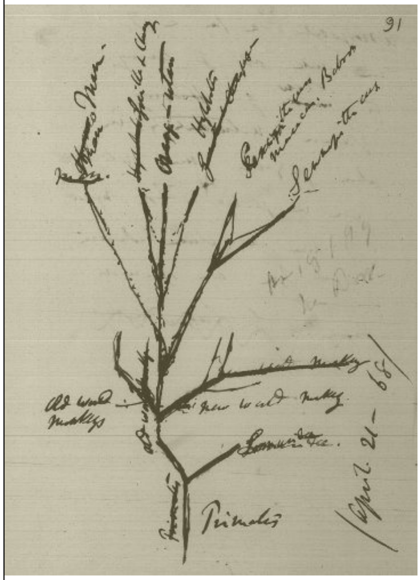
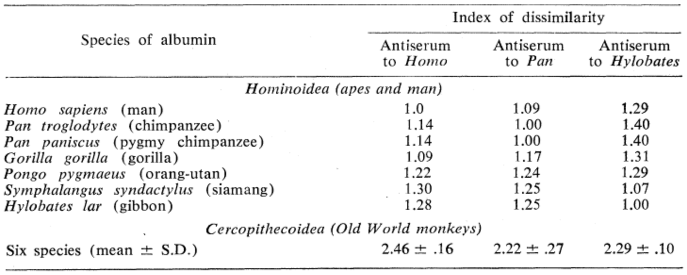
The Chimp-Human-Gorilla Trichotomy

March 2, 2015



Darwin's sketch of hominoid tree

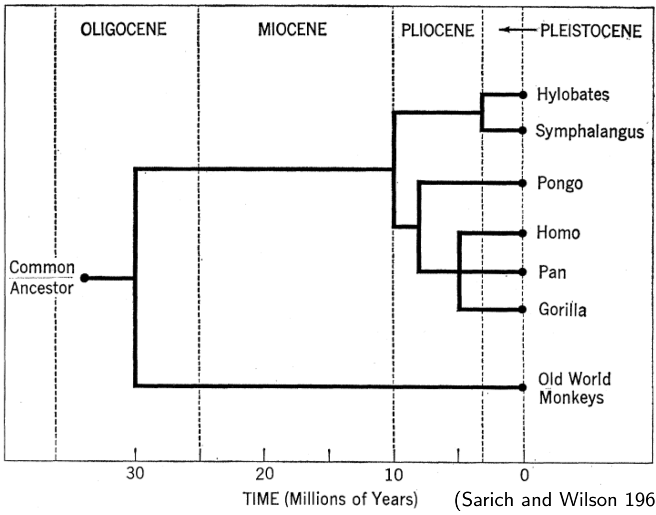
Data of Sarich and Wilson (1967)



Species of albumin	Index of dissimilarity		
	Antiserum to *Homo*	Antiserum to *Pan*	Antiserum to *Hylobates*
Hominoidea (apes and man)			
Homo sapiens (man)	1.0	1.09	1.29
Pan troglodytes (chimpanzee)	1.14	1.00	1.40
Pan paniscus (pygmy chimpanzee)	1.14	1.00	1.40
Gorilla gorilla (gorilla)	1.09	1.17	1.31
Pongo pygmaeus (orang-utan)	1.22	1.24	1.29
Symphalangus syndactylus (siamang)	1.30	1.25	1.07
Hylobates lar (gibbon)	1.28	1.25	1.00
Cercopithecoidea (Old World monkeys)			
Six species (mean ± S.D.)	2.46 ± .16	2.22 ± .27	2.29 ± .10

1. Inject rabbit with blood from species X.
2. Let rabbit's immune system form antibodies.
3. Mix blood from rabbit with blood from species Y.
4. Strength of immune reaction ↔ similarity of X and Y.

Primate tree from immunological data

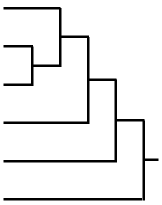


(Sarich and Wilson 1967)

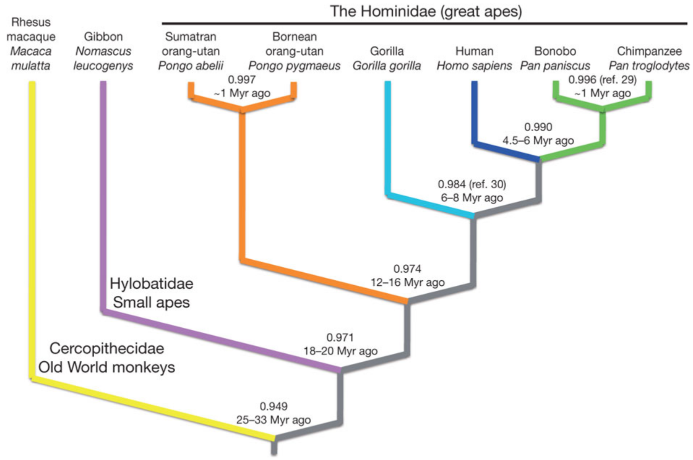
Primate tree from transposable elements

Species	Transposon blocks				
Human	○	●	●	●	●
Bonobo	●	●	●	●	●
Chimp	●	●	●	●	●
Gorilla	○	○	●	●	●
Orangutan	○	○	○	●	●
Gibbon	○	○	○	○	●
# of transposons	1	7	30	15	20

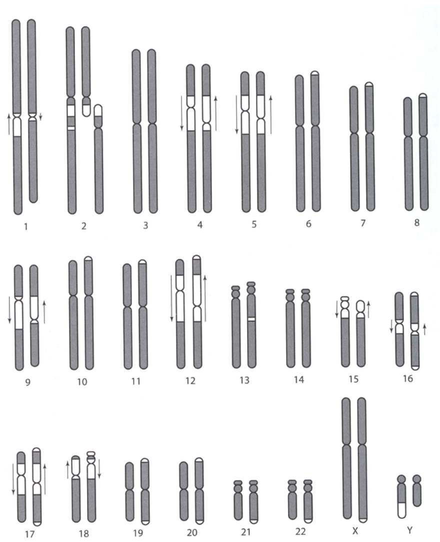
Key: ●,present; ○,absent



Primate tree from full genomes

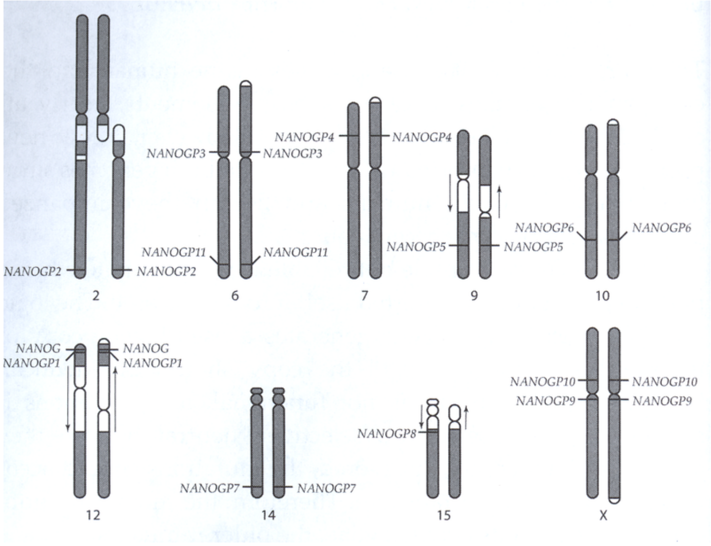


(Locke et al 2011)



Human and chimp genomes differ by 10 major rearrangements.

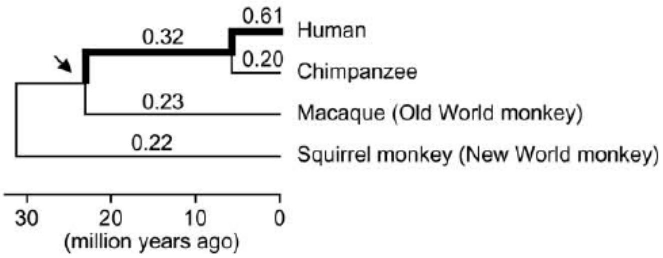
Human and chimp Nanog pseudogenes



The K_a/K_s ratio

- A *synonymous site* is one at which any mutation would be synonymous.
- A *non-synonymous site* is one at which no mutation would be.
- Many sites contribute a fraction to each category.
- In comparison between two species, K_a is number of non-synonymous changes per non-synonymous site.
- K_s: synonymous changes per synonymous site.
- Functional constraint: $K_a/K_s < 1$.

Weaker selective constraint in hominin brains



Dorus et al (2004)

The numbers are K_a/K_s ratios.

All are < 1: evolve slower than pseudogenes.

But selective constraint is weaker in hominin brains.

Chimps and humans

Nielsen et al (2005) study nearly 14,000 genes in chimps and humans.

Look for genes that evolve *faster* than pseudogenes ($K_a/K_s > 1$) in either chimp or human.

Fast adaptive evolution in sensory perception, immunity, tumor surpression and spermatogenesis.

Not in genes expressed in brain.

Details from Nielsen et al (2005)

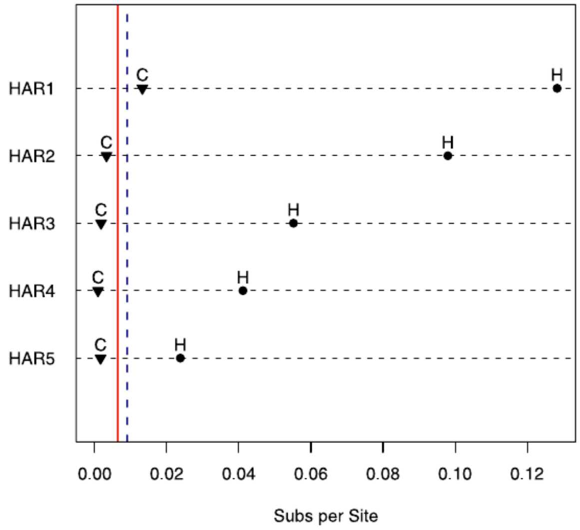
Biological Process	Genes	*p*-value
Immunity and defense	417	0.0000
T-cell-mediated immunity	82	0.0000
Chemosensory perception	45	0.0000
Unclassified	3,069	0.0000
Olfaction	28	0.0004
Gametogenesis	51	0.0005
Natural killer-cell-mediated immunity	30	0.0018
Spermatogenesis and motility	20	0.0037
Inhibition of apoptosis	40	0.0047
Interferon-mediated immunity	23	0.0080
Sensory perception	133	0.0160
B-cell- and antibody-mediated immunity	57	0.0298

Human-accelerated regions

Pollard et al (2006) scanned the entire genome for regions that are

- at least 100 nucleotides,
- conserved in vertebrates,
- but evolved rapidly in hominins.
- Found 202 such “Human-Accelerated Regions,” or HARs.
- The fastest is HAR1, which codes for RNA involved in development of neocortex.

Rates of evolution in top 5 HARs



Changes in gene regulation

- Most HARs are *noncoding* but near genes—probably involved in gene regulation.
- Supports King-Wilson hypothesis: human evolution was mainly about changes in gene regulation.

Human-accelerated regions

- A *selective sweep*—when an advantageous mutation spreads through the population.
- Removes variation from region near the mutant nucleotide.
- 2 of top 5 HARs show evidence of a selective sweep.
- In other cases, sweeps may have occurred too long ago to be detected.

Has there been enough time for mutation to erase the effects of ancient sweeps in the hominin lineage?

- Suppose gene diversity is 0 just after the sweep.
- It will get half-way to the equilibrium gene diversity in about N generations, where N is the population size.
- Perhaps 200,000 years, if $N = 10,000$.
- A sweep 2 my ago would be completely invisible.