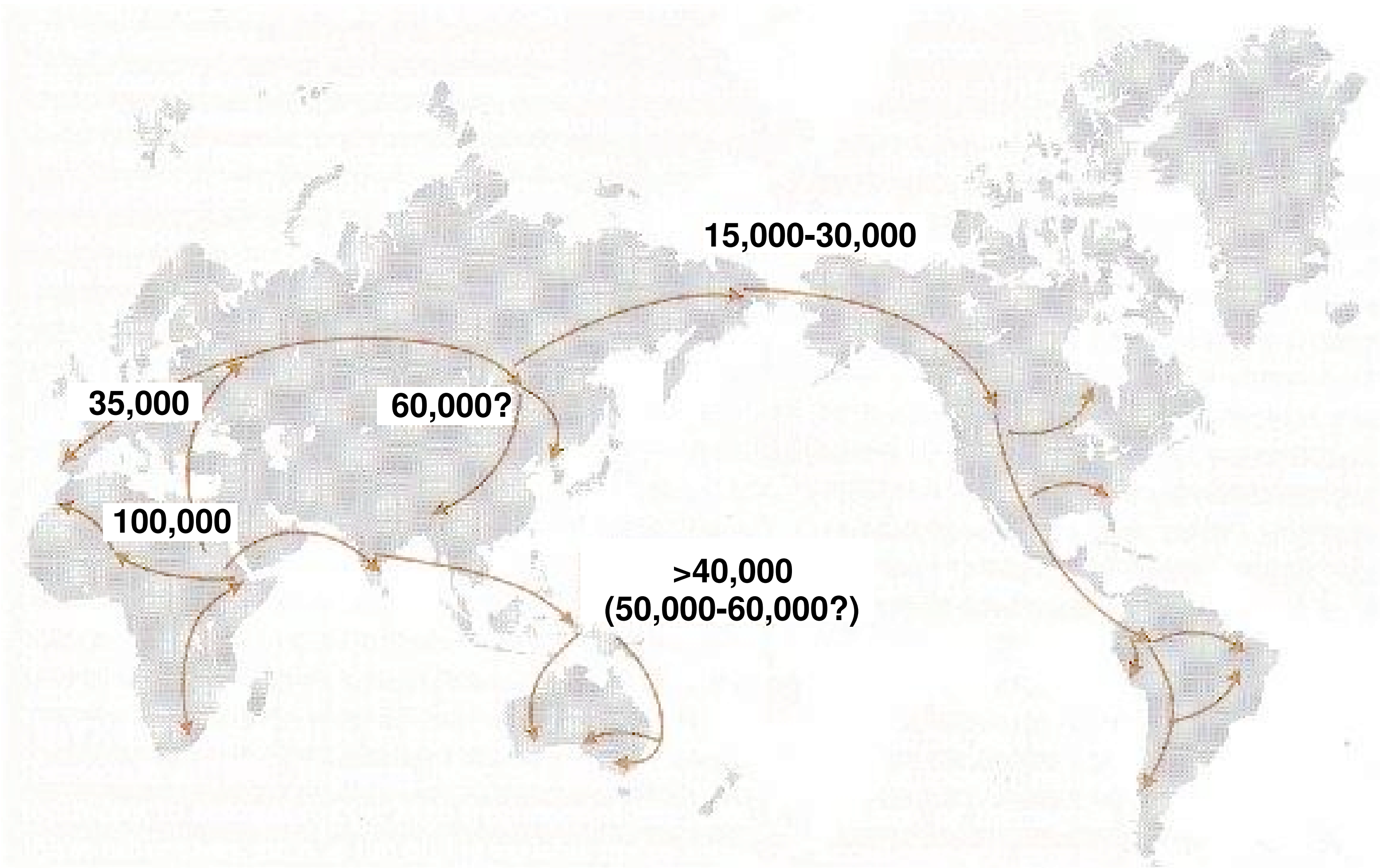
- Ruvolo et al (1993) used similar data and dated Eve to 129,000 - 536,000 YA
- Horai et al (1995) used entire mitochondrial genomes (!) to date Eve to 125,000 - 161,000 YA
- Bowcock et al (1994) used microsatellite data to confirm that the greatest genetic diversity occurs in Africa
- Goldstein et al (1995) used this microsatellite data to date Eve to 75,000 - 287,000 YA

These last studies are particularly important.

It is possible for a single gene (or a completely linked segment like the mitochondrial genome) to provide a biased historical picture. [For example, a beneficial mutation may have recently appeared and fixed.]

Several unlinked genes are needed to get a reliable picture of the phylogeny of a species.

Although the debate continues and has not been definitively settled, the balance of evidence suggests that modern *Homo sapiens* did evolve relatively recently (100,000-300,000 YA) from populations of archaic *Homo sapiens* within Africa and then migrated throughout the world.



SOURCES:

- HIV transmission and the Tree of Life figures and discussion: Freeman and Herron (1998) Evolutionary Analysis. Prentise Hall.
- Ancient DNA figures and discussion: Li (1997) Molecular Evolution. Sinauer Associates, MA.
- Mitochondrial Eve figures and discussion: Futuyma (1998) Evolutionary Biology. Sinauer Associates, MA.
- Take a walk through human prehistory.