

Monkey Business in the Chimp Genome

Jeffrey Tomkins, PhD



THE ORIGIN OF SPECIES

BY MEANS OF NATURAL SELECTION,

OR THE

PRESERVATION OF FAVOURED RACES IN THE STRUGGLE
FOR LIFE.

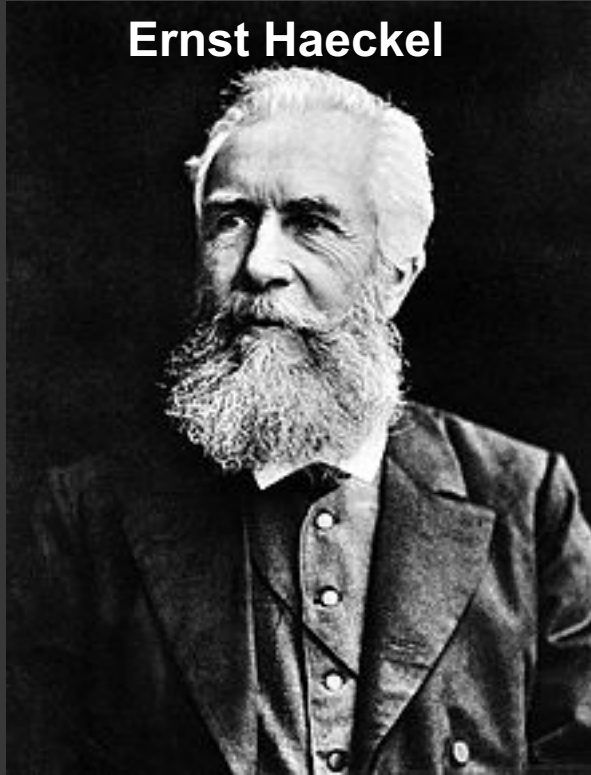
THE
DESCENT
OF
MAN

CHARLES
DARWIN

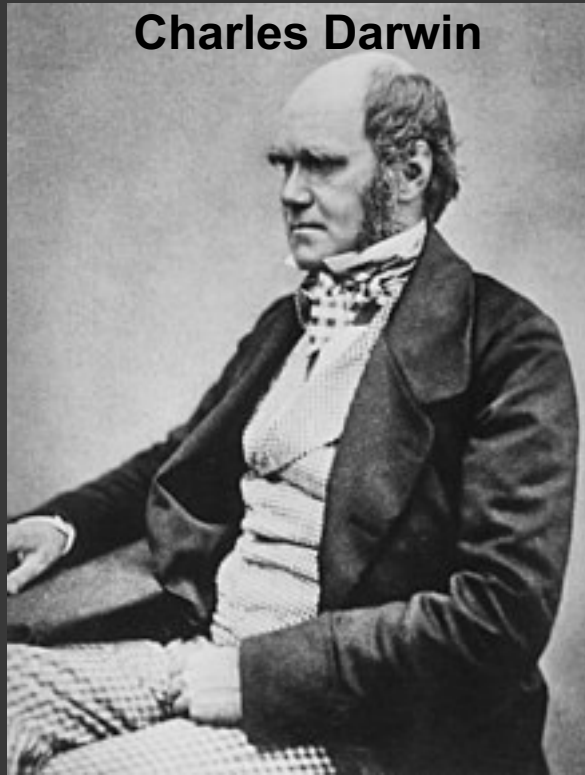
With an introduction by H. James Birx

GREAT MINDS SERIES

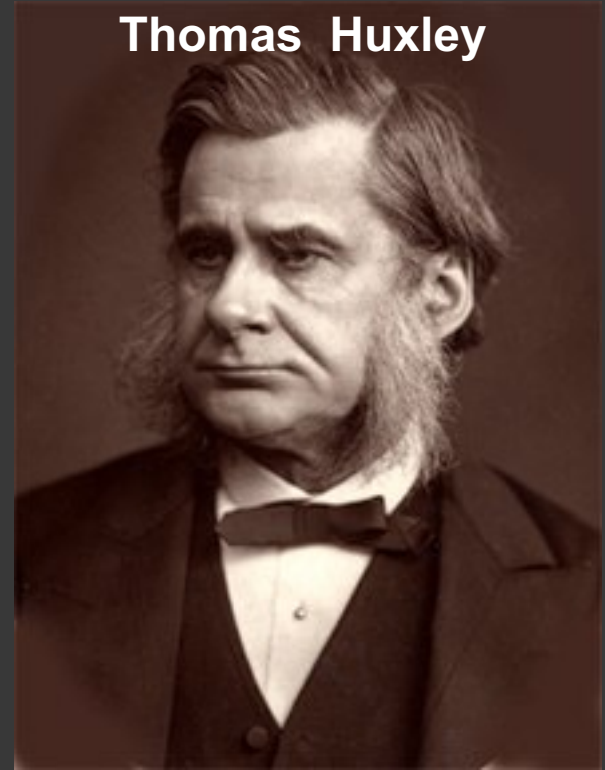
Ernst Haeckel



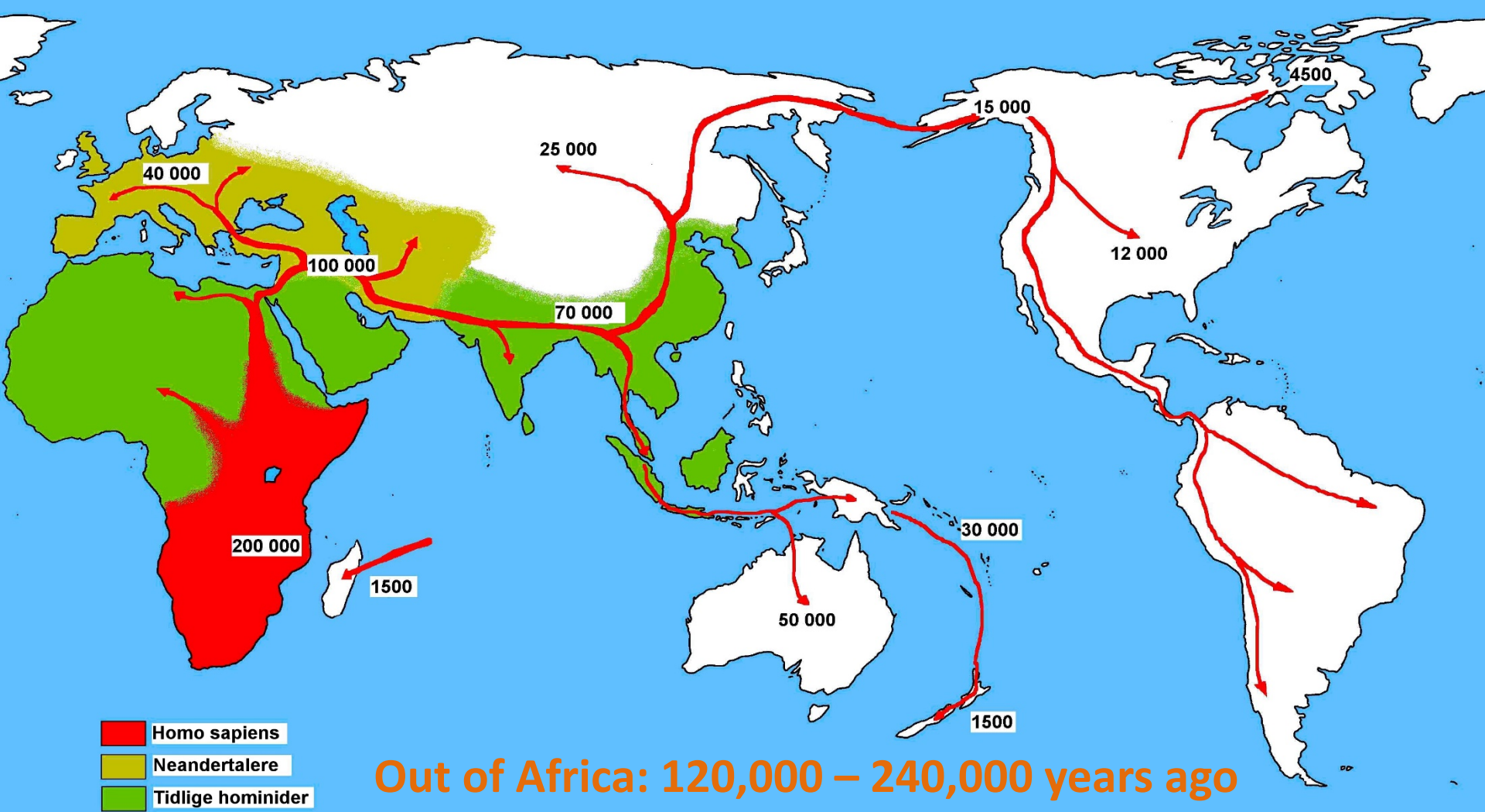
Charles Darwin



Thomas Huxley

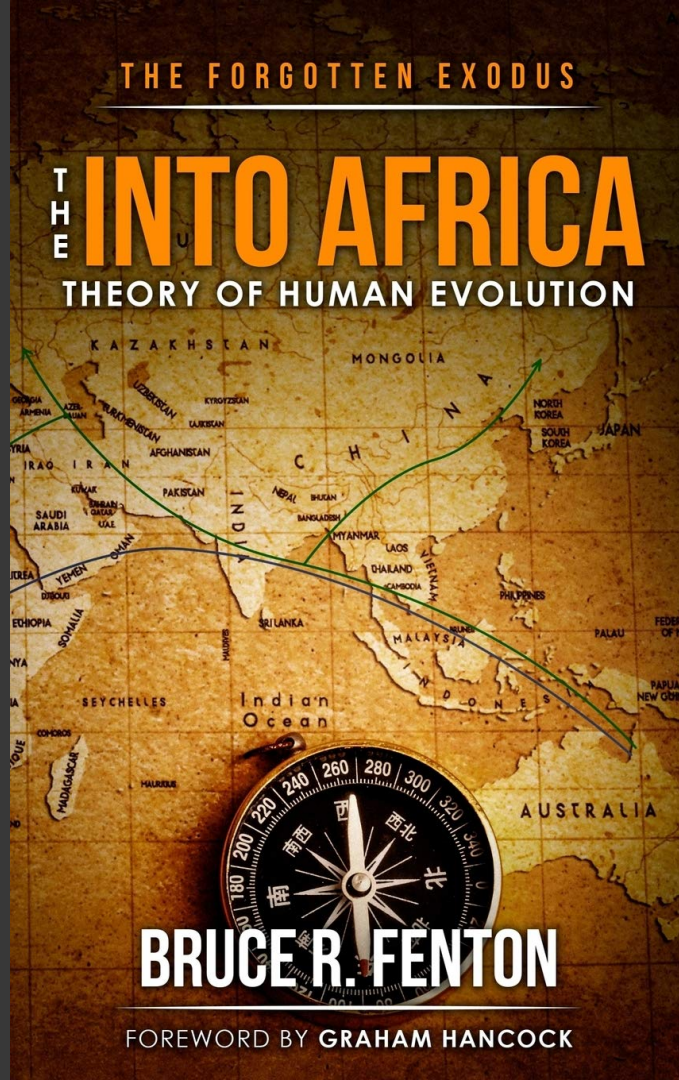


The idea of “human evolution”



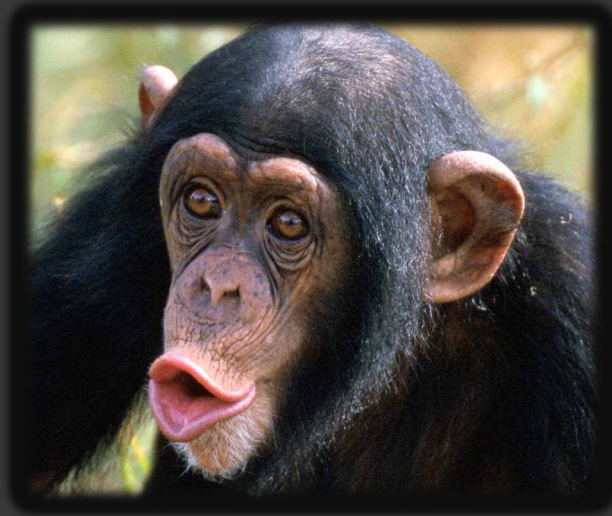
Locations of *H. erectus* fossils

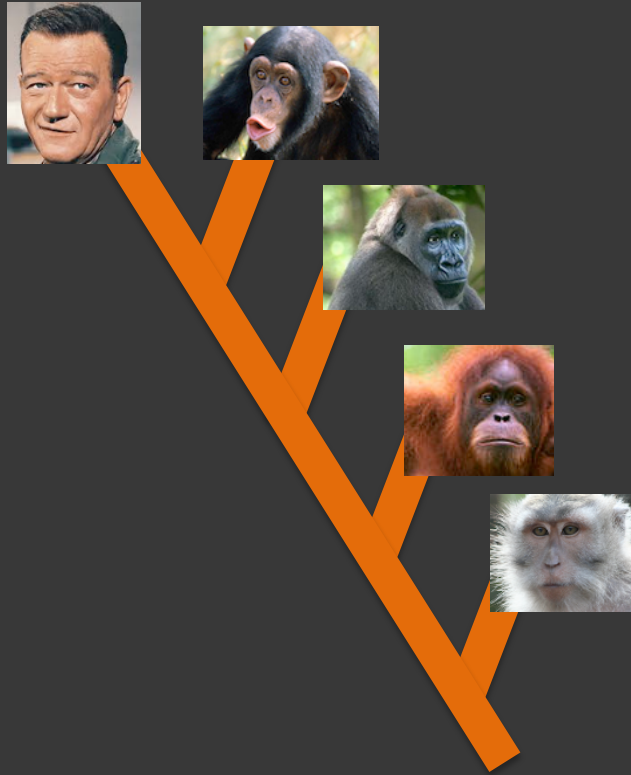






**Chimpanzee was chosen as the closest
living ancestor to human**





**Standard evolutionary
tree (phylogeny) for
human evolution**

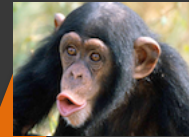
Morphological and molecular mosaics between humans and apes

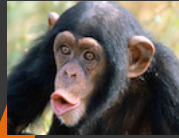
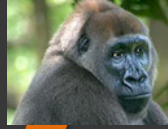
Journal of Biogeography (J. Biogeogr.) (2009)

**SPECIAL
PAPER**

Evolution of the second orangutan: phylogeny and biogeography of hominid origins

John R. Grehan^{1*} and Jeffrey H. Schwartz²





Alpha motif protein 11



ACAP3

“in 30% of the genome, gorilla is closer to human or chimpanzee than the latter are to each other.”



Sally, A. et al. 2012. Insights into hominid evolution from the gorilla genome sequence. *Nature*. 483 (7388): 169-175.

“For about 23% of our genome, we share no immediate genetic ancestry with our closest living relative, the chimpanzee”



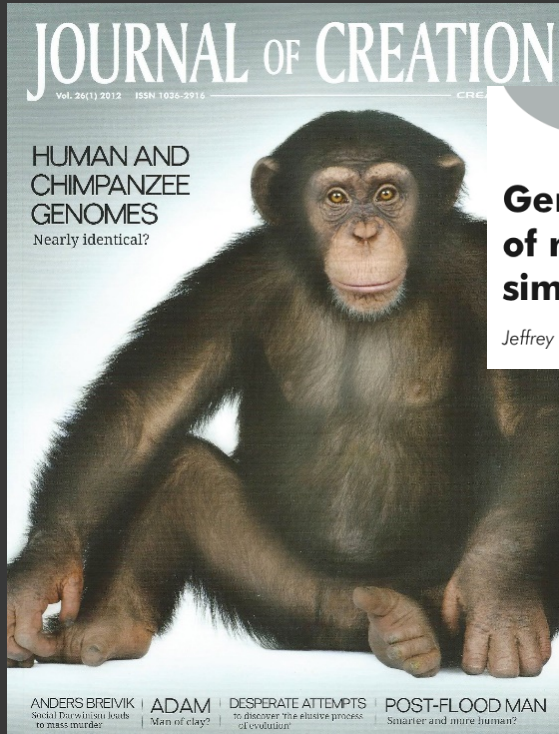
Ebersberger, I. et al., 2007, “Mapping human genetic ancestry.” *Journal of Molecular Biology and Evolution*

**Is the DNA of human and
chimpanzees 98 to 99% identical**



**“About two thirds could be
unambiguously aligned to DNA
sequences in humans”**

Ebersberger, I. et al. 2002. Genomewide Comparison of DNA Sequences between Humans and Chimpanzees. *American Journal of Human Genetics*. 70 (6): 1490-1497.



PAPERS

Genomic monkey business—estimates of nearly identical human-chimp DNA similarity re-evaluated using omitted data

Jeffrey Tomkins and Jerry Bergman

**Human and chimp
genomes only 66 to 87%
similar when omitted
data is factored back in.**



AN GENO

articles

Initial sequencing and analysis of the human genome

International Human Genome Sequencing Consortium*

* A partial list of authors appears on the opposite page. Affiliations are

The human genome holds an extraordinary trove of information for biology, medicine and evolution. Here we report the results of an international collaboration to determine the draft sequence of the human genome. We also present an initial analysis of the data.



biology, medicine and evolution. Here we report the results of an international collaboration to determine the draft sequence of the human genome. We also present an initial analysis of the data.

The Sequence of the Human Genome

J. Craig Venter,^{1*} Mark D. Adams,¹ Eugene W. Myers,¹ Peter W. Li,¹ Richard J. Mural,¹ Granger G. Sutton,¹ Hamilton O. Smith,¹ Mark Yandell,¹ Cheryl A. Evans,¹ Robert A. Holt,¹ Jeannine D. Gocayne,¹ Peter Amanatides,¹ Richard M. Ballew,¹ Daniel H. Huson,¹ Jennifer Russo Wortman,¹ Qing Zhang,¹ Chinnappa D. Kodira,¹ Xiangqun H. Zhang,¹ Lin Chen,¹ Marian Skupski,¹ Gangadharan Suthandharan,¹ George L. Gabor Miklos,² Catherine Nelson,³ Victor A. McKusick,⁶ Norton Zinder,⁷ A. Carolyn Slayman,¹⁰ Michael Hunkapiller,¹¹ R. Michael Flanigan,¹ Liliana Florea,¹ Aaron Halpern,¹ Clark Mobarry,¹ Knut Reinert,¹ Karin Remington,¹ Vivien Bonazzi,¹ Rhonda Brandon,¹ Michele C.

Vol 437 | September 2001 | doi:10.1038/nature04072

nature

ARTICLES

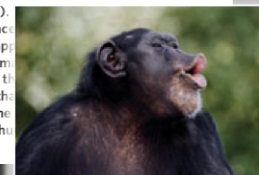


Zuoming Deng,¹ Valerie E. Gabrielian,¹ Wei J. Heiman,¹ Maureen E. Yiding Lei,¹ Zhenya Li, Arkulov,¹ Natalia Miloslavskaya,¹ Beena Neelam,¹ Debajyoti Sengupta,¹ Jingtao Sun,¹ Zhongyuan Wides,¹³ Chunlin Xia, Longyu Zhang,¹ Qi Zhang,¹ Shaying Zhao,¹² Denis M. Kravchik,¹ Trevor J. Badger,¹ Mary B. A. Center,¹ Ming Lai Chao,¹ Susanne Dietz,¹ Kristin R. Hart,¹ Jason Haver

Initial sequence of the chimpanzee genome and comparison with the human genome

The Chimpanzee Sequencing and Analysis Consortium*

Here we present a draft genome sequence of the common chimpanzee (*Pan troglodytes*). Compared with the human genome, we have generated a largely complete catalogue of the genetic differences between the human and chimpanzee species diverged from our common ancestor, constituting approximately 3 million single-nucleotide changes, five million insertion/deletion events, and various chromosomal rearrangements. This catalogue to explore the magnitude and regional variation of mutational forces shaping the genomes of the two species. The strength of positive and negative selection acting on their genes. In particular, we find that the human and chimpanzee protein-coding genes are highly correlated and dominated by the deleterious alleles. We also use the chimpanzee genome as an outgroup to investigate human evolution and identify signatures of selective sweeps in recent human evolution.

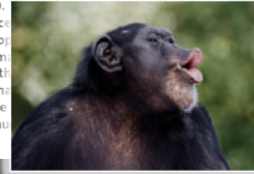


ARTICLES

Initial sequence of the chimpanzee genome and comparison with the human genome

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Here we present a draft genome sequence of the common chimpanzee (*Pan troglodytes*). By comparing this sequence with the human genome, we have generated a largely complete catalogue of the genetic differences between the two species. The human and chimpanzee species diverged from our common ancestor, constituting approximately 1% of the genome. This catalogue includes single-nucleotide changes, five million insertion/deletion events, and various chromosomal rearrangements. We use this catalogue to explore the magnitude and regional variation of mutational forces shaping the genomes of the two species, and to estimate the strength of positive and negative selection acting on their genes. In particular, we find that the human and chimpanzee protein-coding genes are highly correlated and dominated by the same set of deleterious alleles. We also use the chimpanzee genome as an outgroup to investigate human evolution, and to identify signatures of selective sweeps in recent human evolution.



$((\% \text{ alignment Identity} \times \text{amount aligned}) / 2004 \text{ human genome size}) \times 100$

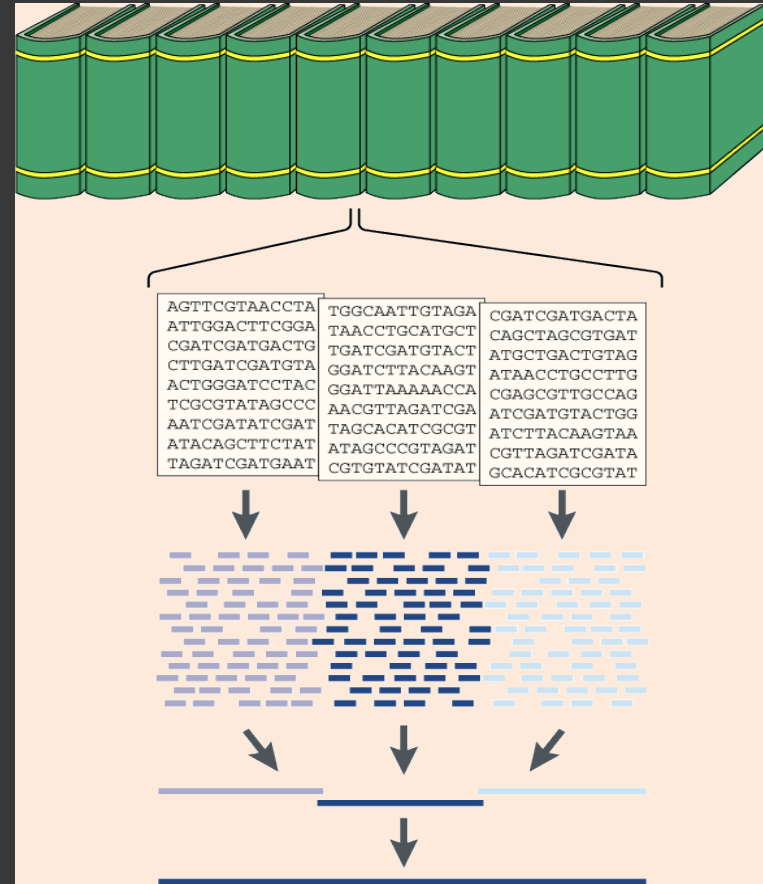
$$((.9577 \times 2.4 \text{ Gb}) / 2.85 \text{ Gb}) = 81\%$$

Cherry Picking the data...



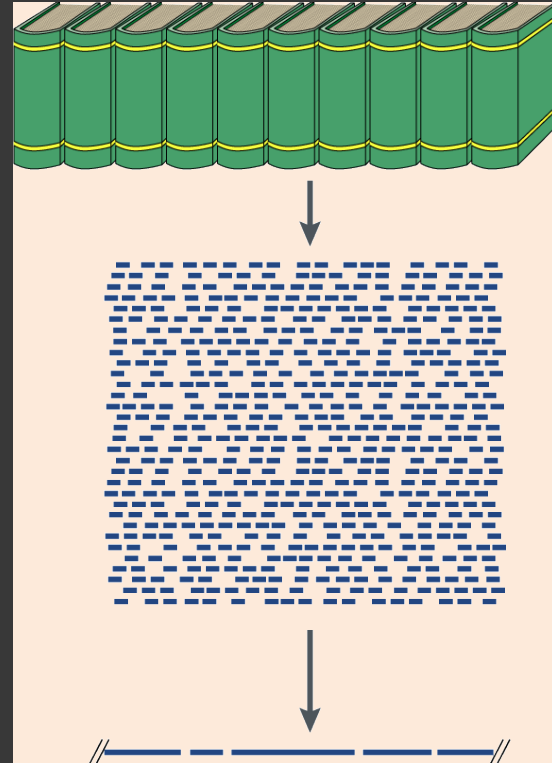
Human Genome Sequencing Project

Page-by-page
sequencing strategy



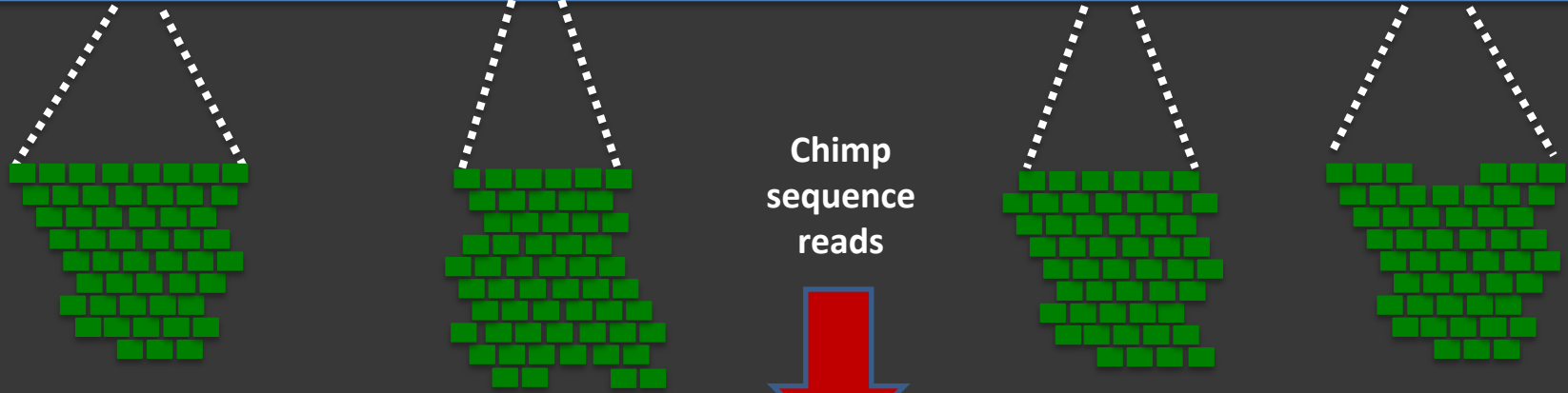
Chimp - All-at-once sequencing strategy

- Shred the whole genome into small pieces
- Decipher the words on each fragment
- Look for overlaps to assemble everything at once
- Align the sequences onto human genome as a scaffold





Human chromosome (reference sequence)



Chimp
sequence
reads



Reconstructed chimp chromosome based on human

Gaps





June 2018

“the higher-quality human genome assemblies have often been used to guide the final stages of nonhuman genome projects, including the order and orientation of sequence contigs and, perhaps more importantly, the annotation of genes”

“This bias has effectively “humanized” other ape genome assemblies”

High-resolution comparative analysis of great ape genomes

Zev N. Kronenberg¹, Ian T. Fiddes^{2,*}, David Gordon^{1,3,*}, Shwetha Murali^{1,3,*}, Stuart Cantsilieris^{1,*}, Olivia S. Meyerson^{4,*}, Jas...

Abundant Human DNA Contamination Identified in Non-Primate Genome Databases

Mark S. Longo, Michael J. O'Neill, Rachel J. O'Neill*

Department of Molecular and Cell Biology, University of Connecticut, Storrs, Connecticut, United States of America

2011

RESEARCH ARTICLE

Human Contamination in Public Genome Assemblies

Kirill Kryukov, Tadashi Imanishi*

Department of Molecular Life Science, School of Medicine, Tokai University, Isehara, Kanagawa, Japan

* imanishi@tokai.ac.jp

2016



Questions:

- Is the chimpanzee genome accurately assembled?
- Is human DNA contamination a problem in the chimpanzee genome?

**What is the actual DNA similarity
between humans and
chimpanzees and how can this be
determined?**



DNA Similarity

Human **TTTCCACCCTTACAGCTAAAT**

| | | | | | | | | | | | | | | | | | | |

Chimp **TTTCCACCCTTACAGCTAAAT**

100%

Human

TTAAGCTCCACCCTTACAGCTAAACGGC

| | | | | | | | | | | | | | | | | | | |

Chimp

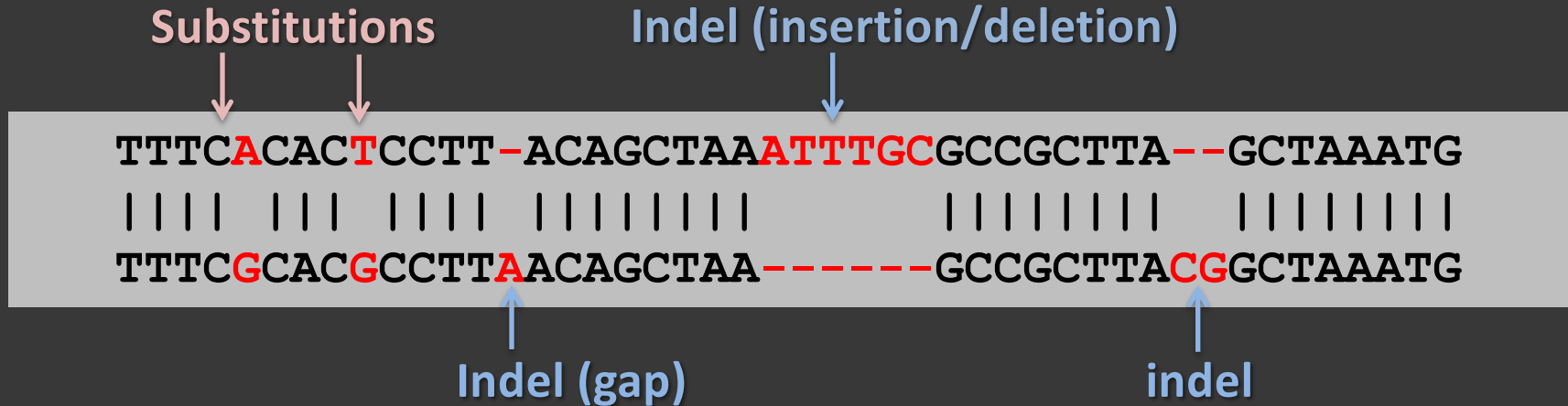
TAAGTTCACACCCTTACAGCTAAACGGC

27/28 bases match

96% similarity

The Big Question...

What gets included and what gets thrown out?



Identity based on:

Substitutions => 46/48 or **98%**

Substitutions + indels => 39/48 or **81%**

Analysis of 101 Chimpanzee Trace Read Data Sets: Assessment of Their Overall Similarity to Human and Possible Contamination With Human DNA

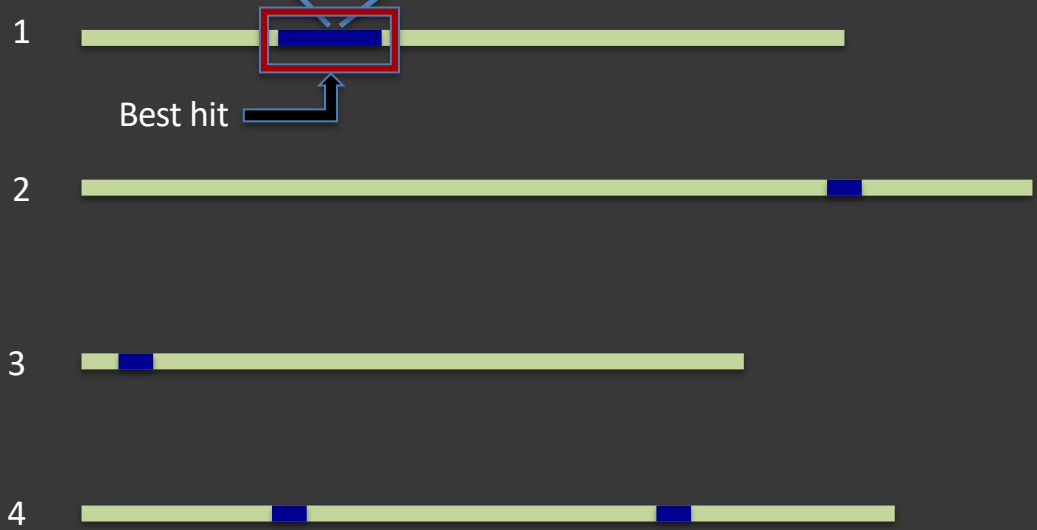
Jeffrey P. Tomkins, Institute for Creation Research, 1806 Royal Lane, Dallas, Texas 75229.

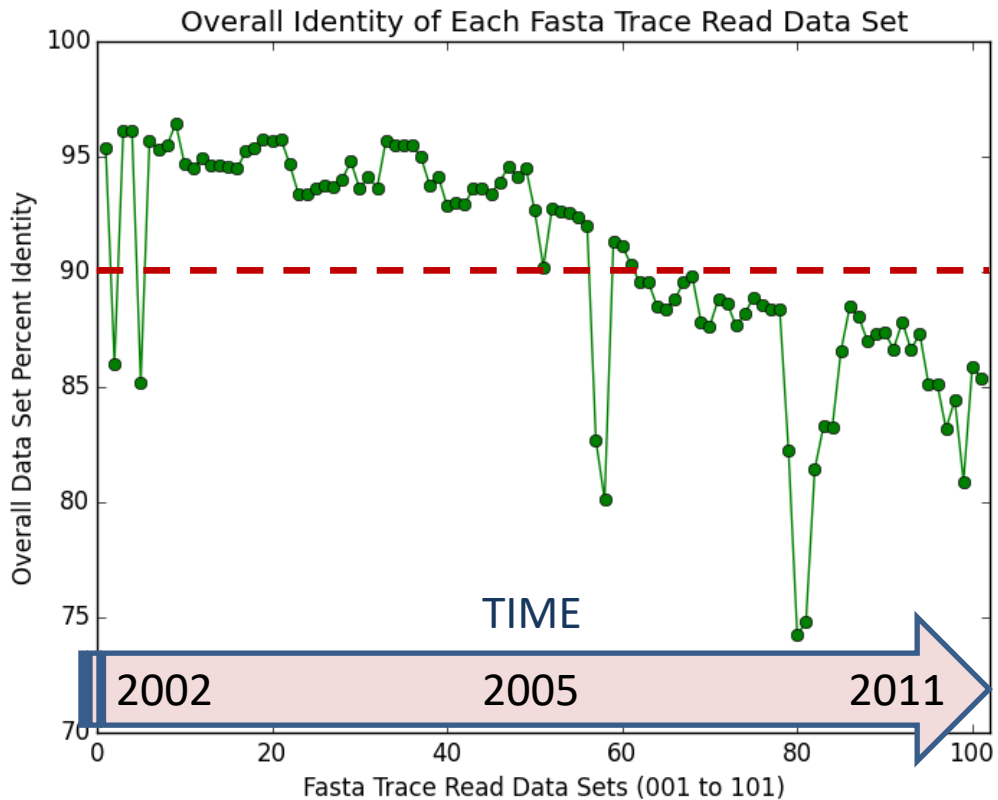
Sampled 25,000 DNA sequences at random from each of 101 data sets – total 2.5 million.

DNA sequences were on average 704 bases long

Query TTTCCGCCCTTACAGCTAAAT
| | | | | | | | | | | | | | | |
Subject TTTCCACCCTT--AGCTAAAT

Chromosome





Years

DNA similarity

2002-2004

92%

Contamination

2005-2011

85%

Research at ICR published 2018...

- 18,000 segments of high-quality chimp unbiased DNA sequence
- Average 30,000 bases each
- Matched (aligned) onto human genome



- Alignments were 10,000 bases on average
- Ave identity of the alignments = **84%**



Richard Buggs, PhD
Professor of Evolutionary Genomics

“The percentage of nucleotides in the human genome that had one-to-one exact matches in the chimpanzee genome was 84.38%” (2018)

[nature](#) > [articles](#) > article

Article | [Open access](#) | Published: 09 April 2025

Complete sequencing of ape genomes

[DongAhn Yoo](#), [Arang Rhie](#), [Prajna Hebbar](#), [Francesca Antonacci](#), [Glennis A. Logsdon](#), [Steven J. Solar](#), [Dmitry Antipov](#), [Brandon D. Pickett](#), [Yana Safonova](#), [Francesco Montinaro](#), [Yanting Luo](#), [Joanna Malukiewicz](#), [Jessica M. Storer](#), [Jiadong Lin](#), [Abigail N. Sequeira](#), [Riley J. Mangan](#), [Glenn Hickey](#), [Graciela Monfort Anez](#), [Parithi Balachandran](#), [Anton Bankevich](#), [Christine R. Beck](#), [Arjun Biddanda](#), [Matthew Borchers](#), [Gerard G. Bouffard](#), ... [Evan E. Eichler](#)  [+ Show authors](#)

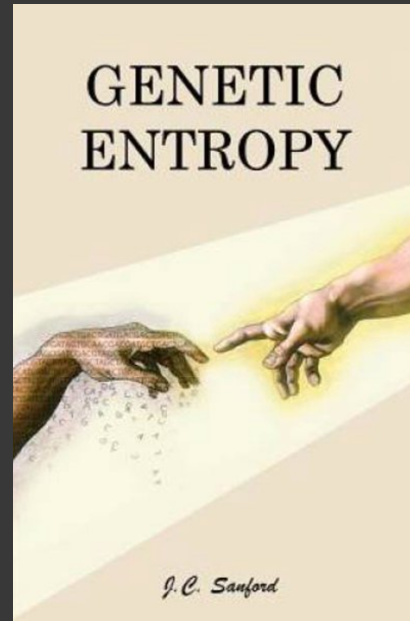
[Nature](#) **641**, 401–418 (2025) | [Cite this article](#)

Chimpanzee genome had a **84%** one-to-one nucleotide autosomal (non-sex chromosomes) DNA identity for compared to human.

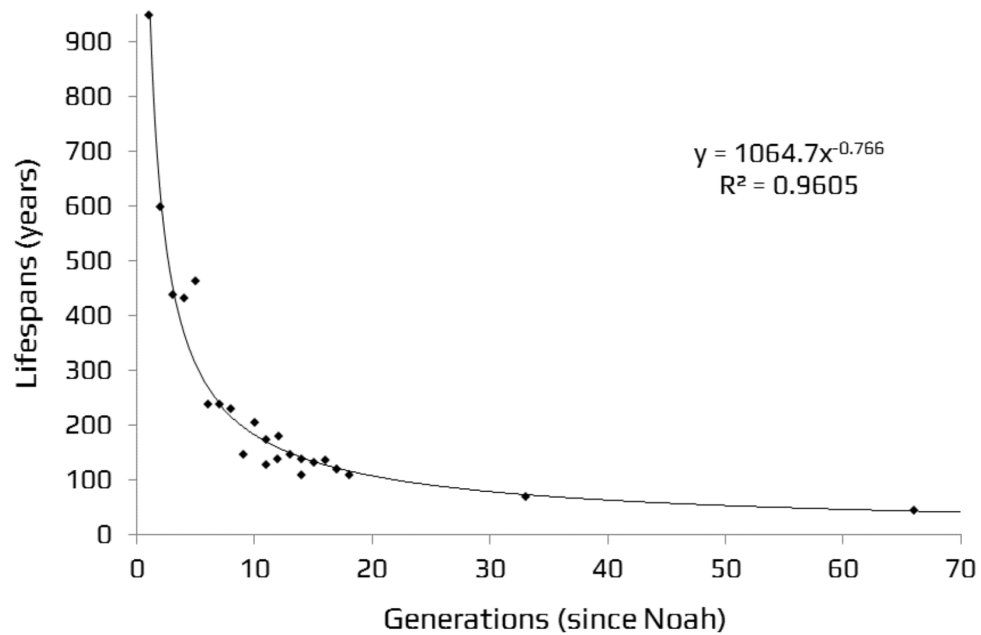
The evolutionary problem with 84%

Theoretical evolutionists need a 98.5 to 99% genome similarity to explain human evolution with known mutation rates in 3 to 6 million years time since a common ancestor with chimps.

The human genome is devolving not evolving

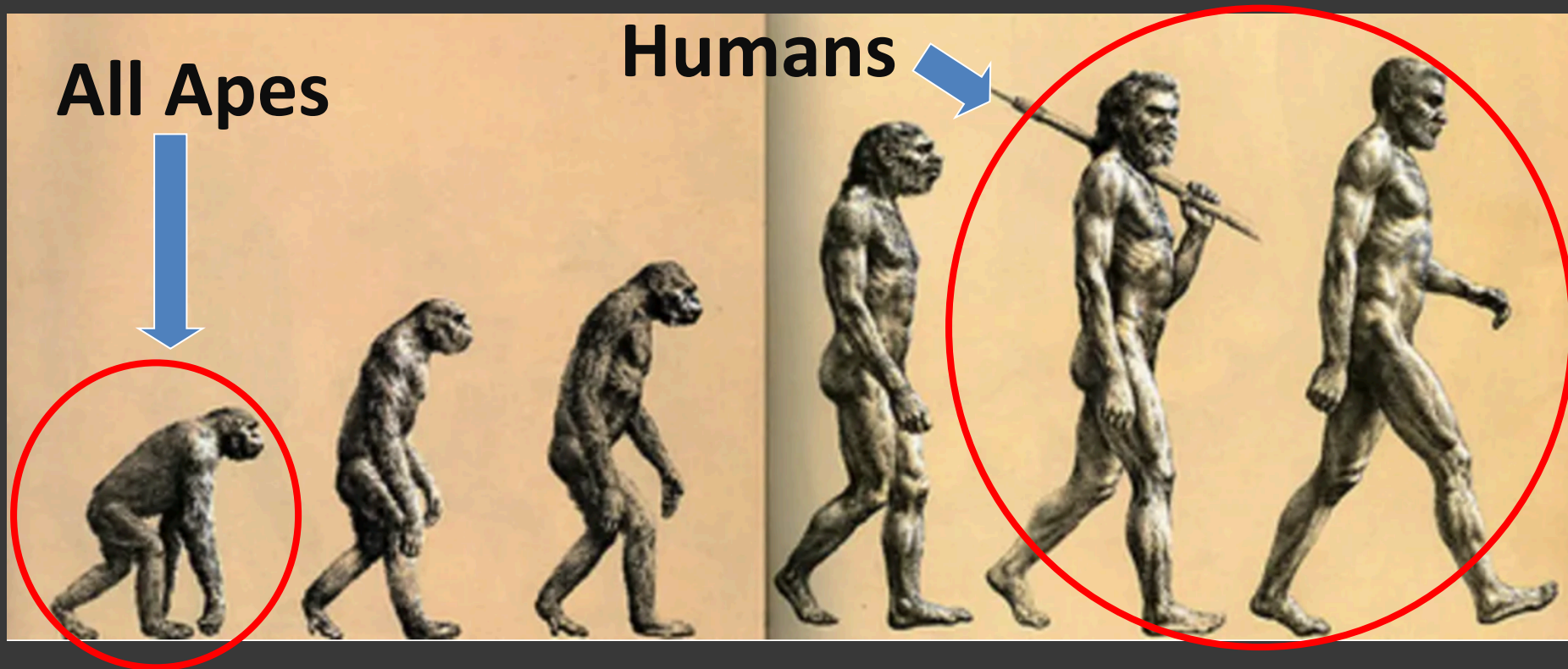


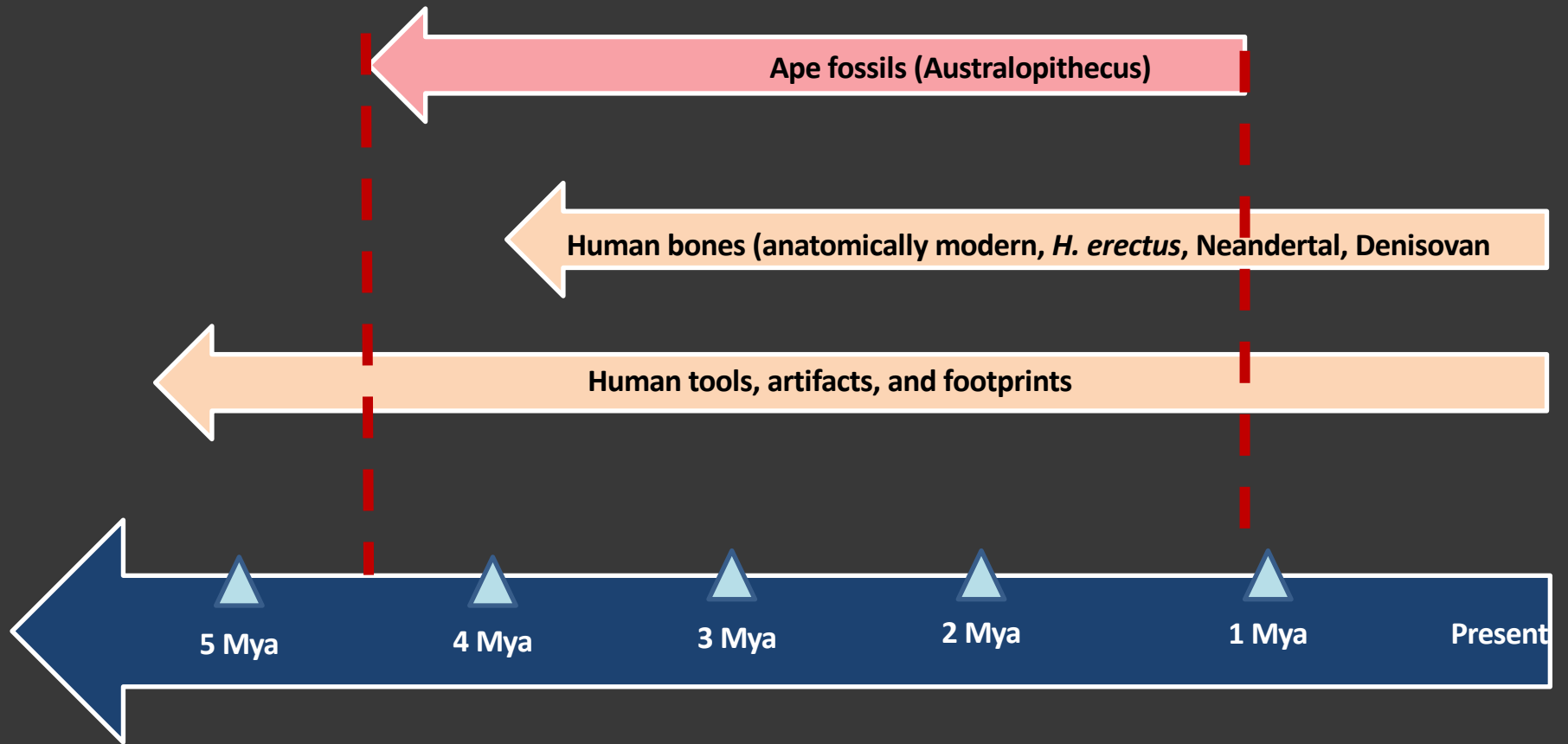
Declining Lifespans of Noah and His Descendants



All Apes

Humans





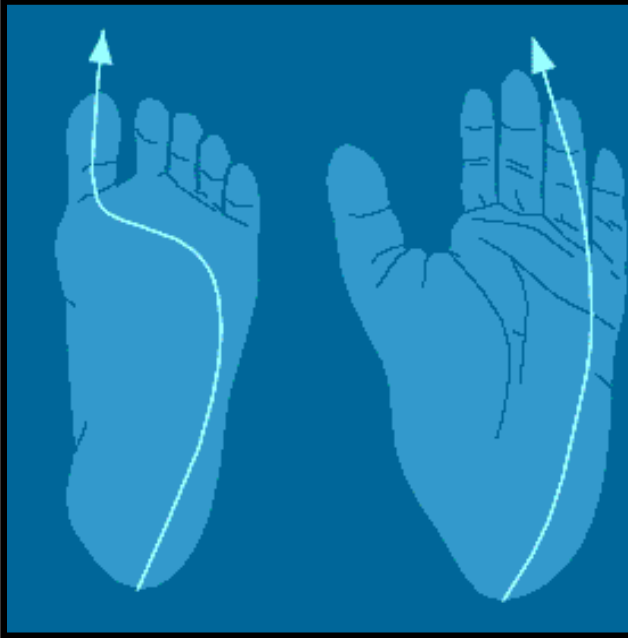
Laetoli Footprints

Footprints discovered in 1978 in Laetoli, Tanzania - dated at 3.5 million years old



Who made
these
footprints?

Ape and Human Footprints



Human

Ape
(Lucy)



Laetoli footprint

“Indistinguishable from those of habitually barefoot Homo sapiens”

Russell Tuttle, “The Pattern of Little Feet,” American Journal of Physical Anthropology, Feb 1989, p. 316.



Olduvai Hominid 1
(anatomically modern
human) discovered in
1913 in same strata as
Australopith fossils



Olduvai Gorge
Tanzania, Bed II



Lucy

- *Australopithecus afarensis* discovered by Donald Johanson in Ethiopia in 1974.
- About 40% complete
- Dated ~3 million years old
- Claimed bipedal (walked upright)

Did Lucy Walk Upright?



I walked over to the cabinet, pulled out Lucy, and shazam! – she had the morphology that was classic for knuckle walkers.”

E. Stokstad, “Hominid Ancestors May Have Knuckle Walked,” *Science*, 2000.



“A. anamensis and A. afarensis
the latter represented by the
famous skeleton known as Lucy –
had wrists capable of locking the
hands in place during knuckle
walking”

“Lucy on the ground with knuckles” Science News,
April 8, 2000
(Reference to p.235 Nature, March 23, 2000)



“Regardless of the status of Lucy’s knee joint, new evidence has come forth that Lucy has the morphology of a knuckle-walker.”

Richmand and Strait, “Evidence that Humans Evolved from Knuckle-Walking Ancestor,” *Nature*, 2000.

“Although the transition from *Australopithecus* to *Homo* is usually thought of as a momentous transformation, the fossil record bearing on the origin and earliest evolution of *Homo* is virtually undocumented.”

PHILOSOPHICAL
TRANSACTIONS B

rstb.royalsocietypublishing.org

Review



Cite this article: Kimbel WH, Villmoare B.

From *Australopithecus* to *Homo*: the transition that wasn't[†]

William H. Kimbel¹ and Brian Villmoare^{2,3}

¹Institute of Human Origins, and School of Human Evolution and Social Change, Arizona State University, Tempe, AZ 85287, USA

²Department of Anthropology, University of Nevada Las Vegas, Las Vegas, NV 89154, USA

³Department of Anthropology, University College London, London UK WC1H 0BW

 BV, 0000-0003-1012-9388

2016

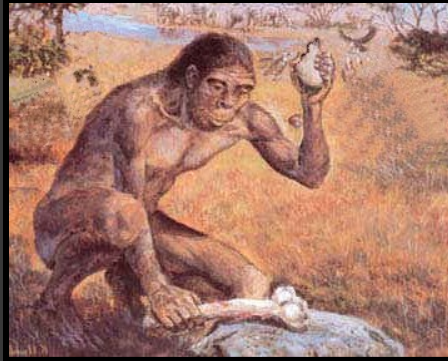
Homo habilis (handy man)



Louis Leakey
(1903-1972)

“Now widely considered an ‘invalid taxon’” (a mixture of ape-like and human fossils)

Nature 377:111, 1995



“...if there weren't a *Homo habilis* we would have to invent one.”

Milford Wolpoff, *American Journal of Physical Anthropology* 89(3), Nov. 1992, p, 402



“Detailed comparison of Neanderthal skeletal remains with those of modern humans have shown that there is nothing in Neanderthal anatomy that conclusively indicates locomotor, manipulative, intellectual, or linguistic abilities inferior to those of modern humans.”

Erik Trinkaus, “Hard Times Among the Neanderthals,”
Natural History, 87:10, p. 58



**Genes for red hair
discovered in
Neanderthal DNA**



Homo erectus

- Sloping forehead
- Pronounced brow ridge



Schwartz J.H. and Tattersall I., *Science* 344:360a, 2014



Turkana Boy 1984, Kenya

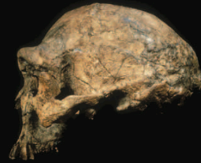


Neanderthal

- Sloping forehead
- Pronounced brow ridge



Homo erectus



ER 3733



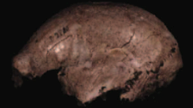
WT 15000



D 2282 r



D 2700



D 2280

Pronounced Brow Ridge





Rugby players with a pronounced supraorbital ridge and sloping forehead

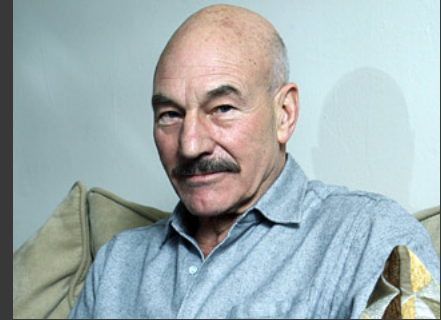
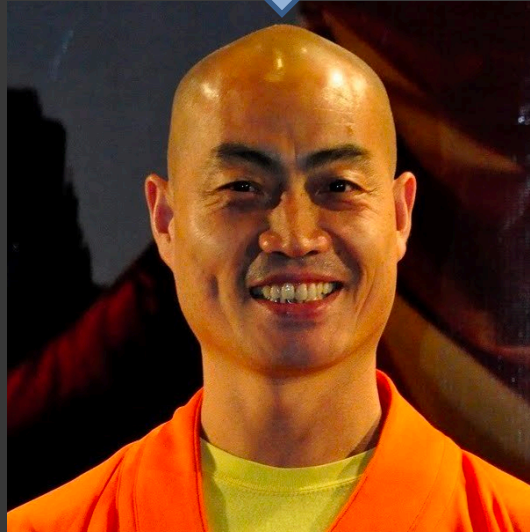
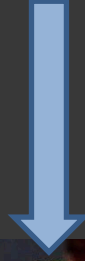
- Sloping forehead
- Pronounced brow ridge



Nikolay Valuev

Former professional boxer, Current Member of Russian Parliament

Pronounced Sagittal Crest

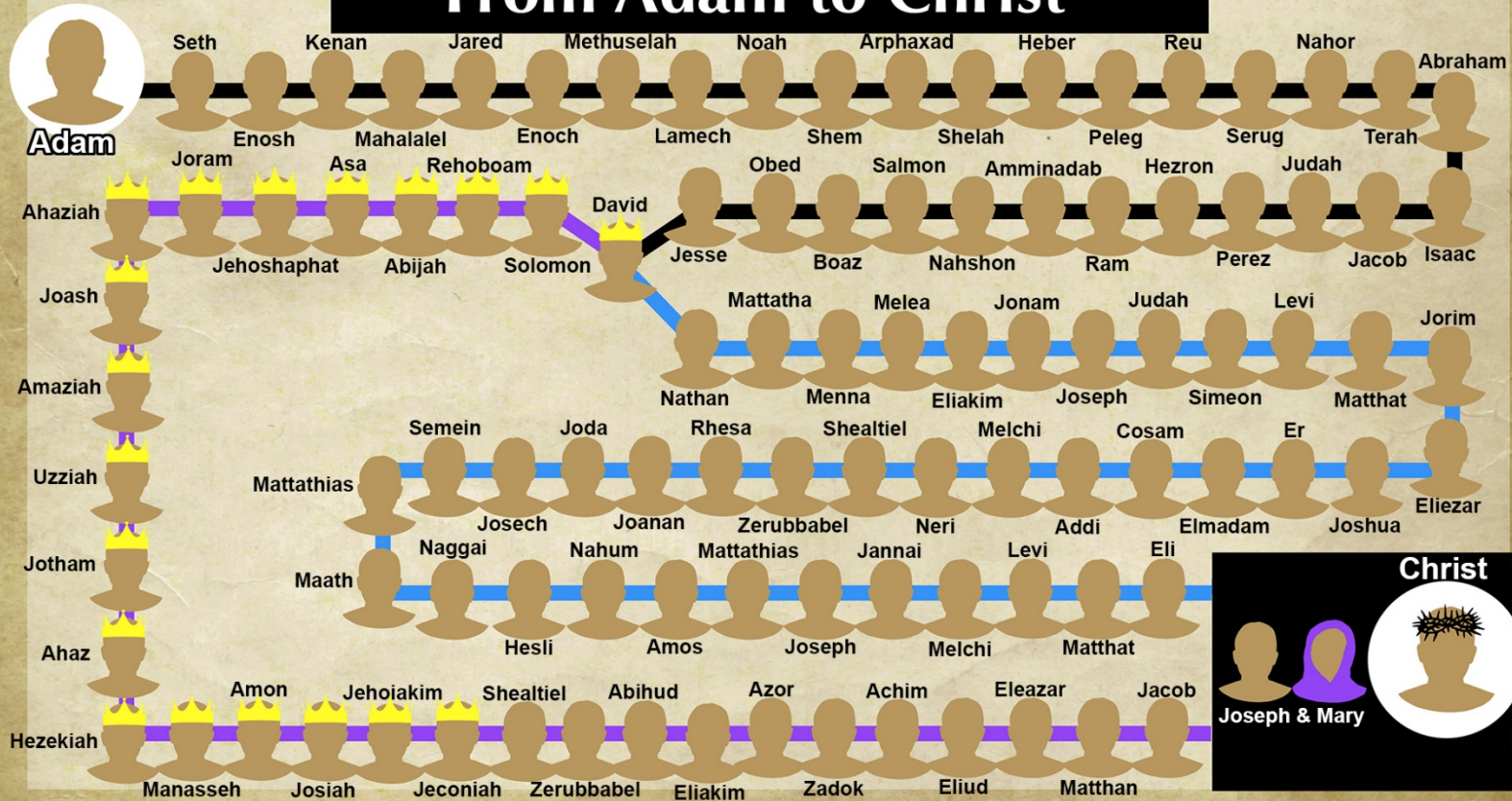


A “Historical” Adam?

April 15, 2010 | By [David Opderbeck](#) (guest author)



From Adam to Christ

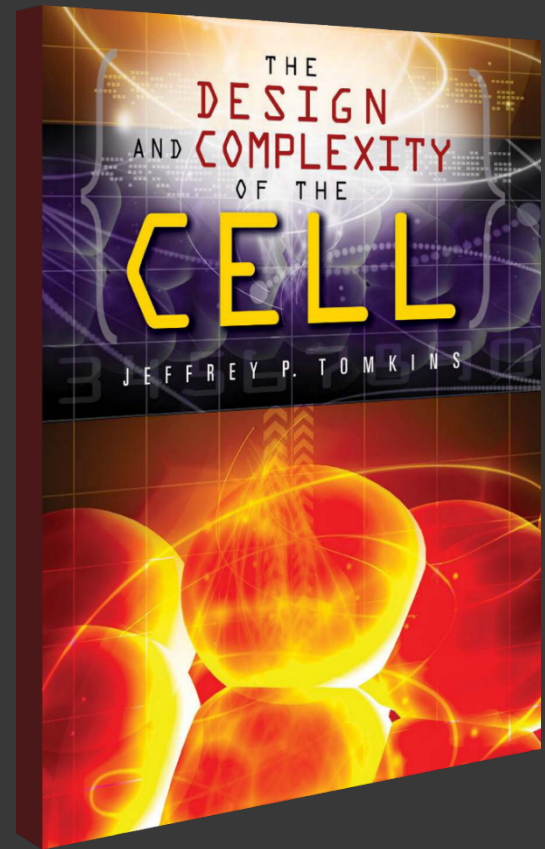
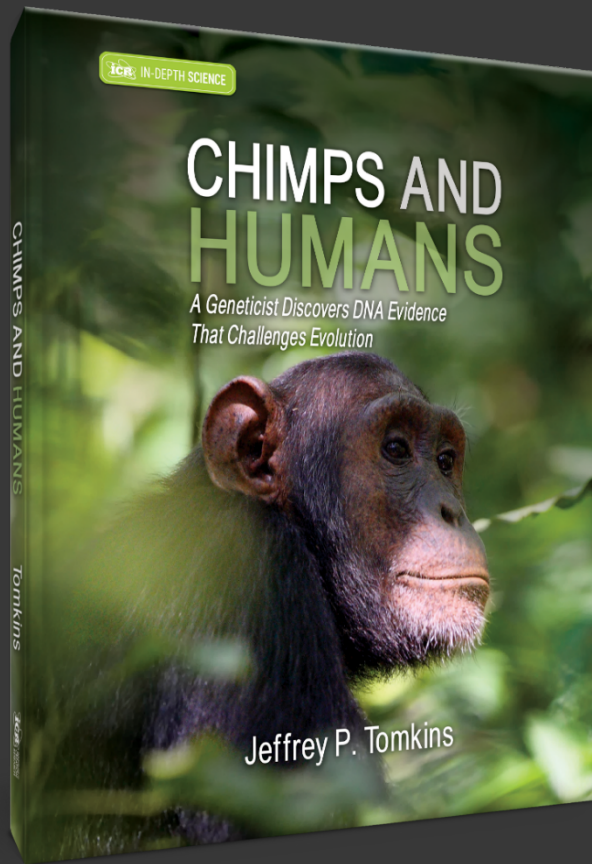


Romans 5:12

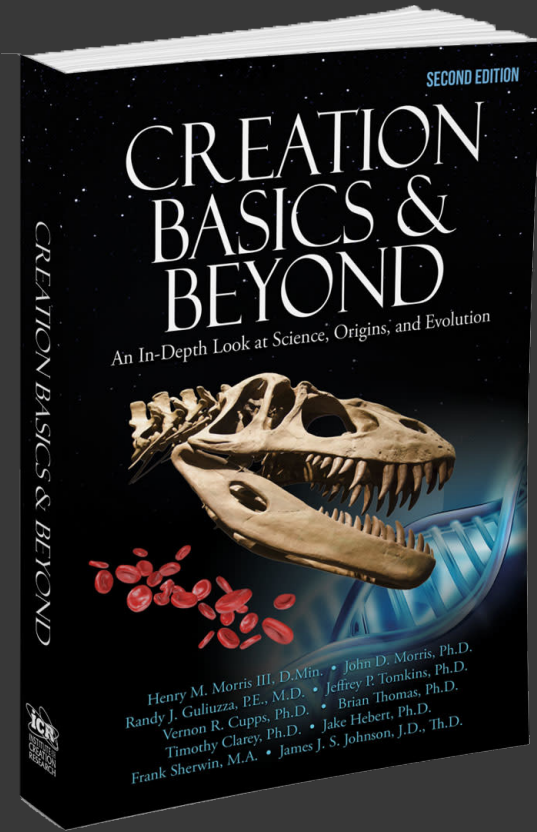
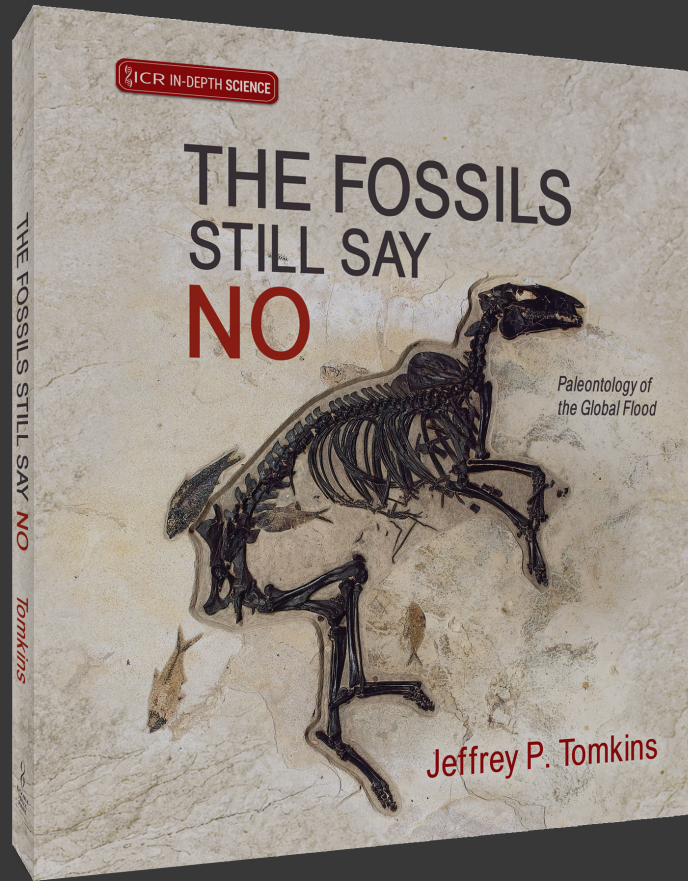
Therefore, just as through one man sin entered the world, and death through sin, and thus death spread to all men, because all sinned.

I Corinthians 15:22

For as in Adam all die, even so in Christ all shall be made alive.



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ACTS & FACTS

A large, detailed illustration of a Tyrannosaurus Rex in a prehistoric landscape. The dinosaur is shown in profile, facing right, with its mouth open, revealing sharp teeth. The background features a hazy, greenish-yellow sky and distant mountains. A small pterosaur is visible in the upper left corner of the sky. The overall scene is set in a lush, prehistoric environment with various plants and foliage.

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SEPTEMBER | OCTOBER
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Natural Selection's
Death-Driven Worldview

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Grand Teton National Park: The
Youngest Rocky Mountains

page 10

**Evolutionary Dinosaur
Myths Debunked**

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The Venus Flytrap's Snap

page 18



SCAN ME



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